Population connectivity and local adaptation in Lake Michigan yellow perch

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ABSTRACT:

Yellow perch (*Perca flavescens*) remain one of the most commercially and recreationally important fishes in the Great Lakes. Similar to many marine and other Great Lakes fishes, yellow perch have a 30-40 day pelagic larval stage as part of their life cycle. During this life stage, larval individuals can disperse hundreds of kilometers or return to their natal population through a combination of passive and active mechanisms (e.g., currents, behavior). This project aimed to identify the extent to which local populations of yellow perch in Lake Michigan are open versus closed at both ecological (population connectivity) and evolutionary (local adaptation) time scales. We used a combination of phenotypic, genomic, and model-based approaches to examine patterns of population connectivity and local adaptation. We first sampled 960 yellow perch from 20 sites circumscribing Lake Michigan. Using a combination of RAD-Seq, biophysical modelling, and eco-genetic modelling we first characterized patterns of population connectivity in Lake Michigan. By far the best predictors of genetic differentiation were connectivity matrices that 1. came from a specific week and year, and 2. resulted in high population connectivity. Thus, these narrow windows of time during which highly dispersive currents occur are driving the patterns of population connectivity in this system. We also found that populations from the northern and southern main basin are slightly divergent from one another, while those from Green Bay and the main basin are highly divergent (FST = 0.11). We next used whole-genome sequencing (~ 12x coverage) on 210 perch sampled from 7 populations. We again found that Green Bay populations are highly divergent from main basin populations. We also included an additional population, Muskegon, which is a drowned river mouth population, and found it to be equally divergent from main basin populations as Green Bay (FST = 0.10). We found substantial genome wide evidence of large, contemporary demographic declines of main basin yellow perch populations that have most likely occurred over the past 200 years. We cannot disentangle the various drivers of those declines (e.g., overfishing, abiotic changes), but the reduction in effective (and almost certainly census) population sizes should be of conservation and management concern. Lastly, after accounting for variation in body size, we found that females inhabiting larger lakes, such as the main basin of Lake Michigan, consistently produced smaller eggs than those in smaller lakes. In summary, we found that main basin yellow perch have high population connectivity, particularly in the southern portion of the lake, while populations from Green Bay and Muskegon Lake are genetically divergent and should be managed separately. There may also be some utility to managing northern and southern main basin perch populations as having lower levels of population connectivity. We also found strong signatures of large, contemporary demographic declines from genome-wide data in main basin populations that suggest that careful management actions are needed.