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Intro

Genetic underpinnings may contribute to any aspect of life history, ecology and physiology. Therefore developing genomic resources and maintenance of genetic diversity within the species are key components to

genetic diversity = closely tied to the evolutionary capacity for adaptation to environmental change

phenotypic variation to allow for a broad respond to climatic factors deeply influencing the Delta. Three key components to

of basic ecology is phenotypic variation; thus, maintenance of genetic diversity is essential as it is tied to the evolutionary capacity for adaptation to environmental change. To assess genetic diversity within delta smelt, contemporary and historical effective population size estimates were made using 2318[tk] samples from 25[tk] generations.

Conservation of genetic diversity within the species will require several components, including an assembled genome to allow for fine-scale genomic change, quantifying genetic diversity through time, and identifying loci to assist in non-lethal monitoring methods of population dynamics, such as sex ratios, of the species.

genetic resources for and monitoring genetic diversity within delta smelt is a critical step to aid in research efforts for making informed decisions to manage this imperiled species. Resource development requires genomic tools for

The abundance of delta smelt (*Hypomesus transpacificus*) has been in decline for decades8,9. 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 identification10–12. 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 2,13. 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.