

## EXTENDED ABSTRACT

### Population Genomics towards Optimizing Muskellunge Management and Conservation in Québec, Canada

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Management of Muskellunge *Esox masquinongy* through most of its natural range has benefited from contemporary ecological and genetic insights, but such information is still lacking in Québec (Canada). Since 2010, the Ministry of Forest, Wildlife and Parks of Québec has collaborated with anglers and international scientists to gather contemporary information related to stock status, recruitment, habitat use, movement, and genomic

structure of Muskellunge. Additionally, gray literature was examined to summarize historical records of extensive stockings that occurred from 1950 to 1997. These stockings were intended to support an existing recreational fishery and create new fishing opportunities. The whole approach aimed to optimize Muskellunge management in Québec.

In the present study, we specifically addressed Muskellunge genetic population structure in the context of demographic con-

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nectivity and adaptive variation of populations in the St. Lawrence River system and inland waters of Québec. Knowledge of genetic structure is essential for proper and sustainable management since it allows identification of groups of individuals that are reproductively isolated and are typically geographically unconnected within a species, therefore implying demographic independence.

Our preliminary analysis was based on Muskellunge from six locations of the St. Lawrence River system and inland waters (Figure 1). A total of 4,009 single nucleotide polymorphisms markers were defined by double-digest restriction site-associated DNA sequencing genotyped on 286 Muskellunge ( $32 < n < 68$  per location).

Genetic structure was assessed using estimates of genetic differentiation among locations ( $F_{st}$ ),  $K$ -mean analysis, and assignment tests (all using GenoDive software). ADMIXTURE analysis and ordinations, including principal component analysis (PCA) and discriminant analysis of principal component (DAPC), were also performed. Both were run with and without a priori knowledge using R software. Although variable levels of differentiation were detected, a moderate level of differentiation ( $F_{ST}$ ) was detected among locations ( $0.003 < F_{ST} < 0.388$ ; mean = 0.146;  $p < 0.02$ ), indicating genetic structure within the system. Three main genetic groups were defined first by ADMIXTURE, PCA, and  $K$ -mean analyses (TRA, CHQ,

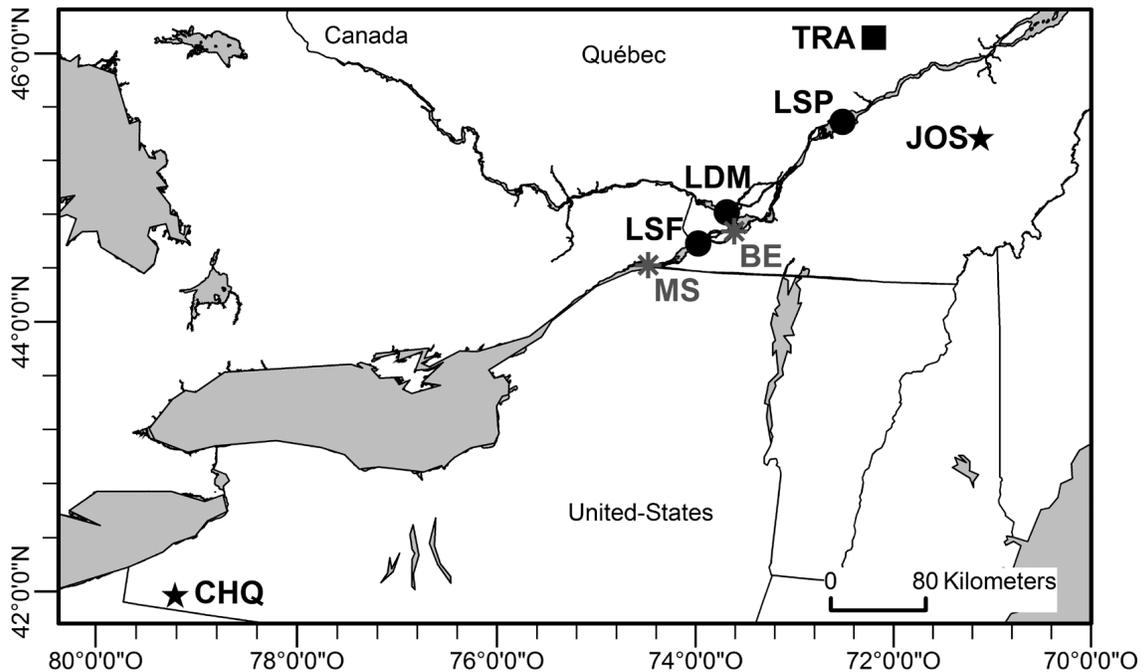


Figure 1.—Locations from which Muskellunge were sampled for genetic analyses, including three important St. Lawrence River angling sectors enhanced by historical stockings (Lake St-François: LSF; Lake des Deux-Montagnes: LDM; Lake St-Pierre: LSP), two source inland lakes used for stocking (Chautauqua Lake: CHQ; Joseph Lake: JOS) and a native inland lake that contains that has never been stocked (Traverse Lake: TRA). Two major physical barriers are present on the St. Lawrence system: Moses-Saunders (MS) and Beauharnois-Les Cèdres hydropower dams (BE).

and JOS; LSF and LSP; and LDM [abbreviations defined in Figure 1 caption]). Then, ADMIXTURE and DAPC analyses allowed us to detect a finer structure within the latter three groups and to evaluate introgression, thus defining five clusters (TRA, CHQ, JOS, LSF and LSP, and LDM). The majority of Muskellunge individuals could be clearly assigned to the putative population of their sampling location ( $\geq 97\%$  for four of six locations; Figure 2), which indicates that assignment tests can be used to trace fish provenance and should be useful for understanding stock structure and helpful for future management purposes. However, assignment was only 50% accurate for Mus-

kellunge from Lake St. François and 75% accurate for Lake St-Pierre (Figure 2).

In all analyses, we were unable to completely discriminate Muskellunge from the Lake St. François and Lake St-Pierre locations, even though they are separated by approximately 200 km and the large Beauharnois-Les Cèdres hydroelectric complex that is a significant barrier to movements. The observed similarity could reflect pronounced genetic exchange prior to the construction of the hydropower dams (1912–1961). Since relatively few generations have occurred since physical separation, it could be that populations did not have enough time to reach a new state of equilibrium that would better

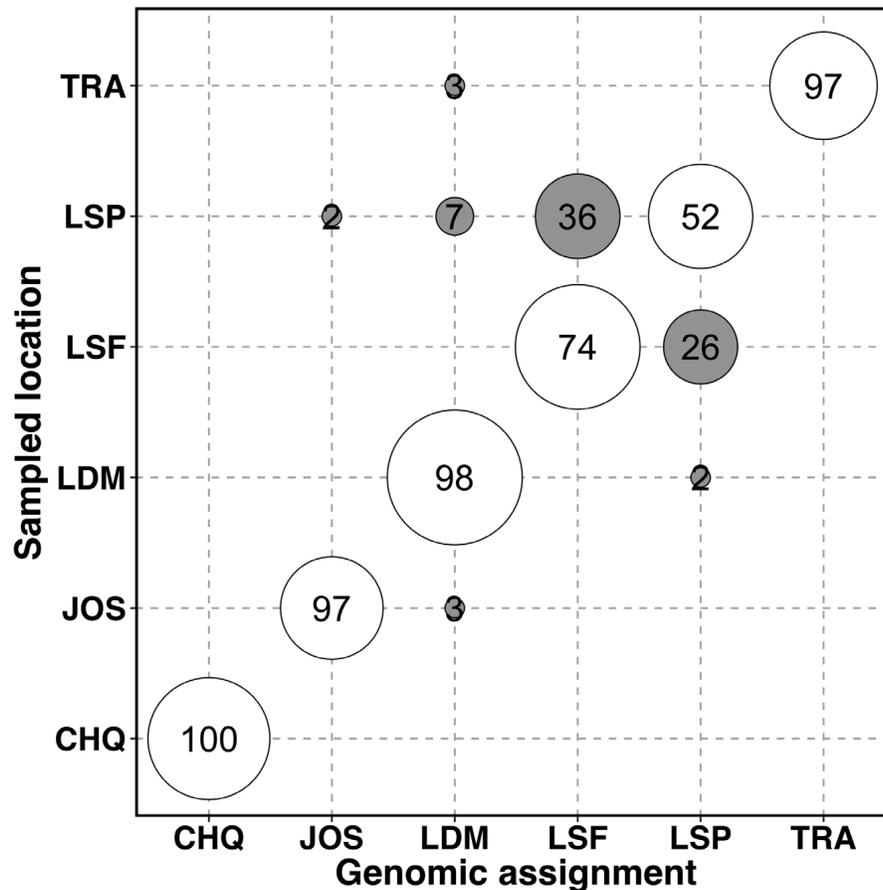


Figure 2.—Percentage of Muskellunge correctly (white) and incorrectly (gray) assigned to the location from which they were sampled. See Figure 1 for descriptions of location codes.

reflect the more limited contemporary gene flow. Alternatively, weak genetic differentiation between these two locations could represent current gene flow. This would involve long distance migration, for instance during reproduction, which would require fish being able to pass through or around the large dam complex. Adult Muskellunge have already been observed to pass through electric dams and other apparently impassable obstacles (e.g., Niagara Falls) where populations on either side of the obstacle showed no genetic differentiation (Kapusinski et al. 2013; Kerr and Jones 2017, this volume). Further support for potential connectivity between these two locations comes from known long-distance migration of spawning Muskellunge, where movements of nearly 100 km have been documented in the upper St. Lawrence River over short time periods (LaPan et al. 1996). It is also plausible that subadult Muskellunge disperse from upstream (Lake St. François) down to Lake St-Pierre, leading to high gene flow between the two populations.

Finer-scale analysis showed a clear distinction between the Lake des Deux-Montagnes location and both Lake St-Pierre and Lake St-François locations. This distinction could be linked to more-pronounced stocking impacts in the Lake des Deux-Montagnes location or to a lack of admixture between the Lake des Deux-Montagnes location and Lake St-Pierre and Lake St-François locations. This lack of admixture might be caused either by demographic (neutral genetic variation) or selective (adaptive genetic variation) pressures driving genetic variation between these sites. High spawning site philopatry in Muskellunge (Jennings et al. 2011) supports the hypothesis of demography driving genetic isolation. Alternatively, adaptive genetic variation could

be driven by variability in biotic and abiotic conditions caused by the encounter of distinct water masses originating from different tributaries and the presence of a deep navigation channel in the system (Hudon and Carignan 2008) that potentially can create a break in connectivity. Studies documenting genetic structure of Northern Pike *E. Lucius* (Ouellet-Cauchon et al. 2014) and Yellow Perch *Perca flavescens* (Leclerc et al. 2008) in the St. Lawrence system noticed a similar lack of gene flow between the south and north corridor of the river, supporting our second hypothesis.

More information regarding hybridization, habitat use, age structure, and adult and subadult movements is needed to discriminate between the alternative scenarios regarding observed structure patterns presented above. To complete the description of the genetic structure of the whole study area, we will analyze an additional 16 sampling locations of the St. Lawrence River, its tributaries, and unconnected lakes that are important angling waters. We will conduct more-detailed analyses of the potential impact of stocking on the genetic structure. Our results will be useful to identify the appropriate spatial scale at which fishery management and habitat protection measures should be applied. Ongoing studies led by the Ministry of Forest, Wildlife and Parks of Québec hopefully will fill other information needs, which are critical to a sound management of Muskellunge in the province.

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