Chapter 1 – Abstract, Acknowledgements, Project Background, Outline

**Abstract**

Delta smelt (*Hypomesus transpacificus*1) is a federally threatened and state endangered fish endemic to the an Francisco Estuary and Sacramento-San Joaquin Delta of North America (SFE). The species is a small, pelagic, mostly annually reproductive fish with freshwater resident, migratory, and semi-migratory life histories2,3. They have previously been thought of as an indicator species for the health of water quality in the SFE. The species has undergone a population collapse associated with drought and anthropogenic effects, and it is now believed stochastic processes may push the species to extinction4,5. 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 understand the species requires the 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 –– which are invaluable resources for current and ongoing research within delta smelt, and evolutionary and conservation genetics. 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 for both measurements within wild delta smelt since 1993. This work contributes to the broad comparative biology and conservation genetic communities, and specifically to delta smelt monitoring, management, and research. To date, our assembled delta smelt genomes are the first to provide male and female specific assemblies, are the first chromosome-level and least fragmented publicly available reference genomes within the *Osmeridae* (smelt) family. Examination of male and female sequencing data shows a discrete difference between sexes and establishes a framework 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 within the cultivated refuge population. Together these components provide necessary resources and research objectives for moving evolutionary biology and delta smelt management forward.

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

Lastly, I would like to acknowledge the adorably derpy *Hypomesus transpacificus,* I am sorry humanity has failed you and I thank you for the few individuals I sacrificed to make this work possible. Perhaps in another universe you are thriving.

**Background of the SFE & delta smelt**

The SFE is a dynamic ecosystem encompassing 1,000 square miles of open water and wetlands in Northern California. Since the area 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. State and federal agencies routinely monitor the relative abundance of fish in the SFE with initiatives like the California Department of Fish and Wildlife (CDFW) Fall Midwater Trawl Survey which began in 1967. Similar to many other estuarine ecosystems throughout the globe6–8, within the SFE many once abundant endemic pelagic fishes, such as delta smelt, have undergone broad declines in population size9,10.

Delta smelt are a small (6 - 9cm), translucent, semi-anadromous species that migrates between fresh and saline water and reproduces annually12. 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 experienced declining populations worldwide1,5,13. Because of their annual life cycle and relatively rapid response to the conditions of their habitat, delta smelt are considered an indicator of the overall health of the SFE ecosystem. Once one of the most abundant and widely distributed fish species in the SFE, delta smelt numbers have been declining since the 1980s14 (Figure 1.1). The species was listed as threatened under the Federal Endangered Species Act (ESA) in 1993 and endangered under the California ESA in 2009. Pelagic productivity and water temperature have been shown to be primary drivers of condition indices ultimately affecting the delta smelt’s fitness11 and it is now believed stochastic processes may push the species to extinction4,5. As a result of their continued decline, resource management agencies, such as CDFW, continue to actively monitor the distribution and abundance of the wild population, and the Genomic Variation Laboratory genetically manages a genetically focused breeding program within a refuge population at the UC Davis Fish Conservation and Culture Laboratory (FCCL).

**Tables & Figures**

Chart, histogram

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**Figure 1.1.** CDFW annual Fall Midwater Trawl delta smelt catch numbers (indices) from 1967 to 2021. CDFW did not sample in 1974 and 1979. Indices taken from CDFW publicly hosted dataset (https://www.dfg.ca.gov/delta/data/fmwt/indices.asp).

**Outline**

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