



Contents lists available at SciVerse ScienceDirect

Journal of Great Lakes Research

journal homepage: www.elsevier.com/locate/jglr

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

Timothy J. Sullivan, Carol A. Stepien*

Great Lakes Genetics Laboratory, Lake Erie Center and Department of Environmental Sciences, The University of Toledo, 6200 Bayshore Road, Toledo, OH 43616, USA

ARTICLE INFO

Article history:

Received 2 December 2011

Accepted 2 December 2011

Available online xxxxx

Communicated by John Farrell

Keywords:

Huron–Erie Corridor

Landscape genetics

Microsatellites

Perca flavescens

Population genetics

Yellow perch

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.

© 2012 International Association for Great Lakes Research. Published by Elsevier B.V. All rights reserved.

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

* Corresponding author. Tel.: +1 419 530 8362 (office).

E-mail address: carol.stepien@utoledo.edu (C.A. Stepien).

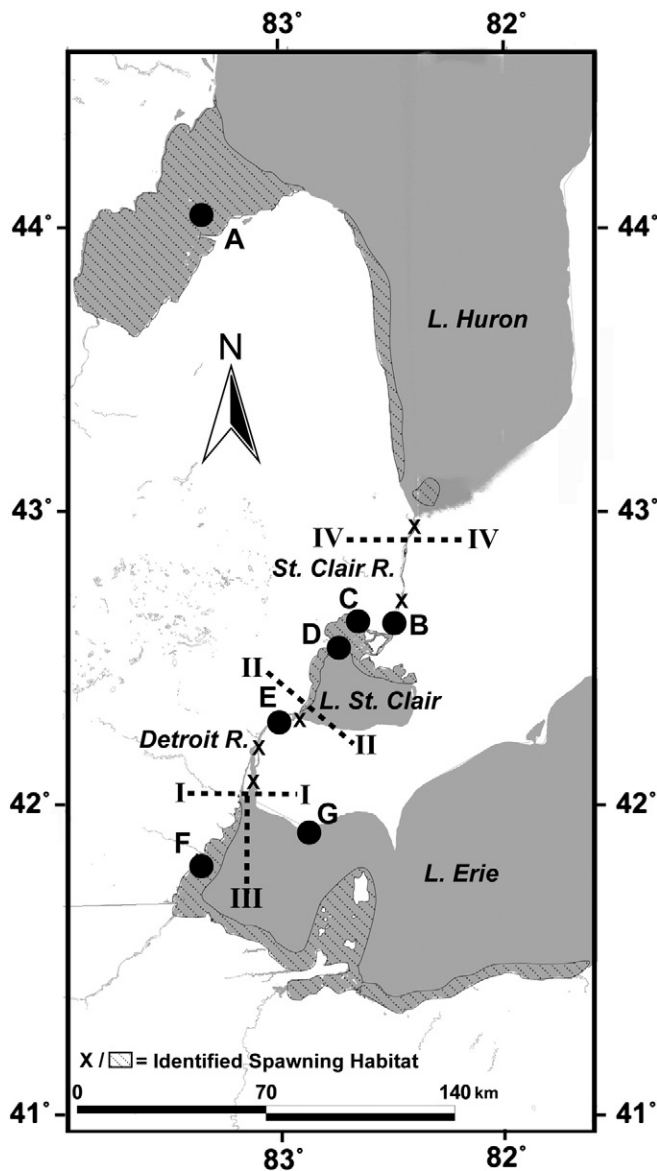


Fig. 1. Map of yellow perch spawning populations sampled (lettered A–G according to Table 1) (Hatch marks and X indicate spawning habitat identified by Goodyear et al., 1982). Lines = primary barriers to gene flow (ranked IV, in order of decreasing magnitude) from Barrier v2.2 (Manni et al., 2004b). 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 m³ removed in all; Moulton and Theime, 2009) and sediment deposition (>41 km²; 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 m² 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 m² 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

Download English Version:

<https://daneshyari.com/en/article/4398431>

Download Persian Version:

<https://daneshyari.com/article/4398431>

[Daneshyari.com](https://daneshyari.com)