Huron-Erie Corridor Initiative Annual Meeting

BRIEFING BOOK

February 7, 2013

Weber's Inn
Ann Arbor, MI

Meeting Materials

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Huron-Erie Corridor (HEC) Initiative
Annual Meeting Agenda

Weber's Inn
3050 Jackson Avenue, Ann Arbor, MI 48103

February 7, 2013
8:30 a.m. – 5:00 p.m.

Theme: ***Approaching our 10th Anniversary! Reassessing our Needs and Shaping a Vision for our Future***

** Denotes Powerpoint presentation*

8:30 – 8:35 **John Hieftje (Mayor, City of Ann Arbor) –** Welcome

8:35 – 8:40 **Mark Cochran (Office of U.S. Representative John D. Dingell) –** Opening Remarks

8:40 – 9:15 ***Russ Strach (USGS) –** Introductions, Opening Remarks
- 2012 Online Survey Follow-up Items:
  - Huron-Erie Corridor Viability Analysis
  - Partnership
    - Team Structure
    - Management Needs
    - Meeting Format

9:15 – 9:45 ***Robin DeBruyne (USGS) –** Huron-Erie Corridor Viability Analysis Update

9:45 – 10:00 ***Rose Ellison (EPA) –** Introduction to Draft Partnership Agreement

10:00 – 10:30 ***Russ Strach (USGS; Facilitator) –** Discussion of Draft Partnership Agreement

10:30 – 11:00 **BREAK** *(refreshments sponsored by Michigan Sea Grant)*

11:00 – 11:10 ***Aaron Jubar (USFWS) –** Sea Lamprey Control Efforts in the HEC

11:10 – 12:00 **Kurt Newman (USGS; Facilitator) –** Management Needs Discussion (10 mins. each)
- ***Michigan Department of Natural Resources:** Todd Kalish
- ***Ohio Department of Natural Resources:** Chris Vandergoot
- ***Ontario Ministry of Natural Resources:** Rich Drouin
- ***Michigan Department of Environmental Quality:** Michelle Selzer
- ***Ontario Ministry of the Environment:** Ted Briggs

12:00 – 1:00 **LUNCH** (*sponsored by Michigan Sea Grant)*

1:00 – 1:40 **Kurt Newman (USGS; Facilitator) –** Management Needs Discussion Cont'd (10 mins. each)
- ***U.S. Fish and Wildlife Service:** Jim Boase
- ***U.S. Army Corps of Engineers:** Hal Harrington
- ***Michigan Sea Grant:** Mary Bohling
- ***Environmental Protection Agency:** Rose Ellison

1:40 – 2:00 **Paul Seelbach (USGS; Facilitator) –** Introduction of Break-out Sessions

2:00 – 2:45 **Break-out Sessions –** Identification of Research Strategies
Session A (Moderators: John Dettmers/Kurt Newman): Fish/Biological
Session B (Moderators: Todd Kalish/Michelle Selzer): Environmental/Water Quality/Habitat
Session C (Moderators: Doug Pearsall/Paul Seelbach): Societal
Session D (Moderators: Rose Ellison/Jen Tewkesbury): Areas of Concern

2:45 – 3:15 **BREAK** *(refreshments sponsored by Michigan Sea Grant)*

3:15 – 4:00 **Break-out Sessions –** Identification of Research Strategies **(*Continued*)**
Session A (Moderators: John Dettmers/Kurt Newman): Fish/Biological
Session B (Moderators: Chris Vandergoot/Michelle Selzer): Environmental/Water Quality/Habitat
Session C (Moderators: Doug Pearsall/Paul Seelbach): Societal
Session D (Moderators: Rose Ellison/Jen Tewkesbury): Areas of Concern

4:00 – 4:30 **Paul Seelbach (USGS; Facilitator) –** Break-out Session Report

4:30 – 4:45 **Lynn Vaccaro (Michigan Sea Grant) –** Outreach/Communications

4:45 – 5:00 **Russ Strach (USGS) –** Closing Remarks

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5:00 – 7:00 **Social & Poster Session** *(sponsored by Great Lakes Fishery Commission & Michigan Sea Grant)*

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Weber's Inn

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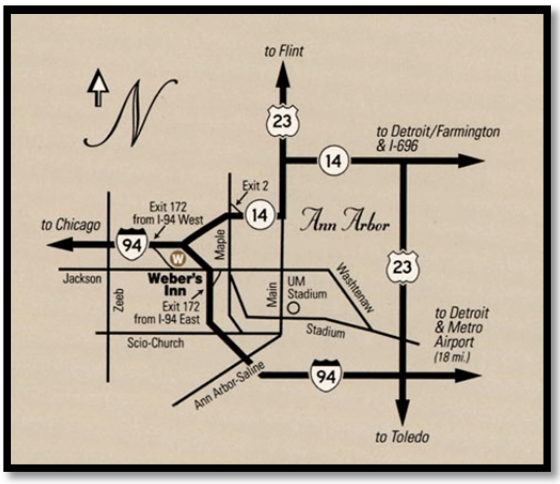

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(DRAFT)
PARTNERSHIP AGREEMENT

St. Clair-Detroit River System Initiative
2013-2023

This draft Partnership Agreement represents the input from a subset of SCDRS Initiative members who participated in a series of four conference calls to gather information. The focus of the four calls was to:

1) Revisit the 2005 Huron-Erie Corridor Initiative Prospectus (Appendix 2)
2) Devise a preliminary list of management priorities/associated information needs for the next 5-10 years
3) Develop potential new membership structure/governance options

PURPOSE OF THE INITIATIVE

The purpose of the Initiative is to promote cooperation among US, Canada, Tribes, First Nations, and other stakeholders, and to advance science that addresses the top priorities of fisheries and aquatic resource managers with jurisdictions within the St. Clair-Detroit River System (SCDRS).

GEOGRAPHICAL EXTENT OF ST. CLAIR-DETROIT RIVER SYSTEM

The international SCDRS includes southern Lake Huron, the St. Clair River, Lake St. Clair, the Detroit River, and western Lake Erie, and includes waters in Michigan, Ohio and Ontario (Appendix 1; *Map of St. Clair-Detroit River System*).

HISTORY OF THE INITIATIVE

Historic impacts and uses of the SCDRS waters for waste disposal, water withdrawals, shoreline development, shipping, urbanization, recreation, and fishing have decreased the ecological resilience of this ecosystem. In 2004, the Huron-Erie Corridor Initiative (HECI) was proposed by the US Geological Survey Great Lakes Science Center (USGS-GLSC) to address high-priority research questions affecting aquatic resources and environments in the SCDRS (see Appendix 2; HECI Prospectus). In 2012, the HECI partners adopted the use of "St. Clair-Detroit River System" to replace the "Huron-Erie Corridor" to more aptly reflect to the strait than the adjacent Great Lakes being referenced (Appendix 1).

Since its inception, Initiative partners have been coming together on a voluntary basis from a vast diversity of sectors with a common agenda. The partners have agreed to: (1) restore/improve the ecological function and resilience within the SCDRS ecosystem; and, (2) maintain healthy, diverse, and productive aquatic ecosystems throughout the SCDRS that will in turn provide societal, economic, and environmental benefits to the Great Lakes region and throughout the U.S. and Canada.

Together, the partners design shared monitoring programs that provide natural resource managers with the quantitative scientific information required to make informed decisions for

managing and restoring native species and habitats in the SCDRS. A collaborative, science-based, adaptive approach is used that allows flexibility to address natural resource issues in this complex and ever-changing environment. The Initiative used various sub-groups of partners who met throughout the years, and the USGS-GLSC served as the organizing entity to provide broader coordination needs and support to staff. The GLSC has hosted and organized an annual meeting each year to share monitoring and scientific information, reaffirm management needs and support, and, in collaboration with partners, develop a work plan for the coming year.

PURPOSE OF THE PARTNERSHIP AGEEMENT

The purpose of the SCDRS Initiative Partnership Agreement is to develop common goals and objectives; identify collective resource management needs and challenges, and research themes and strategies; and, provide for recognized membership and governance. This document provides a strategic vision for the next ten years and lays out a common agenda toward restoring and building ecological resilience within the SCDRS. This document also builds on the science and collaboration forged in the 2005 prospectus and anticipates a transition period as new management needs are identified to guide future science initiatives.

OBJECTIVES OF THE PARTNERSHIP AGREEMENT

The following objectives were developed by the Initiative partners to achieve the goals of restoring and building ecological resilience within the SCDRS:

1) Provide a basis for effective collaboration and communication on the SCDRS through an established partnership.
2) In coordination with fisheries and aquatic resource managers, identify resource management challenges and issues and develop management-driven research strategies to address the most vexing priorities in the SCDRS.
3) Identify critical and emerging SCDRS research challenges through on-going censuses and adaptive processes.

MANAGEMENT PRIORITIES

A sub-committee of SCDRS Initiative partners that identified themselves as having an interest in shaping this agreement convened for a series of four teleconferences; one per month from September thru December, 2012. The sub-committee identified the following four broad categories of management priorities: (1) Fish/Biological, (2) Environmental/Water Quality/Habitat, (3) Societal, and (4) Areas of Concern. Key priorities identified under each category are summarized below.

Fish/Biological

- Determine the extent to which fish populations are discreet to the SCDRS versus their relative contribution to fish populations in Lakes Erie and Huron. Determine fish habitat use for spawning versus transitory purposes and complexity of habitats necessary to restore locally-adapted native fishes.
- Evaluate SCDRS role, potential contribution, and possible actions for cisco recovery in Lake Erie (in coordination with Lake Erie Cisco Management Plan; Lake Erie Committee - Cold Water Task Group).

- Identify sea lamprey spawning locations within the SCDRS and seek understanding of the contributions to populations in Lakes Erie and Huron.
- Develop and implement standardized long-term fish population monitoring plans in the SCDRS in coordination with the appropriate existing committees and task groups.
- Identify and describe invertebrate community composition/dynamics connected to the beneficial use impairment (BUI) involving benthos.

Environmental/Water Quality/Habitat

- Address Michigan water quality regulatory categories/headings that are not currently being met.
- Restore soft edges/wetlands/channel complexity throughout the corridor.
- Reduce water turbidity in Canadian waters (e.g., Thames River plume)/reduce impacts on fish spawning.
- Assess and identify proportional nutrient loading in the SCRDRS contributing to harmful and toxic algal blooms in western Lake Erie.
- Understand the relationship between water quality and chironomid mouthpart deformities in the SCDRS/identification of impairments.

Societal

- Identify landscape-scale features that could contribute to establishment of "Biodiversity Investment Areas" (clusters of places, called ecoregions, that have exceptional biodiversity value), or other designations that recognize the uniqueness and importance of the SCDRS.
- Provide science to support blue economies.
- Better understand ecosystem services (current and potential) and the human values surrounding them.
- Better understand importance of rivermouth and delta areas for people, fish, and other native species.
- Evaluate scientific remedies to address occurrences of human pollutants (including sewage overflows) in the SCDRS.

Areas of Concern

- Address Detroit River AOC-specific Management Needs, including the following:
    - Re-designate (i.e., remove): Tainting of Fish and Wildlife Flavor BUI; and potentially, Fish Tumors and other Deformities BUI.
    - Initiate action to address sources identified by MDEQ impacting the Degradation of Aesthetics BUI.
    - Initiate a comparison study of fish tissue contaminant levels for Fish and Wildlife Consumption BUI to demonstrate whether or not there is a statistically significant difference in fish tissue concentrations of contaminants causing fish consumption advisories in the Detroit River AOC compared to associated Great Lakes or a control site.
    - Initiate a study to identify source(s) of impairment that are continuing to impact the Bird or Animal Deformities or Other Reproductive Problems BUI.
    - Revise or contribute to the revision of the 2009 plan for restoration of the Fish & Wildlife habitat BUIs.

    - Identify strategies and approach to forge consensus on approaching the Restrictions on Dredging Activities and Beach Closings BUIs.
    - Initiate restoration action at target sediment and habitat sites.
- Address St. Clair River AOC-specific Management Needs, including the following:
    - Complete all management action in the AOC by 2014
    - Re-designate (i.e., remove): Bird or Animal Deformities or Other Reproductive Problems; Degradation of Benthos; Beach Closings BUIs; and potentially, Restrictions on Fish and Wildlife Consumption, BUIs.
    - Develop consensus on appropriate removal criteria for Restrictions on Drinking Water Consumption or Taste and Odor Problems BUI. Facilitate broader involvement of relevant local officials in existing spills planning and notification functions by 2014.
    - Manage design and implementation of all target habitat restoration sites by 2014.

In addition to identifying the specific management priorities listed above, the partnership agreement sub-committee also identified key management documents with supplemental information, including the draft Fish Community Objectives for the St. Clair System[1], the Lake Erie Environmental Objectives[2], and the Environmental Objectives for Lake Huron[3]. EPA and DEQ staff also provided management priorities for Michigan AOCs beyond the Detroit River and St. Clair River (this information is summarized in the DEQ briefing item submitted for the 2013 steering committee meeting).

RESEARCH STRATEGIES

To effectively address legacy pollutants, damage to fish and wildlife habitats, and ongoing degradation to the environment, managers need objective, quantitative, scientific information to inform decisions. In many instances basic scientific information on habitat conditions, species presence/absence, and trend data are lacking. Strategies to address each management priority are determined through discussions and consensus among the steering committee. At the 2013 steering committee meeting, resource managers will identify the scientific information needed to better manage natural resources, and as well as research strategies for the next ten years of the Initiative (2013-2023).

(Note: this section will be completed after the 2013 meeting, using ideas generated during the break-out sessions).

Fish/Biological

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[1] Draft Fish Community Objectives for the St. Clair System - http://www.glfc.org/lakecom/lec/LEC_docs/other_docs/scsfcgo.pdf
[2] Lake Erie Environmental Objectives - http://www.glfc.org/lakecom/lec/LEC_docs/other_docs/EOs_July5.pdf
[3] Environmental Objectives for Lake Huron - http://www.glfc.org/lakecom/lhc/lheo.pdf

Environmental/Water Quality/Habitat

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Societal

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Areas of Concern

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GOVERNANCE STURCTURE/MEMBERSHIP PROCESS

The Initiative is a bi-national, collaborative partnership with more than 30 organizations, including U.S. and Canadian natural resource-related agencies, Tribes/First Nations, units of local government, industry and university partners, non-profit organizations, and interested citizens. Resource managers, scientists and other stakeholders use a consensus-building, multi-disciplinary approach to identify management and research priorities, develop funding strategies, and increase public involvement in the Initiative.

(Note: The following four governance structure options will be presented at the 2013 meeting; steering committee will seek consensus on the preferred option).

Option A - Informal/loose structure (status quo): USGS-GLSC facilitator, steering committee comprised of entire partnership.

Governance Structure:

- **Facilitator** – The Director of the USGS-GLSC facilitates or delegates facilitation of steering committee meetings.
- **Steering Committee** – The entire partnership comprises the steering committee.

Membership Process: The steering committee maintains an open membership. Any interested stakeholder may contact USGS-GLSC and ask to become a member. There is no limit to the number of members allowed per member organization.

Pros:

- This model has worked fine so far.

Cons:

- Decision making is open to a diverse group of members who may not be in a position to make decisions on behalf of their organizations; therefore, reaching consensus can be difficult when decision making involves members who may not be bound or affected by the decisions made.
- Lacks formal recognition of possibility for ad hoc teams to emerge.

Option B - Informal/loose structure (status quo) + ad hoc teams: USGS-GLSC facilitator, steering committee comprised of entire partnership, and ad hoc teams.

Governance Structure:

- **Facilitator** – The Director of the USGS-GLSC facilitates or delegates facilitation of steering committee meetings.
- **Steering Committee** – The entire partnership comprises the steering committee.
- **Ad Hoc Teams** – The steering committee may request, as the need arises, expert advice or study on problems identified by the committee. Issue-based ad hoc teams may be assembled in the form of special topic work groups, task forces, implementation committees, etc. The ad hoc teams report back to the steering committee.

Membership Process: The steering committee maintains an open membership. Any interested stakeholder may contact USGS-GLSC and ask to become a member. There is no limit to the number of members allowed per member organization. Appointment to ad hoc teams is determined based on the issue and who has jurisdiction over the decision.

Pros:

- Adds recognition of possibility for ad hoc teams to emerge.

Cons:

- Decision making is open to a diverse group of members who may not be in a position to make decisions on behalf of their organizations; therefore, reaching consensus can be difficult when decision making involves members who may not be bound or affected by the decisions made.

Option C – Small steering committee comprised solely of management agency representatives: Would establish a meeting chair-person, steering committee comprised solely of management agency representatives, members-at-large, and ad hoc teams.

Governance Structure:

- **Chair and Vice-chair –** The chair and vice-chair are nominated by the steering committee from candidates who are recognized as being leading management agency representatives by their peers. Chair and vice-chair will be confirmed by consensus of the steering committee. Each will serve a term of two-years, with the vice-chair assuming the role of chair at the end of their term. The steering committee will in turn nominate and confirm a new vice-chair every other year to maintain the leadership process.
- **Steering Committee –** The steering committee is comprised of a single representative from the each of the following natural resources-related agencies with management jurisdiction in the SCDRS:
    - Essex Region Conservation Authority
    - Michigan Department of Natural Resources
    - Ohio Department of Natural Resources
    - Ontario Ministry of Natural Resources

- Michigan Department of Environmental Quality
- Ontario Ministry of the Environment
- U.S. Fish and Wildlife Service
- U.S. Army Corps of Engineers
- Walpole Island First Nation

Other steering committee members will include a single representative from each of the following two agencies because of their large fiduciary roles in the Initiative:

- Michigan Sea Grant
- U.S. Environmental Protection Agency

- **Members-at-Large –** The members-at-large are those who lead science to inform the management priorities of the steering committee, as well as all other interested stakeholders belonging to the partnership.
- **Ad Hoc Teams** – The steering committee may request, as the need arises, expert advice or study on problems identified by the committee. Issue-based ad hoc teams may be assembled in the form of special topic work groups, task forces, implementation committees, etc. The ad hoc teams report back to the steering committee.

Membership Process: Each of the management and fiduciary agencies listed above is responsible for identifying one representative from the agency to serve on the steering committee. Any interested stakeholder may contact USGS-GLSC and ask to become a member-at-large. There is no limit to the number of members-at-large allowed per member organization. Appointment to ad hoc teams is determined based on the issue and who has jurisdiction over the decision.

Pros:

- Decision making by organizations with the authority and resources to act on the decisions made**.**

Cons:

- Management agency representatives cannot effectively set priorities for science organizations without balanced input. Scientist representation on the steering committee lacking; management decisions could suffer without science advisory role.

Partnership Agreement Sub-committee Recommended Option

Option D – Small steering committee comprised of management agency representatives *and* scientists: A chair, steering committee comprised of management agency representatives and scientists, members-at-large, and ad hoc teams.

Governance Structure:

- **Chair and Vice-chair –** The chair and vice-chair are nominated by the steering committee from candidates who are recognized as being leading management agency representatives by their peers. Chair and vice-chair will be confirmed by consensus of the steering committee. Chair and vice-chair will rotate between management representative and science representative. Each will serve a term of two-years, with the vice-chair assuming the role of chair at the end of their term. The steering committee will in turn nominate

and confirm a new vice-chair every other year to maintain the leadership process.

- **Steering Committee –** The steering committee is comprised of a representative from the each of the following management and science agencies:
    - Department of Fisheries and Oceans Canada
    - Essex Region Conservation Authority
    - Michigan Department of Natural Resources
    - Ohio Department of Natural Resources
    - Ontario Ministry of Natural Resources
    - Michigan Department of Environmental Quality
    - National Oceanic and Atmospheric Administration
    - Ontario Ministry of the Environment
    - U.S. Army Corps of Engineers
    - U.S. Fish and Wildlife Service
    - U.S. Geological Survey
    - Walpole Island First Nation

  Other steering committee members will include a single representative from each of the following two agencies because of their large fiduciary roles in the Initiative:
    - Michigan Sea Grant
    - U.S. Environmental Protection Agency
- **Members-at-Large –** The members-at-large are those who lead science to inform the management priorities of the steering committee, as well as all other interested stakeholders belonging to the partnership.
- **Ad Hoc Teams** – The steering committee may request, as the need arises, expert advice or study on problems identified by the committee. Issue-based ad hoc teams may be assembled in the form of special topic work groups, task forces, implementation committees, etc. The ad hoc teams report back to the steering committee.

Roles and Responsibilities: Steering committee membership does not confer management decision-making authority to science organizations, nor does it confer science decision-making authority to management organizations. Rather, steering committee membership is intended to foster a collaborative and efficient environment for integrating management priorities with appropriate science strategies based on the best available science and lessons learned from ongoing management and science actions.

Membership Process: Each of the management, science, and fiduciary agencies listed above is responsible for identifying one representative from their agency to serve on the steering committee. Any interested stakeholder may contact USGS-GLSC and ask to become a member-at-large. There is no limit to the number of members-at-large allowed per member organization. Appointment to ad hoc teams is determined based on the issue and who has jurisdiction over decision.

Pros:

- Decision making authority for SCRDRS priorities is granted to management agency representatives and scientists, resulting in more balanced representation in the decision making process.

Cons:

- Large size of steering committee could reduce efficiency.

DECISION PROCESS

For deliberations under the Initiative, decisions shall be made by consensus among the steering committee. When consensus cannot be achieved, the majority opinion shall be used. Decisions will be made using the best available science and information, in the context of social, economic, and ecological needs.

MEETING SCHEDULE

The membership at large meets once per year, typically in February or March. The steering committee may meet more frequently on an ad-hoc basis depending on need. Meetings are generally one-day sessions where partners gather and provide updates about their respective management needs, as well as ongoing research and monitoring work underway in the SCDRS to address these needs.

ST. CLAIR-DETROIT RIVER SYSTEM INITIATIVE PARTNERS

We, the undersigned, pledge that in the best interest of the natural resources of the SCDRS, we will contribute technical support, financial assistance and/or in-kind services **as available and on a voluntary basis** to support the Initiative.

The SCDRS Initiative partnership is composed of U.S. and Canadian natural resource-related agencies, tribal/First Nation authorities, local units of government, industry and university partners, non-profit organizations, and interested citizens concerned with the long-term restoration and use of the SCDRS. The SCDRS Initiative partnership will work together to restore, manage, and protect the SCDRS and will operate according to the aforementioned guidelines.

Name	Agency	Date
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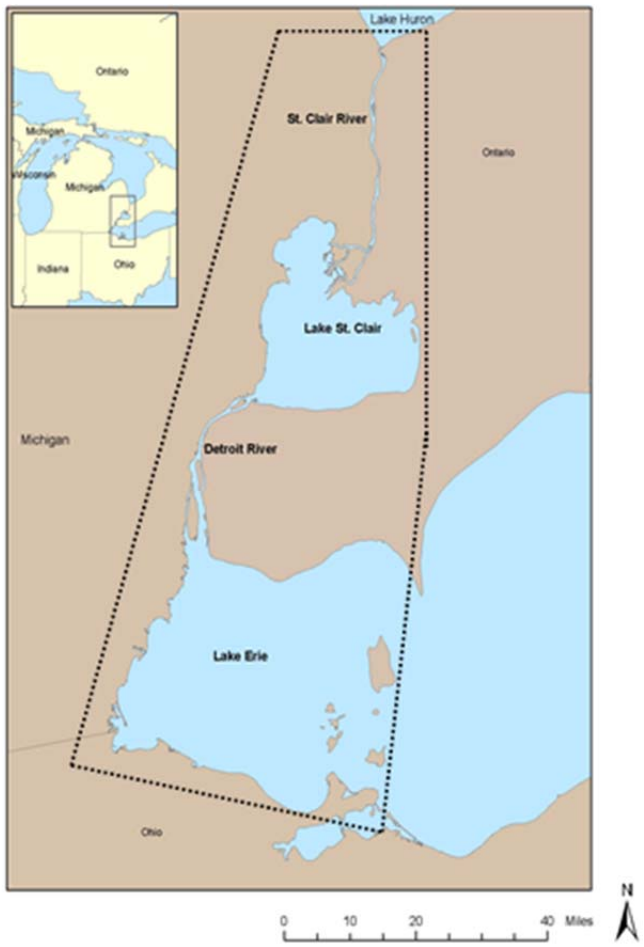
APPENDICES

APPENDIX 1 – Map of the St. Clair - Detroit River System



APPENDIX 2 – HECI Prospectus (May, 2005)

The Huron-Erie Corridor Initiative
USGS Great Lakes Science Center

Purpose

In 2004, the Huron-Erie Corridor Initiative was proposed by the U.S. Geological Survey Great Lakes Science Center (GLSC) to address high priority research issues affecting aquatic resources and environments in the Huron-Erie Corridor (HEC). The HEC includes the waters of southern Lake Huron, the St. Clair River, Lake St. Clair, the Detroit River, and western Lake Erie. Conflicting uses of the HEC waters for waste disposal, water withdrawals, shoreline development, shipping, recreation, and fishing have decreased the ecological resilience of this ecosystem. Managers need quantitative scientific information to make better-informed decisions regarding aquatic natural resources in the HEC.

The purpose of the HEC Initiative is to create relevant new science to better address the needs of fisheries and aquatic resource managers in the HEC. The Initiative is a bi-national, collaborative partnership of over twenty organizations, including government, industry, tribal, and university participants. Resource managers, scientists, and other stakeholders are using a consensus-building, multidisciplinary approach to identify research themes and priorities, develop funding strategies, and increase public involvement in the Initiative.

Introduction

The Huron-Erie Corridor includes one of the busiest navigation centers in the United States and is an international trade route with Canada and overseas markets. Over $80 billion/year in trade between the U.S. and Canada is carried out across the HEC. Over 5 million people live within an hour's drive of this Corridor. The Detroit River International Wildlife Refuge and the Ottawa National Wildlife Refuge are also located within the HEC. Habitat in these waters is used by over 60 species of spawning fish, and is home to sixteen threatened or endangered fish species. The Corridor is also part of the central Great Lakes flyway for millions of migratory waterfowl, and contains some of the largest and most diverse wetlands left in the region.

A number of factors have resulted in detrimental environmental changes in the HEC ecosystem. For example, the dredging of river bottoms for navigation has caused changes to natural flow regimes in the HEC as well as the loss of substrates required by spawning fish and benthic communities. Discharges of sewage and industrial waste into HEC waters have had negative effects on water quality with consequences to both wildlife and human health. Invasive aquatic species that entered the Lakes through shipping channels have severely altered populations of native fish and mussels. Shoreline development and changing land use have resulted in the loss or degradation of coastal habitats such as wetlands and beaches.

To address these use-conflicts effectively, we must communicate and work with scientists, managers, and other stakeholders throughout the HEC to determine present and future science needs and priorities. Partners who are already collaborating with USGS scientists in the HEC encompass a wide variety of local, state, federal, and provincial agencies, as well as non-governmental organizations and private industry. A multidisciplinary steering committee has been formed that is comprised of scientists, managers, and other stakeholders with a strong

interest in the aquatic ecosystems of the HEC. An organizational meeting was held in February 2005 at which resource managers identified the scientific information they needed to better manage natural resources in the HEC. A study design framework (Gillespie et al. 2002) was used as a part of this process. The meeting clarified goals and objectives of the HEC Initiative and identified areas of needed scientific expertise.

Research Themes

The broad interrelated biological management-driven research themes of the HEC Initiative will include: 1) Restoration ecology of native species and their habitats, 2) Effects of aquatic invasive species on native aquatic species, and 3) Conservation biology of native species. Specifics of each theme will be determined through discussions and consensus with interested partners. Restoration of ecological resilience within the HEC is considered an overriding focus of this Initiative.

Restoration Ecology of Native Species and Their Habitats

Sixteen species of fish classified as threatened or endangered inhabit the HEC. Habitat loss and alteration of habitat are major factors that have contributed to the decline of many of these species. Native fish populations have been greatly affected by habitat alterations in the HEC. Millions of tons of cobble and gravel were removed from the St. Clair and Detroit Rivers to build the cities of Detroit and Windsor and create navigation channels (Larson 1981). These gravel substrates provide spawning and nursery habitat for walleye, lake sturgeon, darters, and other native fish species. Substrate removal has contributed to fish population declines.

Changes in water velocity and temperature have also affected native aquatic species in the HEC. Creation of a deep-draft (27 ft.) shipping channel (Larson 1981) reduced water velocity over spawning substrates at 13 historic reputed fish spawning sites in the St. Clair and Detroit Rivers (Goodyear et al. 1982). Large-volume discharges of heated water from numerous industries, power plants, and municipal sewage treatment plants on both sides of the river may have affected the thermal "window" for spawning fish. Lake sturgeon, for example, spawn at water temperatures between 11-15°C. Due to the higher water temperatures, sturgeon may be spawning prior to production of suitable food resources in their nursery habitat downstream, reducing their survival and successful recruitment.

Since 1998, in collaboration with its partners, the GLSC has conducted research to gather information needed for the successful restoration of a remnant population of native lake sturgeon in the Detroit River, including stock size assessment and habitat evaluation (Hill and Manny 1999, McClain and Manny 2000, Alpena FRO 2003, MDNR 2002), spawning success and early life history (Nichols et al. 2003), extent and composition of known-active and historic-reputed spawning grounds (Manny and Kennedy 2002), sturgeon movements (Boase 2003; Caswell et al. 2004), and body burden of contaminants in lake sturgeon (Begnoche et al. 2003). One strategy being used by GLSC scientists and partners to restore lake sturgeon populations is to create spawning habitat in the Detroit River near Belle Isle to replace habitat lost from dredging. This habitat was constructed in June 2004 and will be closely monitored to assess the success of the project (Read et al. 2003).

Successful restoration/rehabilitation of native aquatic species and habitats in the HEC also requires knowledge of the hydrology of the system. For example, low velocity, vegetated habitat, important in the life history of many aquatic organisms, is largely lacking in many parts of the HEC. We will be combining the biological and hydrological components of this project through collaboration with the USGS Water Resources Discipline (WRD). The WRD can

provide the expertise necessary to determine where to best focus our efforts for restoring low velocity, vegetated habitat as well as other natural flow regimes in the system.

Effects of Invasive Species on Native Aquatic Species

Non-native aquatic organisms were first discovered in the Great Lakes in the early 1800's, with the total number of established species now estimated at 162 (Ricciardi, 2001). More than one-third of these organisms have been introduced in the past 30 years, coinciding with the opening of the St. Lawrence Seaway (GLC 1992) and resulting in both biologic and economic consequences to the Great Lakes region. The most problematic invasive species include alewife, common carp, Eurasian ruffe, quagga mussel, rainbow smelt, round goby, sea lamprey, spiny waterflea, and zebra mussel. These species alone have contributed to massive extinctions of native fauna and severe alterations of food webs in the Great Lakes. Negative effects of invasive species include competition with native species for food, habitat, and spawning sites, and predation on native species.

Invasive species have had major economic impacts in the Great Lakes region as well. For example, zebra mussels have caused millions of dollars of damage to municipal and industrial water intake pipes. Sea lamprey have greatly reduced populations of commercial and sport fishes, such as lake trout and lake whitefish, resulting in lost income for commercial and recreational fisheries. Round gobies prey on lake sturgeon eggs contributing to the decline of sturgeon populations (Nichols et al. 2003).

Great Lakes managers and resource users presently need information on all aspects of potential and existing invasive species, including basic biology, geographic distribution, and potential impact on existing biota. Working together and using a proactive research approach we will develop strategies that can help managers respond effectively to current and potential invasive species issues in the HEC.

Conservation Biology

Conserving the aquatic biological diversity of the HEC is an essential component of this Initiative. Maintaining healthy and productive aquatic ecosystems throughout the Corridor benefits the human population as well as the organisms inhabiting these waters. Over 500,000 boats are registered in Michigan and use the HEC waters for sport and commercial fishing and other recreational activities. HEC waters are also a source of drinking water and process water for industry. Changing land use, invasive species, coastline development, and many other factors have impacted native species and their habitats within the HEC. The Restoration Ecology and Invasive Species research themes already discussed interrelate well with the Conservation Biology theme because research results should ultimately contribute to the maintenance of biological diversity and ecosystem resiliency. For example, the lake sturgeon restoration discussed above facilitates the conservation biology of other species, such as native darters. In addition, the GLSC has created a land use map of the Corridor which can serve as a baseline to monitor changes in land use and predict potential ecological impacts of those changes.

Research Needs and Potential Strategies

The development of research strategies and relevant new science are key objectives of the HEC Initiative. Our partners believe that habitat restoration should be a primary research focus

in the HEC. Initial research needs and priorities have been determined through discussions with the HEC Initiative steering committee. It was decided, by consensus, that initial research should focus on: 1) Compiling historic HEC habitat and data resources, 2) Current habitat function, and 3) Roadblocks to habitat restoration. A set of preliminary hypotheses are currently being developed on how historic loss of habitat and changes in ecosystem function will impact future habitat restoration efforts. Many factors may change habitat or ecosystem function. Two primary factors of importance in the HEC relate to water flow regimes and invasive species. Altered flow regimes may disrupt the linkage between fish spawning and nursery habitat by sweeping drifting fry past suitable nursery areas. Habitat function may also be lost due to altered predation pressures by invasive species such as the round goby, reducing recruitment of native fish from spawning areas.

It is essential that we use a multidisciplinary ecosystem approach as we develop these strategies. To create an effective experimental design requires scientific expertise in a number of areas including biology, hydrology, ecology, water quality, and statistical design. It is also important to work with partners that represent federal, tribal, state, provincial, and local agencies as well as non-governmental organizations, universities, and industry. All stakeholders will play a critical role in the success of this project and the HEC Initiative as a whole.

Goals and Objectives of the HEC Initiative

1) Identify key aquatic research issues in the HEC using a consensus building and adaptive management approach.
2) Develop a research strategy to address resource management issues in the HEC that are identified.
3) Create relevant new science to better address the needs of fisheries and aquatic resource managers in the HEC.
4) Provide managers with the scientific information they need to address aquatic resource issues in the HEC.

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Huron-Erie Corridor Initiative
BRIEFING ITEM

February 7, 2013

Name: Nick Mandrak
Agency: Great Lakes Laboratory for Fisheries and Aquatic Sciences, Fisheries and Oceans Canada

Briefing Item Type: Information
Permission to post on HECI Website: No

Title: Fish Community Sampling in the Huron-Erie Corridor

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Huron-Erie Corridor Initiative
BRIEFING ITEM

February 7, 2013

Name: Susan Doka
Agency: Great Lakes Laboratory for Fisheries and Aquatic Sciences, Fisheries and Oceans Canada

Briefing Item Type: Informational
Permission to post on HECI Website: Yes

Title: St. Clair River - Detroit River AOCs: Fish Habitat Assessments

Fisheries and Oceans Canada is currently engaged in fish habitat and supply modelling in the St. Clair and Detroit rivers. Our modelling is meant to inform reasonable targets for Area of Concern delisting, and to assess progress on beneficial use impairments identified in Canadian remedial action plans. Our models are spatially explicit and classify fish habitat based on depth, vegetation cover, substrate and temperature, according to expert opinion and documented preferences for representative fish guilds. To this end we have been collecting habitat data in the Detroit and St. Clair rivers, including: 1) submerged aquatic vegetation cover using hydroacoustics which identify percent cover, edge of bed, and maximum depth of colonization; 2) Substrate size distribution using ponar samples; and 3) Temperature data using temperature loggers deployed during the summer months.

Recently we have finished compiling complimentary datasets from partner organizations and local stakeholders. We have mapped these data to identify gaps in our spatial coverage. We have been standardizing substrate observations to a modified Wentworth scale, collecting those data in a geodatabase, and including metadata such as the data source and whether the data are quantitative or qualitative samples.

Our objectives for 2013 are: 1) to complete the compilation of substrate data and create a single, seamless spatial layer; 2) To create a digital elevation model incorporating both bathymetric and terrestrial elevation, and improve upon this model as data allow; 3) To process raw hydroacoustics data into a GIS-compatible spatial layer; and 4) To scope models for predicting submerged aquatic vegetation and classify emergent wetlands.

We hope to continue to fill important data gaps and improve our spatial data layers to quantitatively assess fish habitat as we have in other AOCs.

Huron-Erie Corridor Initiative
BRIEFING ITEM

February 7, 2013

Name: Michelle Selzer, Lynda Krupansky, Melanie Foose, and Jennifer Tewkesbury

Agency: Michigan Dept. of Environmental Quality, Office of the Great Lakes

Briefing Item Type: Information

Permission to post on HECI Website: Yes: Office of the Great Lakes Website: www.michigan.gov/deqogl; and the General DEQ Website: www.michigan.gov/deq

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Title: Update of on-going and planned water quality-related activities in the HEC.

Lake Coordination (Selzer):

- Planning a Great Lakes Challenges Forum with the International Joint Commission. Conference being held on Thursday, March 14, 2013 at Oakland University in Rochester, MI.
- Partnering with the River Raisin Partnership organization to find ways to enhance state and local collaboration in the River Raisin Watershed.
- Working with the Natural Resources Working Group comprised of state, federal, university, and non-profits organizations to develop realistic outcomes and a framework for concerted action to address non-point source issues in the River Raisin Watershed.
- Partnering with the Detroit Climate Action Collaborative to develop a city of Detroit Climate Change Action Plan. The plan will be used as a guide to reduce greenhouse gas emissions and to increase the resilience of the city's social, built and natural environment.
- Participating in the South East Michigan Council of Governments Regional Green Vision for Southeast Michigan. The primary goal of this regional vision is to help benchmark the current green infrastructure levels through data collection and envision the future of green infrastructure through various analyses of the data.
- Continuing to engage in the Lake St. Clair Partnership. Next meeting is scheduled for February 4th.
- Participated in the 6th Binational Lake St. Clair Conference at MacRay Harbor on November 29-30. Proceedings of the conference are at: http://glc.org/stclair/conf2012_proceedings.html

Coastal Management Program (Krupansky):

- The Coastal Management Program has a grant opportunity (up to $100,000) for a variety of coastal projects related to public access creation and improvement, coastal habitat stewardship, coastal hazard management, coastal water quality protection, and coastal community development with an emphasis on planning and zoning. Deadline is March 29, 2013.

Detroit River Area of Concern (Foose):

- Current PAC Support grant developing data set on locations/hot spots of contaminated sediments.
- Targets for Fish and Wildlife Habitat and Populations plan drafted; however update in progress to include in-river aquatic sites.
- Tainting of Fish BUI in process of being removed; potential for spring bi-national celebration of BUI removal.
- Statewide assessment of Aesthetics BUI completed.
- Statewide assessment of Bird and Animal Deformities BUI completed.

St. Clair River Area of Concern (Foose):

- Added cost to Agriculture and Industry BUI removed in 2012.
- Degradation of Aesthetics BUI removed in 2012.
- Analysis and data collection of contaminated sediments completed on Canadian side.
- Delisting targets for Fish and Wildlife Habitat BUI were finalized in 2012. Habitat restoration and enhancement design work currently in progress as a result of direct EPA funding.
- Statewide assessment of Bird and Animal Deformities BUI completed.

Rouge River Area of Concern (Tewkesbury):

- Ongoing are discussions related to a collaboration of state and federal partners to promote the implementation of a habitat enhancement project in the concrete channel and its probable long term impacts on the Rouge River AOC.
- There is growing interested by state and federal partners for a fish passage and habitat restoration project at the Henry Ford Estate Dam. Specifically, partners are working on data supporting the need for the project, its potential positive impacts, and creative design solutions.
- Completed the Wayne Road Dam Removal and Habitat Improvements Project on the lower Rouge in the Fall of 2012, reconnecting 22 miles of the river to the Great Lakes system and the Detroit River.
- Completed the Danvers Pond Dam Removal Project and Stream Restoration on the upper Rouge in the Fall of 2012.
- Completed the Feasibility Study and Remedial Investigation for a Great Lakes Legacy Act contaminated sediment project on the Lower Rouge River Old Channel. Currently working on the design phase of the project and potential project partnerships.
- Currently working to produce an AOC BUI Report Card to share with stakeholders and potential partners.

Clinton River Area of Concern (Tewkesbury):

- Completed design phase of the Clinton River Spillway Habitat Enhancement Project. Currently seeking funds for implementation through various sources.
- Completed implementation of habitat restoration work at the Lake St. Clair Metropark Coastal Wetland Project site with post monitoring activities planned for the Spring of 2013.
- Completed streambank restoration and angler access projects on the Clinton River at Yates Park in Rochester Hills through funding awarded by Miller-Coors to the Clinton River Watershed Council.
- Completing post monitoring analysis of the Paint Creek Dam Removal project and its impact on benthic populations.
- Completing Pre-Assessment of Benthic Populations in the AOC to assess Degradation of Benthos BUI and prioritize areas for restoration.

River Raisin Area of Concern (Foose):

- The Statewide assessment of the Bird and Animal Deformities BUI is completed. The observational data shows that the BUI is still impaired for the productivity of bald eagles. Additional raw monitoring data collected indicates productivity of bald eagles has increased in the previous three years and to the level where the BUI may be removed; however additional monitoring of bald eagle populations may be needed for definitive removal of the BUI.
- Contaminated sediment removal process on-going.
- Phase I of the River Raisin Fish Passage project complete which included complete removal of two dams and rock ramps at four other dams in the Lower river. Phase II of the fish passage projects in progress – permits have been applied for. Post monitoring of the dam removal projects may be a future research need/desire.
- Wetland restoration projects currently ongoing at the Sterling State Park.

Huron-Erie Corridor Initiative
BRIEFING ITEM

February 7, 2013

Name: Mike Thomas and Todd Wills
Agency: Michigan DNR Lake St. Clair Fisheries Research Station

Briefing Item Type: Information
Permission to post on HECI Website: Yes

Title: Assessment Program Summary for 2012 – Lake St. Clair Fisheries Research Station (LSCFRS)

All fisheries surveys scheduled for LSCFRS staff in 2012 were completed. These included long-term fish community surveys (Lake St. Clair trap net survey, Lake St. Clair fish community trawl survey) as well as long-term targeted surveys (St. Clair River sturgeon setline survey, Lake Erie walleye fall gill net survey). Field work was also completed for 3 short-term projects: a fish community survey in Southern Lake Huron, the Middle Channel Reef post-construction juvenile lake sturgeon survey, and a cormorant nest survey. A brief description of each of these surveys follows:

1. Lake St. Clair Fish Community trap net survey – This survey consists of small mesh trap nets fished from late April through mid-May at 4 sites in Anchor Bay, Lake St. Clair. The principal species captured include smallmouth bass, rock bass, channel catfish, northern pike, muskellunge, white bass, white perch, yellow perch, freshwater drum, and various species of suckers. This survey was conducted in the 1970's and early 1980's. The current survey period dates from 2002. Smallmouth bass are jaw tagged to evaluate movement and survival. Gametes from ripe muskellunge are utilized for hatchery propagation. Value-added sampling includes samples collected for disease surveillance, contaminant monitoring, parasite investigations, and genetic studies. This survey also is a component of MDNR invasive species monitoring efforts in the HEC.

2. Lake St. Clair Fish Community trawl survey – This survey includes 10m headrope bottom trawling in Anchor Bay, Lake St. Clair during late May and early September. Total effort ranges from 6 to 16 trawl tows per year. The survey has been conducted annually since 1996. This gear is most efficient at capturing small fish and provides an index of abundance for many of the forage species (alewife, rainbow smelt, trout-perch, spottail shiner, sand shiner, logperch, round goby, etc.). The September trawls also provide an index of yearclass strength for yellow perch and smallmouth bass as age 0 fish each year. Value-added sampling includes samples collected for disease surveillance, diet studies, contaminant monitoring, and genetic studies. This survey also is a component of MDNR invasive species monitoring efforts in the HEC.

3. St. Clair River sturgeon setline survey – The sturgeon setline survey has been conducted annually since 1997, except for 2003. This survey is conducted each year beginning in late May and

continuing for 3 or 4 weeks. The survey gear includes 8 setlines (each with 25 hooks) baited with round gobies. Annual effort typically ranges from 80 to 100 overnight sets. Two hook sizes have been used to sample a broader size range of lake sturgeon. All lake sturgeon captured are scanned for PIT tags and examined for external tags. First time captures are tagged with a PIT tag and external tag, except external tags are no longer applied to juveniles less than 36" TL. This survey is the principal source of mark-recapture data used in estimating the abundance of lake sturgeon in the St. Clair River. Other value-added sampling includes samples collected for parasite investigations, disease surveillance, and genetic studies.

4. Lake Erie walleye fall gill net survey – This survey consists of 1300' experimental multifilament gill nets fished overnight at 2 index locations in Michigan waters of Lake Erie. Each index site is sampled twice during early October. This survey has been ongoing since 1978. The gill net gangs are canned on 6' strings so sample the upper portion of the water column. Walleye are generally the dominant species in the catch, but gizzard shad, white perch, white bass, are also caught in substantial numbers. This survey provides an annual index of abundance by year-class for walleye in the Michigan waters of Lake Erie. These data are pooled with Ohio DNR fall gill net data and included in the walleye statistical catch-at-age population model used in estimating walleye abundance for interagency quota allocation purposes. Value added sampling includes samples collected for diet studies and contaminant monitoring. This survey also is a component of MDNR invasive species monitoring efforts in the HEC.

5. Southern Lake Huron Nearshore Fish Community Survey – A one-time snapshot survey of the nearshore fish community in southern Lake Huron was conducted in July 2012 as part of a lakewide monitoring project. This work replicated (to some degree) work conducted at this same location in 1970. The survey included habitat mapping with sidescan sonar (Hummingbird) and underwater camera, 10m headrope bottom trawls, small mesh trap nets, experimental mesh gillnets, and micro-mesh gill nets. All sampling was conducted between the 2 m and 25 m contours. Principal species captured in the sampling included rainbow smelt, trout-perch, round gobies, yellow perch, and white bass.

6. Middle Channel Reef Juvenile Sturgeon Assessment – 2012 was the second year of sampling as part of the assessment of the Middle Channel Reef construction project. A total of 45 tows were made with a 5m headrope bottom trawl in the shallow delta habitat suspected to support juvenile lake sturgeon. Sampling occurred in April and August in 2012. Principal species captured in this assessment work have included sand shiners, spottail shiners, logperch, round gobies, yellow perch and smallmouth bass. No juvenile lake sturgeon have been captured during this assessment effort.

7. Cormorant Nest Survey – LSCFRS staff have conducted visual counts of cormorant nests by boat on Lake St. Clair on an intermittent basis, beginning in 2004. Nests have only been documented on the navigational structures along the shipping channel near the head of the Detroit River. No cormorant nests in trees or on the ground have been observed around LSC or in the St. Clair River delta. This is a one-day survey with the small vessel. In 2012, 5 navigation structures combined for a total of 97 nests.

Huron-Erie Corridor Initiative
BRIEFING ITEM

February 7, 2013

Name: Rose Ellison
Agency: US EPA – Great Lakes National Program Office

Briefing Item Type: Information
Permission to post on HECI Website: Yes

Title: Update of US EPA's on-going and planned activities in the HEC.

EPA is continuing to focus on the removal of impairments to beneficial uses (BUIs) in the St. Clair River and Detroit River AOCs. In this regard, the tables below provide a description of current and future actions.

St. Clair River AOC

BUI	Current activities	Future steps
Tainting of Fish and Wildlife Flavor	Re-designated, 2011.	n/a
Restrictions on Dredging Activities	Re-designated, 2011.	n/a
Degradation of Aesthetics	Re-designated, 2012.	n/a
Added Costs to Agriculture or Industry	Re-designated, 2012.	n/a
Bird or Animal Deformities or Other Reproductive Problems	MDEQ completed assessment, 2012. BUI determined to be unimpaired.	Convene technical review committee to examine re-designation of BUI.
Degradation of Benthos	DEQ to complete review of available benthos data.	Convene technical review committee to examine re-designation of BUI.
Beach Closings	Port Huron CSO elimination by 2016, Chrysler Beach TMDL 2018.	Convene technical review committee to examine re-designation of BUI.
Restrictions on Fish and Wildlife Consumption,	Currently under assessment by MDCH.	• If assessment shows no impairment, convene technical review committee to re-designate BUI . • If impaired, determine whether impairment caused from inside or outside AOC
Restrictions on Drinking Water Consumption or Taste and Odor Problems	Determine appropriate endpoint for removal criteria.	• Document status of industry/regulatory efforts to prevent spills; • Identify facilities, sources and pathways, significant enough to cause facility shutdown; • Ensure facilities are in compliance with spill planning and prevention regulations; • Ensure engagement and communication re: spill planning, notification and response are acceptable to local municipalities and PAC.
Loss of Fish and Wildlife Habitat	• Revised plan for removal of Fish & Wildlife BUI completed, 2012; • Restoration Design for all target habitat sites on-going.	• 2013/14, complete habitat restoration actions for all target habitat sites identified in revised Fish & Wildlife plan.

Detroit River AOC

BUI	Current activities	Future steps
Restrictions on Drinking Water Consumption or Taste and Odor Problems	Re-designated, 2011.	n/a
Tainting of Fish and Wildlife Flavor	Proposed for re-designation.	Bi-national review for re-designation by Four Agency Management committee. Re-designate in 2013.
Fish Tumours and other Deformities	MDEQ assessment, 2011-2012, indicates BUI likely unimpaired. Awaiting final results.	If found unimpaired, convene technical review committee to examine re-designation of BUI.
Degradation of Aesthetics	MDEQ completed assessment, 2012. BUI remains impaired.	Address source of impairment identified in assessment.
Restrictions on Fish and Wildlife Consumption	MDCH assessment determined fish consumption advisories more restrictive than non-AOCs.	Study contaminants in fish tissue from AOC compared to control site.
Bird or Animal Deformities or Other Reproductive Problems	MDEQ completed assessment, 2012. BUI remains impaired.	Conduct study to identify source of impairment.
Degradation of Benthos	Effort underway to identify target sediment sites.	GLLA site characterization of identified target sediment sites.
Loss of Fish and Wildlife Habitat & Degraded Fish and Wildlife Populations	• Completion of restoration actions at Blue Heron Lagoon & South Fishing Pier; • Design of Fort Wayne reef site	• Revise Fish & Wildlife BUI removal plan • Begin construction of Fort Wayne reef • Planning and permitting for remaining reef sites
Restrictions on Dredging Activities	MDEQ completed assessment, 2011. BUI remains impaired.	TBD
Beach Closings	Impaired	TBD

Lake St. Clair

Through GLRI US EPA has been supporting target projects identified the USACE Strategic Implementation Plan (SIP) for Lake St. Clair (http://www.semcog.org/lakestclair.aspx). Since 2010, EPA has funded six projects identified in the SIP that directly relate to Lake St. Clair, including: Macomb County Illicit Discharge Elimination Program; Restoring the Lake Erie Corridor through Green Streets; Eliminating E. Coli Sources Impacting Beach Closures; Metro Beach Parking Lot Reconstruction; Metro Beach Marsh Restoration; and, Restoration of Fish Spawning Habitat in the St. Clair River (Middle Channel reef project).

Future management needs for Lake St. Clair is somewhat uncertain. According to the new Great Lakes Water Quality Agreement (GLWQA), management actions for Lake St. Clair (as well as the St. Clair and Detroit Rivers) are to be developed through the Lakewide Action and Management Plan (LAMP) for Lake Erie. US and Canadian co-leads for management of the new LAMP annex have recently been identified. How the Annex co-leads will implement the new provisions of the GLWQA and whether it will impact future priorities for Lake St. Clair is not known at this time. Until then, US EPA will continue to support implementation of the SIP and 2005 Lake St. Clair and St. Clair River Comprehensive Management Plan.

Huron-Erie Corridor Initiative
BRIEFING ITEM

February 7, 2013

Name: Paul Evanoff
Agency: SmithGroupJJR

Briefing Item Type: Information
Permission to post on HECI Website: Yes

Title: Belle Isle Habitat Restoration Projects at Blue Heron Lagoon and South Fishing Pier

Belle Isle South Fishing Pier Habitat R

Belle Isle Blue Heron Lagoon Habitat Restc

South Fishing Pier, Belle Isle Park

Detroit, Michigan

As part of a multi-year, multi-phased effort to improve the ecological quality of the Detroit River by increasing fish and wildlife habitat, SmithGroupJJR designed 2.5 acres of protected coastal wetland and shallow water nursery habitats at the South Fishing Pier.

SmithGroupJJR began working on the project in 1996 during the preparation of the *Belle Isle Piers Fishery Habitat Enhancement* report. This area will be located immediately downstream from the sturgeon spawning reef restoration project, which SmithGroupJJR previously designed and implemented. The newly constructed reef is the site of reproduction for 16 species of native fish where spawning was nonexistent; however, the fate of the fish larvae is largely unknown as little nursery habitat exists along the urban center. The new wetland and shallow nursery habitat, which will be constructed on the river bottom through earthwork enhancements and the introduction of habitat structure composed of rock, submerged woody debris, and aquatic plantings, will provide a critical refuge for the fish larvae to grow in a protected environment.

Size
2.5 acres

Estimated Completion Date
2012

Estimated Construction Cost
$600,000

Grant Funding
$600,000
Great Lakes Restoration Initiative

Blue Heron Lagoon Habitat Restoration Belle Isle Park

Detroit, Michigan

The Blue Heron Lagoon is a 41-acre lake/wetland on the east end of Belle Isle that discharges to the Detroit River. Direct access for fish from the river to the lagoon is prohibited by sheet pile walls, grates, and drop structures. SmithGroupJJR designed a habitat restoration project that will reconnect and naturalize the mouth of the lagoon to the Detroit River, restoring fish access to all 41 acres of the wetlands, shallow, and deep water habitats providing critical wildlife and fish nursery habitat that is severely limited along the Detroit River. The project's four critical components include:

- *Costal Wetland Restoration*: Up to 5 acres of new shallow and deep-water habitat will be provided within the existing Blue Heron Lagoon, which will function as a nursery for targeted fish species.
- *Channel Restoration/Naturalization*: Fish passage will be restored at the existing outlet to the river and a second inlet/outlet will be created through the existing peninsula.
- *Spawning Reef Enhancements*: The existing high-quality rock reef that SmithGroupJJR previously designed, located immediately upstream of the project area, will be expanded to provide greater spawning habitat and increased connectivity to the costal wetland and channel restoration.
- *Existing Upland Recreation Amenity Restoration*: Recreation resources, native vegetation, and other elements of the SmithGroupJJR *Blue Heron Lagoon Natural Area Restoration Master Plan*, impacted by the work will be restored. Trail restoration includes over 150 linear feet of a concrete and steel bridge spanning a new inlet, which is designed to support emergency and maintenance vehicles.

SmithGroupJJR's work will also involve collaboration with critical stakeholders, including Friends of the Detroit River, the EPA, the Detroit Recreation Department, the U.S. Geological Survey, and the U.S. Army Corps of Engineers.

Size
41 acres

Estimated Completion Date
2012

Estimated Construction Cost
$1.1 million

Grant Funding
$1.1 million
Great Lakes Restoration Initiative

Huron-Erie Corridor Initiative
BRIEFING ITEM

February 7, 2013

Name: David Mifsud
Agency: Herpetological Resource and Management, LLC (HRM)

Briefing Item Type: Information
Permission to post on HECI Website: Yes

Title: HEC Amphibian and Reptile Project Updates

HRM has continued to work on a number of innovative projects in the past year within the HEC. Our work with the Michigan Herp Atlas project and the development of an online data submittal system and database has been very successful. We are in the process of securing funds to run conservation workshops throughout Michigan to educate participants about the importance of amphibians and reptiles and encourage attendees to contribute to the database. We are also working on funding for a smartphone application (app). We will continue to encourage agencies, researchers, and conservation organizations to provide data and partner with us on this project. This project is quickly becoming the most compressive database on the distribution of all species of amphibian and reptile in Michigan!

We are working with the St. Clair Community Foundation to conduct baseline wildlife surveys associated with a restoration project in the Upper St. Clair River. We are also actively creating restoration designs associated with that project including the creation of Mudpuppy habitat. We are also conducting wildlife monitoring on Belle Isle associated with habitat restoration, and developing a statewide Best Management Practices Manual focused on Amphibians and Reptiles for the Michigan Department of Environmental Quality. This project is a collaboration, and multiple agencies and organizations are involved with providing topics, resources, and critical review. This will be the first of its kind in Michigan and an important resource on reducing impacts to herpetofauna as well as providing resources and design concepts to restore and improve habitat for these imperiled indicator species.

Huron-Erie Corridor Initiative
BRIEFING ITEM

February 7, 2013

Name: Robert Reider
Agency: DTE Energy

Briefing Item Type: Information
Permission to post on HECI Website: Yes

Title: Clean Water Act Section 316(b) Rule (Cooling Water Intake Structures)

A proposed rule covering existing facilities that use > 2 million gallons per day (MGD) design intake flow (DIF) was published in April 2011 and was originally scheduled to be finalized in July 2012. However, in July 2012 EPA announced that the release date of the final rule had been extended to no later than June 27, 2013. As currently proposed, power plants with a DIF $\geq$ 50 MGD must submit to the permitting authority the results of several studies within 6 months of the effective date of the rule. These studies pertain to CWIS design (existing and proposed possible changes), and physical and biological characterizations.

Huron-Erie Corridor Initiative Steering Committee
BRIEFING ITEM

February 7, 2013

Name: Doug Pearsall
Agency: The Nature Conservancy

Briefing Item Type: Information
Permission to post on HECI Website: Yes

Title: Lake Erie Biodiversity Conservation Strategy

The Nature Conservancy, working with the Michigan Natural Features Inventory and Nature Conservancy of Canada, has just completed biodiversity conservation strategies—or "blueprints"—for Lake Erie and Lake Michigan, funded by US EPA through the Great Lakes Restoration Initiative with additional funding provided by Environment Canada for Lake Erie. Four blueprints have now been completed, covering all the lakes except Superior. These blueprints are being reviewed by LAMPs; the Lake Ontario LAMP has already produced their own biodiversity conservation strategy, incorporating five of the six recommendations from the Lake Ontario blueprint. TNC and NCC will continue to work with the LAMPs and other partners to promote and improve the strategies contained in the blueprints and to provide technical support to regional and local conservation efforts.

The Lake Erie Biodiversity Conservation Strategy[1] distinguishes the Huron – Erie Corridor (St. Clair River, Lake St. Clair, and the Detroit River) as one of four "reporting units" and provides information on the status of biodiversity and critical threats to biodiversity for the HEC (Table 1). Top threats include AIS, shoreline alterations, pollution from agricultural sources, invasive terrestrial species, housing and urban development, and climate change. Further information on key strategies is available in the report.

Table 1. Viability and threat status of biodiversity conservation targets in the Huron - Erie Corridor

Target	Viability Status	Threat Status
Nearshore Zone	Fair	Very High
Aerial Migrants	Good	Medium
Coastal Terrestrial Systems	Fair	Very High
Coastal Wetlands	Fair	High
Connecting Channels	Fair	Very High
Islands	Fair	High
Native Migratory Fish	Fair	High
Overall	Fair	Very High

[1] Full report is available here: http://conserveonline.org/workspaces/greatlakesblueprints/documents/all.html

Huron-Erie Corridor Initiative Steering Committee
BRIEFING ITEM

February 7, 2013

Name: Doug Pearsall
Agency: The Nature Conservancy

Briefing Item Type: Information
Permission to post on HECI Website: Yes

Title: Western Lake Erie Coastal Conservation Vision

TNC is developing a strategic vision for coastal restoration and management along the 150-mile shoreline of the Western Lake Erie Basin[1]. Through this six-year initiative, we are coupling an analysis of the actions and outcomes required to achieve a healthy western Lake Erie with a deeper understanding of the human communities that rely on the ecosystem so that both ecological and sociocultural goals can be pursued in tandem. This is a new and essential conservation approach for the Conservancy. We no longer expect to conserve nature apart from the needs of people, least of all in coastal areas, which not only support our economies and recreational pursuits but are the most biologically diverse areas of the Great Lakes. Planning for ecological outcomes by integrating stakeholder values illuminates key factors of feasibility, opportunities for synergies between conservation and other seemingly unrelated endeavors, and the opportunity to achieve outcomes that demonstrate the central role of conservation in Michigan's economic and ecological well-being and future prosperity. This new approach also focuses the Conservancy's work under an ecosystem services framework, which connects ecosystems and biodiversity with the environmental capital upon which our society and economy depends.

During this first year, we established an interdisciplinary project team whose members have expertise in restoration, social science, natural science, geographic information systems (GIS), conservation planning, and project management. We also made progress on each of the three objectives:

- **1: Working with partners and stakeholders, map and prioritize actions to improve ecosystem health and meet the needs of people.** We identified and engaged stakeholders through formal and informal meetings and interviews; identified ecological and sociocultural goals; compiled data and maps; and established conservation targets.
- **2: Implement and learn from early "no-regrets" restoration projects.** Several ongoing projects are in place to manage invasive species, create fish passage, restore lakebed, and restore coastal wetland and terrestrial habitat.
- **3: Promoting broad scale adoption and implementation of the vision.** Engaging partners has set the stage for future promotion and engagement.

[1] project scope includes the Western Basin and Detroit River, along with a 10km inland coastal area

Huron-Erie Corridor Initiative Steering Committee
BRIEFING ITEM

February 7, 2013

Name: Emily Bouckaert[1], Nancy Auer[1], Ed Roseman[2], Jim Boase[3]
Agency: [1]Michigan Technological University, [2]USGS Great Lakes Science Center, [3]US Fish and Wildlife Service

Briefing Item Type: Information
Permission to post on HECI Website:

Title: Assessment of lake sturgeon spawning efficacy on a constructed reef at Fighting Island, Detroit River.

Objectives: Assess and measure the use by lake sturgeon on a constructed reef spawning area at Fighting Island, Detroit River. We measured egg and larval abundances above and below the constructed reef in 2010, 2011, and 2012.

Results Overview: In 2008, an artificial spawning reef was constructed near Fighting Island in the Detroit River to enhance spawning habitat for native fishes including lake sturgeon (*Acipenser fulvescens*). In this system, much of the natural lake sturgeon spawning habitat has been degraded or eliminated as a result of channelization, dredging, and substrate removal. The Fighting Island reef consists of 12 experimental reef beds containing four different substrate treatments. In 2010, viable eggs and larvae were collected in a small-scale pilot study. No eggs or larvae were detected at the site in 2011. In 2012, the four reef beds closest to Fighting Island were sampled for fish larvae in order to evaluate the effectiveness of this artificial reef project. These four reef beds were composed of four different substrates: limestone shot rock (5.1-30.5 cm), limestone sorted rock (5.1-30.5 cm), rounded rock (5.1-30.5 cm), and a 1:1:1 mix of all three types (5.1-30.5 cm).We detected the presence of lake sturgeon eggs on all substrate types on May 9th, and began larval lake sturgeon sampling using D-Frame drift nets on May 15th. Night sampling was conducted biweekly until June 5th. In total, 30 lake sturgeon larvae were collected directly downstream of the four reef beds and 3 larvae were collected upstream in control sites. Approximately 45.5% of the larvae were collected on May 15th, and zero larvae were collected on June 5th. Additionally, the majority of larvae (~45.5%) were collected between 20:00 and 22:00 hours. A repeated measures ANOVA found no significant difference in average CPUEs (larval sturgeon/hr/night) between sampling sites located directly downstream of the four reef bed treatments. Our results indicate that the Fighting Island reef is producing viable lake sturgeon larvae, and that differences in substrate type among these reef beds appears to not affect egg deposition or the number of larvae that are produced.

Roseman, E.F., B.A. Manny, J. Boase, G. Kennedy, M. Child, J. Craig, K. Soper, and R. Drouin. 2011. Lake Sturgeon Response to a Spawning Reef Constructed in the Detroit River. Journal of Applied Ichthyology 27(Suppl 2):66-76.

Huron-Erie Corridor Initiative
BRIEFING ITEM

February 7, 2013

Name: Jim Diana, Maureen Lynch
Agency: University of Michigan School of Natural Resources & Environment

Briefing Item Type: Information
Permission to post on HECI Website: Yes

Title: Juvenile Fish Assessment in St Clair River, Middle Channel Reef Project

Objectives: To assess juvenile fish community composition and wetland habitat usage in the St Clair River delta and to assess short-term growth of rock bass *Ambloplites rupestris*.

Results Overview: Sampling took place in May-Aug and in October of both 2011 and 2012. Samples were taken at nine sites throughout the middle channel and connected bays. Each month, two hoop nets and two minnow trap gangs were set for two consecutive 24-hour soaks at each site for a total of 8 units of effort per month, per site. After each soak, fish were collected, identified to species, and released. From a total of 610 units of effort, 40,147 fish from 28 species were collected. Catch was heavily dominated by emerald shiner *Notropis atherinoides* as well as other cyprinids, with 93.25% of the total catch from this family. Rock bass *Ambloplites rupestris* was the most abundant species when cyprinids were excluded from analysis, with 1348 individuals. When cyprinids and gobiids were removed to focus solely on juvenile fish, total catch was reduced to 2,273 individuals, with a species richness of 20. Of that 20, 11 species were considered rare, comprising less than one percent of total catch.

Mixed model ANOVAs and Canonical Correlation Analyses were run to analyze the data. General trends showed catch per unit effort (CPUE) highest in bay sites in June and October. Both CPUE and species richness were significantly influenced by the interaction of site and month factors, indicating spatial and temporal changes throughout the study. CPUE and rare species richness were greater at the bay sites than at the channel sites, and overall fish species richness was correlated with vegetation species richness, which was also higher at bay habitats. CPUE did increase in the downstream sites, but overall species richness and rare species richness were positively correlated with upstream sites. Length-adjusted RNA:DNA ratios of rock bass tissue, however, did not display clear trends by month or location, indicating that growth may not vary significantly over such a relatively small spatial extent.

The data show that while the community associations vary by site and month throughout the summer, the bay habitats consistently have higher abundance and diversity of YOY fish, indicating that these habitats may be critical nursery grounds and should be highlighted as conservation and restoration priorities.

Future Plans: Sampling will continue through the summer of 2013, we will again sample in May and October at all wetland sites. In addition, we will focus on locating the habitat of juvenile lake sturgeon spawned on the new reef, and will utilize hydrodynamic models as well as larval fish collections to improve the detection of juvenile lake sturgeon. In addition to our standard sampling, this will include spotlight surveys of littoral areas and modified minnow traps for deepwater sampling in the river.

Huron-Erie Corridor Initiative
BRIEFING ITEM

February 7, 2013

Name: Mark DuFour and Dr. Christine Mayer
Agency: University of Toledo – Lake Erie Center

Briefing Item Type: Information
Permission to post on HECI Website: Yes

Title: Estimating larval walleye (Sander vitreus) export from the Detroit River.

Overview

Larval fish in large river systems are extremely variable; however estimates of abundance and mortality are important for understanding the quality of these systems as reproductive and nursery habitats and their role in population recruitment. In concert with inherent variability, estimating larval fish abundance is difficult as logistics often cause sampling to be restricted and incomplete. Therefore, acknowledging and accounting for uncertainty in the estimation process is an important step in providing managers with useful information on temporal trends in larval fish abundance.

Objectives

- Estimate daily and annual abundance of larval fish exiting large tributaries of the Great Lakes while accounting for spatial and temporal uncertainty.
- Use these results to identify temporal tends within and among systems as well as relative contributions from each system.

Results

Estimated daily export of larval walleye began in late April and peaked in mid-May during 2011, with the extent of the hatching season spanning just less than one month (Figure 1). Export in 2012 began two weeks earlier but remained at low levels until early May; declining abruptly after. The hatching season in 2012 extended for just over a month. The concentrated and slightly delayed hatching season from 2011 produced substantially more fish (~50 million) then the protracted earlier season in 2012 (~ 20 million). A high degree of uncertainty in the 2011 daily estimates is reflected in the wide annual distribution; spanning potential values of annual abundance. A comparison of annual larval walleye abundance from the three major Lake Erie spawning tributaries indicates that both the Maumee and Detroit Rivers are important producer systems. Percent contribution from the Detroit was 51% in both 2011 and 2012 with the Maumee contributing 38% and 47% respectively (Figure 2).

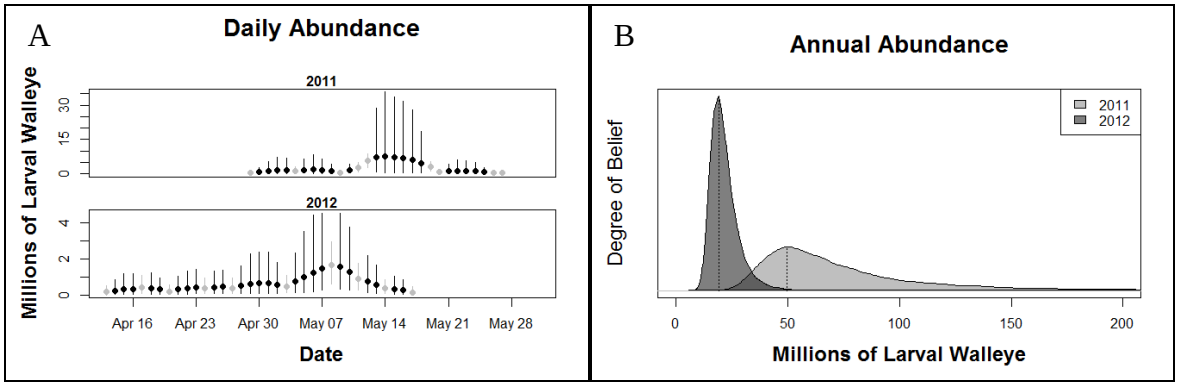

Figure 1. A) Estimated daily exports of larval walleye from the Detroit River (2011-2012) are represented by mean (dots) and 95% credible intervals (bars). Gray values correspond to sampled days while black values represent unsampled days. B) Estimated annual abundance are displayed as distributions spanning potential values with the most probable value (dashed line) occurring at the peak of the distribution.

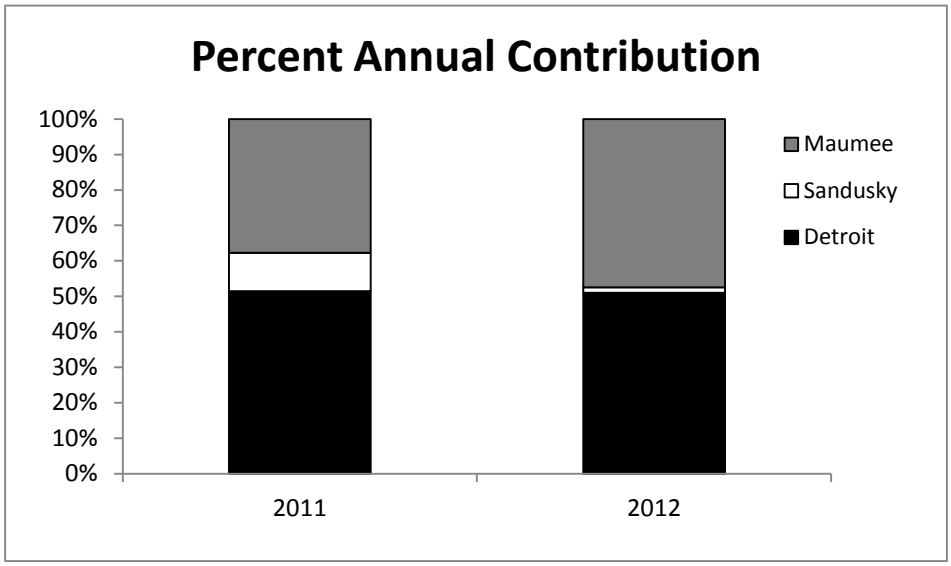

Figure 2. A comparison of the relative annual contributions of larval walleye from three major Lake Erie spawning tributaries indicates that the Maumee and Detroit systems are important producers. Mean values from estimated annual distributions were used in this comparison.

Future Directions

- Estimate contribution from Ohio reef complex.
- Relate relative contributions from individual sub-stocks to indices of recruitment.

Huron-Erie Corridor Initiative
BRIEFING ITEM

February 7, 2013

Name: Doug Larson[1], Scott McNaught[1], and Edward Roseman[2]
Agency: [1]Central Michigan University, Mt. Pleasant, MI, [2]USGS Great Lakes Science Center, Ann Arbor, MI

Briefing Item Type: Information
Permission to post on HECI Website: Yes

Title: Assessment of Nursery Habitat Use by Larval Fishes in the St. Clair River Delta, MI

Recruitment of larval fishes into wetland nursery areas is critical to the large-scale restoration of river ecosystems; however, habitat factors necessary for good recruitment have not been widely studied.

Prior to the construction of new spawning habitat in the St. Clair River, we surveyed twenty wetland sites in the North and Middle Channels of the delta between May and July 2010 and 2011. Larval fish were collected weekly with a 0.5-m conical net and quatrefoil light traps to assess community composition and abundance. We measured a wide range of abiotic and biotic factors to establish differences between nursery area sites. Nursery area use was quantified by number of individuals of each species and total abundance of fish collected. We used principal component analysis to reduce abiotic variables and copepod density to a single variable, lentic-lotic input. We then compared that variable to the general larval fish community composition derived from non-metric multidimensional scaling (NMDS).

Community composition was significantly negatively correlated with lentic-lotic input (-0.573, $p<0.001$), suggesting that, for certain species, habitat restoration should focus on reconnecting river channels with functional lentic, wetland ecosystems. Larval fish community composition also showed a species specific relationship with relative submerged aquatic vegetation density (Multi-Response Permutation Procedures, $p=0.003$).

Results of these analyses suggest that restoration efforts in wetland nursery areas should focus on establishing vibrant submerged aquatic vegetation as a means to improve larval fish prey recruitment.

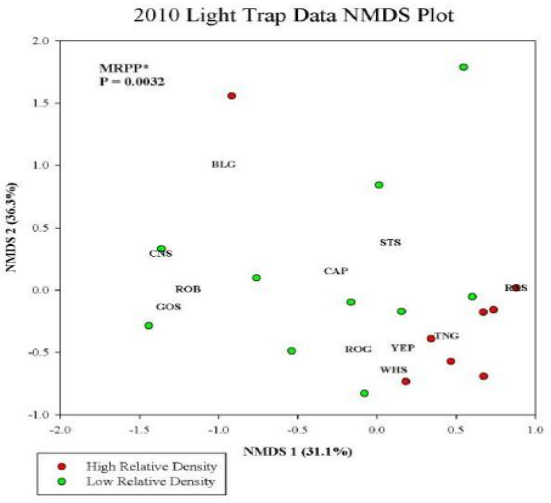

Figure 2. Community Composition as described by Relative Density of Submerged Aquatic Vegetation. NMDS; MRPP = 0.003.

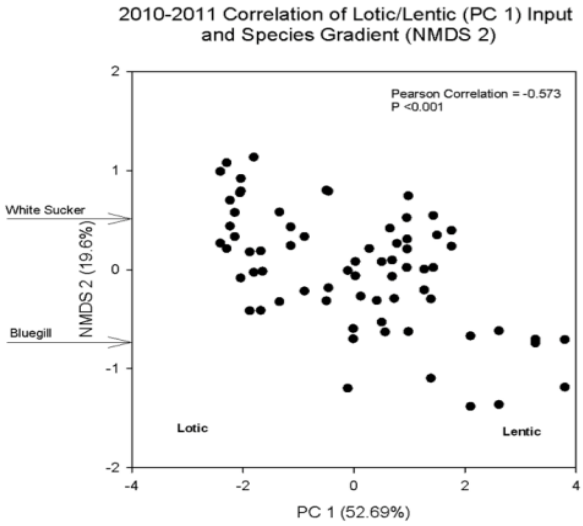

Figure 1. Correlation of Lentic-Lotic Input with Community Composition. Pearson Correlation = -0.573, P<0.001

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Genetic connectivity and diversity of walleye (*Sander vitreus*) spawning groups in the Huron–Erie Corridor

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ABSTRACT

The Huron–Erie Corridor (HEC) connects the upper and lower Great Lakes, providing key fish passage. A century of channelization, dredging, and pollution has led to habitat loss and declining fish numbers. Since 2004, the multi-agency HEC initiative augmented fish spawning habitat at Belle Isle and Fighting Island in the Detroit River, whose populations are examined here. We analyze genetic patterns among seven spawning groups ($N = 311$) of walleye *Sander vitreus*, a key fishery species, using nine nuclear DNA microsatellite loci and mitochondrial DNA control region sequences. Results reveal that all spawning groups contained appreciable genetic diversity (microsatellites: $H_O = 0.72$; mtDNA: $H_D = 0.73$) and showed a mixture of connectivity and divergence. Genetic relationships did not fit an isolation by geographic distance hypothesis, with some closely spaced populations being very different. Notably, the Flint River–Lake Huron spawning group was the most divergent, showing no genetic exchange. The Belle Isle and Fighting Island populations markedly differed, with the latter showing some genetic exchange with the Grosse Ile (Detroit River) and the Huron River (northwest Lake Erie) populations to the south. Walleye spawning at Fighting Island experienced no significant change in overall genetic diversity pre- versus post-habitat augmentation, but the allelic frequency changed. Our results comprise an important baseline for future population analyses and habitat assessment of these habitat augmentation areas. Despite habitat degradation and pollution, it appears that historic walleye spawning groups have persisted along the HEC, meriting continued genetic monitoring and further restoration efforts to conserve and enhance this important and diverse fishery.

Introduction

Understanding the genetic connectivity (i.e., gene flow) and divergence of populations is fundamental to develop appropriate management strategies for ecologically and economically valuable species. Notably, identifying barriers to gene flow reveals important ecological information on species movement, dispersal, behavior, survival, and reproduction patterns that may be used to identify evolutionary significant units or other conservation management designations (see Sork and Waits, 2010; Waples, 1995; Wofford et al., 2005).

Aquatic populations may maintain gene flow through connecting channels that serve as migration corridors among watersheds (LeClerc et al., 2008; Robinson et al., 2002). Vagile fishes use such avenues to disperse to spawning sites, nursery habitats, and feeding grounds (Meeuwig et al., 2010; Sheer and Steel, 2006). Some widely distributed species may exhibit high gene flow across their connected range, with low overall population structure and little specialization (Boulet et al., 2007; Hughes, 2007). On the other hand, species having spawning site fidelity may show marked genetic structure and local adaptedness, despite apparent ample opportunity for migration and gene flow among adjacent locations. Notably, populations of salmonid fishes and other species, including walleye *Sander vitreus* (Percidae: Teleostei) are genetically structured due to spawning site philopatry and natal homing (Banks et al., 2000; Jennings et al., 1996; Nielsen and Fountain, 1999; Stepien and Faber, 1998; Utter et al., 1989). Throughout most of the year, walleye move widely and intermingle within and among bodies of water, with some individuals traveling 50–300 km (Colby et al., 1979). In the spring walleye return to spawn at rocky shoals believed to be their natal sites (Jennings et al., 1996; Stepien and Faber, 1998; Wang et al., 2007).

Anthropogenic activities, such as exploitation, stocking, and habitat fragmentation and channelization may disrupt or increase genetic exchange across migration corridors, changing relationships among sub-populations. Such factors may lower genetic diversity and increase genetic drift, or may act to homogenize formerly different groups (Laroche and Durand, 2004; Wofford et al., 2005) and lead to declines in adaptedness and fitness (Leberg, 1992; Schindler et al., 2010).

Walleye distribution and genetic patterns

The walleye is one of the most ecologically and economically valuable fishes in the Great Lakes, constituting a keystone species as a primary predator (Locke et al., 2005; Nate et al., 2011; Roseman et al., 2010)

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and supporting large sport and commercial fisheries (Schmalz et al., 2011). Its native distribution ranges from the Mackenzie River in the Northwest Territories of Canada, south to the US Gulf Coast, and northeastward to New Hampshire and Quebec (Page and Burr, 2011). Over the past century, stocking transplants – many originating from western Lake Erie in the Great Lakes – introduced walleye throughout most of the continental US and southern Canada (summarized by Billington et al., 2011).

Broad and fine-scale spatial genetic patterns of walleye spawning groups have been defined across North America using mitochondrial (mt) DNA (Billington et al., 1992; Gatt et al., 2000, 2002; Stepien and Faber, 1998) and nuclear DNA microsatellite (μsat) loci (Stepien et al., 2009, 2010, 2012; Strange and Stepien, 2007). Results have shown that many walleye spawning groups exhibited little genetic connectivity (e.g., gene flow) and significantly diverged in genetic composition, including between and within lakes, their basins, and connected tributaries (Stepien et al., 2009, 2010). The largest genetic divisions across their native range separated populations outside of the Great Lakes region from those within (Stepien et al., 2009). The Great Lakes region was colonized by walleye originating in three Pleistocene glacial refugia: the Atlantic coastal, Mississippian, and Missourian (Billington et al., 1992; Gatt et al., 2000; Stepien and Faber, 1998; Ward et al., 1989). Primary population demarcations within the Great Lakes separate the upper Lakes (Lakes Superior, Michigan, and Huron) from the lower Lakes (Lakes Erie and Ontario), with significant genetic barriers between most of the lakes and some within them (Stepien et al., 2009, 2010; Strange and Stepien, 2007). The genetic patterns of the upper Great Lakes are likely a result of fish colonizing from the Mississippian and Missourian glacial refugia. The lower Great Lakes populations also were largely founded by the Mississippian refugium, with some contribution from the Atlantic Coastal refugium (Billington et al., 1992; Gatt et al., 2000; Stepien and Faber, 1998; Ward et al., 1989). A recent investigation evaluated three closely-related Lake Erie spawning runs over 15 years, showing overall within-site genetic consistency, and some genetic connectivity and divergence among them (Stepien et al., 2012).

Little is known of the genetic connectivity or divergence among walleye spawning groups in connecting channels, such as the HEC. Those spawning groups may be locally adapted, with unique ecological and physiological variations that may aid their response to external pressures such as spawning habitat loss, exploitation, invasive species, and climate change (Kerr et al., 2010; Stepien and Faber, 1998). Such perturbations likely have impacted walleye populations across the Great Lakes for more than a century, especially along fragile and degraded connecting channels, including the HEC. Defining the patterns of genetic connectivity and divergence of HEC walleye spawning groups may aid managers to maintain and enhance the fishery across this highly impacted system.

Degradation and augmentation of fish habitat along the Huron–Erie Corridor

The HEC is one of four connecting channels within the Great Lakes; it links Lakes Huron and Erie via the St. Clair River, Lake St. Clair, and the Detroit River (Fig. 1). The HEC constitutes a major international shipping route, supporting over $80 billion USD in annual trade (USGS, 2010). It once housed productive spawning and nursery habitats for many ecologically and economically important fish species, including lake trout *Salvelinus namaycush*, lake sturgeon *Acipenser fulvescens*, and walleye (Manny et al., 2010). The first reported habitat modifications began in 1874 with the construction of a shipping channel (914 m long, 91 m wide, and 6 m deep) near Bois Blanc Island in the Detroit River, which eliminated fish spawning habitat in that area. Since that time, the HEC underwent a series of detrimental habitat modifications and fragmentation, including loss of coastal wetlands, armoring of shorelines, channelization, dredging, and industrialization (Bennion and Manny, 2011; Hartig et al., 2009; USGS, 2010).

In addition to habitat loss, industrial outputs along the HEC resulted in heavy metal contamination and declining fish health and numbers throughout the mid to late 20th century (Hartig et al., 2009). Fish health problems included neoplasms, tumors, and lesions on walleye, brown bullhead *Ameirus nebulosis*, white sucker *Catostomus commersonii*, and other species (Manny and Kenaga, 1991). During the 1970s, walleye populations crashed and the entire fishery (commercial and recreational) was closed along the HEC due to high mercury levels in fish tissues.

In 2004, the HEC Initiative partnered 27 federal, state, and provincial agencies and local groups with the goal of restoring aquatic habitat (USGS, 2010). Two artificial reefs were installed in the Detroit River in waters ≥6 m deep: one in 2004 off the northeastern corner of Belle Isle (site C in Fig. 1) and another in 2008 at Fighting Island offshore from LaSalle, Ontario (site D in Fig. 1) (HTG, 2009, 2011; Habitat Task Group of the Lake Erie Committee, Great Lakes Fishery Commission). Pre-construction assessment of spawning habitat revealed that walleye spawned at the Belle Isle site (Manny et al., 2007) and walleye and lake whitefish *Coregonus clupeaformis* spawned on suboptimal substrates at Fighting Island (HTG, 2009; Roseman et al., 2011). Prior to installation of these artificial reefs, the Belle Isle and Fighting Island sites contained suboptimal habitat for walleye spawning with thin patches (<8 cm thick) of sand and small-diameter gravel on hardpan clay, lacking interstitial spaces to protect fish eggs from predation or dislodgement (Manny, 2006; Roseman et al., 2011). In 2004, 1080 m^2 of broken limestone (41–61 cm diameter), metamorphic cobble and gravel (20–30 cm), and coal cinders (2–8 cm) were deposited at the Belle Isle reef site to augment the spawning substrate (Manny et al., 2005). In 2008, 3300 m^2 of four different bed materials were deposited at the Fighting Island site, including a wide size range of broken limestone (5–50 cm) and rounded rock (10–25 cm; HTG, 2009, 2011) to provide an interstitial space gradient so that fish eggs would not be swept away by the current (Roseman et al., 2011). Prior to our study, it was unknown if walleye spawning at Belle Isle and Fighting Island belonged to historical spawning groups or were migrants from other locations.

Use of the Huron–Erie Corridor by walleye

Ripe walleye have been tagged and recorded to travel through the HEC in the spring to reach their spawning grounds (Ferguson and Derkson, 1971; Wang et al., 2007). Historically, walleye were known to spawn at sites along the HEC, most of which were sampled in the present study, with major runs occurring in Lake Huron's Saginaw Bay, the Thames River of Lake St. Clair (site B; Fig. 1), and the Hen Island shoals in northwestern Lake Erie (site G; Goodyear et al., 1982; Wolfert, 1963; known spawning sites are marked with Xs in Fig. 1). Along the remainder of the HEC, smaller walleye spawning runs were located in the Flint River (site A), St. Clair River (including at its connection to Lake Huron), Detroit River (sites C–E), including its lower reaches and mouth, and the Huron River (site F; Fielder et al., 2006; Goodyear et al., 1982). Historical walleye spawning runs likely occurred at Belle Isle (site C) and Fighting Island (site D), where the artificial reefs were constructed (HTG, 2009; Manny et al., 2007).

Walleye spawning in the HEC have experienced varying degrees of habitat degradation, exploitation, and stocking (Thomas and Haas, 1994). Saginaw Bay comprises the largest commercial walleye fishery in Lake Huron (Fielder and Baker, 2004). This population experienced spawning habitat loss in the Saginaw River and its tributaries, including the Flint River (site A), due to construction of several dams. The walleye run in the Flint River is relatively small and provides one of the sole sources of natural recruitment to Saginaw Bay (Leonardi and Gruhn, 2001). The lower reaches of the Flint River were stocked with walleye in 1976 (Leonardi and Gruhn, 2001) and the Saginaw River and Bay have been stocked on a regular basis since 1989 (USFWS/GLFC, 2010) from a western Lake Erie source. There thus is

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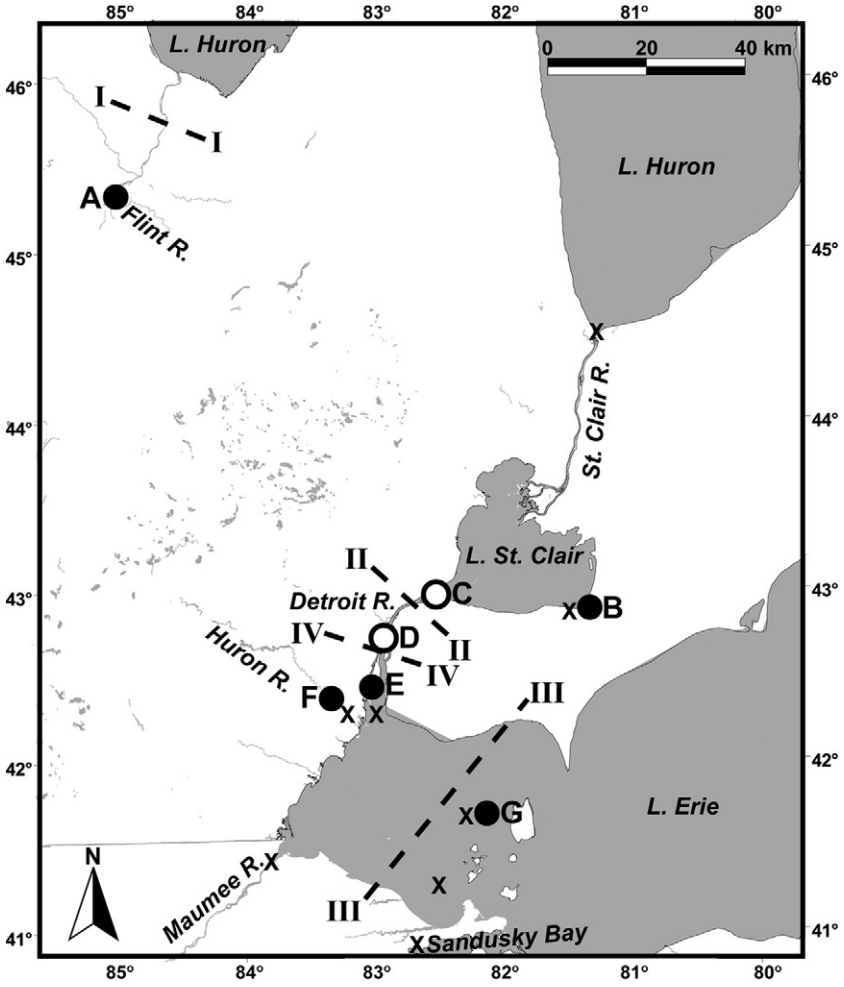

Fig. 1. Walleye spawning groups sampled in the Huron–Erie Corridor with their primary population genetic barriers (dashed lines; I = strongest) from Manni et al. (2004). Barrier analysis using nine nuclear microsatellite loci. X = approximate locations of the historical walleye spawning grounds reported by Wolfert (1963) and Goodyear et al. (1982). A—Flint River, B—Thames River, C—Belle Isle, D—Fighting Island, E—Grosse Ile, F—Huron River, and G—Hen Island. Open circles denote the two Detroit River habitat augmentation sites.

the potential that some stocked individuals may have migrated into the Flint River and affected the genetic composition, which is evaluated here. Walleye populations from the Thames River (site B), Detroit River (sites C–E), and Hen Island (site G) are reported to be self-sustaining and have not been stocked despite anthropogenic pressures (WTG, 2005; Walleye Task Group of the Lake Erie Committee, Great Lakes Fishery Commission; USFWS/GLFC, 2010; Thomas and Towns, 2011). The Huron River (site F) of northwestern Lake Erie was dammed, reducing habitat, and has a smaller native spawning run near its mouth that has experienced low levels of exploitation (Leonardi and Thomas, 2000). In the past, some of its impoundments upstream from that spawning site were sporadically stocked, however, the spawning site itself was not stocked (Leonardi and Thomas, 2000; USFWS/GLFC, 2010).

The HEC serves as an important dispersal route for post-spawn walleye, indicated by mark-and-recapture study results. Tagged walleye have been reported to move from (1) Lake Huron down into the St. Clair River, (2) the Thames River up into Lake Huron (Ferguson and Derkson, 1971), and (3) the western basin of Lake Erie up into Lakes St. Clair and Huron (Haas et al., 1985; Todd and Haas, 1993; Wang et al., 2007). Notably, ~68% of spent walleye captured in southern Lake Huron originated from Lake Erie spawning sites where they were tagged during the spawning run (Belore et al., 2010; McParland et al., 1999). Belore et al. (2010) found that walleye in the western basin of Lake Erie moved northward along the HEC after spawning and were unlikely to travel eastward. Post-reproductive walleye from particular spawning groups thus appear to move in consistent patterns to mix among lake systems throughout most of the year, and likely then return to their natal locations during spring spawning runs (Belore et al., 2010; Jennings et al., 1996; Todd and Haas, 1993).

The objective of our study was to evaluate the genetic connectivity, diversity, and divergence patterns of walleye spawning groups in the HEC. We analyzed 311 walleye from seven spawning sites in the HEC and outlying populations (A–G; Fig. 1), with a dual approach of nine nuclear DNA μsat loci and mtDNA control region sequences. This approach allowed us to compare patterns at multiple evolutionary and temporal scales (Avise, 2004; Wang, 2010, 2011), since the μsat loci addressed contemporary microevolutionary processes, such as migration, gene flow, and genetic drift, whereas the mtDNA control region sequences revealed historical context, such as origins from Pleistocene glaciation refugia. Specific hypotheses (stated as null/alternative) tested in the present study included:

H1. Walleye spawning groups across the HEC had similar/different levels of genetic diversity.

H2. Their relationships reflected genetic connectivity/divergence among spawning groups and between the sexes.

H3. Genetic composition at the HEC Detroit River Fighting Island reef site remained similar/changed after habitat augmentation.

Hypothesis 3 was limited to early findings; additional samples will be needed to evaluate long-term effects and trends in these habitat augmentation areas.

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Materials and methods

Sample collection and DNA extraction

Walleye fin clips (1–2 cm^2 of pectoral or caudal fins) were collected by federal and state fishery biologists during spring spawning runs at seven sites in the HEC, totaling 311 individuals and representing the major and minor spawning runs along the HEC (Fig. 1, Table 1; all available samples were analyzed). Sampled sites included: the Flint River–Lake Huron (site A, coordinates 43.3300 N, −84.0543 W), Thames River (B, 42.3171 N, −82.4363), Belle Isle (C, 42.3469 N, −82.9533 W), Fighting Island (D, 42.2378 N, −83.1295 W), Grosse Ile (E, 42.1177 N, −83.1781 W), Huron River (F, 42.0899 N, −83.2902 W), and Hen Island (G, 41.8024 N, −82.7804 W). All individuals were verified as in spawning condition, and most were released after fin-clipping, measurement of standard length (SL, mm) and sex determination. A total of 51 spawning females (1–23 per site), 146 spawning males (12–40 per site), and 10 unsexed individuals (3–7 per site) were recorded from samples for which sex data were available. Sex and length data were not taken for walleye spawning in the Thames River (B) and Hen Island (G). To test effects of habitat augmentation on genetic diversity and composition (Hypothesis 3), spawning walleye were collected from the Detroit River Fighting Island reef pre- (2008 $N=20$), and post- (2010 $N=28$) habitat augmentation (Table 1). Tissue samples were immediately placed in 95% ethanol, stored at room temperature, and archived in the Great Lakes Genetics Laboratory at the University of Toledo's Lake Erie Center (Oregon, OH). DNA was extracted using Qiagen DNEASY extraction kits (Qiagen Inc., Valencia, CA), then assessed for quality and quantity on 1% agarose mini-gels stained with ethidium bromide.

Nuclear microsatellite data collection

Allelic variation at nine μsat loci (*Svi*2, 4, 6, 7, 17, 18, 33, L6, and L7) was analyzed to test for population genetic structure (e.g., Stepien et al., 2009, 2010; Strange and Stepien, 2007; Table 2). Polymerase chain reaction (PCR) amplifications were conducted in 48 well plates with 10 μl reactions containing 0.6 units *Taq* polymerase, 50 μM dNTPs, 50 mM KCl, 1.5 mM $MgCl_2$, 10 mM Tris–HCl, 0.5 μM of each primer, and ~80 ng of template. A positive control (designated Lake Erie walleye tissue, sample AYD03 from the Maumee River 2006 spawning run) and a negative control (no template) were included in all reaction runs. PCR cycling parameters consisted of 2 min at 94 °C for initial denaturation, followed by 35 cycles of denaturation (94 °C, 30 s), primer annealing (1 min) at specific temperatures (given in Table 2), and polymerase extension (72 °C, 30 s), followed by a final extension at 72 °C for 5 min. Three sets of loci were multi-plexed as single PCR reactions: *Svi*4 and 33, *Svi*2, 6, and 7, and *Svi*L6 and L7. *Svi*17 and 18 were run individually. Amplification products were diluted 1:50, of which 1 μl was added to 13 μl of formamide and Applied Biosystems (ABI, Fullerton, CA) Gene Scan 500 size standard in 96-well plates, denatured for 2 min at 95 °C, and analyzed on an ABI 3130xl Genetic Analyzer with Genemapper v3.7. To minimize analyzer runs, *Svi*17 and 18 were pooled and visualized with different dye colors. Output profiles were checked manually to confirm allelic size variants. Repeat number and size, and number of alleles per locus, are reported in Table 2.

Table 2
Summary of genetic variation per microsatellite locus across the seven walleye spawning groups and temporal comparison at the Fighting Island reef, totaling 311 individuals in the Huron–Erie corridor, showing annealing temperature (T_A), number of alleles (N_A), allelic size range (base pairs, bp), inbreeding coefficient (F_{IS}, average divergence within a spawning group), genetic deviation across all combined samples (F_{IT}), and mean genetic divergence among loci (F_{ST}).

Locus	Source	T_A (°C)	N_A	Size range	F_{IS}	F_{IT}	F_{ST}
*Svi*4	Borer et al. (1999)	60	8	106–122	−0.027	−0.021	0.007
*Svi*6	″	60	16	126–168	−0.017	−0.008	0.009
*Svi*17	″	54	8	102–118	0.014	0.023	0.009
*Svi*18	″	65	7	114–126	0.123	0.137	0.016
*Svi*33	″	60	13	82–106	0.016	0.019	0.004
*Svi*L6	Wirth et al. (1999)	54	16	104–140	0.003	0.002	0.001
*Svi*L7	″	54	25	174–238	0.031	0.039	0.008
*Svi*2	Eldridge et al. (2002)	60	13	188–222	−0.037	−0.012	0.024
*Svi*7	″	60	13	140–178	0.068	0.094	0.028
Total	–	–	119	–	0.017	0.030	0.013

MtDNA control region sequence data

A subset of the 311 individuals representing the seven HEC walleye spawning groups was amplified and sequenced for the mtDNA control region ($N=195$, 20–25 per site; Table 1), with the primers LW1-F (Gatt et al., 2000) and HN20 (Bernatchez and Danzmann, 1993). PCR reactions contained 50 mM KCl, 1.5 mM $MgCl_2$, 10 mM Tris–HCl, 50 μM of each dNTP, 0.5 μM each of the forward and reverse primers, 30 ng DNA template, and 1 unit of *Taq* polymerase in a 25 μl reaction. Amplification procedure was an initial denaturation for 2 min at 94 °C, followed by 42 cycles of 40 s at 94 °C, 40 s at 48 °C, and 1.5 min at 72 °C, with a final extension of 5 min at 72 °C. A 4 μl aliquot of each PCR product was visualized on a 1% agarose mini gel stained with ethidium bromide, and successful reactions were purified using a QIAGEN PCR Purification

Table 1
Genetic variation of the seven walleye spawning groups (sites are labeled according to Fig. 1) using nine nuclear microsatellite loci and mitochondrial DNA control region sequences, including the number of individuals (N), observed heterozygosity (H_O), inbreeding coefficient (F_{IS}), total number of alleles (N_A) or haplotypes (N_H), allelic richness (A_R), number of private alleles (N_{PA}) or haplotypes (N_{PH}), i.e., those found only in that spawning group, proportion of private alleles (P_{PA}) and haplotypes (P_{PH}), and gene diversity (H_D). Bold rows indicate means of designated sites.

Site	Microsatellites							Control region				
	N	H_O	F_{IS}	N_A	A_R	N_{PA}	P_{PA}	N	H_D	N_H	N_{PH}	P_{PH}
A. Flint R.–L. Huron (1998)	44	0.76±0.05	−0.018±0.024	74	7.2±0.9	1	0.01	25	0.58±0.02	5	1	0.20
B. Thames R. (2004)	39	0.74±0.04	0.008±0.034	84	7.7±0.9	2	0.02	25	0.72±0.01	4	0	0.00
C. Belle Isle (2006) – post	40	0.73±0.03	0.018±0.030	88	7.8±1.0	6	0.07	25	0.78±0.01	5	0	0.00
D1. Fighting Is. (2008) – pre	20	0.72±0.04	−0.009±0.045	67	7.3±1.3	1	0.01	20	0.70±0.02	5	0	0.00
D2. Fighting Is. (2010) – post	28	0.69±0.04	0.056±0.025	70	7.2±1.0	1	0.01	25	0.74±0.01	5	0	0.00
Mean Fighting Is. (pre and post)	**24**	**0.71±0.04**	**0.023±0.035**	**69**	**7.3±1.2**	**1**	**0.01**	**23**	**0.72±0.02**	**5**	**0**	**0.00**
E. Grosse Ile (2001)	35	0.73±0.05	0.013±0.030	84	8.1±1.1	1	0.01	25	0.77±0.01	4	0	0.00
Detroit R. – Mean (C, D2, and E)	**34**	**0.72±0.04**	**0.029±0.030**	**81**	**7.7±1.0**	**3**	**0.03**	**25**	**0.76±0.01**	**5**	**0**	**0.00**
Mean L. St. Clair (B, C, D2, and E)	**36**	**0.72±0.04**	**0.023±0.030**	**82**	**7.7±1.0**	**3**	**0.03**	**25**	**0.75±0.01**	**4**	**0**	**0.00**
F. Huron R. (2003 $N=20$, 2010 $N=20$)	40	0.73±0.03	0.019±0.040	84	7.8±1.0	2	0.02	25	0.78±0.01	5	1	0.20
G. Hen Is. (2003)	65	0.68±0.03	0.045±0.020	85	7.1±0.8	5	0.06	25	0.78±0.01	5	0	0.00
Mean Northwest L. Erie (E and F)	**53**	**0.71±0.04**	**0.032±0.030**	**85**	**7.5±0.9**	**4**	**0.04**	**25**	**0.78±0.01**	**5**	**1**	**0.20**
Total (all sites A–G)	311	0.72±0.03	0.028±0.017	119	13.2±1.9	–	–	195	0.73±0.01	8	–	–
Mean (all sites A–G)	**39**	**0.72±0.04**	**0.017±0.031**	**80**	**7.5±1.0**	**2**	**0.03**	**24**	**0.73±0.01**	**5**	**1**	**0.20**

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Kit. DNA sequencing was outsourced to the Cornell University Life Sciences Core Laboratories Center, which used ABI Automated 3730 DNA Analyzers. HEC walleye spawning group mtDNA control region sequences totaled 733 bp and were checked, identified, and aligned with BioEdit v7.05 (Hall, 1999). We related the haplotypes to those of Stepien and Faber (1998), who sequenced the entire mtDNA control region (totaling ~1086 bp) for 179 walleye across the Great Lakes and recovered 14 haplotypes (GenBank accession # U90617). We trimmed the original sequences of Stepien and Faber (1998) to match our 733 bp, omitting their 5′ repeat section, which left seven of their original haplotypes (designated here as A1–7, National Institutes of Health (N. I. H.) GenBank numbers U90617 and JX442946-52; http://www.ncbi.nlm.nih.gov/).

Genetic data analyses

The nine μsat loci were tested for conformance to Hardy–Weinberg equilibrium (HWE) expectations and linkage disequilibrium (LD), using a Markov Chain Monte Carlo (MCMC) chain of 10,000, 1000 batches, and 10,000 iterations in Genepop v4.0 (Rousset, 2008). Levels of significance were adjusted with the standard Bonferroni correction (Zar, 1999). The program Micro-checker v2.2.3 (van Oosterhout et al., 2004) was used to evaluate loci for null alleles, scoring errors, or large allele dropout. Per-locus calculations included: number of alleles (N_A), inbreeding (F_{IS}), overall genetic deviation across all samples (F_{IT}), and divergences (F_{ST}) in *F*stat v2.9.3.2 (Goudet, 1995, 2002).

Genetic diversity comparisons (Hypothesis 1) among the spawning groups and sampling years included: observed (H_O) and expected (H_E) heterozygosities in Genepop, and F_{IS}, N_A, and allelic richness (A_R) in *F*stat for the nine μsat loci, and haplotype diversity (H_D) and number of haplotypes (N_H) calculated in Arlequin v3.5.1.3 (Excoffier and Lischer, 2010) for the mtDNA control region sequence data. Number and proportion of private alleles (N_{PA}) and private haplotypes (N_{PH}), i.e., those unique to a given spawning group or system, were calculated with Convert v1.31 (Glaubitz, 2004). Proportion of private alleles (P_{PA}) and proportion of private haplotypes (P_{PH}) were determined by dividing the number of private alleles/haplotypes for a given population sample by its total number of alleles/haplotypes. Standard errors were calculated in Microsoft Office Excel 2003 (Redmond, WA). To test for significant differences in H_O and A_R, a Friedman rank sum test in R v2.14.2 (R Development Core Team, 2011) was employed, with the loci treated as blocks. To test hypotheses of genetic diversity patterns (Hypothesis 1) and genetic connectivity/divergence among walleye spawning groups along the HEC (Hypothesis 2), just the samples from Fighting Island post-habitat augmentation were used.

To examine whether the relationships reflected genetic connectivity (gene flow) or divergence among spawning groups (Hypothesis 2), females versus males, or a change in genetic composition pre- versus post-habitat augmentation at the Fighting Island Reef site (Hypothesis 3), exact tests of differentiation (χ^2) were used to test for differences in genetic composition among pairs of samples (Raymond and Rousset, 1995), using a MCMC chain of 10,000, 1000 batches, and 10,000 iterations in Genepop. These tested whether the seven spawning groups represented a single panmictic group or multiple sub-populations. Two different analyses tested for differences between the sexes, one included all available data (μsats: 51 females, 146 males; mtDNA: 29 females, 110 males) and the other evaluated samples from Grosse Ile (site E) that had a more even distribution of females and males (μsats: 23 females, 12 males; mtDNA: 13 females, 12 males). Probability values were adjusted using the sequential Bonferroni correction (Rice, 1989). Number of genetic migrants (N_M) between spawning groups was calculated in Arlequin, following Slatkin (1991) to evaluate how much genetic exchange may have occurred.

Three additional approaches further evaluated genetic connectivity and divergence patterns (Hypothesis 2): (1) Analysis of Molecular Variance (AMOVA; Excoffier et al., 1992), (2) Barrier v2.2 (Manni et al., 2004), and (3) isolation by distance via Mantel's (1967) test. AMOVA tests assessed hierarchical relationships among samples (i.e., lakes versus spawning groups) in Arlequin. Barrier tested for significant discontinuities in gene flow (connectivity) by identifying which neighboring samples were distinguished by higher than expected genetic divergence (measured as θ_{ST} (Weir and Cockerham, 1984) in *F*stat) in relation to geographical coordinates (latitude and longitude). Support for the barriers was assessed in two ways: (1) relative number of supporting loci (per LeClerc et al., 2008; Strange and Stepien, 2007), and (2) bootstrap analysis of 2000 multilocus matrices in Geneland v3.3.0 (Guillot and Santos, 2009; Guillot et al., 2005). Those with locus and bootstrap support values higher than 50% were reported here. Fit to a genetic isolation ($\theta_{ST}/(1-\theta_{ST})$) by geographic distance model (shortest connected waterway using the path option in Google Earth® (Google, 2010)) was tested with Isolde in Genepop, which predicted a linear relationship (Rousset, 1997), using Mantel's (1967) procedure and 10,000 MCMC permutations. Origins of individuals spawning at Fighting Island pre- and post-habitat augmentation (Hypothesis 3) were compared using a Bayesian approach in Geneclass2 (Piry et al., 2004), which assigned individual fish to one of the seven HEC walleye spawning samples via 10,000 simulations per Rannala and Mountain (1997) and Cornuet et al. (1999). A χ^2 contingency was used to test for significant difference between individuals that self- or misassigned (Zar, 1999).

Results

Genetic diversity of walleye spawning groups along the HEC (Hypothesis 1)

The nine μsat loci were unlinked, and the samples and the loci conformed to HWE expectations following Bonferroni correction. Only two possible cases of null alleles were detected: locus *Svi*7 from the Thames River (B) spawning group and *Svi*18 in the Huron River (F). Since null alleles were not detected at those loci in the five other HEC spawning groups, the populations were in HWE, and there were no signs of heterozygote deficiency, scoring error, or stuttering, all loci were included in our analyses (see van Oosterhout et al., 2004). Loci *Svi*2, 7, and 18 had the highest F_{ST} values (0.024, 0.028, and 0.016) and thus contributed more to divergence among the spawning groups (Table 2).

Overall, 119 alleles were recovered from 311 walleye at the nine μsat loci, with 74–88 alleles per spawning group (mean = 80) and allelic richness (A_R) values of 7.1–8.1 (mean = 7.5 ± 1.0; Table 1). Walleye spawning at the Detroit River Belle Isle (C) augmentation site had the most alleles (88, $A_R = 7.8 \pm 1.0$), followed by Hen Island (G, 85, $A_R = 7.1 \pm 0.8$), the Thames River (B, 84, $A_R = 7.7 \pm 0.9$), Grosse Ile (E, 84, $A_R = 8.1 \pm 1.1$), and the Huron River (F, 84, $A_R = 7.8 \pm 1.0$). The population spawning at Grosse Ile (E) had the highest μsat allelic richness. Allelic richness did not significantly differ among the seven spawning groups, based on the Friedman rank sum test ($\chi^2 = 8.90$, df = 6, $p = 0.1800$).

For the mtDNA control region sequence data (733 bp), eight haplotypes (GenBank accession #s JX442946-49 and JX44953-56) were identified among 195 HEC spawning walleye (Fig. 2; Table 1). Four haplotypes were common throughout the data set (these matched haplotype #s A1–4 of Stepien and Faber (1998); GenBank # U90617 and # JX442946-49). We discerned four new haplotypes that were unique from those of Stepien and Faber (1998), which here are designated as B8-11, GenBank # JX442953-56. Haplotype A1 (GenBank # U90617, JX442946) was the most abundant overall, characterized 37% of the samples, and reached its highest proportion (60%) in the Flint River (A). Haplotype A3 (GenBank # JX442948) was the next most abundant and occurred in 31% of the samples, whereas haplotypes A2 (GenBank # JX442947) and A4 (GenBank # JX442949) represented 17 and 12%, respectively. Similar number of haplotypes were found in all spawning groups, with Flint River (A), Belle Isle (C), Fighting Island (D2), Huron River (F), and Hen Island (G) having five each and the

Thames River and Grosse Ile with four (Fig. 2; Table 1). The newly discovered haplotypes were: B8 (GenBank # JX442953) from Fighting Island (D1) and Hen Island (G), B9 (GenBank # JX442954) from Belle Isle and Fighting Island (D2), B10 (GenBank # JX442955) from the Huron River (F), and B11 (GenBank # JX442956) from the Flint River (A).

Numbers of private μsat alleles ranged from 1–6 per spawning group (mean = 2), with the most at Belle Isle (C, 6 alleles, proportion (P_{PA}) = 0.07) and Hen Island (G, 5, 0.06), a moderate number at Thames River (B, 2, 0.02) and Huron River (F, 2, 0.02), and the least in the Flint River (A, 1, 0.01), Fighting Island (D2, 1, 0.01), and Grosse Ile (E, 1, 0.01; Table 1). Two private haplotypes were recovered in the mtDNA control region dataset, one in the Flint River (A) and one in the Huron River (F).

The spawning groups had similar μsat heterozygosities (mean $H_O = 0.72 \pm 0.03$), ranging from 0.68 ± 0.03 at Hen Island (site G) in Lake Erie to 0.76 ± 0.05 at Flint River (A). Heterozygosity values at the habitat augmentation sites were relatively high: 0.73 ± 0.03 at Belle Isle (C) and 0.69 ± 0.04 at Fighting Island (D2). The Friedman rank sum test results showed no significant differences in observed heterozygosity values of walleye spawning groups across the HEC ($\chi^2 = 3.17$, df = 6, $p = 0.7900$). The Flint River (A) sample in Lake Huron suggested some slight heterozygote excess or outbreeding ($F_{IS} = -0.018 \pm 0.024$), which was not significant. The other six samples (B–G) indicated slight inbreeding depression ($F_{IS} = 0.008 \pm 0.034$–0.056 ± 0.025; Table 1), which also was not significant. The Flint River–Lake Huron (A) had the lowest mtDNA haplotypic diversity (0.58 ± 0.02), whereas the other spawning groups had similar diversity levels (0.72 ± 0.01–0.78 ± 0.01).

Genetic divergence and connectivity among walleye spawning groups along the HEC (Hypothesis 2)

Several HEC walleye spawning groups significantly differed in genetic composition according to the μsat data (Table 3). The Flint River (A) spawning group was the most divergent ($\chi^2 = 63.5$-Inf, $p \leq 0.0001$), followed by the Fighting Island sample post-habitat augmentation (D2), which significantly differed from Belle Isle (C, $\chi^2 = 46.1$, $p = 0.0003$) and Hen Island (G, $\chi^2 = 43.8$, $p = 0.0006$), but was less divergent from the Thames River (B, $\chi^2 = 35.0$, $p = 0.0100$), Grosse Ile (E, $\chi^2 = 35.3$, $p = 0.0090$), and Huron River samples (F, $\chi^2 = 31.5$, $p = 0.00$). Walleye spawning at Belle Isle (C) also significantly differed from the Hen Island spawning group (G, $\chi^2 = 46.8$, $p = 0.0002$) and slightly differed from the Thames (B, $\chi^2 = 31.2$, $p = 0.00$) and Huron (F) river samples ($\chi^2 = 34.3$, $p = 0.010$). Appreciable genetic connectivity (Table 3) was evident among walleye spawning in the Thames River (B), Grosse Ile (E), Huron River (F), and Hen Island (G, $\chi^2 = 18.2$–27.7, $p = 0.00$–0.40). Estimated migration values among those four spawning groups (B, E–G) were high; values for Thames River (B) were 65 individuals exchanged with Hen Island (G), 307 with Grosse Ile (E), and calculated as infinite with the Huron River (F; Table 3). The Grosse Ile sample additionally showed high gene flow, with migration estimated from 76 individuals with Hen Island (G) to 114 with the Huron River (F; Table 3). In contrast to the higher-resolution μsat data, no significant differences were recovered from the mtDNA control region sequence data ($\chi^2 = 0.0$–5.2, $p = 0.0700$–1.0000). Thus, the mtDNA data were not used for Barrier, AMOVA, or isolation by distance analyses.

The overall genetic composition of females ($N = 51$ μsats: $N = 51$; mtDNA: $N = 29$) and males (μsats: $N = 146$; mtDNA: $N = 110$) did not significantly differ (μsats: $\chi^2 = 16.50$, $p = 0.5600$; mtDNA: $\chi^2 = 0.24$, $p = 0.8900$). The genetic composition of females and males spawning at a single site likewise did not significantly differ (μsats: $N = 146$: $\chi^2 = 20.18$, $p = 0.3200$; mtDNA: $\chi^2 = 4.41$, $p = 0.1100$).

Barrier analysis recovered four primary barriers to gene flow (Fig. 1), in which genetic divergence was significantly greater than expected. The primary division (barrier I; 98% bootstrap support, 100% of the loci) distinguished the Lake Huron (Flint River, site A) spawning group from all other samples. The second (II; 96%, 100% loci) separated the walleye spawning groups in the Thames River (B) and Belle Isle (C). The third (III; 87%, 100% loci) barrier separated walleye spawning at Hen Island (G), and the next (IV; 72%, 89% loci) denoted the Detroit River Fighting Island group (D2).

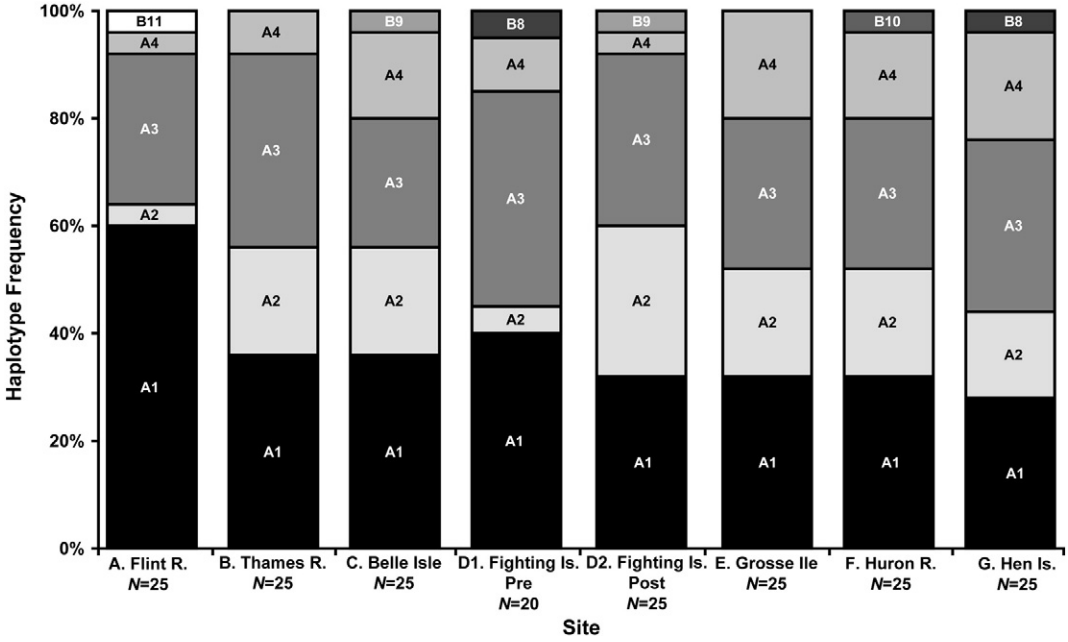

Fig. 2. MtDNA control region haplotype frequency distribution in the seven Huron–Erie Corridor walleye spawning groups, including pre- and post-habitat augmentation comparisons. Each haplotype is represented by a single color. Haplotype numbering follows Stepien and Faber (1998), for A1–4 (GenBank #s U90617, and JX442946-49). Haplotypes B8–11 are new haplotypes recovered in this study, which are GenBank # JX442953-56. Note: Haplotypes A5–7 of Stepien and Faber (1998) were not recovered in the HEC in our study; thus those numbers are not used here.

Table 3
Pairwise tests of genetic divergence among the seven Huron–Erie corridor walleye spawning samples, including pre- and post-habitat augmentation at Fighting Island based on nine microsatellite loci. Exact tests of differentiation are below the diagonal with *p*-values in parentheses and genetic migration estimates (N_M) are above.

Site	A.	B.	C.	D1.	D2.	E.	F.	G.
A. Flint R.	–	14	9	7	6	7	7	12
B. Thames R.	77.4[a] (<0.0001)	–	195	43	33	307	Inf	65
C. Belle Isle	111.6[a] (<0.0001)	31.2* (0.0280)	–	30	45	158	214	47
D1. Fighting Is. Pre	72.2[a] (<0.0001)	23.3 (0.1780)	29.4* (0.0430)	–	37	187	35	45
D2. Fighting Is. Post	96.1[a] (<0.0001)	35.0* (0.0100)	46.1[a] (0.0003)	32.7* (0.0180)	–	150	32	47
E. Grosse Ile	116.7[a] (<0.0001)	20.9 (0.2870)	26.7 (0.0840)	19.0 (0.3950)	35.3* (0.0090)	–	114	76
F. Huron R.	63.5[a] (<0.0001)	18.2 (0.4460)	34.3* (0.0120)	25.8 (0.1040)	31.5* (0.0250)	23.9 (0.1570)	–	61
G. Hen Is.	Inf[a] (<0.0001)	26.3 (0.0940)	46.8[a] (0.0002)	23.3 (0.1780)	43.8[a] (0.0006)	27.7 (0.0670)	27.5 (0.0700)	–

Inf = infinite value denoted by computer programs Genepop and Arlequin. Note: no significant differences were recovered using the mtDNA control region sequence data for the exact tests of differentiation and its N_M values were mostly infinite (Inf).

* Significant at $\alpha = 0.05$.

[a] Remains significant following sequential Bonferroni correction (Rice, 1989).

Hierarchical relationships among population groups analyzed with AMOVA showed significant delineation among the three Lakes (1.07%, $p<0.0001$) and among spawning groups within them (0.42%, $p=0.0100$). Relationships among the spawning sites (Fig. 3) did not fit a genetic isolation by geographic distance model ($p=0.0800$), with the best-fit regression line explaining 69% of the variation ($y=0.010x-0.03$, $R^2=0.69$). Comparisons of the Flint River (A) group with all other samples showed much greater difference than would be predicted by geographic isolation. This result was similar to the Barrier analysis and χ^2 findings, indicating that the Flint River–Lake Huron spawning group is very genetically distinct. When the Flint River (A) comparisons were excluded from analysis, the remaining HEC samples likewise did not follow an isolation by distance model ($y=-0.001x+0.006$, $R^2=0.001$, $p=0.5800$). Thus, the relationships among spawning groups across the HEC appeared independent of geographic distance.

Genetic composition pre- and post-habitat augmentation (Hypothesis 3)

Genetic comparisons of walleye spawning at the Fighting Island reef (D) pre- and post-habitat augmentation (Fig. 2, Table 1) showed a slight decrease in observed μsat heterozygosity (0.72 ± 0.04 to 0.69 ± 0.04), an increase in mtDNA haplotypic diversity (0.70 ± 0.02 to 0.74 ± 0.01), and a greater number of μsat alleles (67–70). Friedman rank sum test results showed no significant differences in observed heterozygosity values of walleye spawning at Fighting Island pre- and post-habitat augmentation ($\chi^2=0.11$, df = 1, $p=0.7400$). Pairwise comparison tests showed a significant difference in genetic composition pre- versus post-habitat augmentation ($\chi^2=32.7$, $p=0.0200$) in the μsat data (the mtDNA control region sequence data did not differ; $\chi^2=2.5$, $p=0.2800$). Pre- and post-habitat augmentation samples each contained a different private allele and a unique haplotype (Fig. 2; Table 1). These results may be due to sample size effects. Apparent inbreeding (heterozygote deficiency) increased pre- to post-habitat augmentation from −0.009–0.056; the latter value was the highest in our dataset (Table 1).

Divergence values for the Fighting Island spawning group before habitat augmentation (D1) indicated more connectivity, suggesting more exchange of reproductive individuals with other spawning populations, than after augmentation (D2). Both samples from Fighting Island significantly diverged from the Flint River (A, $\chi^2=72.2$–96.1, $p\leq0.0001$) and Belle Isle populations (C, $\chi^2=29.4$–46.1, $p=0.0003$–0.0400; Table 3). However, the earlier sample was genetically similar to other HEC spawning groups ($\chi^2=19.0$–25.8, $p=0.1000$–0.4000). Following the habitat augmentation, divergence increased, with the Fighting Island walleye appearing more genetically distinct ($\chi^2=31.5$–46.1, $p=0.0003$–0.0300; Table 3). Walleye from Fighting Island

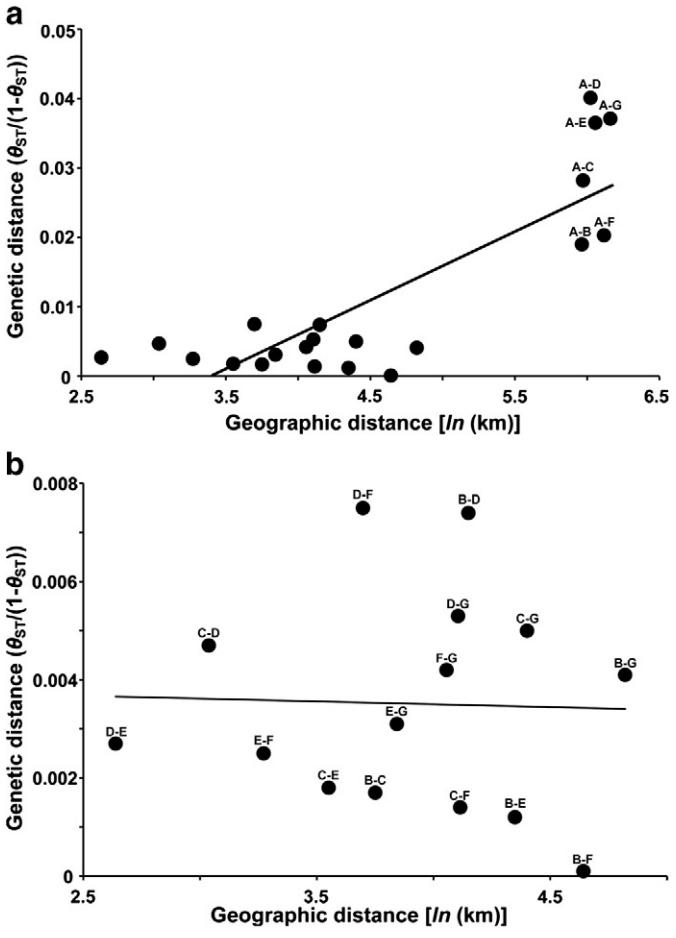

Fig. 3. Relationship between genetic divergence $[\theta_{ST}/(1-\theta_{ST})]$ of walleye spawning groups and geographic distance (natural logarithm of nearest waterway distance in kilometers (km)) using the nine nuclear microsatellite loci for a) all seven sites sampled ($y=0.010x-0.03$, $R^2=0.69$, $p=0.08$) and b) excluding the Flint River–Lake Huron outlier comparisons ($y=-0.001x+0.006$, $R^2=0.001$, $p=0.58$). Comparisons between sites are labeled as: A—Flint River, B—Thames River, C—Belle Isle, D—Fighting Island, E—Grosse Ile, F—Huron River, and G—Hen Island.

in both samples most closely resembled those spawning at Grosse Ile (E) just to the south (Fig. 1), with N_M estimates (representing possible reproductive migrants) of 150 and 187 individuals, respectively (Table 3). Overall estimated N_M values ranged from 30–187 in the earlier sample versus 33–150 post-habitat augmentation. Likely returns numbered 37 individuals between the two sampling dates (88 according to the mtDNA data; Table 3). Congruently, both samples from Fighting Island showed low self-assignment values (Table 4), with no significant difference in those self-assigning and assigning to other samples between the two dates (χ^2 contingency test = 3.12, $p = 0.0800$, 1 df). Many misassigning individuals traced to Grosse Ile (E, 40% pre- and 25% post-augmentation), similar to the N_M results. Others that misassigned traced to the Thames River (B, 20% pre- and 7% post-habitat augmentation), Belle Isle (C, 20% and 14%), Huron River (F, 20% and 29%), and Hen Island (G, 0% and 11%). Before spawning habitat augmentation, 40% of walleye spawning at Fighting Island misassigned to the north (sites B–C) and 60% to the south (E–G). Following augmentation, 21% misassigned to the north and 65% to the south (Table 4). This trend, however, was not significant (χ^2 contingency test = 1.13, $p = 0.2900$, 1 df).

Discussion

Genetic trends in relation to our hypotheses

Our results reveal relatively similar levels of genetic diversity among samples across the HEC, supporting null Hypothesis 1. Walleye spawning in the HEC thus have unique variability despite over a century of habitat degradation. The population reproducing at the Belle Isle habitat augmentation site in the Lake St. Clair system had the most alleles, high allelic richness, and the greatest number and proportion of private alleles. The Fighting Island spawning group also showed appreciable genetic diversity. Walleye from the Flint River–Lake Huron site did not reproduce with those from other HEC locations (rejecting null Hypothesis 2). Walleye spawning at the Belle Isle and Fighting Island habitat augmentation sites housed unique variability and diverged from most other groups (also rejecting null Hypothesis 2). Both augmentation sites thus appear to house different and potentially native spawning groups of walleye. More genetic connectivity and gene flow characterized most other groups spawning in Lake St. Clair and northwestern Lake Erie (supporting null Hypothesis 2). Overall patterns among spawning populations did not fit a hypothesis of genetic isolation with geographic distance, with some HEC spawning groups located in close proximity being very divergent.

The genetic composition of walleye spawning at the Fighting Island reef habitat augmentation site in the Detroit River changed pre- versus post-habitat augmentation (rejecting null Hypothesis 3 for genetic composition). In contrast, the overall amount of genetic diversity was similar between the two (failing to reject the null hypothesis). The results likely were influenced by sample size. Fewer individuals self-assigned pre- versus post-habitat augmentation, with most individuals originating from the south in both samples. Numbers from the south increased in the later sample. This represents an important baseline and suggests that walleye spawning at the Fighting Island site originated from a variety of source populations, which should be further investigated with additional samples and years.

Walleye genetic diversity patterns (Hypothesis 1)

The genetic diversity levels for spawning groups along the HEC appear typical for walleye populations, suggesting that despite over a century of exploitation, stocking, habitat loss, and degradation, genetic integrity likely has been maintained. In our study, walleye spawning in the Lake St. Clair basin displayed intermediate diversity levels, having high numbers of μsat alleles and mtDNA haplotypes, greatest allelic richness, and high number and proportion of private alleles. The Belle Isle habitat augmentation site had the most μsat alleles, one of the highest allelic richness values, and the most private alleles, reflecting a diverse genetic history. Walleye spawning at the seven sites along the HEC had mean genetic diversity (observed heterozygosity) values (0.72 ± 0.04) similar to those reported across the Great Lakes (0.71 ± 0.01) and across their native range (0.68 ± 0.01) by Stepien et al. (2009, 2010) using the same nine μsat loci.

Mean mtDNA control region haplotypic diversity of the HEC walleye spawning groups (0.73 ± 0.01) was similar to values from Stepien and Faber (1998) across Lakes St. Clair and Erie populations (0.69 ± 0.05). Our diversity values were higher than those calculated from mtDNA restriction fragment length polymorphisms by Gatt et al. (2002) for walleye spawning in Lake Huron's Georgian Bay (0.49 ± 0.06). That population experienced a decline in haplotypic diversity over three decades (from 0.50 in the 1960s to 0.15 in the 1990s) attributed to exploitation and stocking. In contrast, Franckowiak et al. (2009) discerned temporal genetic consistency over 50 years (1952–2002) for walleye spawning in Escanaba Lake, Wisconsin ($H_O = 0.76 \pm 0.01$) using eight μsat loci (six of those used here). Likewise, Stepien et al. (2012) found temporal consistency of three Lake Erie spawning groups from 1995 to 2008, including the Maumee River (0.71 ± 0.01, $N = 250$), Sandusky River (0.74 ± 0.01, $N = 227$), and Van Buren Bay Reefs (0.76 ± 0.02, $N = 249$), using the nine μsat loci employed here. The Maumee River is thought to be the largest Lake Erie spawning group (Mion et al., 1998) and experiences high exploitation (Schmalz et al., 2011), yet houses a genetically diverse spawning run. In conclusion, despite a history of exploitation and habitat loss along the HEC, its walleye diversities are relatively high, likely due to the prevalence of large connected populations across this region.

Genetic divergence and connectivity of walleye spawning groups along the HEC (Hypothesis 2)

Comparisons among the HEC walleye spawning groups using mtDNA control region sequence data showed no differences among them, whereas the nuclear μsat loci discerned significant differences. This difference is attributable to the slower evolutionary rate of mtDNA control region sequences compared to nuclear μsat loci (Hewitt, 2001; Wang, 2010, 2011). Mitochondrial DNA sequences have 1/4 the effective population size of nuclear DNA, rendering mtDNA more subject to declines in variability from population bottlenecks. We sampled many more μsat alleles per population (here 70–88 alleles per spawning group) and many more loci with the μsat data set compared to the mtDNA control region sequence data (4–5 haplotypes with 1–2 base pair differences).

The seven walleye spawning groups along the HEC are believed to trace to colonists from the Mississippian and Atlantic coastal glacial refugia (Billington et al., 1992; Gatt et al., 2000; Stepien and Faber, 1998; Stepien et al., 2009; Ward et al., 1989). Our study recovered four

Table 4
Geneclass2 analysis showing the percentage of walleye spawning at the Detroit River Fighting Island habitat augmentation site that self-assigned or assigned to other HEC spawning locations. Bold = percentage that self assign, underlined = highest percentage assigned to a given group, and () = number of individuals assigning to a given location.

Site	B. Thames R.	C. Belle Isle	Bold D. Self	E. Grosse Ile	F. Huron R.	G. Hen Is.
D1. Fighting Is. — pre	20 (4)	20 (4)	**0**	40 (8)	20 (4)	0
D2. Fighting Is. — post	7 (2)	14 (4)	**14 (4)**	25 (7)	29 (8)	11 (3)

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common mtDNA control region haplotypes (A1–4) that characterized all of our HEC sites. Common haplotypes A1 and A3 were identified as originating from the Mississippian glacial refugium, whereas common haplotype A4 came from the Atlantic coastal refugium (Billington et al., 1992; Stepien and Faber, 1998). We also found four rarer haplotypes that differed by 1–2 base pairs from the more common ones.

Our analyses using the nine nuclear μsat loci showed pronounced genetic differences between walleye spawning in the Flint River–Lake Huron from other sites in the HEC, which were much greater than those predicted by geographic distance. Walleye spawning in different Great Lakes do not appear to exchange genes (Stepien et al., 2009), although they move among systems during non-spawning times (Vandergoot et al., 2010; Wang et al., 2007). Studies of other Great Lakes fishes likewise showed marked difference of spawning groups in Lake Huron from those in Lakes St. Clair and Erie, including yellow perch *Perca flavescens* (Sepulveda-Villet and Stepien, 2012; Sullivan and Stepien, this issue) and smallmouth bass *Micropterus dolomieu* (Stepien et al., 2007).

Divergence of the Flint River–Lake Huron walleye gene pool from those in Lakes St. Clair and Erie may have occurred more recently than the Pleistocene glaciations, reinforced by behavioral isolation and spawning site philopatry, since we recovered this pattern with the μsat data alone. Tagging studies showed that Flint River post-spawn walleye had limited migration, traveling only to inner Saginaw Bay (~50 km) and remaining there until the spring, when they migrated back into the river to spawn (Leonardi and Gruhn, 2001). In comparison, some individuals from other walleye spawning groups traveled longer distances (e.g., ~165 km from the western basin of Lake Erie to Lake Huron; Ferguson and Derkson, 1971; Haas et al., 1985; Todd and Haas, 1993; Wang et al., 2007). Moreover, the Saginaw River and Bay system connected with the Flint River has been stocked with individuals from the western basin of Lake Erie since 1989 (USFWS/GLFC, 2010), which may have obscured the mtDNA signal. However, our nuclear DNA data and the relatively high and unique diversity of the Flint River spawning group supports its historical genetic signature. This appears congruent with the observation of behavioral isolation by migration patterns (Leonardi and Gruhn, 2001).

Walleye spawning groups along the lower HEC showed a mixed pattern of genetic divergence and connectivity. The Belle Isle population significantly differed from others, including Fighting Island located only ~21 km away, indicating that Belle Isle likely houses a historical spawning group. Habitat along its north side was left relatively undisturbed by human activities during the history of the HEC (Bennion and Manny, 2011), likely providing a long-term refuge for spawning walleye that led to this genetic divergence. Similarly, Wilson et al. (2007), described a previously undocumented walleye spawning population in Lake Superior's Nipigon Bay, where habitat degradation and loss had occurred (Ryder, 1968). Managers had stocked Nipigon Bay with walleye from other areas; however, the population genetically differed from the stocked individuals, indicating persistence of a native population (Wilson et al., 2007). Our study likewise indicates that walleye spawning at Belle Isle have high genetic diversity and are genetically distinct, supporting retention of a historical genetic signature. Manny et al. (2007) found evidence for walleye spawning at Belle Isle in the spring of 2004 – before the installation of the artificial reef – further supporting the existence of a native population. The Belle Isle spawning group thus may provide an important genetic resource in the HEC restoration project, meriting conservation.

The other HEC walleye spawning groups – Thames River, Fighting Island, Grosse Ile, Huron River, and Hen Island – displayed more inter-migration and connectivity, but significant difference between the Fighting Island and Hen Island populations. Using lower resolution allozyme and mtDNA restriction fragment length polymorphism markers, McParland et al. (1999) found no differences in spawning walleye collected from our sites in Lakes St. Clair (Thames River) and Erie (Huron River), along with Chickenolee Reef in western Lake Erie. Stepien et al. (2012) found only a slight difference with μsat data between the Maumee and Sandusky River spawning groups (two of Lake Erie's largest spawning runs, located in close proximity; Mion et al., 1998), compared to a larger genetic divergence from other populations. Walleye spawning in some western Lake Erie sites thus may comprise a single connected spawning group, which may extend into the HEC.

The observed genetic connectivity and greater homogeneity among some HEC walleye spawning groups could be the product of population exploitation along the HEC. This would lead to loss of rare alleles and haplotypes and increased presence of common ones, similar to the pattern observed by Gatt et al. (2002) in Georgian Bay walleye spawning runs (whose populations were extensively stocked). However, the seven HEC walleye spawning groups sampled here are self-sustaining via natural reproduction and recruitment (Leonardi and Thomas, 2000; Leonardi and Gruhn, 2001; WTG, 2005; Thomas and Towns, 2011). Our results showed that these spawning groups possessed high diversity levels in both the nuclear and mtDNA data sets, typical of walleye populations within and outside of the Great Lakes region.

The high genetic connectivity observed among some of the HEC walleye spawning groups also may be influenced by anthropogenic habitat degradation. Walleye homing behavior could be more facultative in degraded areas due to disruption of habitat and associated chemical cues (Backhouse-James and Docker, 2012; Colby and Nepszy, 1981; Olson and Scidmore, 1962). Olson and Scidmore (1962) stated that with increased stream flow (as occurred from modification of the Detroit River), eggs and larvae would have less time to imprint, which would increase straying and lead to genetic homogenization. Optimal egg deposition for walleye in river systems occurred at velocities of 0.4–1.0 m/s (Bozek et al., 2011; Paragamian, 1989), whereas present-day estimates were 0.76–1.68 m/s for the Detroit River (U.S. Army Corp. of Engineers, 2006), indicating that it might be difficult for eggs to remain in place (see Manny et al., 2005; Roseman et al., 2011). Roseman et al. (2011) documented a decline in water velocity to 0.3–0.8 m/s at the Fighting Island site after installation of the artificial reefs. This suggests that artificial habitats may improve egg retention and imprinting of walleye to natal sites, ultimately leading to localized adaptation.

Spawning runs of chinook salmon *Oncorhynchus tshawytscha* showed greater genetic connectivity after logging and mining had decimated historical spawning runs in the Sacramento and San Joaquin River drainages, measured from 10 μsat loci (Williamson and May, 2005). This greater genetic homogeneity was attributed to increased straying by ripe adults. A similar pattern of increased genetic connectivity might account for low divergence among walleye spawning groups along much of the HEC, whose natal sites may have been highly degraded.

In contrast to our results for walleye, Sullivan and Stepien (this issue) found great genetic divergence and no connectivity among yellow perch spawning groups across the HEC. This may be due to higher spawning group fidelity of yellow perch and their more limited migration (Rawson, 1980). Studies showed that the related European perch discriminates kin from non-kin via olfactory cues, and schools of full and half-sib groups were maintained throughout their lives (Behrmann-Godel and Gerlach, 2008; Gerlach et al., 2001). Thus, family groups of the European perch appear to move and reproduce together, genetically diverging from non-kin groups (Gerlach et al., 2001). This life history pattern remains to be tested for yellow perch and walleye.

Lack of genetic isolation by geographic distance along the HEC (Hypothesis 2)

Broad-scale genetic relationships of walleye spawning groups across North America were explained by a general pattern of genetic isolation by geographic distance, but did not follow this relationship across finer scales (e.g., within lakes or among more closely spaced

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spawning samples; Stepien et al., 2009, 2010; Strange and Stepien, 2007). Spawning groups along the HEC, likewise, did not fit an isolation by distance pattern. Moreover, walleye spawning at neighboring sites along the HEC, especially at Belle Isle, significantly differed from other groups, including Fighting Island and the Thames River. Other spawning groups showed more genetic similarity to those farther away (e.g., between the Thames River in Lake St. Clair and Hen Island in northwestern Lake Erie).

Yellow perch likewise exhibited isolation by distance across its broad-scale range (Sepulveda-Villet and Stepien, 2012; Sepulveda-Villet et al., 2009), but not along the HEC (Sullivan and Stepien, 2013) or within Lake Erie (Sepulveda-Villet and Stepien, 2011). Similarly, analyses of smallmouth bass using eight μsat loci recovered an overall pattern of genetic isolation by geographic distance across its broad-scale range, but spawning groups in adjacent Lake Erie tributaries were more divergent than expected (Stepien et al., 2007). Thus, the genetic compositions of walleye, yellow perch, and smallmouth bass spawning groups often are much more divergent than predicted by geographic proximity.

Effects of habitat augmentation on genetic composition (Hypothesis 3)

We discerned a significant difference in the genetic composition of walleye spawning at Fighting Island pre- (spring 2008) and post- (2010) installation of the artificial reef in fall 2008. In the later sample, overall μsat heterozygosity and number of alleles were greater. Results indicated that approximately equal numbers of walleye self-assigned and misassigned to other samples pre- and post-habitat augmentation. Thus, the overall amount of straying did not appear to change. More individuals spawning at Fighting Island originated from the south (60% pre- and 65% post-habitat augmentation) compared to the north (40% pre- and 21% post-augmentation). These results may be due to sampling variability, with 20 individuals sampled pre-habitat augmentation and 28 post-habitat augmentation. Our study represents an important baseline comparison and should be investigated with more samples and additional sampling years.

Apparent declines in μsat heterozygosity at Fighting Island following habitat augmentation should be further evaluated with additional samples and timepoints. This decline might be followed by an eventual increase, i.e., a genetic "restoration" or "rescue" (Hedrick, 2005; Tallmon et al., 2004), as individuals spawned at other locations may arrive to spawn at the new habitat. It will be interesting to discern whether this spawning population experiences increased reproductive migration, and to identify the origin of any new immigrants. Alternatively, migration could lead to decline of the historical genetic signature at Fighting Island via dilution of unique alleles and adaptations. The present study thus represents an important baseline and points to the need for continued long-term monitoring of these spawning groups to include additional generations of walleye.

Summary

Our results show that genetic connectivity and divergence patterns of walleye spawning groups varied along the HEC. The Flint River–Lake Huron spawning population was very different from the others, showing no genetic exchange, which was much greater than that predicted by isolation by distance. Across the remainder of the HEC, the Belle Isle spawning group significantly diverged, with high genetic diversity and more unique alleles, indicating persistence of this native spawning population. Likewise, the group spawning at Fighting Island differed from some nearby populations. There was greater genetic similarity and more connectivity among the other Lake St. Clair and northwestern Lake Erie samples. The Fighting Island walleye spawning population may have lost some overall genetic diversity, and appeared to exchange genes with the nearby Grosse Ile group (which appeared greater in the pre-augmentation sample). Further study is needed to evaluate these long-term population trends. In conclusion, despite habitat degradation and pollution, it appears that historical walleye spawning groups have persisted along the HEC, meriting conservation and further restoration efforts.

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Genetic diversity and divergence of yellow perch spawning populations across the Huron–Erie Corridor, from Lake Huron through western Lake Erie

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ABSTRACT

The yellow perch *Perca flavescens* supports one of the largest Great Lakes fisheries, whose populations have varied due to environmental changes, including exploitation and habitat degradation. The Huron–Erie Corridor (HEC) connects the upper and lower Great Lakes, running from Lake Huron through the St. Clair River, Lake St. Clair, and Detroit River to western Lake Erie; it serves as an essential fish migration corridor, and contains key spawning and nursery grounds. Its shipping importance led to its extensive channelization and dredging, destroying and degrading habitats. Since 2004, the HEC Initiative has restored some fish spawning and nursery grounds. Our objective is to assess the genetic diversity, connectivity, and divergence of yellow perch spawning populations along the HEC to provide a baseline for assessing future patterns, including responses to improved habitat. Genetic variation of seven spawning populations ($N = 248$), four in the HEC, one in Lake Huron, and two in western Lake Erie, are analyzed at 15 nuclear microsatellite loci. Results showed appreciable genetic diversity of the seven spawning populations (mean observed heterozygosity = 0.637 ± 0.020, range 0.568–0.699), which significantly differed in genetic composition ($\theta_{ST} = 0.011$–0.099, $p < 0.0001$–0.0007), suggesting a history of genetic isolation; relationships did not follow a pattern of genetic isolation by geographic distance. Notably, some nearby spawning populations were very genetically distinctive, with high genetic diversity and high proportions of private alleles, as characterized by the Belle Isle restoration site in the Detroit River. Our study provides a genetic benchmark to assess ongoing and future habitat restoration efforts across the HEC and beyond.

Introduction

Maintaining genetic distinctiveness and diversity of populations may be important for conserving their long-term stability and ability to respond to changing environmental conditions (Allen et al., 2010; Keller et al., 2011; Miller et al., 2012). Habitat loss and fragmentation can reduce population sizes and impede the movement of individuals among locations, increasing the potential for inbreeding and fitness decline (Lande, 1998; Mills and Smouse, 1994; Sato, 2006). Population genetic diversity and structure also may be influenced by behavioral processes such as natal homing and spawning site fidelity (Miller et al., 2012; Stepien and Faber, 1998; Stepien et al., 2009), which may enhance specialization of reproductive groups and increase genetic divergence. In aquatic ecosystems, the rehabilitation of habitat in natural connecting channels can be an effective means to restore population structure and preserve locally adapted population groups (Bini et al., 2003; Isaak et al., 2007).

The study of landscape genetics examines the role of landscape ecology on the spatial distribution of genetic variation (Manel et al., 2003; Storfer et al., 2007). An understanding of these patterns may guide conservation and management decisions to restore or enhance habitat, thereby retaining or increasing population genetic diversity and local adaptations. Here we employ a landscape genetics approach to analyze fishery stocks, which are defined as population subunits that share a common gene pool, freely interbreed, and are genetically distinguishable from other such groups (Hallerman et al., 2003). We test the genetic diversity and connectivity among spawning populations of an important fishery – the yellow perch *Perca flavescens* (Teleostei: Percidae) – along the Huron–Erie Corridor (HEC) that links the upper and the lower Great Lakes. The overall aim is to understand the genetic variation, divergence, and similarity of yellow perch stocks within a complex and highly disturbed connecting channel.

History of the Huron–Erie Corridor

The HEC is one of the four connecting channels within the Great Lakes, which links Lake Huron with Lake Erie through the St. Clair River, Lake St. Clair, and the Detroit River (Fig. 1). This area encompasses some of the Great Lakes' most diverse wetlands and contains over 65 fish species, of which 16 are threatened or endangered (Manny et al., 2004, www.huron-erie.org). The HEC comprises the major shipping corridor between the upper and the lower Great Lakes (US Army Corps of Engineers, 2004), where large channelization projects have

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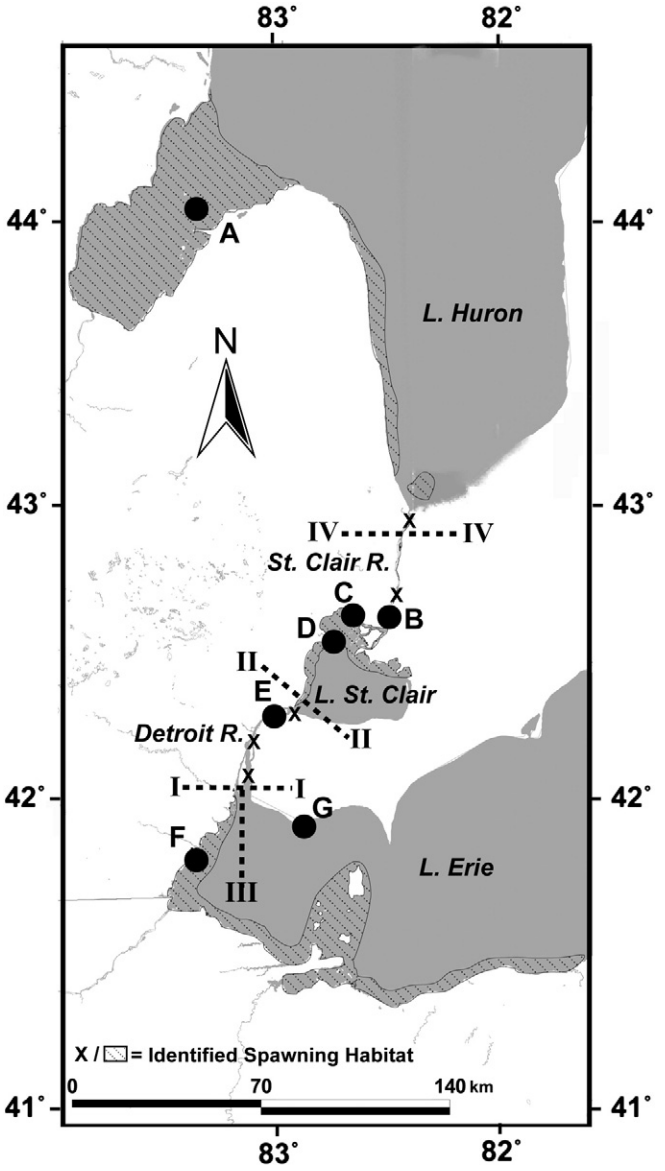

Fig. 1. Map of yellow perch spawning populations sampled (lettered A–G according to Table 1) (Hatch marks and X indicate spawning habitat identified by Goodyear et al., 1982). Lines = primary barriers to gene flow (ranked IV, in order of decreasing magnitude) from Barrier v2.2 (Manni et al., 2004b). Barrier support is indicated by percent bootstrap support and number of supporting loci (Barrier I: 56%, 13 loci; Barrier II: 59%, 11 loci; Barrier III: 58%, 12 loci; Barrier IV: 73%, 11 loci).

restructured much of its habitats (Bennion and Manny, 2011). Many of these modifications occurred within the Detroit River, leading to 96.5 km of shipping channel dating from the 1874 construction of the Livingston Channel through the 1968 completion of its modifications (Bennion and Manny, 2011). Fish habitats of the Detroit River have been subjected to continuous dredging (~46,000,000 m^3 removed in all; Moulton and Theime, 2009) and sediment deposition (>41 km^2; Bennion and Manny, 2011). HEC habitats were altered by increased industrialization, levels of contaminants (Manny and Kenaga, 1991), and human population growth, along with shoreline armoring, bulkheading, and dyking (HTG, 2009; Leach, 1991; Leslie and Timmons, 1991). Today less than 3% of its original coastal wetland areas remain (Bennion and Manny, 2011). These habitat losses and alterations likely affected populations of yellow perch and other fishes along the HEC.

The Huron–Erie Corridor Initiative was formed in 2004, with the goal of rehabilitating fish spawning habitat in the Detroit and St. Clair rivers (www.huron-erie.org), when 1080 m^2 of rock-cobble and ash cinders were placed at the head of the Belle Isle (site E; Fig. 1) in the Detroit River (HTG, 2009). In 2008, Fighting Island in the middle Detroit River (Ontario) was similarly enhanced with 3300 m^2 of habitat (HTG, 2009). An assessment by federal and state biologists has concluded that these two spawning habitats successfully attract large numbers of fishes, increasing species diversity and abundances (HTG, 2009; Manny et al., 2007).

Although the extent of spawning habitat and size of yellow perch populations in the HEC have not been explicitly documented, Goodyear et al. (1982) described many regional spawning and nursery habitats (Fig. 1; Hatching). In Lake Huron, most yellow perch spawning and nursery habitats are located in Saginaw Bay (site A; Fig. 1), with additional nearshore spawning in southern Lake Huron. Along the HEC, spawning has been documented in and above the St. Clair River delta, throughout most nearshore areas of Lake St. Clair, including Anchor Bay (site C; Fig. 1) and L'anse Creuse Bay (D; Fig. 1), and along Belle Isle (E; Fig. 1), Crystal Bay, and Grosse Ile in the Detroit River (Goodyear et al., 1982). An 2–6.5 million yellow perch spawn in western Lake Erie near Monroe, Michigan (F; Fig. 1; Thomas and Haas, 2000); other large numbers spawn in Sturgeon Creek, Ontario (G; Fig. 1) and throughout the Lake Erie Islands (HTG, 2009).

Tagging studies of yellow perch indicate that the HEC is important for allowing passage of individuals between riverine and lacustrine habitats, and between overwintering grounds and spawning sites (Haas et al., 1985). The genetic diversity, divergence, and connectivity of the yellow perch spawning populations (stocks) along Lake Huron, the HEC, and western Lake Erie are analyzed here and compared to those throughout the geographic range. The genetic variability of these HEC spawning stocks will likely provide a foundation for assessing the effects of present and future restoration.

Yellow perch populations, life history, and previous genetic investigations

Yellow perch populations reach their greatest abundances in the Great Lakes watershed, where they support economically important commercial and sport fisheries (Clapp and Dettmers, 2004; YPTG, 2006). Population sizes of yellow perch in western Lake Erie were ~16–64 million throughout the 1990s (Thomas and Haas, 2000), with ~130 million living in Lake Erie as a whole today (YPTG, 2011). Yellow perch stocks likely have been influenced by exploitation, pollution, habitat degradation, and competition with exotic species (Marsden and Robillard, 2004; Trautman, 1981; YPTG, 2011).

Cued by gradual changes in water temperature and photoperiod in late spring (Jansen et al., 2009), yellow perch aggregate to spawn on shallow reef complexes or in slow-moving tributaries 0.5–8 m in depth (Craig, 2000; Krieger et al., 1983). Males move into the nest areas first (Scott and Crossman, 1973), followed by females who drape egg masses on submerged macrophytes or rock, which are fertilized by 2–5 males (Mangan, 2004; Robillard and Marsden, 2001). Males generally linger post-spawn, potentially fertilizing eggs from several females, with neither sex providing parental care (Craig, 2000). A study of yellow perch tag returns determined that post-spawning movements are moderate; individuals tagged at Lake Erie spawning sites did not move upstream through the HEC, whereas some of those tagged in Lake St. Clair migrated to nearby tributaries (Haas et al., 1985).

Kin recognition and aggregative homing of yellow perch during reproduction may lead to genetic divergence of spawning populations over time. Kin recognition has been implicated in the closely related European perch *Perca fluviatilis*; chemical and physical cues are used to recognize relatives, with whom individuals preferentially associate (Behrmann-Godel et al., 2006; Gerlach et al., 2001). Studies of yellow perch spawning in Nova Scotia, Canada showed that removal of egg masses from a spawning site led to significantly fewer egg masses at that site in subsequent years, as compared to control locations (Aalto and Newsome, 1990). Those results revealed that yellow perch did not follow a pattern

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of random spawning site selection, but likely returned to given spawning sites (Aalto and Newsome, 1990).

Previous genetic studies examined diversity and divergence among yellow perch spawning populations in Lake Erie, the Great Lakes, and across their native range, using these same 15 nuclear microsatellite loci (Sepulveda-Villet and Stepien, 2011, 2012), providing an important comparison to the present study. Notably, Lake Erie spawning populations (Sepulveda-Villet and Stepien, 2011) had appreciable genetic diversity (mean $H_O = 0.533 \pm 0.010$; range = 0.479–0.593) and their genetic compositions significantly differed among sites (mean $\theta_{ST} = 0.233 \pm 0.020$; 0.000–0.665). Diversity levels were similar among spawning populations across the Great Lakes (mean $H_O = 0.551 \pm 0.013$; 0.478–0.635) and somewhat lower in other areas of their native range (0.533 ± 0.016; 0.333–0.670), especially in isolated populations (Sepulveda-Villet and Stepien, 2012). Sepulveda-Villet and Stepien (2012) also identified high genetic divergence among Great Lakes spawning populations ($\theta_{ST} = 0.127 \pm 0.007$; 0.008–0.282) as well as across the North American native range ($\theta_{ST} = 0.235 \pm 0.006$; 0.008–0.472); divergence levels were especially pronounced among isolated populations. Those results indicate that high divergence and moderate diversity characterize yellow perch spawning populations, which might also be predicted across the HEC.

Our study compares the genetic diversity, divergence, and connectivity of yellow perch spawning populations in Lake Huron, the HEC, and western Lake Erie. Specific hypotheses tested are: (1) genetic diversity levels of spawning populations significantly differ, (2a) their levels of divergence significantly vary, and (2b) genetic divergence follows an isolation by geographic distance pattern. The present investigation provides a fine-scale analysis of yellow perch genetic diversity, divergence, and connectivity along an extensively altered connecting channel.

Materials and methods

Sample collection, DNA extraction, and amplification

Adult spawning-condition yellow perch ($N = 248$) were collected by state and federal agency biologists and via hook-and-line fishing by us under permits issued to our laboratory from seven spawning sites in Lake Huron, the HEC, and western Lake Erie (lettered A–G in Fig. 1). Each collection was made from a single spawning location and year, except for samples from Saginaw Bay (site A) where samples from throughout the bay from two collection years were tested for difference; none was found, and thus they were pooled (Table 2). Pectoral fin clips were preserved in 95% EtOH in the field and stored at room temperature prior to DNA extraction.

Genomic DNA was extracted and purified from the fin clip by using DNeasy Quiagen kits (QUIAGEN, Inc., Valencia Ca.), whose aliquots were frozen, labeled, and archived. Genetic variation was analyzed by using 15 nuclear DNA microsatellite loci following Sepulveda-Villet and Stepien (2011) including: *Svi*2, 3, and 7 from Eldridge et al. (2002), *Svi*4, 17, and 33 from Borer et al. (1999), *YP*13 and 17 from Li et al. (2007), and *Mpf*1-7 from Grzybowski et al. (2010).

Polymerase chain reactions (PCR) consisted of 50 mM KCl, 1.5 mM $MgCl_2$, 10 mM Tris–HCl, 50 μM of each deoxy-nucleotide, 0.5 μM each of the forward and reverse primers, 2% dymethyl sulfoxide (DMSO), 5–30 ng DNA template, and 0.6–1.2 μM of Taq polymerase per 10 μL of reaction volume. Positive and negative controls were included in each reaction. An initial cycle of 2 min at 94 °C was used for strand denaturation, followed by 40 cycles of denaturation (94 °C, 30 s), primer annealing (1 min) at a primer-specific temperature (T_A; Table 1), and polymerase extension (72 °C, 30 s). A final extension at 72 °C for 5 min was included to minimize partial strands.

Forward primers were synthesized with one of four 5′ fluorescent labels, allowing pool-plexing during analysis (grouped as follows: *Svi*2 + 7, *Svi*3 + 33, *Svi*4 + 17, *YP*13 + 17, *Mpf*1 + 2 + 5 + 6, and *Mpf*3 + 4 + 7). Amplification products were processed for allelic length determination by diluting at a ratio of 1:50 with ddH_2O, with a 1 μL aliquot added to 13 μL of a formamide and ABI GeneScan-500 size standard solution, loaded onto 96-well plates, and denatured for 2 min at 95 °C. The denatured products were analyzed on our ABI 3130XL Genetic Analyzer with GeneMapper 3.7 software (Applied Biosystems Inc., Foster City, CA). We reviewed output profiles manually to confirm correct identification of allelic size variants.

Microsatellite data analyses

Population samples were tested for conformance to Hardy–Weinberg Equilibrium (HWE) expectations at each locus, with significance estimated by using the Markov Chain Monte Carlo method (MCMC) via 1000 randomization procedures (Guo and Thompson, 1992) in Genepop v4.0 (Rousset, 2008; http://mbb.univ-montp2.fr/MBB/subsection/downloads.php?section=2). Any deviations were analyzed for excess or deficiency of homozygotes, and loci were tested for linkage disequilibrium (LD). Levels of significance for both tests were adjusted by using sequential Bonferroni corrections (Rice, 1989) to minimize Type 1 error. Possible presence of null (nonamplified) alleles was tested with Micro-Checker v2.3.3 (van Oosterhout et al., 2004, 2006; http://www.microchecker.hull.ac.uk). To test hypothesis 1, whether genetic diversity differs among spawning populations, expected and observed heterozygosity values (H_E and H_O) were calculated in Genepop v4.0, and number of alleles (N_A) and allelic richness (A_R; number of alleles per locus independent of sample size, adjusted by rarefaction per El Mousadik and Petit, 1996) were determined in *F*STAT v2.9.3.2 (Goudet, 2002; http://www2.unil.ch/popgen/softwares/fstat.htm). We tested for significant differences in observed heterozygosity or allelic richness (hypothesis 1) among samples with Friedman sum rank tests in the R statistical software suite v2.14.0 (R Development Core Team, 2011; http://www.r-project.org/), with the loci treated as blocks per spawning population. The number of private alleles (N_{PA}; those occurring only in a single spawning population) was computed in Convert v1.31 (Glaubitz, 2004; http://www.agriculture.purdue.edu/fnr/html/faculty/rhodes/students%20and%20staff/glaubitz/software.htm).

To investigate hypothesis 2a, whether genetic compositions significantly differ among yellow perch spawning populations, unbiased θ estimates of *F* statistics (Weir and Cockerham, 1984) and their levels of significance were evaluated in *F*STAT. Models using θ_{ST} (the F_{ST} estimate of Weir and Cockerham, 1984) have been shown to better resolve relationships among such recently diverged populations

Table 1
Summary statistics for 15 microsatellite loci across Huron–Erie Corridor yellow perch spawning populations, including: PCR annealing temperature (T_A), number of alleles per locus (N_A), allelic size range in base pairs (bp), mean deviation from Hardy–Weinberg equilibrium within subpopulations (F_{IS}), and among subpopulations (F_{ST}).

Locus	T_A (°C)	N_A	Size range (bp)	F_{IS}	F_{ST}
*Svi*2	54	5	206–216	0.130	0.088
*Svi*3	54	10	130–152	0.102	0.032
*Svi*4	62	33	114–188	−0.060	0.030
*Svi*7	53	11	158–212	−0.106	0.013
*Svi*17	60	16	148–184	0.012	0.013
*Svi*33	60	40	100–190	−0.024	0.021
*YP*13	54	8	235–271	0.187	0.312
*YP*17	56	6	208–223	0.066	0.077
*Mpf*1	56	35	227–321	0.020	0.009
*Mpf*2	56	41	215–321	0.024	0.005
*Mpf*3	54	20	107–149	−0.095	0.049
*Mpf*4	58	31	159–239	0.167	0.047
*Mpf*5	54	17	127–163	0.021	0.124
*Mpf*6	54	9	124–160	−0.027	0.038
*Mpf*7	53	20	142–194	0.029	0.066
Total	–	309	–	0.024	0.057

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(Balloux and Lugon-Moulin, 2002). Pairwise comparisons between samples also were conducted by using a nonparametric (exact *G*) procedure (Raymond and Rousset, 2005), with probability estimated from MCMC in Genepop v4.0; this approach does not assume a normal distribution and is not influenced by sample size, but may have less statistical power (Goudet et al., 1996). In all pairwise comparisons, sequential Bonferroni corrections were used to minimize the potential for Type 1 statistical error (Rice, 1989). Lastly, numbers of migrants (N_M) among spawning populations were estimated in Arlequin v3.5.1.3 (Excoffier and Lischer, 2010), following Slatkin (1991).

To further evaluate connectivity and divergence patterns (hypothesis 2a), we used Barrier v2.2 (Manni et al., 2004a,b; http://www.mnhn.fr/mnhn/ecoanthropologie/software/barrier.html) to identify discontinuous groups of sampling sites independent from an a priori knowledge of their relationships. Pairwise θ_{ST} estimates were mapped onto a matrix of sample site geographic coordinates (latitude and longitude). The resulting "barriers" denote populations whose genetic distances are greater than predicted from spatial proximity. Relative support for each barrier was evaluated by the number of loci that supported it, and by bootstrap analysis of the multilocus θ_{ST} matrix with 2000 iterations in Geneland v3.1.4 (Guillot et al., 2005a,b, 2008; http://www2.imm.dtu.dk/~gigu/Geneland/) through R. Genetic barriers supported by a majority of loci and bootstrap values ≥50% are reported.

Patterns of genetic connectivity and stock structure (hypothesis 2a) were further evaluated by using a Bayesian approach in Structure v2.3.3 (Pritchard and Wen, 2004; Pritchard et al., 2000; http://pritch.bsd.uchicago.edu/structure.html) to identify similar groups of individuals, regardless of their true sample origin. Membership to groups was analyzed by 10 independent runs at $K=1$ (a single spawning group, i.e., panmixia) to $K=14$ (double the *N* of spawning sites sampled), with burn-ins of 100,000 and 500,000 replicates. We analyzed consistency among runs, compared the probabilities of individual assignments to groups, and calculated log-likelihood values. Optimal *K* scenarios were determined from the Δ*K* likelihood evaluations of Evanno et al. (2005).

Partitioning of genetic variation among Lake Huron, the HEC, and western Lake Erie, and among individual spawning populations (hypothesis 2a) was analyzed with Analysis of MOlecular VAriance (AMOVA; Excoffier et al., 1992) in Arlequin v3.5.12 (Excoffier and Lischer, 2010; Excoffier et al., 2005; http://cmpg.unibe.ch/software/arlequin35/). We additionally tested for correspondence between genetic distances ($\theta_{ST}/1-\theta_{ST}$) and geographic distances (hypothesis 2b), measured as the shortest waterway distances between each pair of samples (both natural log transformed and nontransformed), by using Isolde in Genepop (Rousset, 1997). The regression line fit and significance were calculated by using Mantel's (1967) procedure with 1000 permutations.

Results

Genetic diversity of yellow perch spawning populations along the HEC (hypothesis 1)

The 15 loci analyzed in this study for 248 spawning individual yellow perch from seven sampling sites did not show null alleles and all samples conformed to HWE and LD expectations after sequential Bonferroni correction (Table 1). Loci *Svi*2, *YP*13, and *Mpf* 5 were the most informative for discerning divergence among spawning populations, as indicated by their higher F_{ST} values (Table 1). In contrast, loci *Svi*17 and *Mpf*1 and 2 had relatively low F_{ST} values and showed more modest differentiation (Table 1).

Numbers of alleles per locus ranged from 5 (*Svi*2) to 41 (*Mpf*2), with the population spawning in the Detroit River having the most (Tables 1 and 2). Spawning populations from Saginaw Bay in Lake Huron (site A in Fig. 1) and Anchor Bay (C) in Lake St. Clair also had high numbers of alleles (180 and 176 respectively; Table 2). Allelic richness significantly differed among yellow perch spawning in Lake Huron, the HEC, and western Lake Erie ($\chi^2=8.9$, df = 2, $p=0.01$), with the HEC having the highest values (14.04 ± 2.34). Allelic richness likewise significantly varied among spawning populations ($\chi^2=30.9$, df = 6, $p<0.0001$), and was greatest (10.51 ± 1.63) at Belle Isle (E) in the Detroit River, followed by Algonac (B) on the St. Clair River (9.25 ± 1.61); both are within the HEC. All spawning populations had private alleles, which numbered from 1 at L'anse Creuse Bay (D) in Lake St. Clair to 28 at Belle Isle (E) in the Detroit River. Yellow perch spawning in the HEC overall had more private alleles (58; proportion = 0.19), than were found in Lake Huron (13; 0.07) and western Lake Erie (8; 0.05). Observed heterozygosity (H_O) differed among spawning populations in Lake Huron, the HEC, and western Lake Erie ($\chi^2=13.7$, df = 2, $p=0.001$), with higher values in Lake Huron (0.678) and the HEC (0.683) than in western Lake Erie (0.587). Observed heterozygosity also significantly differed among individual spawning sites ($\chi^2=30.5$, df = 6, $p<0.0001$), ranging from 0.699 (E; Belle Isle, MI; Detroit River) to 0.568 (F; Monroe, MI; western Lake Erie). These results show that levels of genetic diversity differ among yellow perch spawning populations, supporting hypothesis 1.

Genetic divergence and connectivity (hypotheses 2a and 2b)

Pairwise θ_{ST} and exact *G* tests discerned that all yellow perch spawning populations significantly differed in allelic composition (Table 3). Migration values (N_M) were low among all populations, indicating spawning group specificity and little gene flow (Table 4). These results support hypothesis 2a, that spawning populations of this area have distinct genetic compositions and low genetic exchange.

BARRIER analyses revealed four major genetic discontinuities among the spawning populations tested (Fig. 1), with the largest genetic barrier (Barrier I; 56%, 13 loci) separating those in Lake Erie from all others (Fig. 1). Barrier II (59%, 11 loci) isolated the population spawning at Belle Isle (E) in the Detroit River from the others. Barrier III (58%, 12 loci) distinguished the spawning populations at Monroe, MI (F) and Sturgeon Creek (G) in western Lake Erie from one another. Barrier IV (53%, 10 loci) divided yellow perch from Saginaw Bay (A) in Lake Huron from those spawning at Algonac (B) in the St Clair River and at Anchor Bay (C) and L'anse Creuse Bay (D) in Lake St. Clair. Overall, high levels of genetic structure indicated little gene flow among spawning populations, with Belle Isle (E) in the Detroit River showing pronounced genetic divergence. These patterns support hypothesis 2a and suggest that divergence patterns vary spatially.

Bayesian Structure analyses (Fig. 2a) identified two likely scenarios ($K=3$ and $K=7$; Fig. 2b). The first scenario, $K=3$, highlighted the unique allelic compositions of populations spawning at Saginaw Bay (A; red color) in Lake Huron and Belle Isle (E) in the Detroit River (green color; Fig. 2a). The remaining sites showed a mixed genetic signature, which appeared consistent with the AMOVA results that found genetic variance was not partitioned among the three hypothesized regions of Lake Huron, the HEC, and western Lake Erie (1.3% variation explained; $p=0.2$, N.S.), but rather among individual spawning populations (4.7% variation explained; $p<0.0001$), congruent with θ_{ST} and exact *G* test results. The Structure analysis ($K=7$) supported seven population groups along the HEC, consistent with pairwise test results, which mirrored findings from BARRIER analysis that showed genetic differences among yellow perch spawning populations from Saginaw Bay in Lake Huron (A), Belle Isle in the Detroit River (E), and the two in western Lake Erie (F and G). Yellow perch spawning at Algonac in the St. Clair River (B), and in Lake St. Clair at Anchor Bay (C) and L'anse Creuse Bay (D) revealed a mixed genetic signature, indicating closer relationships to one another although all significantly differed. The mixed signature of individuals at Algonac in the St. Clair River (B), and in Lake St. Clair at Anchor Bay (C) and L'anse Creuse Bay (D) may be due in part to reduced assignment success that comes with lower F_{ST} values less than 0.03

Table 2
Geographic and genetic parameters of yellow perch spawning populations, including: location, sample size (N), observed heterozygosity (H_O) ± standard error (s.e.), deviation from Hardy–Weinberg equilibrium within subpopulations (F_{IS}) ± s.e., total number of alleles across all loci (N_A), allelic richness (A_R) ± s.e., number of private alleles (N_{PA}), and proportion of private alleles (P_{PA}). Total values are calculated across all sites as a single unit. Mean values are averages of the seven spawning sites.

Water body	Locality	Year	Lat. (°N)	Long. (°W)	N	H_O	F_{IS}	N_A	A_R	N_{PA}	P_{PA}
L. Huron	A) Saginaw Bay, MI	2004 (32) 2007 (24)	43.4292	−83.7536	56	0.678 ± 0.055	0.092 ± 0.039	180	8.58 ± 1.27	13	0.07
St. Clair R.	B) Algonac, MI	2011	42.6524	−82.5139	23	0.690 ± 0.065	0.075 ± 0.035	148	9.25 ± 1.61	11	0.07
L. St. Clair	C) Anchor Bay, MI	2009	42.6319	−82.7764	47	0.619 ± 0.072	−0.046 ± 0.023	176	8.51 ± 1.53	12	0.07
	D) L'anse Creuse Bay, MI	2003	42.2457	−83.1198	23	0.633 ± 0.071	0.026 ± 0.034	140	8.71 ± 1.50	1	0.01
Detroit R.	E) Belle Isle	2011	42.3469	−82.9533	48	0.699 ± 0.063	0.098 ± 0.037	222	10.51 ± 1.63	28	0.13
HEC	(B–E)	–	–	–	141	0.683 ± 0.055	0.075 ± 0.034	275	14.04 ± 2.34	52	0.19
	F) Monroe, MI	2009	41.8683	−83.3178	30	0.568 ± 0.071	−0.123 ± 0.036	127	7.10 ± 1.11	3	0.02
	G) Sturgeon Creek, ON	2010	42.0083	−82.5875	21	0.576 ± 0.078	0.012 ± 0.038	121	7.77 ± 1.48	5	0.04
Western L. Erie	(F–G)	–	–	–	51	0.587 ± 0.074	−0.041 ± 0.027	171	11.26 ± 2.13	8	0.05
Total	Across all samples (A–G)	–	–	–	248	0.678 ± 0.062	0.084 ± 0.031	302	20.02 ± 3.26	–	–
Mean	7 spawning populations (A–G)	–	–	–	35	0.637 ± 0.020	0.019 ± 0.031	159	8.62 ± 0.41	10	0.06

Table 3
Pairwise genetic divergences between yellow perch spawning populations, with θ_{ST} values below the diagonal and χ^2 values from exact (G) tests of differentiation above the diagonal. Inf. = infinite value, as indicated by Genepop. All comparisons remained statistically significant after sequential Bonferroni correction (Rice, 1989); p values are in italics below each metric. Mean values are the average θ_{ST} divergence from all other spawning populations ± standard error.

Location	A	B	C	D	E	F	G
A) Saginaw Bay, MI	–	Inf. *<0.0001*	Inf. *<0.0001*	Inf. *<0.0001*	Inf. *<0.0001*	Inf. *<0.0001*	Inf. *<0.0001*
B) Algonac, MI	0.039 *<0.0001*	–	89.0 *<0.0001*	86.1 *<0.0001*	Inf. *<0.0001*	166.7 *<0.0001*	138.5 *<0.0001*
C) Anchor Bay, MI	0.055 *<0.0001*	0.011 *0.0007*	–	92.3 *<0.0001*	Inf. *<0.0001*	Inf. *<0.0001*	Inf. *<0.0001*
D) L'anse Creuse Bay, MI	0.040 *<0.0001*	0.019 *0.0003*	0.022 *<0.0001*	–	Inf. *<0.0001*	126.2 *<0.0001*	Inf. *<0.0001*
E) Belle Isle, MI	0.086 *<0.0001*	0.046 *<0.0001*	0.068 *<0.0001*	0.077 *<0.0001*	–	Inf. *<0.0001*	Inf. *<0.0001*
F) Monroe, MI	0.074 *<0.0001*	0.038 *<0.0001*	0.030 *<0.0001*	0.043 *<0.0001*	0.072 *<0.0001*	–	Inf. *<0.0001*
G) Sturgeon Creek, ON	0.099 *<0.0001*	0.037 *<0.0001*	0.030 *<0.0001*	0.048 *<0.0001*	0.078 *<0.0001*	0.052 *<0.0001*	–
Mean θ_{ST}	0.066 ± 0.010	0.032 ± 0.006	0.036 ± 0.009	0.042 ± 0.009	0.071 ± 0.006	0.052 ± 0.007	0.057 ± 0.011

(Latch et al., 2006). Overall, our results indicated that all sites sampled from Lake Huron, the HEC, and western Lake Erie contain distinct and divergent spawning populations.

Genetic relationships among the spawning populations did not follow a pattern of isolation by geographic distance (nontransformed; $y = 0.0001 \times + 0.04$, $R^2 = 0.24$, $p = 0.16$; Fig. 3), with some nearby groups being very different. For example, those spawning at Belle Isle (E) in the Detroit River were more genetically distinct than predicted by geographic distance. The natural log transformed regression discerned congruent results ($y = 0.012 \times - 0.002$, $R^2 = 0.21$, $p = 0.16$; not shown). Our results thus did not reject null hypothesis 2b, indicating that factors other than geographic distance regulate gene flow and divergence among spawning populations in the HEC.

Discussion

Genetic diversity of yellow perch (hypothesis 1)

Our results showed that overall genetic diversity levels of yellow perch spawning populations across Lake Huron, the HEC, and western Lake Erie were higher (mean $H_O = 0.637 \pm 0.020$; range = 0.568–0.699) than those across Lake Erie (0.533 ± 0.010; 0.479–0.593; Sepulveda-

Table 4
Estimated effective number of migrants per generation among spawning populations from the equation $F_{ST} = 1/(4N_M - 1)$ (Slatkin, 1991). Mean values are the average N_M ± standard error from all other spawning populations.

Location	A	B	C	D	E	F	G
A) Saginaw Bay, MI	–						
B) Algonac, MI	25	–					
C) Anchor Bay, MI	16	84	–				
D) L'anse Creuse Bay, MI	22	50	44	–			
E) Belle Isle, MI	10	22	14	12	–		
F) Monroe, MI	12	26	34	22	12	–	
G) Sturgeon Creek, ON	9	26	34	20	12	18	–
Mean N_M	16 ± 2.7	39 ± 9.9	38 ± 10	28 ± 6.1	14 ± 1.7	21 ± 3.5	20 ± 3.7

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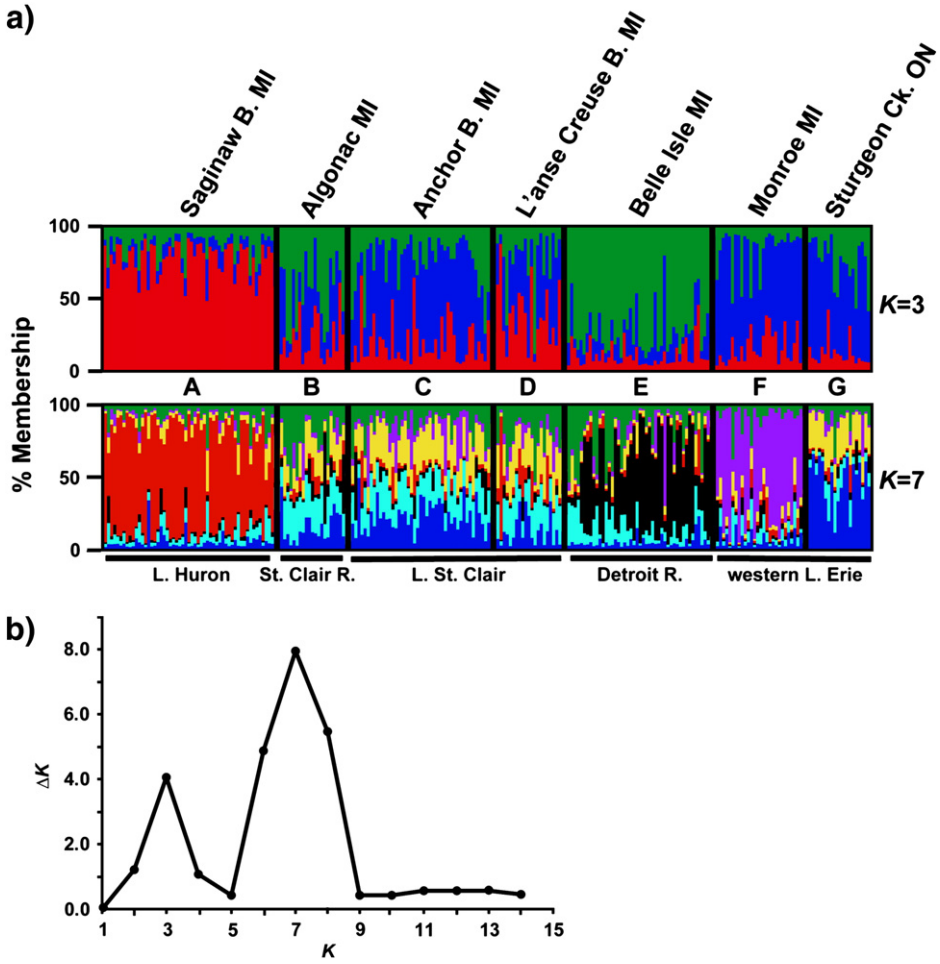

Fig. 2. a) Estimated yellow perch population structure from Bayesian Structure analysis (Pritchard and Wen, 2004; Pritchard et al., 2000) for $K = 3$ and 7 groups determined from ΔK evaluations (Evanno et al., 2005). Black lines separate different spawning populations, with each individual fish as a thin vertical line colored according to its estimated group membership. b) Results of ΔK computation (Evanno et al., 2005), for each scenario tested ($K = 1$–14) showing support for $K = 3$ and 7. (For interpretation of the references to color in this figure, the reader is referred to the web version of this article.)

Villet and Stepien, 2011), the entire Great Lakes (0.551 ± 0.013; 0.478–0.635; Sepulveda-Villet and Stepien, 2012), or their native North American range (0.533 ± 0.016; 0.333–0.670; Sepulveda-Villet and Stepien, 2012). Those studies were done in our laboratory with the same 15 microsatellite loci; thus these values are directly comparable. Our study and the others focused on variation at neutral markers, which does not directly address whether habitat alterations resulted in changes that influenced overall fitness. However, several recent studies have linked such variation at neutral loci as predictive of trends at adaptive loci in a variety of fishes (Allendorf et al., 2010; Tymchuk et al., 2010).

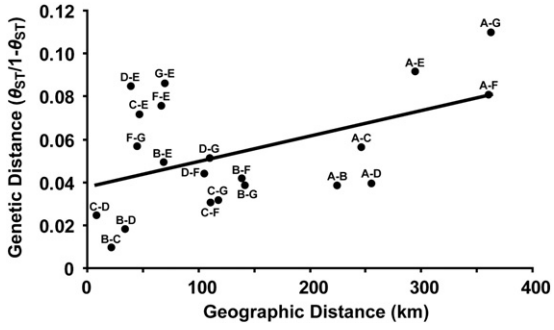

Fig. 3. Mantel (1967) regression of the pairwise relationship between genetic distance ($\theta_{ST}/1-\theta_{ST}$) and geographic distance (km) for yellow perch spawning populations ($y = 0.0001 \times + 0.04$; $R^2 = 0.24$, $p = 0.16$, N.S.).

An early study of yellow perch genetics using allozymes (H_O range = 0.000–0.039, Todd and Hatcher, 1993) recovered modest overall levels of genetic diversity, attributed to the lower resolution power of those genetic markers compared to the microsatellite loci used here. More recent studies of genetic diversity using mtDNA control region sequences (mean $H_D = 0.395 \pm 0.026$, range = 0.000–0.822, Sepulveda-Villet et al., 2009) and microsatellite loci (mean $H_O = 0.533 \pm 0.016$; range = 0.333–0.670; Sepulveda-Villet and Stepien, 2012) recovered greater diversity levels across the North American range of yellow perch. Similar values also have been recovered from populations of their close percid relatives: the European perch (mtDNA control region sequences; mean $H_D = 0.340 \pm 0.330$; range = 0.000–0.870; Nesbo et al., 1998, 1999) and the ruffe *Gymnocephalus cernua* (mtDNA control region sequences; 0.732 ± 0.025; Stepien et al., 1998, 2005). These levels of genetic diversity are consistent with those predicted for freshwater fishes based on results summarized by DeWoody and Avise (2000). In contrast, genetic variability levels are somewhat higher in walleye *Sander vitreus* than in yellow perch using mtDNA control region sequences (mean $H_D = 0.690 \pm 0.001$, range = 0.360–0.790; Faber and Stepien, 1998) and microsatellite loci (mean $H_O = 0.698 \pm 0.013$; range = 0.512–0.783; Stepien et al., 2009). These differences in average levels of genetic variability of populations may reflect a life history

trend for yellow perch remaining in kin-related groups as has been shown for the European perch (Behrmann-Godel and Gerlach, 2008). This merits experimental investigation.

Along the HEC, levels of yellow perch genetic diversity appear lower than those of walleye spawning populations (mean $H_O = 0.722 \pm 0.009$; range = 0.680–0.760; Haponski and Stepien, in press), which may reflect lower gene flow among yellow perch spawning populations. Like yellow perch, walleye diversity in the HEC was somewhat higher than its values across Lake Erie (0.704 ± 0.011; 0.660–0.780; Strange and Stepien, 2007), the Great Lakes (0.711 ± 0.011; 0.650–0.780; Stepien et al., 2009, 2010), and the native North American range (0.684 ± 0.02; 0.512–0.783; Stepien et al., 2009). Thus, genetic diversity levels of both percid species are higher in the HEC than in other spawning populations range-wide. These relatively high diversity levels in Lake Huron, the HEC, and western Lake Erie are not consistent with reduced population levels that might be predicted from a history of severe habitat loss, degradation, and population fragmentation (Mills and Smouse, 1994). In contrast, smaller populations of stream-dwelling char *Salvelinus leucomaenis* (Morita and Yamamoto, 2002) from Japan and the killifish *Aphanius fasciatus* (Angeletti et al., 2010) from wetlands in central Italy, linked low genetic diversity to habitat degradation and decreased population connectivity, which improved after restoration. The abundance of percid spawning habitat and their large population sizes in the Great Lakes likely have maintained the genetic diversity of spawning populations despite habitat changes along the HEC. Our results indicate that the HEC houses diverse spawning populations of both yellow perch and walleye (Haponski and Stepien, in press), which should be monitored as restoration efforts continue to ensure retention of their respective unique genetic signatures.

Genetic composition, divergence, and connectivity of yellow perch stocks (hypothesis 2a)

Marked genetic differences between upper and lower Great Lakes spawning populations indicate low genetic exchange that likely stemmed from former drainage isolation and post-glacial colonization pathways (see Sepulveda-Villet and Stepien, 2012). Our results indicate a large genetic break separated yellow perch spawning population groups between the upper and lower Great Lakes (also see Sepulveda-Villet and Stepien, 2012), along with spawning populations of smallmouth bass (Stepien et al., 2007) and walleye (Haponski and Stepien, in press; Stepien et al., 2009, 2010). Differentiation among these fish reproductive populations likely became pronounced when the early Lake Huron and Lake St. Clair/Erie systems had separate drainages following the glaciations, dating to ~14 kya (Lewis et al., 1994, 2008). Similar genetic patterns among these species reflect congruent biogeographic histories. These patterns likely did not result from recent habitat loss or fragmentation (Bessert and Orti, 2008; Laroche and Durand, 2004), as their appreciably high genetic diversity levels exclude recent genetic bottlenecks.

Kin group recognition and fidelity may result in high genetic divergence among yellow perch spawning populations located in close proximity due to behavioral isolation (Behrmann-Godel and Gerlach, 2008; Gerlach et al., 2001). Although spawning fidelity of kin-groups has not been investigated for yellow perch, the closely-related European perch has been shown to use olfactory cues to discriminate kin from unrelated individuals (Behrmann-Godel and Gerlach, 2008; Behrmann-Godel et al., 2006; Gerlach et al., 2001). Those studies indicated that European perch clustered in long-term population groups composed of full and half siblings (Behrmann-Godel and Gerlach, 2008; Gerlach et al., 2001). Reproductive success was significantly lower in non-kin groups, reducing pre-zygotic and post-zygotic fitness. Notably, kin-groups exhibited higher fertilization rates and higher hatching success (Behrmann-Godel and Gerlach, 2008). A similar reproductive strategy by yellow perch may explain the high genetic divergence we find among spawning populations across the HEC (mean $\theta_{ST} = 0.051 \pm 0.005$; range = 0.011–0.099; here), Lake Erie (mean $\theta_{ST} = 0.233 \pm 0.020$; range = 0.000–0.665; Sepulveda-Villet and Stepien, 2011), and their Great Lakes range (mean $\theta_{ST} = 0.127 \pm 0.007$; range = 0.008–0.282; Sepulveda-Villet and Stepien, 2012). This merits further investigation.

Genetic isolation is not explained by geographic distance (hypothesis 2b)

Our findings showed no significant relationship between genetic distance and geographic distance among yellow perch spawning populations along the HEC, similar to patterns found in Lake Erie (Sepulveda-Villet and Stepien, 2011). Instead, some proximate groups were distinguished by high genetic divergence, and some of those separated by larger geographic distances appeared genetically more similar (here and Sepulveda-Villet and Stepien, 2011). Similarly, genetic isolation by geographic distance did not explain relationships among walleye spawning populations along the HEC (Haponski and Stepien, in press). Some walleye spawning populations showed greater similarity among more distant groups, while some closely spaced ones were more divergent (Haponski and Stepien, in press; Stepien et al., 2009, 2010). Thus relationships among reproductive populations of both percids likely are regulated by homing behavior to natal sites and possible fidelity of kin groups.

Significance of the Belle Isle restoration site

Our results show that the yellow perch spawning population at Belle Isle (E) is genetically diverse ($H_O = 0.699 \pm 0.063$; $P_{PA} = 0.126$) and significantly differs from the populations sampled. Similarly, Haponski and Stepien (in press) discerned high genetic diversity of walleye spawning at Belle Isle ($H_O = 0.730 \pm 0.030$; $P_{PA} = 0.068$). Restoration efforts at the Belle Isle reefs likely have provided increased spawning habitat for many lithophilic spawners including several sucker species (*Moxostoma* and *Hypentelium*), sturgeon (*Ascipenser fulvescens*), lake whitefish (*Coregonus clupeaformis*), and walleye (Haponski and Stepien, in press; HTG, 2010; Manny et al., 2007; Roseman et al., 2007). Further restoration efforts targeting nearshore phytophilic spawners (i.e., vegetation and woody debris) likely will increase spawning habitat areas for additional species, including the yellow perch. Such habitat enhancement may conserve and augment population genetic diversity, leading to long-term adaptive potential and stability of fishery stocks along the HEC. Future monitoring efforts and genetic assessments are important to track this trend.

Conclusions

Our landscape genetic analysis of yellow perch spawning populations discerned appreciable genetic diversity and distinctiveness in the HEC. These genetic patterns likely have been maintained despite habitat loss, degradation, and fragmentation. Pronounced yellow perch population structure likely denotes fidelity to specific spawning groups (Aalto and Newsome, 1990; Sepulveda-Villet and Stepien, 2011), little exchange of individuals among them (Haas et al., 1985), and potential kin-recognition, as implicated for European perch (Behrmann-Godel et al., 2006). As spawning habitat is restored, this genetic diversity will underlie the long-term success of yellow perch and other populations along the HEC.

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Huron-Erie Corridor Initiative
BRIEFING ITEM

February 7, 2013

Name: Lynn Vaccaro, Jen Read, Mary Bohling, Elizabeth LaPorte, Jim Diana
Agency: Michigan Sea Grant

Briefing Item Type: Information
Permission to post on HECI Website: Yes

Title: Current and Planned Reef Construction

Michigan Sea Grant has been working with a number of project partners (USGS, USFWS, MDNR, JJR-Smith Group, MI Wildlife Conservancy) to coordinate the construction of several spawning reefs in the Huron Erie Corridor.

Middle Channel Reef, St. Clair River – Project partners were awarded a grant from NOAA's Restoration Center (with GLRI funds) in late 2010. In May and June of 2012, a marine construction company, Faust Corporation, built a new spawning reef project in the Middle Channel of the St. Clair River. The project includes nine reef beds made from three types of loose rock – angular limestone, rounded field stone and a mixture – covering an acre of the river bed. Although reef construction occurred later in the spring than expected, spawning ready adult lake sturgeon were observed on the reef even before the final reef bed was completed! Preliminary assessments indicated that sturgeon were depositing eggs on the reef and these eggs produced viable larvae. Greg Kennedy's dive team collected fantastic video footage of sturgeon and eggs on the reef! Project partners will conduct a more thorough post-construction assessment during the spring and summer of 2013.

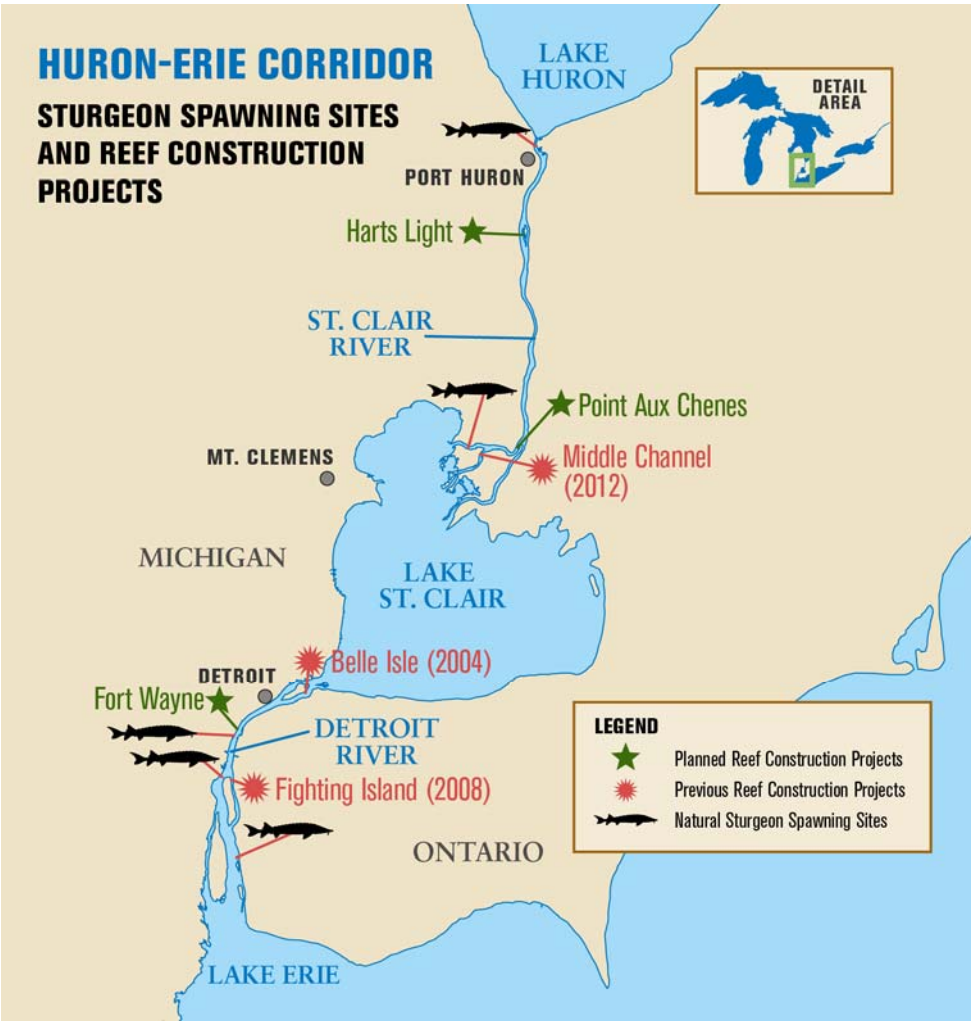
Fort Wayne Reef, Detroit River – Project partners were awarded a grant from the Sustain Our Great Lakes program (run by the National Fish and Wildlife Foundation, with GLRI funds) in late 2012. Plans include building another reef project in Detroit River, just offshore from Fort Wayne, in fall of 2013. A single large reef will be built using 4 - 8 inch angular limestone to maximize cost efficiency. Project partners will conduct pre and post construction assessment of the restoration area and connected shoreline habitats during 2013 and the spring 2014.

Two New Reefs, St. Clair River – The USGS is leading efforts to build two additional reef projects in the St. Clair River, most likely in the vicinity of Algonac (Point Aux Chenes) and St. Clair Township (Harts Light). Michigan Sea Grant will oversee the contracts for reef design and construction and lead outreach efforts. Reef construction is anticipated in fall of 2013.

Outreach – Michigan Sea Grant will continue promoting these and other efforts to restore fish and wildlife habitat throughout the Huron Erie Corridor. A variety of web and print-based outreach tools will

be used to communicate project activities, findings and impacts to HEC partners, stakeholders, media and the general public. In 2012, two public events and a promotional video helped us share the early successes of the Middle Channel Reef. In 2013 and 2014, Michigan Sea Grant will work with partners to host another public event, organize a webinar about restoration best practices, develop a print publication about fish habitat and enhance existing online curriculum resources.

For more information about these projects visit:
http://www.miseagrant.umich.edu/explore/restoration/



Map showing approximate location of existing and planned spawning reef construction projects in the Huron Erie Corridor.

Huron-Erie Corridor Initiative
BRIEFING ITEM

February 7, 2013

Name: James Boase and Justin Chiotti
Agency: U.S. Fish and Wildlife Service Alpena FWCO – Waterford Substation

Briefing Item Type: Information
Permission to post on HECI Website: Yes

Title: Adult Fish Community Assessments Associated with the Middle Channel Reef Project in the St. Clair River

Methods: The Service has been deploying gill nets to monitor the adult fish community before and after the construction of the middle channel reef. Experimental gill nets are fished once per week in the spring and early summer (April through June) and fall (November, December) at the middle channel reef and at a control site near the head of Russel Island. Three gill nets are set at each location. Gill nets consist of mesh sizes ranging from 75 to 150 mm in 12.5 mm increments with each net having 14 panels (2 of each mesh size). Nets dimensions are 2 m tall x 7.6 m panels x 14 panels (with randomly placed mesh sizes) for a total length of 106 m. Common biological metrics are collected from each fish species including genetic samples and aging structures from select sport fish.

Results:
Overview of adult fish community assessment effort associated with the Middle Channel Reef Project.

Year	Season	Middle Channel Reef Effort in Hours (# of Weeks)	Control Site Effort in Hours (# of Weeks)
2010	Spring	184 (6 weeks)	-
	Fall	-	-
2011	Spring	445 (7 weeks)	266 (5 weeks)
	Fall	135 (2 weeks)	111 2 (weeks)
2012	Spring	113 (2 weeks)	143 (2 weeks)
	Fall	219 (4 weeks)	194 (4 weeks)

Spring (Middle Channel Reef vs Control): We have captured a total of 205 fish during our spring assessments on the Middle Channel Reef representing 19 different fish species. The most common being White Bass (0.06/hr), White Sucker (0.06/hr), Walleye (0.04/hr), and Silver Redhorse (0.03/hr). Fish species captured at the reef site which have not been captured at the control site include: Chinook Salmon,

Freshwater Drum, Rainbow Trout, Round Goby, and Smallmouth Bass. We have captured a total of 100 fish at the control site representing 16 different fish species at the control site. The most common fish species are White Sucker (0.11/hr), Walleye (0.03/hr), White Bass (0.02/hr), Rock Bass (0.02/hr). Fish species captured at the control site and not found at the Middle Channel Reef include: Common Carp, Golden Redhorse, and Largemouth Bass. Due to minimal effort in the spring of 2012 comparisons between pre and post construction cannot be made.

Fall (Middle Channel Reef vs Control): We have captured a total of 45 fish during our fall assessments on the Middle Channel Reef representing 10 different fish species. The most common collected were Walleye (0.05/hr) and Northern Pike (0.03). Fish species captured at the reef site which have not been captured at the control site include: Smallmouth Bass. We have captured a total of 46 fish at the control site in the fall, representing 14 different fish species. The most common fish species include: Shorthead Redhorse (0.03/hr), Walleye (0.03/hr), Lake Sturgeon (0.02/hr), Silver Redhorse (0.02/hr), and Gizzard Shad (0.02/hr). Fish species collected at the control site and not at the reef site include: Lake Sturgeon, Rainbow Trout, White Perch, and Golden Redhorse.

The control site near the head of Russel Island and Pt. Aux Chene seems to be an important area for juvenile lake sturgeon. Between 2011 and 2012 a total of 10 juvenile Lake Sturgeon (0.01/hr) have been captured at this location ranging in size from 335 – 870 mm.

2013 Field Work: The Service plans to continue deploying gill nets weekly during the spring and fall in 2013 at the Middle Channel Reef and control location.

Huron-Erie Corridor Initiative
BRIEFING ITEM

February 7, 2013

Name: James Boase and Justin Chiotti
Agency: U.S. Fish and Wildlife Service Alpena FWCO – Waterford Substation

Briefing Item Type: Information
Permission to post on HECI Website: Yes

Title: Adult Lake Sturgeon Setline Assessments

Detroit River Update: The Fish and Wildlife Service has been conducting setline assessments in the Detroit River annually beginning in 2002 to obtain information on adult and subadult Lake Sturgeon. This data is used to obtain growth information, genetics, distribution, potential spawning sites, and population demographic information. To date, 234 sturgeon have been tagged. Using this mark-recapture data, the estimated population size of adult and subadult lake sturgeon in the Detroit River is near 4,000 individuals. In the spring of 2012, 11 Lake Sturgeon were implanted with transmitters to monitor the movement of these fish throughout the St. Clair-Detroit River System as part of a larger project funded by the Great Lakes Fishery Trust.

Southern Lake Huron Update: In 2012, setlines were also deployed in the Upper St. Clair River and Southern Lake Huron near Port Huron to collect fish as part of the Great Lakes Fishery Trust Lake Sturgeon movement project. A total of 36 adult Lake Sturgeon were collected and 26 of these fish received transmitters.

Ultrasound: An ultrasound unit was purchased by the Service in 2012 in order to evaluate the utility of this gear to determine sex and maturity status of Lake Sturgeon in the field. The Great Lakes Fishery Trust Lake Sturgeon movement project provided us with the opportunity to test the ultrasound on fish of known sex since a small incision would be needed to insert transmitters. In 2012, ultrasound images were taken of 70 Lake Sturgeon.

Genetics: Blood samples and pictures of the head region of Lake Sturgeon were collected from fish that received transmitters in Southern Lake Huron. The blood samples and pictures will be used to determine if a distinction can be made between river and lake resident sturgeon.

This work is conducted in cooperation with the USGS Great Lakes Science Center, Michigan Department of Natural Resources, Great Lakes Fish Commission, Ontario Ministry of Natural Resources, and West Virginia University.

Huron-Erie Corridor Initiative
BRIEFING ITEM

February 7, 2013

Name: Justin Chiotti[1], Pete Hrodey[2], James Boase[1], Eric Stadig[1], and Ed Roseman[3]
Agency: [1]U.S. Fish and Wildlife Service, Alpena FWCO – Waterford Substation
[2] U.S. Fish and Wildlife Service, Marquette Biological Station
[3] U.S. Geological Survey, Great Lakes Science Center

Briefing Item Type: Information
Permission to post on HECI Website: Yes

Title: Using Fyke Nets to Assess the Near-Surface Fish Assemblage in the St. Clair Detroit River System

Invasive species assessments such as the USFWS Sea Lamprey Control – Adult Assessment Program can provide insight into important information regarding non-target fish populations. A juvenile sea lamprey monitoring study provided us with a unique opportunity to utilize by-catch data to describe the near-surface fish assemblage in the St. Clair-Detroit River System (SCDRS). Floating fyke nets were attached to navigational buoys in the lower St. Clair and upper and lower Detroit Rivers during November through December 2011 and 2012.

Over 7,000 fish were collected in 2011 and nearly 3,000 in 2012. Fish species composition was consistent between the lower St. Clair and upper and lower Detroit River with brook silversides, emerald shiners, and bluegill representing a large proportion of the catch. The contribution of rainbow smelt in the lower Detroit River was much higher in 2011 (33%) when compared to 2012 (2%). Shannon-Weiner diversity indices were similar between the lower Detroit and lower St. Clair regions (1.3 and 2.0, respectively). The upper Detroit River showed the lowest diversity value (0.70), likely driven by a high abundance of brook silversides (Figure 1). Simlarly, species richness was greatest in the lower Detroit River, followed by the upper Detroit and the lower St. Clair (Figure 2). A total of ten unidentified Coregonines 51 to 75 mm total length were captured in the Livingstone Channel in the lower Detroit River. These fish are currently being identified to species using molecular techniques at the USGS Great Lake Science Center. The high number of littoral fishes and correlation between fish species captured in fyke nets with USGS bottom trawl data in Southern Lake Huron provides evidence that the connecting channel between Lakes Huron and Erie is an important vector for the downstream movement of fish. These findings highlight the utility of non-target data and demonstrate how cooperation between fisheries programs can prove instrumental in determining fish assemblages in large river systems.

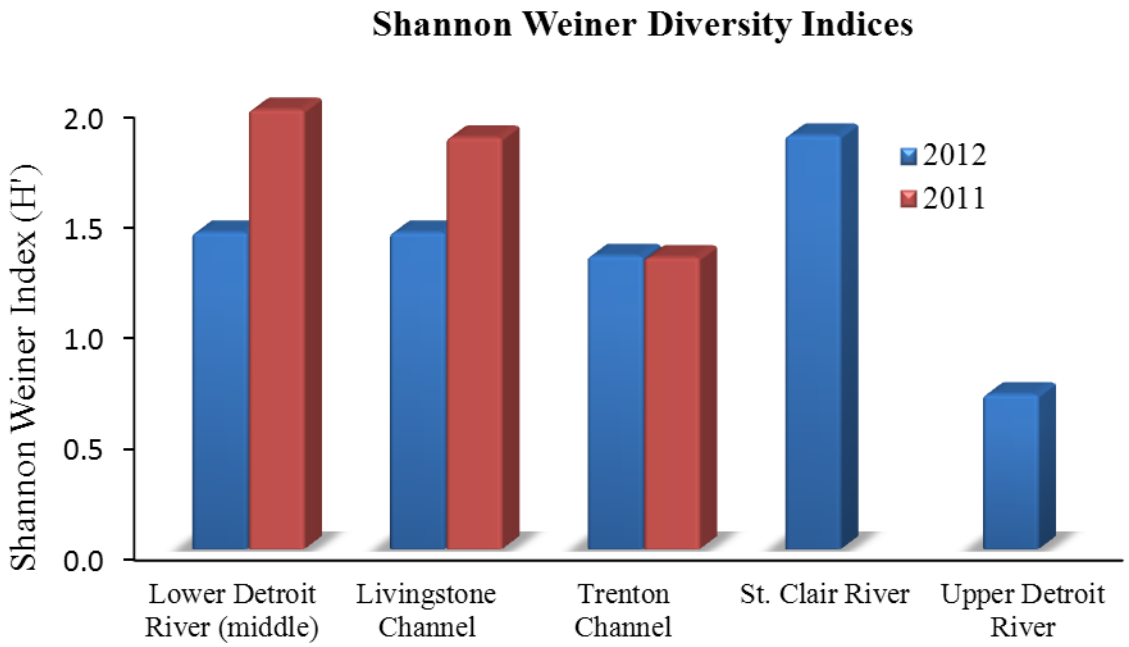


Figure 1. Shannon Weiner Diversity Indices calculated using fish assemblage data collected at different sites in the St. Clair and Detroit Rivers.

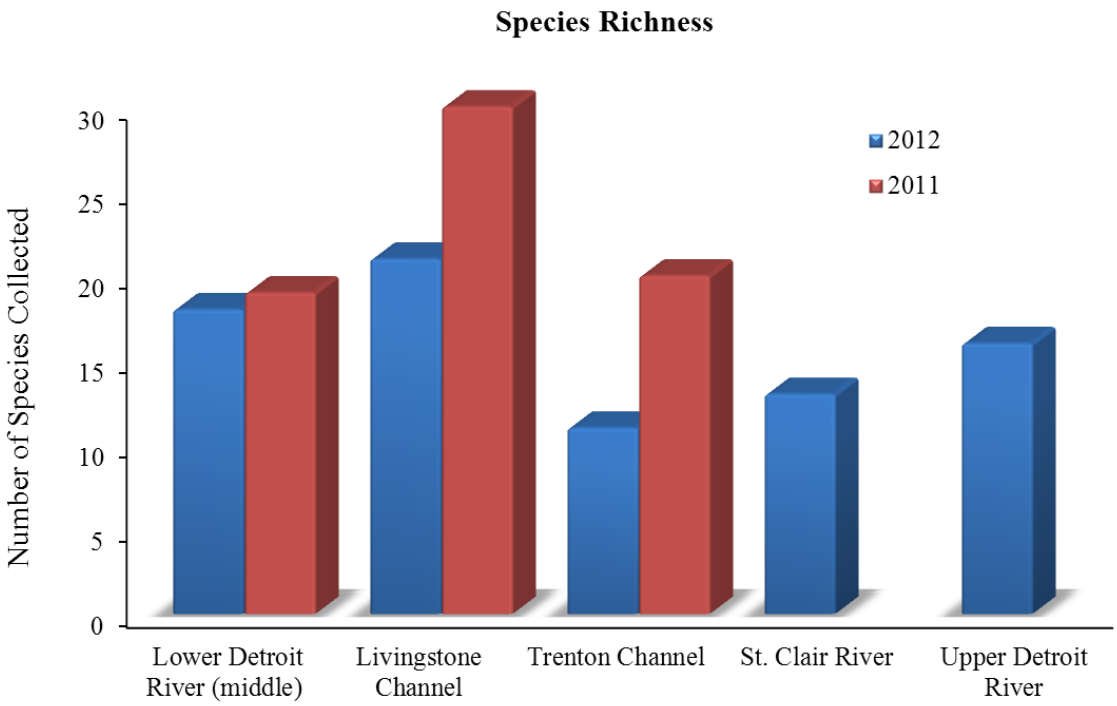


Figure 2. Number of fish species captured at different sites in the St. Clair and Detroit Rivers.

Huron-Erie Corridor Initiative
BRIEFING ITEM

February 7, 2013

Name: Justin Chiotti, James Boase, and Margaret Hutton
Agency: U.S. Fish and Wildlife Service Alpena FWCO – Waterford Substation

Briefing Item Type: Information
Permission to post on HECI Website: Yes

Title: Juvenile Lake Sturgeon Assessments in the St. Clair and Detroit Rivers

Objectives:

1) To evaluate the distribution and abundance of juvenile lake sturgeon in the Detroit and St. Clair Rivers
2) Collect biological information from other fish species encountered during the surveys to obtain benthic fish community information

The Fish and Wildlife Service has been conducting juvenile Lake Sturgeon assessments in the St. Clair River, Detroit River, and Western Lake Erie, since 2010 evaluating habitat restoration efforts and to gain a better understanding of juvenile distribution and abundance in this system. Juvenile Lake Sturgeon (< 500 mm) have been targeted using otter trawls (4.9 and 6.1 m head rope; 3 mm and 32 mm cod end, respectively) and monofilament gill nets (25, 38 and 51 mm gillnet). To date, efforts have included 88, 39, and 93 bottom trawls in the Detroit River, Lake Erie, and St. Clair Rivers, respectively for a total sampling area of 375,000 meters^2. Monofilament gill net efforts include 119 hours in the Detroit River and 530 hours in the St. Clair River in 2012. From the combined trawl and gill net effort, six YOY (134-190 mm) and one juvenile lake sturgeon (476 mm) have been captured. Three YOY were captured in a bottom trawl along the east side of Fighting Island in the Detroit River in 2010, two were captured in a bottom trawl near the head of Dickinson Island in 2011, and one was captured in a gill net (38 mm mesh) near the head of Dickinson Island in 2012. There are an estimated 50,000 adult lake sturgeon utilizing the SCDRS, and while good numbers of juveniles over the age of 3 have been observed, different locations and techniques should be considered for the collection of younger age classes.

All other fish species captured during these assessments are noted. The most common fish species captured during the Detroit River and Lake Erie trawl surveys include: Spottail Shiner (61%), White Perch (9%), Gizzard Shad (5%), and Smallmouth Bass (4%). The most common fish species captured in the St. Clair River trawl surveys include: Spottail Shiner (49%), Log Perch (10%), Rainbow Smelt (8%) and Round Goby (7%). Catches in the gill nets primarily include: Rock Bass (24%), White Perch (21%), Stonecats (8%), Yellow Perch (7%), Northern Madtom (7%), Walleye (6%), and Channel Catfish (6%).

2013 Field Plans: The Service plans to continue these surveys in the fall of 2013, spending more time sampling in the upper sections of the St. Clair River. More effort will be devoted towards gill netting because of the positive results obtained during the 2012 sampling season, however trawling will also continue.

Assessments conducted in cooperation with: Michigan DNR, Ontario Ministry of Natural Resources, and U.S. Geological Survey

Huron-Erie Corridor Initiative
BRIEFING ITEM

February 7, 2013

Name: Stephen Hensler and James Boase
Agency: U.S. Fish and Wildlife Service Alpena FWCO – Waterford Substation

Briefing Item Type: Information
Permission to post on HECI Website: Yes

Title: U. S. Fish and Wildlife Service Early Detection Monitoring for Aquatic Invasive Species

In response to the Great Lakes Restoration Initiative Action Plan, the U. S. Fish and Wildlife Service will be collecting field samples in 2013 as part of a new early detection monitoring program for aquatic invasive species. The eventual goal of this program will be to detect both fish and invertebrates, but activities in the coming field season will focus on fish. All locations sampled (e.g., St. Clair River, Lake St. Clair, Detroit River) will be divided into grids, and specific sampling sites within grids will be chosen for all sampling methods using a probabilistic approach where target organisms or signs of their presence are most likely to be found.

Sampling will begin in April with water samples being collected for environmental DNA (eDNA) analysis focused on detection of silver and bighead carp. One hundred water samples will be collected in the St. Clair River, Lake St. Clair, and Detroit River each for this work. Ichthyoplankton sampling will follow the eDNA work and will occur from late May through July. All larval fish sampling will occur at night with net tows occurring in open water areas and light traps being deployed in backwater areas and near macrophyte-covered nursery areas. Post-larval and adult fish will be targeted during sampling efforts in August and September. Fish will be collected via standard fyke and mini-fyke net collections, baited minnow traps, night electrofishing (10-minute runs), and night bottom trawling. Other methods may be used (e.g., seining, micro-mesh gill netting) if time and conditions permit.

Huron-Erie Corridor Initiative
BRIEFING ITEM

February 7, 2013

Name: Peter Hrodey, Jessica Barber, and Michael Twohey[1]
Agency: [1]U.S. Fish and Wildlife Service, Marquette Biological Station

Briefing Item Type: Information
Permission to post on HECI Website: Yes

Title: Detroit and St. Clair River Sea Lamprey Transformer Fyke Netting

Objectives:
1. Capture metamorphosing sea lampreys during the peak of their downstream fall outmigration from three locations within the HEC.
2. Determine if marked transformers from the St. Clair River can survive migration through the HEC.
3. Determine the relative contribution of each study reach to the overall HEC source population.

Update: Despite a recent intensive effort to reduce numbers of sea lampreys in Lake Erie, we have noted an increase in the population. Large-scale habitat restoration initiatives, along with increased water quality standards, may have led to improved sea lamprey spawning and rearing habitat in the Lake Erie basin. In response, we increased our efforts to identify sources of sea lampreys in tributaries to the lake. Efforts to identify the source of parasites in the usual suite of Lake Erie tributaries have been unsuccessful, which suggests the source may be within the Huron-Erie corridor (HEC; St. Clair and Detroit rivers).

Results:

2011 – Assessments began on November 21st and continued until December 22nd. Fyke nets sampling the water surface were attached to coast guard buoys and fished overnight. Water temperatures during the assessment period ranged from 2.2 – 7.0° C. Fyke nets were fished at 20 different locations in the river for a total of 2,462 hours of effort. A total of four sea lamprey transformers were captured. The first sea lamprey was captured in the Livingstone Channel on 12/2 at a water temperature of 6.2° C. The remaining three lampreys were captured in Fighting Island Channel (west of Fighting Island) on 12/19-12/20 at water temperatures ranging between 2.7 – 3.6° C.

2012 – Juvenile sea lamprey trapping was conducted at three locations within the Huron-Erie Corridor (HEC) between November 27th and December 14th. This work continued the efforts started in the lower Detroit River during 2011, but expanded to include more stations further upstream in the system (Belle Isle and the lower St. Clair River). A total of 31 floating fyke nets were deployed in U.S. waters during the course of the survey. Nets were fished on a near continuous basis and checked every 48hrs. Eighteen

juvenile sea lampreys were collected during the nearly 9900 hours of sampling effort put forth by Service field crews, two with coded wire tags indicating that migration through Lake St. Clair is possible.

2013 – There are currently no plans to repeat the work during the fall of 2013; any new and/or continued efforts would be dependent upon available funding, etc.

Huron-Erie Corridor Initiative
BRIEFING ITEM

February 7, 2013

Name: Jeremy Moore[1], Annette Trowbridge[2], Zachary Jorgenson[2], Steve Choy[3], JoAnn Banda[4], Dan Gefell[5], Luke Iwanowicz[6], Kathy Lee[7], Patricia Mazik[8], Vicki Blazer[6], Lisa Williams[1]

Agency: [1]US Fish and Wildlife Service, East Lansing, MI, USA
[2]US Fish and Wildlife Service, Bloomington, MN, USA
[3]US Fish and Wildlife Service, Green Bay, WI, USA
[4]US Fish and Wildlife Service, Columbus, OH, USA
[5]US Fish and Wildlife Service, Cortland, NY, USA
[6]US Geological Survey, Leetown, WV, USA
[7]US Geological Survey, Mounds View, MN, USA
[8]West Virginia Cooperative Fish and Wildlife Unit, University of West Virginia, Morgantown, WV, USA

Briefing Item Type: Information
Permission to post on HECI Website: Yes

Title: Early Warning Program to Detect and Identify Contaminants of Emerging Concern and Their Effects to Fish and Wildlife

The purpose of the study is to understand contaminants of emerging concern (CECs) with respect to source, routes of exposure, and impacts to Trust Resources. A CEC is defined as a new substance, chemical, or metabolite, or an older substance with a newly expanded distribution, altered release, or a newly detected presence in the environment. Priority contaminants include fragrances, herbicides, pesticides, insecticides, hormones, pharmaceuticals, polycyclic aromatic hydrocarbons (PAHs), plant sterols, plastics, flame retardants and wastewater treatment plant indicators. The U.S. Fish and Wildlife Service's Environmental Contaminants Program established three goals in order to address CECs in the Great Lakes Basin. The Fish and Wildlife Service (Service) is determining the extent that CECs may present risk to fish and wildlife, will recommend resource management actions or controls/regulations to prevent/reduce adverse impacts, and is coordinating and collaborating with other Federal agencies (U.S. Geological Survey and U.S. Environmental Protection Agency) to ensure efficient and effective research.

The Service's objectives, while pursuing these goals include: measuring select CEC concentrations across time, space, water, sediment, and fish in locations characterized as Areas of Concern (AOCs) by the USEPA. The Service is comparing CEC concentrations between selected AOC locations in the Great

Lakes Basin, between sites within each of the selected AOCs to determine possible sources of introduction, determining if CECs analyzed are associated with exposure effects in fish, and selecting CECs that are a higher concern than others. CECs were selected on basis of usage, toxicity, potential estrogenic activity, and persistence in the environment. They have at least some basis in scientific literature, along with established or customized analytical methods. AOCs, such as the Detroit River, are being studied because they are areas with known emerging contaminants, sensitive or listed species, areas downstream of municipal wastewater discharges or receiving waters for industrial facilities, and areas susceptible to agricultural or urban contaminations, or harbors or ports.

Sites were sampled in the Detroit River in September of 2010, May of 2011 and May of 2012. Sites were also sampled in the River Raisin in May of 2012. Water and bottom sediment samples were analyzed at the USGS National Water Quality Laboratory for a broad suite of organic compounds that are indicators of industrial, domestic, and agricultural wastewaters. A suite of bioindicators are being assessed for 2-3 species of fish. Bioindicators that are being assessed include: Genotoxic/blood cell results, molecular analyses, histopathology/reproductive endpoints, and *in vitro* screening assays. The choice of species is based on a number of criteria and includes brown bullhead (*Ameirus nebulosus)* or white sucker (*Catostomus commersonii*) and largemouth bass (*Micropterus salmoides*) or smallmouth bass (*Micropterus dolomieu*). Brown bullheads have been extensively used at Great Lakes AOCs for monitoring the "tumor and deformities" beneficial use impairment (BUI). Largemouth and smallmouth bass have been used in numerous studies on the effects of exposure to emerging contaminants and have been shown to be sensitive species, particularly in terms of endocrine disruption.

The Service is establishing a database resulting from a literature search and this study and will use that database to compare concentrations of select CECs at AOCs to known effect concentrations. We will determine areas most at risk to cause effects in fish and wildlife, and analyze select response endpoints to determine possible CEC exposure and compare those responses between locations to determine areas of increased exposure effects. Finally, the Service will establish a spatially-explicit relational database for collecting project study information and related literature, while exploring recommendations from other Federal agencies to ensure research is contributing to the protection of fish, wildlife, and habitat.

Huron-Erie Corridor Initiative
BRIEFING ITEM

February 7, 2013

Name: Aaron Jubar and Fraser Neave
Agency: U.S. Fish and Wildlife Service and Department of Fisheries and Oceans, Canada (Sea Lamprey Control Program)

Briefing Item Type: Information
Permission to post on HECI Website: Yes

Title: Sea Lamprey Control in the Huron-Erie Corridor

Issue: Recent increases in sea lamprey abundance in Lake Erie may be attributed to increased larval abundance or increased survival of juvenile sea lampreys produced in the Huron-Erie Corridor (HEC).

Background: Larval sea lampreys were first discovered in the St. Clair River in July 1975. Abundance remained relatively low through the 1990's, and reports of parasitic sea lampreys attached to fish in Lake St. Clair were rare. Therefore, it was hypothesized that survival of juvenile sea lampreys from the St. Clair River and recruitment to the parasitic population in Lake Erie was minimal or non-existent. To date, larval sea lampreys have not been collected in the Detroit River, but improvements in the quality of water and spawning habitat increase the potential of sea lamprey recruitment.

To reduce sea lamprey abundance in Lake Erie, in 2008-2010, all streams known to contain larval sea lampreys tributary to the main basin of Lake Erie were treated with lampricides in two consecutive years. Despite these efforts, sea lamprey abundance and wounding on lake trout continue to be greater than targets. Increased assessment, designed to identify unknown source(s) of sea lampreys, failed to identify any untreated sources in tributaries to the main basin of Lake Erie. Increased assessment of sea lamprey production potential in the HEC occurred concurrently with assessment of Lake Erie tributaries. These efforts included increased larval assessment in the primary and secondary tributaries in the HEC, evaluation and mapping of habitat, angler interviews in the western basin of Lake Erie, and assessment of the contribution of juvenile sea lampreys to Lake Erie from the HEC. Results suggest that the larval population may be more widely distributed and greater in abundance than previously thought, that juvenile sea lamprey abundance may be on the increase in western Lake Erie, and that juvenile sea lampreys produced in the HEC are contributing to Lake Erie.

Future plans include increased assessment designed to guide potential control with lampricides and continued evaluation of the contribution of juvenile sea lampreys from the HEC to Lake Erie. Results of ongoing and future assessments will be used to determine if control in the HEC is warranted, and if so, how it will be directed and implemented.

Huron-Erie Corridor Initiative
BRIEFING ITEM

February 7, 2013

Name: Mary Anne Evans
Agency: USGS Great Lakes Science Center

Briefing Item Type: Information
Permission to post on HECI Website: No

Title: Western Lake Erie *Microcystis* sp. bloom initiation study

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Huron-Erie Corridor Initiative Steering Committee
BRIEFING ITEM

February 7, 2013

Name: Greg Kennedy, Jaquie Craig, Stacey Ireland
Agency: USGS Great Lakes Science Center

Briefing Item Type: Information
Permission to post on HECI Website: Yes

Title: Egg deposition in the St. Clair-Detroit River System

Objectives: Assess and measure the community composition, phenology, and spatial extent of egg deposition by lithophylic broadcast spawning fishes in the St. Clair (SCR) and Detroit (DR) rivers.

Milestones: Spawning reefs were constructed in the DR at Belle Isle (2004) and Fighting Island (2008) and in the SCR at Middle Channel (2012). The SCR also has an old coal cinder reef used by spawning lake sturgeon located in the North Channel near Algonac, which is a byproduct of the shipping industry. Intensive longitudinal studies of fish egg deposition occurred in the DR during 2007-2008, and then again in 2011. Intensive longitudinal studies of fish egg deposition occurred in the SCR during 2010, 2011, and 2012. Multiple habitat types were sampled in each river including main channels, channel fringes, shallow island margins, rivermouths, and open lake areas. Additional sampling occurred to document egg viability for lake sturgeon at the Fighting Island reef in 2010 and 2012, the Algonac reef in 2010, 2011, and 2012, and the Middle Channel reef in 2012. This year's highlights were that lake sturgeon spawned on the Middle Channel reef as it was being constructed, and lake whitefish eggs were collected from the SCR (main channel, approximately 4 km downstream of the city of St. Clair) for the first time since we started sampling for them in 2010.

Results Overview, 2012: This spring the DR was sampled with less intensity than in years past. The objective was to use the Fighting Island reef as a control for the Middle Channel reef; sites were limited to the Fighting Island area (2 upstream, 6 reef, 2 downstream). Sampling focused primarily on lake sturgeon spawning and we did not set our gear until after the majority of walleye were done spawning, resulting in a 3-week sampling season. A total of 1,276 eggs was collected from all sites, of which 567 were lake sturgeon. On-reef egg density by species and week is shown in the table below.

Reef-only mean egg densities (eggs/m^2) at Fighting Island reefs, 24 April – 15 May 2012. (* not sampled throughout entire spawning period)

	Week 1	Week 2	Week 3	Season Total
all species	232	377	21	630*
walleye	222	27	20	269*
sucker spp.	6	2	0	8*
lake sturgeon	0	329	0	329
other	4	19	1	24*

The number of sampling sites in the SCR was also reduced (n = 16), but still covered the entire length of the river and the full 10-week sampling season. The contrast in egg production between the two rivers is stark; a total of 108 eggs were collected from the SCR, of which 76 were lake sturgeon collected at the Algonac and Middle Channel reefs. Of notable mention is that 62 lake sturgeon eggs (222 eggs/m^2) were collected on the Middle Channel site as the reef was being constructed. The rest of the reef was constructed after our sampling season ended. All other sites yielded less than 40 eggs/m^2 except for the Algonac reef (58 eggs/m^2, suckers and lake sturgeon).

Fall sampling for fish eggs on the DR occurred over 4 weeks and was river-wide (19 sites), including the Belle Isle reefs, Fighting Island reefs, and pre-assessment for the Fort Wayne reefs. A total of 741 lake whitefish eggs was collected and eggs were found at all but one site over the 4-week sampling period. We ran into the unfortunate situation of massive gear loss at the Fort Wayne pre-assessment sites, but despite that, we did learn that lake whitefish are reproducing there on the natural substrate. Lake whitefish egg densities (eggs/m^2) for the reef sites were: Belle Isle = 313, Fort Wayne pre-construction = 164, Fighting Island = 96. The other non-reef sites in the river all yielded less than 40 eggs/m^2 except for the site immediately downstream of the Fighting Island reefs, which produced 397 eggs/ m^2.

As with the DR, fall sampling on the SCR was also river-wide (28 sites) and ran for 6 weeks. This was the first fall sampling season in which we collected lake whitefish eggs from the SCR since our sampling program began in 2010. Three eggs were collected from a site just downstream of the city of St. Clair, the only site to produce any eggs. This sampling season was the first full post-assessment of the Middle Channel reefs and they produced no lake whitefish eggs.

2013-14 Plans: Future plans for studying egg deposition as a measure of spawning habitat quality include: SCR – post-assessment of the Middle Channel reef, and pre-assessment at Hart's Light near Marine City and in the North Channel at Pointe aux Chenes; DR – pre-assessment at Fort Wayne (modified) and Grassy Island, post-assessment of the reef expansion at Fighting Island. We are considering the possibility of choosing several index stations throughout both rivers for annual monitoring.

Huron-Erie Corridor Initiative

BRIEFING ITEM

February 7, 2013

Name: Bruce Manny
Agency: USGS Great Lakes Science Center

Briefing Item Type: Information
Permission to post on HECI Website: Yes

Title: Remediate BUI 14 (Loss of Fish & Wildlife Habitat): Establish fish spawning habitat in the St. Clair and Detroit River Areas of Concern.

To remediate beneficial use impairment 14--Loss of fish and wildlife habitat in the St. Clair River and Detroit River Areas of Concern, with financial support from the Great Lakes Restoration Initiative, Environment Canada, and more than 12 other organizations, spawning habitat has been established in the Detroit River at Belle Isle in 2004, at Fighting Island in 2008, and in the St. Clair River at Middle Channel in 2012. All three spawning habitats were immediately used for spawning by native fishes, including the State- and Provincially-threatened lake sturgeon, walleye, lake whitefish, and the Federally endangered Northern madtom, as well as more than 10 species of other native fish. All these spawning habitats were established with the cooperation and assistance of over 15 State, Federal, and Provincial agencies and other entities, including the Essex Region Conservation Authority and Michigan Sea Grant.

Funding has been received to establish fish spawning habitats in the St. Clair River at two locations identified by a geospatial model of water depth and velocity in the river, namely at Harts Light and Pt. aux Chenes. Each spawning site will be 1-2 acres in size by a minimum of 2 feet thick, comprised of broken limestone, 5-8 inches in diameter, on an area of clean river bottom, in greater than 30 feet of water, flowing at 1-3 feet per second.

These two new spawning sites will be monitored and assessed by USGS, USFWS, and our other partners before and after construction to determine fish species using the sites for reproduction. After construction, assessments will include adult fish using the new habitat, eggs deposited per unit area on the spawning habitat and larval fish drifting off the spawning habitat.

These two new spawning habitats bring our total remediation effort to date to five spawning habitats, three in the St. Clair River (Middle Channel, Harts Light, and Pt. aux Chenes, and two in the Detroit River (Belle Isle and Fighting Island).

Several more sites for establishment of fish spawning habitat have been identified in each of these two rivers, if more funding is available. Our goal is to fully remediate a huge loss of fish spawning habitat that resulted from construction of shipping channels in these two rivers many years ago.

Benefits of this habitat remediation are expected to include higher numbers of adult native fishes, such as the State- and Provincially-threatened lake sturgeon, the Federally endangered Northern madtom, lake whitefish, and walleye, being produced each year in the Huron-Erie Corridor, repopulating the Corridor and adjacent waters of Lakes Huron and Erie.

Collaborators on this part of our initiative include: USEPA, USFWS, Michigan Sea Grant, The University of Michigan Water Center, OMNR, Smith Group JJR, Michigan Dept. of Natural Resources, and our partners in this St. Clair Detroit River System Initiative.

Huron-Erie Corridor Initiative Steering Committee
BRIEFING ITEM

February 7, 2013

Name: Ed Roseman, Stacey Ireland, Jaquie Craig, Robin DeBruyne
Agency: USGS Great Lakes Science Center

Briefing Item Type: Information
Permission to post on HECI Website: Yes

Title: Larval fish studies in the St. Clair-Detroit River System.

Objectives: Assess and measure the community composition, phenology, species abundances, spatial extent, movement, and production of larval fishes in and transported through the system.

Milestones: Intensive longitudinal studies of larval fish occurred in the DR during 2005, 2006, 2011, and 2012 with smaller spatial scope collections occurring in 2007, 2008, 2009, and 2010. Intensive longitudinal studies of larval fish occurred in the SCR during 2010, 2011, and 2012. Multiple habitat types were sampled in each river including main channels, channel fringes, deltaic wetlands, river mouths, and open lake. Additional sampling occurred to assess larval lake sturgeon produced at the constructed Fighting Island reef of the DR and in the North Channel reef of the SCR.

Results Overview: While many of the same native and invasive species were found in both systems, the DR had about an order of magnitude more larval fish than the SCR and the phenology of fish early life history events was delayed in the SCR compared to the DR, likely due to water warming rates being slower in the SCR. In the DR, we found lake whitefish, walleye, yellow perch, *Morone* spp. (white bass/white perch), suckers, lake sturgeon, and several native forage fish species to be relatively abundant in the middle and lower river as well as at sites in Lake Erie near the river mouth. In the SCR, walleye, yellow perch, and suckers were found in lower abundances than in the DR. Transient coldwater fishes such as deepwater sculpin, rainbow smelt, cisco, and lake whitefish were found in both rivers in low abundances. Invasive species were found in both rivers and included rainbow smelt, round gobies, tubenose gobies, white perch, and common carp. Lake sturgeon were collected in the DR immediately below the Fighting Island reef and in the North and Middle Channels of the SCR. Collections of larval and juvenile native lampreys (*Ichthyomyzon* and *Lampetra* species) occurred in the North Channel of the SCR concurrent with collections of lake sturgeon. All larval fish samples from previous years have been sorted, identified and measured. Databases have been updated and QA/QC'd.

2013-14 Plans: Sampling will continue in both rivers during 2012-13 with an emphasis on pre- and post-construction assessments of constructed habitats such as Middle Channel reef, Hart's Light, Pt. Aux Chenes in the SCR and at Fort Wayne reef, Belle Isle (reefs, connectivity and wetland restoration), northeast Grassy Isle in the DR, and assist with planning new restoration projects. In the lower DR and river mouth area, intensive collections will occur to satisfy data needs for collaborative bio-physical modeling efforts, genetics, and micro-elemental stock analyses. Sampling for larval lake sturgeon is scheduled to occur in the SCR at the Middle Channel reef.