Saving San Francisco Bay-Delta Native Fishes: Hatchery Management and Reintroduction Strategy Modeling

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Native fishes in the San Francisco Bay-Delta and Central Valley have recently seen a drastic decline in abundance, resulting in an increasing need to bring these fish into conservation hatcheries to prevent their extinction. A number of mandated hatchery-related projects exist in the Central Valley as part of NOAA Fisheries and US Fish and Wildlife Biological Opinions. Current and proposed hatchery operations make it imperative that we study appropriate genetic management, as planning for hatchery genetic management is necessary to determine the best management strategies that account for possible reintroductions and dynamics between hatchery and wildfish populations. Ideally, fish hatcheries would be managed to promote the long-term genetic and demographic viability of their populations, but genetic management is often lacking due to logistical constraints. Many captive fish populations accumulate detrimental genetic changes that decrease the genetic integrity of wild populations when their stocks are used for reintroduction. To improve fish hatchery management and reintroduction success, this study evaluates three methods of incorporating molecular data into hatchery management plans and their utility in preserving the genetic integrity of wild supplemented populations in the context of hatchery activities in the San Francisco Bay-Delta and Central Valley. Methods of molecular data incorporation include pedigree reconstruction and molecular relatedness estimation. Individual-based demogenetic simulations are used to model hatchery genetic management strategies for four proposed hatchery species and three species currently captively-bred in the San Francisco Bay-Delta. As hatchery genetic management is a relatively contemporary idea, in addition to improving the logistics of hatchery genetic management, this study aims to establish a new culture of hatchery management, which should incorporate considerations of the genetic health of both captive and wild populations in the San Francisco Bay-Delta.

Keywords: Fish hatcheries, modeling, individual-based model, simulations, genetic management, pedigree reconstruction

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Genetic Analysis of Natural and Hatchery Origin Steelhead in the Central Valley Reveals Population Structure and Odavdarigins

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Steelhead (*Oncorhynchus mykiss*) that spawn in the Sacramento, San Joaquin and their tributary rivers form the Central Valley Steelhead Distinct Population Segment (DPS), which is listed as threatened under the US and California Endangered Species Acts. There are four hatchery programs in the basin that produce steelhead, and two of the associated stocks, Nimbus and Mokelumne River, are excluded from the DPS, due to a past practice of using broodstock imported from other basins. We use a combination of different genetic markers and analytical techniques to elucidate the population structure and origins for Central Valley steelhead. We present data for 112 genes, a combination of single nucleotide polymorphism (SNP) and microsatellite markers, collected from almost all of the numerically significant populations of steelhead below barrier dams, as well as from many populations of resident trout above barrier dams. We describe analyses that help to understand both historical and present migration between populations and to define the genetic impacts of releases of both hatchery steelhead and rainbow trout in the Central Valley. The use of data from other steelhead DPSs in California further helps to unravel the effects of recent events from the long-term history of Central Valley steelhead. Additionally, analyses of approximately 4,000 adult returns to the four hatchery programs were analyzed with 95 SNP markers and the data used to understand migration between them and potential levels of inbreeding in hatchery mating. These genotypes serve as intergenerational genetic tags that form the basis for future ecological investigation of steelhead in the Delta, including evaluation of stock-specific rates of migration and their underlying genetic mechanisms.

Keywords: Steelhead, genetics, single nucleotide polymorphisms, hatcheries, genetic stock identification

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Estimates of Hatchery Contribution to California's Central Valley Chinook Salmon Populations: Results of 2010 and 2011 Coded-Wire Tag Recovery Data

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Annually, over 32 million fall-run Chinook salmon are produced at five hatcheries in California's Central Valley (CV). Production from these hatcheries contributes to a major ocean and inland fisheries and annual escapement. Until 2007, releases of fall-run Chinook were not marked and coded-wire tagged with consistency. Beginning with brood year 2006, a minimum 25% of production releases of fall-run Chinook have been adipose fin clipped and coded-wire tagged in the Central Valley Constant Fractional Marking Program (CFM). This program is a cooperative effort of the California Department of Fish and Game, Department of Water Resources, U.S. Bureau of Reclamation, U.S. Fish and Wildlife Service, East Bay Municipal Utility District, and Pacific States Marine Fisheries Commission. The remaining Merced Hatchery fall-run, Coleman Hatchery late-fall, and Feather River Hatchery spring-run Chinook are 100% marked and tagged. Coded-wire tags are recovered from adult fish in ocean and inland fisheries and inland escapement. 2010 and 2011 are the first years that the majority of fall-run Chinook recovered in harvest and escapement were marked and tagged at a minimum 25% rate. Brood years 2006-2009 were represented by age two, three, and four Chinook recovered in 2010 and 2011.

This work evaluates the 2010 and 2011 CV fall, late-fall, and spring-run Chinook coded-wire tag recovery data. Estimates of hatchery and natural proportions in escapement to the CV are reported in addition to estimates of hatchery contribution to ocean harvest. Stray and recovery rates as they pertain to release strategy are also reported.

Results of the CFM program, along with aging work will provide the best opportunity to manage CV Chinook based on scientifically defensible data. Age-specific rates of ocean harvest, maturation, survival, and straying can be calculated. Such analyses may provide the basis for changing hatchery practices, release strategies, and improving fisheries management.

Keywords: Chinook salmon, coded-wire tag, marking, hatcheries, fisheries management, salmon escapement

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Application of Genetic Methods to Salvaged Winter-Run Chinook Salmon

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Current monitoring methods at the South Delta export fish salvage facilities are insufficient for detecting and estimating loss of Endangered Species Act (ESA) listed salmonids. Current salvage monitoring is incapable of determining stock (race, tributary of origin) specific mortality, with long-term genetic information suggesting approximately 40% of the winter-run juveniles identified using length-date criteria are not actually winter run in origin. Additionally, salvage loss cannot be scaled to stock abundance, which is an ongoing issue under litigation. The fundamental inadequacies of current methods hinder establishing appropriate operation triggers (including real-time monitoring) and prevent us from effectively evaluating the efficacy of flow alterations, barrier operations, predator control and other conservation measures.

In coordination with Department of Water Resources, California Department of Fish and Game, National Marine Fisheries Service, US Fish and Wild Service, and other resource management agencies, we have implemented a pilot genetic monitoring program (2011 and 2012 water years) that will accomplish two objectives for South Delta export loss monitoring: 1) We will compare single nucleotide polymorphism (SNP) genotypes to reference allele frequencies to rapidly and accurately detect and quantify loss of natural origin winter-run Chinook salmon; and 2) As a pilot study, we will investigate whether the fraction of stock-specific juvenile production lost to South Delta water exports can be estimated using Parental Based Tagging (PBT) methods on natural-origin winter-run Chinook. As current regulatory actions associated with loss are derived from a length-at-date model (i.e., Delta Model), we will compare our direct observations from genetically-partitioned salvage loss to current regulatory take determinations. Further, the statistical importance of race determination method to the overall mathematical variability associated with loss estimation will be reported.

Keywords: Delta salvage, loss estimation, genetic monitoring, mixed-stock analysis, parental-based tagging

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Results of Parentage Based Tagging at the Feather River Hatchery: Pedigree Reconstruction and Ocean Tag Recoveries

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Hatcheries in California produce and release millions of juvenile salmon and steelhead annually. This production is intended to mitigate for the loss of natural spawning and rearing habitat due to the construction of large dams. Parentage based tagging (PBT) is a genetic method for identifying the origin and cohort of hatchery salmon, crucial information for modern stock assessment models that is currently supplied by the aging coded wire tag program. PBT takes advantage of the fact that every fish already has a uniquely identifying tag, its sequence of nucleotide variation, which is passed from one generation to the next. So by genotyping a single pair of parents, 100% of their offspring are "tagged", thereby providing age and source population when offspring are encountered in fisheries, ecological sampling or at escapement. PBT also produces pedigree information, which allows inference about the inheritance of life history traits, variance in reproductive success, domestication selection and inbreeding; all critical concerns of Central Valley hatchery programs.

This talk will briefly review the methodological considerations of implementing a PBT program. We will present the results of reconstructing multigenerational pedigrees of spring-run Chinook salmon sampled from 2006-2011 at the Feather River Hatchery. We will also demonstrate the PBT recovery of Feather River spring and fall Chinook in 2010 and 2011 mixed-stock ocean fisheries off of California. Having shown that PBT works, we will argue that widespread implementation of genetic tagging at California hatcheries can provide high quality data for informing management and conservation of the species.

Keywords: Chinook salmon, genetics, hatchery, Central Valley, parentage based tagging (PBT)

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