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Heritage strain and diet of wild young of year and yearling lake trout in the main basin of Lake Huron

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ABSTRACT

Restoration of lake trout *Salvelinus namaycush* stocks in Lake Huron is a fish community objective developed to promote sustainable fish communities in the lake. Between 1985 and 2004, 12.65 million lake trout were stocked into Lake Huron representing eight different genetic strains. Collections of bona fide wild fish in USGS surveys have increased in recent years and this study examined the ancestry and diet of fish collected between 2004 and 2006 to explore the ecological role they occupy in Lake Huron. Analysis of microsatellite DNA revealed that both pure strain and inter-strain hybrids were observed, and the majority of fish were classified as Seneca Lake strain or Seneca Lake hybrids. Diets of 50 wild age-0 lake trout were examined. Mysis, chironomids, and zooplankton were common prey items of wild age-0 lake trout. These results indicate that stocked fish are successfully reproducing in Lake Huron indicating a level of restoration success. However, continued changes to the benthic macroinvertebrate community, particularly declines of Mysis, may limit growth and survival of wild fish and hinder restoration efforts.

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Introduction

Restoration of self-sustaining lake trout *Salvelinus namaycush* stocks in Lake Huron is a fish community objective developed to promote sustainable fish communities (DesJardine et al. 1995). Lake trout were extirpated between 1945 and 1955 and subsequent restoration efforts have included sea lamprey *Petromyzon marinus* control, gear restrictions, harvest quotas, stocking of hatchery-reared fish, and designation of biological refuges for lake trout reproduction (Eshenroder et al. 1995). Studies to evaluate the success of lake trout restoration efforts are listed as research priorities by all management agencies in the Great Lakes region (Eshenroder et al. 1999).

Since 1985, 12.65 million lake trout from eight strains have been planted into Lake Huron in efforts to rehabilitate populations (Table 1). Numerous genetic and tagging studies on lake trout strain performance in Lake Ontario (Marsden et al. 1989, Grewe et al. 1994, Perkins et al. 1995), Lake Michigan (McKee et al. 2004), and Lake Huron (Page et al. 2003, Stott et al. 2004) suggest that the Seneca Lake strain has been most successful in the Great Lakes. Although stocked fish support substantive recreational, commercial, and subsistence fisheries, the goal of self-sustaining lake trout populations remained elusive, primarily because of chronic recruitment failure of naturally reproduced fish as evidenced by predominance (>96%) of marked hatchery fish in agency surveys. Reasons for recruitment failure were not known, but hypotheses included the vulnerability of lake trout eggs and/or fry to predation (Savino and Henry 1991; Chotkowski and Marsden 1999; Biga et al. 1998; Horns and Magnuson 1981), alewife suppression, contaminants, and inability of hatchery fish to identify historic spawning sites or engage in successful spawning behavior (Eshenroder et al. 1995).

Age-0 and yearling lake trout were collected in USGS surveys on Six Fathom Bank and Yankee Reef between 1994 and 2002 (Desorcie and Bowen 2003) and appeared in bottom trawl samples during subsequent spring and fall surveys conducted in 2004, 2005, and 2006 (Riley et al. 2007, Roseman et al. 2008). These lake trout were likely naturally produced because they lacked fin clips and were smaller than the typical size of lake trout stocked (this study 46–86 mm; clipped fish >100 mm in fall) into Lake Huron (Riley et al. 2007). An average of 3.4 million age-1 lake trout was stocked annually during 2000–2006 (Bence et al. 2008; GLFC 2009). Most wild lake trout were collected from northern sampling stations adjacent to the northern lake trout refuge (Fig. 1). Age-0 lake trout were rare in collections prior to those years. In this paper, we couple an examination of the diet and genetic strain identity of wild age-0 lake trout in order to assess their ecological role in Lake Huron in respect to lake trout restoration.

Information on diets of wild age-0 and yearling lake trout in the Great Lakes is limited and restricted to Lake Superior, where wild populations exist (Hudson et al. 1995, Swedberg and Peck 1984). Those studies reported benthic macroinvertebrates, zooplankton, and small fish in age-0 lake trout diets, emphasizing the importance of their feeding on lower trophic levels during their first year. Benthic foodweb components are undergoing rapid and dramatic change in Lake Huron as evidenced by the decline in abundance and distribution

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Table 1
Numbers of lake trout stocked in the main basin of Lake Huron, 1985-2004.

Year	GLW	LLW	LOW	SAW	SIW	SLW	SMD	STW	Total
1985						52791	180536		233327
1987						94963	92603		187566
1989						74400	981350		1055750
1990			56650			10350	71700		138700
1991						55500	71500		127000
1992		718300	57000				363400		1138700
1993		436300	118700				473800		1028800
1994		555300				37900	197900		791100
1995		89875	55000			93854	247776		486505
1996		178150				366590	148600		693340
1997		59900		63600		434300	238900		796700
1998	330000	174400		310000	410000	719400	251500		2195300
1999						407190	133500		540690
2000		205230				352344	115894		673468
2001						407294	60754		468048
2002	21600	77969		8816	13666	356687	167924	43439	690101
2003		75953				434119	160600		670672
2004		79998				582654		71630	734282
Total	351600	2651375	287350	382416	423666	4480336	3958237	115069	12650049

GLW—Green Lake, LLW—Lewis Lake, LOW—Lake Ontario wild, SAW—Apostle Islands Lake Superior, SIW—Isle Royale Lake Superior, SLW—Seneca Lake wild, SMD—Marquette domestic, STW—Traverse Bay Lake Superior. From Great Lakes Fishery Commission fish stocking database: http://www.glfc.org/fishstocking/index.htm; April 23, 2007.

of *Diporeia* (Nalepa et al. 2008) and declining abundances of benthic fishes (Riley et al. 2008; Roseman and Riley 2009). Understanding how recent trophic changes in Lake Huron might affect lake trout ecology is equally as important as assessing the performance of stocked fish. To this end, examination of the diets of juvenile fish may reveal important information on resource use and potential bottlenecks limiting lake trout recruitment.

Methods

Bottom Trawl

Wild age-0 lake trout used in the diet study came from two different surveys. Forty-five fish were examined from collections made during standard USGS trawl sampling performed in May and October of 2004–2006 at five ports in U.S. waters of Lake Huron: Detour, Hammond Bay, Alpena, Au Sable Point (Tawas), and Harbor Beach (Fig. 1). Sampling also occurred at Goderich, Ontario during autumns 2004–2006 using the same trawling regime as other ports. At each port, 10-min on-contour trawl tows were made at approximate 9 m depth intervals on fixed transects from 9 to 110 m in depth. The 27, 37, 46, 55, 64, and 73 m depths are common to all ports, but the number of shallower and deeper tows varies among ports due to variation in bathymetry and bottom composition. Most lake trout used in this study were collected from 37 to 73 m depths. For all trawl tows, a 21-m wing trawl was fished on bottom at a speed of about 2.5 km/h from the USGS R/V *Grayling*. Results on the distribution of catches of wild lake trout in these surveys were reported in Riley et al. (2007). An additional five fish were collected using a 12-m trawl towed off the east side of Six Fathom Bank during June 2006. Methods of trawling were identical to deployment of the 21-m net.

All lake trout captured were measured in the field (total length [TL] to the nearest mm) and preserved individually in 95% ethanol. In the laboratory, fish were removed from ethanol, patted dry, measured (nearest mm TL), and weighed to the nearest 0.001 g.

Genetics

Total DNA was extracted from the wild caught lake trout and representatives of three hatchery strains (Lewis Lake from Jordan River National Fish Hatchery-LLW, Marquette-SMD from Marquette State Fish Hatchery, and Seneca Lake-SLW from Jordan River National Fish Hatchery). A previous genetic study of lake trout from Lake Huron showed that these three strains accounted for the majority of wild lake trout captured (Page et al. 2003). In addition, these strains accounted for the majority (>80%) of the stocking in the areas were sampled and tagging data indicated that most lake trout stocked into northern Lake Huron remained in that area (Madenjian et al. 2004).

The microsatellite loci *Sfo*1, *Sfo*8, *Sfo*11, *Sfo12*, *Sfo*18, *Sfo*23 (Angers 1995), *Sfo*C38 (GeneBank accession #AY168189), *Sfo*C88 (GeneBank accession #AY168192), *Sfo*C113 (GeneBank accession #AY168193), *Sfo*C115 (GeneBank accession #AY168194), *Sfo*D75 (GeneBank accession #AY168198), *Sfo*D105 (GeneBank accession # not available; King et al. 2002), *Ssa*85 (O'Reilly et al. 1996), *Scou*19 (Taylor et al. 2001), *Ogo*1a (Olsen et al. 1998), *Oneu9*, *Oneu*10 (Scribner et al. 1996) *Sco*202, *Sco*211, and *Sco*215 (DeHaan and Ardren 2005) were amplified in wild caught and hatchery lake trout. Genomic DNA (100 ng) was amplified in a 15μL reaction with 0.35 mM deoxynucleoside triphosphates (dATP, dTTP, dCTP, dGTP), 0.4μM of each primer (one primer of each pair was 5'-labelled), 2 mM $MgCl_2$, 1U *Taq* DNA polymerase (Promega Co.), and 1× reaction buffer supplied by Promega Co. The PCR profile was similar for each primer set; only the annealing temperatures differed. Samples were preheated at 95 °C for 2 min prior to the amplification cycle. The amplification cycle included 95 °C for 45 s, annealing at temperature for 45 s, and 72 °C for 1.5 min; which was repeated for 35 cycles , with a final extension for 5 min at 72 °C. The PCR products were analyzed using capillary electrophoresis on an ABI 3100-AVANT Genetic Analyzer (Applied Biosystems, Foster City, CA), following the manufacturer's specifications. Fragment sizes were determined in reference to a size standard (ROX-400) run in each lane using the manufacturer's software.

Individual assignment tests were conducted using Bayesian methodology, implemented in the program STRUCTURE (Pritchard et al. 2000) to determine the origins of recaptured lake trout and to verify that the hatchery strains were genetically distinct. First we used the genotypes from the lake trout from the three hatchery strains and determined to determine how many genetic clusters were present. We ran 100,000 iterations following a burn-in of 100,000 iterations, assuming correlated allele frequencies, and did not use information on the origins of the hatchery fish. We then used the most likely value of *K* (the number of populations) and ran the simulation again, this time including the wild caught lake trout. The simulation conditions were the same, except we used the population information for the hatchery strains (i.e. we set POPFLAG = 1 for the hatchery fish and POPFLAG = 0 for the wild caught lake trout and looked back one generation; GENSBACK = 1). We assigned the wild-caught individuals