



Stock structure, dynamics, demographics, and movements of walleyes spawning in four tributaries to Green Bay



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ABSTRACT

To test assumptions related to the current conceptual model for walleye *Sander vitreus* management in Green Bay, we evaluated whether: 1) spawning aggregations in the Fox, Menominee, Oconto, and Peshtigo rivers represent genetically distinct stocks; 2) population dynamics and demographics vary among walleye spawning at these locations; 3) walleye spawning in these rivers contribute to the fishery in northern Green Bay, and 4) walleye spawning in these rivers exhibit spawning site fidelity or if they stray among rivers. Genetic differentiation among the four tributaries was low and sex-specific total length (TL), mean TL at age 5, and age-class diversity were generally similar among rivers and observed differences were not consistent. Movements of walleye inferred from angler tag returns suggest that walleye spawning (and tagged) in the four tributaries typically remain within southern Green Bay; however, this assertion may be confounded by the distribution of angling effort that provides tag recoveries. Straying rates among rivers ranged from 0 to 23% and were likely sufficient to preclude genetic differentiation among stocks. Collectively, results suggest that walleye spawning in the Fox, Menominee, Oconto, and Peshtigo rivers do not function as separate stocks and do not significantly contribute to the fishery outside of southern Green Bay. The primary assumption of the current conceptual model that remains to be tested is whether the walleye fishery in southern Green Bay is supported primarily by fish spawning in these four rivers, or if there are substantial contributions from fish spawning at other unknown locations.

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Introduction

Green Bay supports one of the most prominent recreational fisheries for walleye *Sander vitreus* in North America. The recreational fishery provides annual harvests that exceed 90,000 fish and provides millions of dollars to local economies. In Michigan waters, walleye also contribute to an important tribal subsistence fishery designated by the Great Lakes Consent Decree for the 1836 Treaty of Washington. As a native top-level predator, walleye play an important role in the Green Bay ecosystem and could influence other species such as yellow perch *Perca flavescens* and lake whitefish *Coregonus clupeaformis* that also support important fisheries within the region (e.g., Schneider et al., 1991). The popularity and socioeconomic importance of all these fisheries makes walleye a species of primary management interest for both the Michigan (MIDNR) and Wisconsin (WDNR) Departments of Natural Resources, who jointly manage this important resource.

The current status of the Green Bay walleye fishery represents the successful culmination of several recovery efforts. By the mid-1900s, walleye stocks in Green Bay had been decimated by a combination of habitat destruction, pollution, overexploitation, and invasive species (Kapusinski et al., 2010; Schneider and Leach, 1977; Schneider et al., 1991). By the 1960s, walleye stocks in northern Green Bay had reached historic lows and only the Menominee River supported a self-sustaining stock in southern Green Bay (Kapusinski et al., 2010). Water quality in Green Bay began to improve following passage of the Clean Water Act in 1972; and in the late 1960s and early 1970s, both the WDNR and MIDNR began to stock walleye into Green Bay and associated tributaries (Hogler and Lange, 2012; Zorn and Schneeberger, 2011). The Wisconsin DNR discontinued walleye stocking in most of southern Green Bay in 1984 after approximately 86 million fry and 3.5 million fingerlings had been stocked (Schneider et al., 1991); however, limited stocking continued in Sturgeon Bay through 2012. Since 1969, MIDNR has stocked >40 million walleye fry and nearly 15 million fingerlings into portions of northern Green Bay and the Cedar River to increase walleye abundance and stocking continues in Michigan waters (Zorn and Schneeberger, 2011). The primary brood source for walleye stocked

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into Wisconsin waters of Green Bay was unspecified inland lakes in northern Wisconsin; whereas, walleye stocked into Michigan waters were obtained from native brood fish collected in Little Bay de Noc (Schneider et al., 1991).

Walleye in southern Green Bay are considered self-sustaining along with several other Michigan stocks in northern Green Bay (Zorn and Schneeberger, 2011). These self-sustaining stocks spawn at many locations within Green Bay and its tributaries (Schneider et al., 1991), providing the potential for a mixed-stock fishery. Schneider et al. (1991) suggested that at least some of these spawning stocks are discrete, but this assertion has never been fully verified. The current conceptual model for walleye management assumes that the fishery in southern Green Bay is largely supported by fish spawning in the Fox, Menominee, Oconto, and Peshtigo rivers. Furthermore, it is assumed that walleye spawning in these rivers do not contribute significantly to the walleye fishery in northern Green Bay. Determining whether walleye spawning in the Fox, Menominee, Oconto, and Peshtigo rivers represent discrete stocks and whether these stocks differ in terms of stock dynamics, demographics, and movements represent important questions for fishery managers. This information is critical to all aspects of the management process, including development of monitoring activities, determining stocking strategies, and implementing harvest regulations; yet, key assumptions related to the current conceptual model have not been tested. Therefore, our objectives were to determine if: 1) spawning aggregations in the Fox, Menominee, Oconto, and Peshtigo rivers represent genetically distinct stocks; 2) population dynamics and demographics vary among walleye spawning at these locations; 3) walleye spawning in these rivers contribute to the fishery in northern Green Bay, and 4) walleye spawning in these rivers exhibit spawning site fidelity or if they stray among rivers.

Methods

Study area

Green Bay is the largest bay of Lake Michigan and with a surface area of approximately 4200 km², is considered the largest freshwater estuary in the world (Sager and Richman, 1991; Smith et al., 1988). Mean and maximum depths are 20 m and 53 m, respectively. The bay features a diversity of substrates, macrophyte types, temperatures, and currents (Smith et al., 1988), and supports prominent recreational (and in some instances, commercial) fisheries for walleye, lake whitefish, yellow perch, muskellunge *Esox masquinongy*, and smallmouth bass *Micropterus dolomieu*. Our study was focused on southern Green Bay, specifically, the portion of the bay south of Chambers Island (Fig. 1). Southern Green Bay is considered eutrophic to hypereutrophic (Smith et al., 1988) and is fed by several tributaries, the largest of which include the Fox, Menominee, Oconto, and Peshtigo rivers (Fig. 1). These tributaries support large spawning runs of walleye and managers currently assume that the fishery in southern Green Bay is mainly supported by walleye spawning in these tributaries.

Sampling and tagging

During late March–mid April of 2012–2016, the WDNR collected walleyes from the Fox, Menominee, Oconto, and Peshtigo rivers using daytime electrofishing during spawning runs; only the Oconto and Peshtigo rivers were sampled in 2012. Electrofishing was conducted in a standardized manner (60 Hz pulsed DC current; 7.5 A; 180 V; 25% duty cycle) to sample each tributary at the same approximate time of the spawning run during each year. In general, samples were collected from each tributary over the course of 2–4 d when water temperatures ranged between 3 and 7 °C. However, samples from the Oconto and Peshtigo rivers in 2012 were collected when water temperatures ranged between 10 and 13 °C. Walleyes were measured for total length (TL; nearest mm), and sex was determined (when possible) based on

extrusion of gametes. During 2013–2015, second or third dorsal spines were removed from sex-specific, length-stratified subsamples (10 fish per 10 mm TL group) for age estimation. In 2014, fin clips were obtained from 60 fish in each river for DNA extractions; fin clips were dried and stored in scale envelopes. During each sampling event, a subsample of walleye were tagged with individually-numbered Floy tags (FD-94; Floy Tag, Inc., Seattle, Washington) printed with contact information for the WDNR. During each year and in each tributary, approximately 10% of the tagged walleye were double-tagged (i.e., affixed with a second Floy tag) for the purpose of estimating tag loss. Tag number, TL, sex, and location were recorded for walleye tagged in previous years that were recaptured during electrofishing sampling. Anglers catching tagged walleye were asked to report the tag number, TL, date, and location of capture.

Genetic stock structure

Fin clips were genotyped using the same suite of 10 microsatellite loci and molecular methods described in Waterhouse et al. (2014). The programs GenAlEx 6.5 (Peakall and Smouse, 2012) and FSTAT (Goudet, 1995) were used to test all loci in each population for deviations from Hardy-Weinberg equilibrium ($\alpha = 0.05$) and calculate the following genetic diversity statistics: mean number of alleles per population (A), allelic richness (A_R), and observed and expected heterozygosities (H_O , H_E). Pairwise F_{ST} values (Weir and Cockerham, 1984) were calculated for each population in GENEPOP 4 (Rousset, 2008) to estimate genetic differentiation among populations; the significance of each value was assessed with exact tests of genetic differentiation (Raymond and Rousset, 1995; $\alpha = 0.05$) implemented in GENEPOP.

Dynamics and demographics

Dorsal spines were viewed in whole or in section by two experienced readers to estimate ages. Ages were assigned to unaged fish using sex specific age-length keys (Isermann and Knight, 2005) that were constructed for each river in each year of sampling. To assess potential differences in dynamics and demographics among rivers, we compared sex-specific TLs, ages, mean TLs at age 5 (as a measure of growth) and age-class diversity as measured by the Shannon index (H'). We selected age 5 as the point to measure growth because at this point most walleye have reached sexual maturity and the period of relatively rapid growth before maturation has been completed. The Shannon index was calculated as:

$$H' = \sum p_i \times \log_e p_i$$

where p_i = proportion of age_i fish in a sample from a river in a specific year. Only data from 2013 to 2015 were used for age-based analyses, and metrics were compared among rivers using single factor ANOVA where each year (and not each fish) was considered an individual observation of each metric for each river. Normality and homogeneity of variance were confirmed using Shapiro-Wilks and Levene's tests, respectively. If ANOVA indicated that a metric differed among rivers, Tukey-Kramer tests were used to conduct pairwise comparisons. Alpha was set at 0.05 for all analyses.

Movements and straying rates

Movements of walleye were inferred from angler tag return data. Displacement distances were calculated as the minimum over-the-water distance (km) between tagging location and return location. We used ANOVA to determine if displacement distance varied in relation to tagging location, season [i.e., spring (March–May), summer (June–August), fall (September–November), winter (December–February)], or sex. Straying of walleye among tributaries was assessed using data from walleye that had been tagged during previous spring sampling

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