Chapter 1 – Abstract, Acknowledgements, Project Background, Outline

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 histories1. 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 extinction2,3. 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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Background 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.4 The SFE is a dynamic ecosystem encompassing 1,000 square miles of open water and wetlands in Northern California. 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 endemic species to the SFE which has undergone a population collapse associated with drought and anthropogenic effects where pelagic productivity and water temperature are primary drivers of condition indices ultimately affecting the species’ fitness5. It is now believed stochastic processes may push the species to extinction2,3. They are a small (6 - 9cm), translucent, semi-anadromous species that migrates between fresh and saline water and reproduces annually6. 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 worldwide3,7,8. 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 1980s9. 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 of the wild population, and the Genomic Variation Laboratory genetically manages a breeding program within a refuge population at the UC Davis Fish Conservation and Culture Laboratory (FCCL).

Outline

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