Chapter 1 – Project Background, Introduction, Acknowledgements, Abstract

Overview of delta smelt

tktkt

Methods of genome assembly

tktktk

Genetic diversity & effective population size

tktktk

Sex determination in teleost fish

tktktkt

Abstract

Acknowledgements

The abundance of delta smelt (*Hypomesus transpacificus*) has been in decline for decades1,2. Genetic tools have been useful for several management concerns: monitoring overall diversity and effective population size () in the wild population, genetic management in the captive population, developing assays to detect hybrids between delta smelt, wakasagi, and longfin smelt, and developing assays for eDNA sampling or species identification3–5. Attempts at quantifying in the wild population have been hampered by several interacting factors including a lack of power from using microsatellite markers and a very large historical 6,7. In order to improve estimates of , we assembled the delta smelt genome. We then leveraged the genome to estimate contemporary and the loss of genome-wide diversity between 1993 and 2020, interrogate domestication selection, and search for a sex marker. While is useful for monitoring purposes, we strongly advice against the use of alone for making management decisions.

For this project our tasks were to: 1) assemble a high-quality reference genome for delta smelt that is publicly available for all researchers, 2) estimate contemporary effective population sizes () for the wild 2017 to 2019 birth year cohorts of delta smelt, 3) search for genetic evidence of domestication selection across the genome, and 4) search for sex-specific markers and/or chromosomes in delta smelt. In order to obtain a more comprehensive understanding of through time, we have expanded Task 2 to include analysis of historical datasets of delta smelt dating back to 1995 and samples collected from 2020. The status of each deliverable is listed in Table 1. We have divided this final report into 4 sections, each with its own background, methods, results and discussion, followed by a final conclusion integrating our findings.