Evaluating the integration of genomics-based mixed stock analysis into statistical catch-at-age model for lake whitefish stock assessment in Lake Michigan

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ABSTRACT:

Understanding stock compositions in complex mixed-stock fisheries can help direct fishing effort away from vulnerable stocks. Moreover, incorporating stock-specific harvest rates inferred by mixed stock analyses into statistical catch-at age modeling (SCAA) models would improve managers' capacity to achieve such stock-specific sustainable management regimes. Our objective was to determine the spatiotemporal patterns of lake whitefish stock mixing throughout Lake Michigan and integrate our mixed stock analysis into 'mixture-informed' SCAA modeling. We applied a newly developed genotyping-in-thousands (GT-seq) panel containing 472 single nucleotide polymorphisms (SNPs) to conduct genetic stock identification (GSI). Using GSI, we quantified contributions from each of six genetically distinct stocks in 44 collections of mixed stock samples from throughout Lake Michigan collected from 1977-2022. Variable mixing was observed between years and seasons within a year for some management zones, with the largest variations in northeast Lake Michigan. Although at varying rates, lake whitefish originating from genetic management zone (GMZ)1N (Northern Green Bay and east Door County) were present in every mixed stock sample across all years of collection and management zones indicating high rates of dispersal. Seasonal mixing rates reflected philopatric behavior with more fish from local genetic stocks being captured in samples closer to the fall spawning season in four management zones (WFM-01, WFM-02, WI-01, WI-02). Based on the variable mixing rates observed within fishery samples we recommend the re-evaluation of stock mixing every few years to follow stock behavior more closely. Additionally, larger sample sizes (n ≥ 100) supported less variable mixing proportion estimations compared to smaller sample sizes. We successfully developed mixture-aware SCAA models to generate stock-specific harvest estimates; however, comparison to existing models proved difficult due to issues with current models identified during this research. Importantly though, this work catalyzed porting of existing SCAA models to a new platform following discontinuation of the previously used software, AD Model Builder. Understanding lake whitefish stock mixing rates using modern, cost-effective genetic tools will improve fisheries management and the ability to make commercial quota decisions based off stock mixing.