Chapter 1 – Project Background, Introduction, Acknowledgements, Abstract

**Abstract**

Delta smelt (*Hypomesus transpacificus*) is a federally threatened and state endangered fish endemic to the San Francisco estuary. The species is a small, pelagic, mostly annually reproductive fish with freshwater resident, migratory, and semi-migratory life histories [tk Campbell et al 2022]. They have previously been thought of as an indicator species for the health of water quality in the Delta and the species has undergone a population collapse associated with drought and anthropogenic effects [tk CITE] where pelagic productivity and water temperature are primary drivers of condition indices ultimately affecting fitness [tk Hammock 2022]. It is now believed stochastic processes may push the species to extinction.2,3 Meaningful conservation management of the species must encompass gaining a better understanding of the life history, ecology, and physiology of the species to effectively preserve biological components contributing to success in the wild. Because genetics, in combination with the environment, influence many aspects of individual and population level phenotypes, building a framework to better understanding the species requires development of genetic resources and monitoring of genetic diversity. Chapter one of this dissertation presents two chromosome-level genome assemblies one male and one female –– invaluable resources for current and ongoing research within delta smelt. Chapter two investigates three novel methods for identifying sex marker(s) within the delta smelt genome. While no specific sequences diagnostic of sex were found, sex-specific discrepancies in kmer were identified. Chapter three uses restriction site-associated DNA sequencing (RADSeq) of \_\_tk\_\_ delta smelt from\_\_tk\_\_ generations to monitor contemporary and historical effective population size, a metric diagnostic of genetic diversity, through time. Results show a sweeping and significant decrease in genetic diversity within wild delta smelt since 1993. This work contributes narrowly to delta smelt monitoring, management, and research as well as to the broader comparative biology community. To date, the assembled delta smelt genome is the first chromosome-level and least fragmented publicly available assembly within the *Osmeridae* (smelt) family. Examination of male and female sequencing data shows a discrete difference between sexes and pushes the marker forward to establish the need for further investigation. Contemporary and historical declines in effective population size support the need for effective conservation management to prioritize preserving genetic diversity as a component of management. Together these components provide necessary research objectives for pushing evolutionary biology and delta smelt management forward.

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This dissertation, like all my published work, is dedicated to Philia.

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**Overview of delta smelt**

In the San Francisco Estuary (SFE), many once abundant native pelagic fishes, such as delta smelt, have undergone broad declines in population size.1 The SFE is a dynamic ecosystem encompassing 1,000 square miles of open water and wetlands in Northern California (Figure 1). Since the Sacramento-San Joaquin Delta (the Delta) became the primary distribution hub of California’s water supply in the 1960’s, the composition of SFE has been heavily altered by anthropogenic activity. Agriculture, water delivery, shipping, and urban development have spurred changes in the way water is distributed throughout the estuarine environment.

Delta smelt is a native species to the SFE which has undergone a population collapse associated with drought and anthropogenic effects. It is now believed stochastic processes may push the species to extinction.2,3 They are a small (6 - 9cm), translucent, semi-anadromous species that migrates between fresh and saline water and reproduces annually.4 Delta smelt are part of the Osmeridae family which represent a prosperous food source for human consumption in Japan, Europe, and North America, and have declining populations worldwide.3,5,6 Because of their annual life cycle and rapid response to conditions of their ecosystem, delta smelt are considered an indicator of the overall health of the SFE ecosystem. Once abundant and widely distributed throughout the SFE, the delta smelt population has been declining since the 1980s.7 Delta smelt have been listed as threatened under the Federal Endangered Species Act (ESA) since 1993 and endangered under the California ESA since 2009. As a result of their continued decline, resource management agencies actively monitor abundance in the wild population.

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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.