

Genetic population structure of Chinook salmon (*Oncorhynchus tshawytscha*) in
California's Central Valley.

**Final Report for CalFed Project “Comprehensive Evaluation of Population
Structure and Diversity for Central Valley Chinook Salmon”.**

John Carlos Garza¹, Scott M. Blankenship², Christophe Lemaire³ and Gregory Charrier

Institute of Marine Sciences, University of California, Santa Cruz, CA 95060, USA

and

NOAA Southwest Fisheries Science Center, Santa Cruz, CA 95060, USA

¹Corresponding Author: John Carlos Garza 110 Shaffer Rd Santa Cruz CA 95060

Tel. (831) 420-3903, fax (831) 420-3977, email: carlos.garza@noaa.gov

²Present address: Washington Department of Fish and Wildlife, Olympia WA.

³Present address: Université d'Angers, Angers, France.

Table of Contents

Table of Contents.....	i
Abstract.....	1
Introduction.....	3
Methods.....	7
Tissue collection and DNA extraction.....	7
Laboratory analysis.....	8
Genetic data analysis.....	9
Results.....	13
Genetic diversity.....	13
Genetic differentiation and phylogeographic analysis.....	14
Genetic Stock Identification.....	17
Discussion.....	21
References.....	36
Figures	
Tables	
Appendix A. Allele frequencies for all population samples	
Appendix B. Full assignment matrices by population sample	

Abstract

An understanding of genetic population structure is an important component of the biological information necessary to effectively formulate strategies for conservation or other management concerns. Molecular genetic data provide estimates of parameters such as population boundaries, historical relationships of populations, kin relatedness and current and historical gene flow. Chinook salmon (*Oncorhynchus tshawytscha*) are a dominant component of the ichthyofauna of California's Central Valley and are currently divided into 3 evolutionarily significant units (ESUs): fall/late fall-run, spring-run and winter-run. Previous studies have collected genetic data for the evaluation of population structure and relationships within ESUs, but very limited information is available on the relationship of populations of more than one ESU that occur in the same tributary river. Here we present a comprehensive evaluation of population structure for Central Valley Chinook salmon populations from all three ESUs. We use genetic data from 20 microsatellite loci, and compare population samples of adult Chinook salmon (N = 2613) from 13 Central Valley locations, as well as the Klamath River as an outgroup. The population samples include four comparisons between spring- and fall-run populations from the same watershed (Feather River, Mill, Deer and Butte Creeks). We also compare population samples taken from hatchery-returning and stream-spawning fish from 3 basins, and from fish sampled in consecutive years in 8 basins.

We report widespread population homogeneity within the fall-run, which indicates substantial recent gene flow between all sampled fall-run populations throughout the Central Valley, and subtle, but significant, differentiation of late fall-run from fall-run populations in the Upper Sacramento and Battle Creek. We also report substantial differentiation of the Merced River Hatchery fall-run stock. Phylogeographic analyses

demonstrate that the two primary remaining spring-run lineages (Butte Creek and Deer/Mill Creeks) are monophyletic, a relationship which had not been previously confirmed. Concordant with previous studies, the nominal “spring-run” from the Feather River are genetically fall-run, although there is subtle, but significant, differentiation between the two groups at the Feather River Hatchery. In addition, we find significant linkage disequilibrium in this population sample, but no others, supporting the hypothesis that it is a remnant of the ancestral Feather River spring-run that has been heavily introgressed with fall-run genes.

The phylogeographic analyses indicate that the spring-run and winter-run are more closely related to each other than either is to the fall-/late fall-run(s). It is unclear whether this is the true evolutionary relationship between these two temporal runs, or if it the result of hybridization of the winter-run in the 1990s. Both the tree analysis and tests of genetic differentiation demonstrate clear differentiation between spring-run and fall-run fish spawning in the same stream for Deer, Mill and Butte Creeks, and no evidence of recent gene flow or hybridization between them. In general, the results from our data indicate that run timing is more important than geography for describing genetic structure in the Central Valley, with spring-run populations from different basins more closely related to each other than are spring-run and fall-run populations from the same basin.

Introduction

Chinook salmon (*Oncorhynchus tshawytscha*) are found throughout the northern Pacific and spawn from Hokkaido, Japan to the Central Valley in California, USA. They reach the largest size of all the Pacific salmonids and have the greatest range in timing of entry into freshwater for reproduction (Healey 1991; Brannon et al. 2004). Chinook salmon populations in the California Central Valley are important in several ways 1) they are the southernmost native Chinook salmon populations, 2) there is greater diversity in timing of freshwater entry for reproduction than in any other part of the range, with 4 distinct temporal runs described historically, and 3) Chinook salmon from the Central Valley are the subject of major commercial and recreational fisheries, comprising the bulk of the salmon harvested off the coasts of California and Oregon. The four historically recognized runs of Central Valley Chinook salmon are classified by the seasonal timing of their freshwater entry and by their stream residence behavior (Healey 1991; Fisher 1994). The four groups of Central Valley Chinook salmon are referred to as winter-run, spring-run, fall-run, and late fall-run Chinook (Fisher 1994; Healey 1994). These groups have been defined as Evolutionary Significant Units (ESUs) for the purposes of management and conservation planning (status review), although the fall-run and late fall-run are grouped into a single ESU because of genetic similarity between them. Both the spring-run and the winter-run ESUs have been listed under the US and state Endangered Species Act (ESA) as threatened and endangered, respectively. These legal protections further emphasize the need for a clear understanding of population structure and evolutionary history.

Determining the magnitude and scope of genetic population structure - the distribution of genetic variation within and between populations and the relative levels of shared ancestry between them - is a fundamental component of evolutionary biology and ecology. Determining the current and historical genetic relationships between populations provides a context for understanding the evolution and maintenance of life history variation and also enhances the efficacy of conservation and management efforts, as well as the effectiveness of genetic monitoring (Bowcock et al. 1994; Beacham et al. 1996). For example, the accuracy of genetic stock identification for estimation of harvest impacts on exploited species depends upon an understanding of genetic population structure. In addition, identifying population boundaries, due to reductions in gene flow, is critical to understanding how populations accumulate local adaptations and become independent evolutionary units, since gene flow mediates the effects between natural selection and genetic drift. It is also crucial in understanding how population dynamics of different populations, runs, or stocks will respond to environmental changes, such as hydrological projects or hatchery operations, global climate change and harvest regulations. Therefore, identifying population genetic boundaries and relationships is critical, since they influence key parameters in biological conservation and management.

Pacific salmonids have been the focus of intensive study of genetic population structure because of their importance in recreational and commercial fisheries, as well as the conservation status of many populations. In addition, the life-history traits of anadromy and natal homing establish an obvious hypothesis about population structure of salmonid populations; that of a series of semi-isolated reproductive units, which may

accumulate local adaptation through the interaction of natural selection, genetic drift and migration (Utter et al. 1989).

The genetics of Chinook salmon have been extensively studied and large-scale genetic population structure for the species has been described primarily using allozyme (protein) electrophoresis data (Utter et al. 1989; Winans 1989; Bartley et al. 1992; Myers et al. 1998; Waples et al. 2004). Although allozyme data have been useful at defining the genetic relationships of the major genetic lineages and over broad geographic distances, the genetic information acquired from protein electrophoresis is generally insufficient to assess population structure within a watershed or between closely related populations (Waples et al. 2004).

In this study, we investigate population differentiation and genetic structure between Chinook salmon populations in California's Central Valley using nuclear microsatellite markers. Our primary objective is to describe population structure and the distribution of genetic variation for Central Valley Chinook salmon populations to help guide management and conservation efforts. A secondary objective is to develop a comprehensive baseline database that will support future research on stock identification, gene flow, effective population sizes, demographic trajectory and hatchery practices of California Chinook salmon. Previous genetic studies on Central Valley Chinook using markers other than allozymes have found genetic differentiation between the major ecotypes (Nielsen et al. 1994; Kim et al. 1999; Banks et al. 2000). Yet, due to limited sampling and information content of previous studies, questions remain about the population boundaries within ESUs and the interactions between ESUs. In order to address ongoing questions about the intricate population structure in the Central Valley,

we have surveyed a large number of Chinook salmon over their entire geographic distribution within the Central Valley using 20 high-resolution microsatellite markers. Of particular emphasis in this study is to assess the degree of interaction between spring-run and fall-run individuals that co-occur in the same drainage. We report measures of genetic diversity, genetic differentiation, phylogeographic relationships between populations and accuracy of identification of the ESU and population of origin for all individual fish.

Materials and Methods

Tissue collection and DNA extraction

Tissues from adult Chinook salmon were collected from 13 basins in the Central Valley, covering a geographic range that comprises the entire Sacramento-San Joaquin River watershed with current anadromous fish access (Figure 1). An additional population sample from the Klamath River in the northern coastal portion of California was included as a genetic outgroup. All of these basins are represented by samples taken from naturally-spawned fish and were therefore collected from carcasses. In addition, samples were taken from fish returning to hatcheries on the Merced, American and Feather Rivers. The Central Valley populations sampled include representatives from the fall/late fall-run, spring-run, and winter-run Evolutionary Significant Units (ESUs). All of the persistent late fall-run, spring-run and winter-run populations of large size, and most of the fall-run populations, are represented in the dataset. The dataset therefore provides a nearly comprehensive analysis of Central Valley Chinook salmon genetic population structure. Comparisons between spring and fall-run ESU populations co-occurring in the same basin were possible for four locations, Mill Creek, Deer Creek, Butte Creek, and Feather River Hatchery. Comparisons between nominal fall-run and late fall-run populations from the same basin were possible for the Upper Sacramento River and Battle Creek, which are the two tributaries with persistent late fall-run populations. With the addition of the Klamath River population, which is part of the Upper Klamath-Trinity Rivers Chinook salmon ESU, but includes both nominal fall-run and spring-run fish, a total of 2613 individual fish were studied. For the Central Valley, a total of 1748 fall-run, 683 spring-run (including those from the Feather River, but see below), 99 winter-run,

and 83 nominal late fall-run individual fish were studied (Table 1). All samples were collected in 2002 and 2003, except the winter-run samples, which were collected between 1995 and 2004 (Table 1). In an attempt to further evaluate the amount of temporal variation in population genetic composition, additional samples were collected from Central Valley Chinook salmon populations in 2004 and DNA extractions were performed. However, tissue quality was found to be very low and little reliable genetic data could be obtained, so these samples were not further analyzed or included in the study. All fish were sampled by staff from the California Department of Fish and Game by excising small pieces of tissue from the caudal fin of either carcasses or live fish (hatchery samples) and drying them on blotter paper. DNA was then extracted from dried fin clips using DNeasy 96 Tissue Kits (Qiagen, Inc) on a Qiagen BioRobot 3000.

Laboratory Analysis

All samples were genotyped with 20 highly variable microsatellite marker loci (Table 2), including genes originally isolated in five different salmonid species. Polymerase chain reaction (PCR) amplification was performed using 20 primer pairs that target these salmonid microsatellite loci. One primer was fluorescently end-labeled and PCR amplifications were performed in 15 μ L reaction volumes, with the following reagent concentrations: 1.5 μ L 10x PCR buffer (Applied Biosystems Inc.), 0.9 μ L $MgCl_2$ (1.5 mM), 0.6 μ L 10 mM dNTP mix (400 μ M final), 0.5 μ L 10 μ M primer mix (0.667 μ M final) and 0.15 units/ μ L *AmpliTaq* DNA polymerase (Applied Biosystems Inc.). Thermal cycling was conducted on Tetrad PTC225 thermal cyclers (MJ Research, Inc.) with the following thermal cycling conditions: 95°C (2 min); 30 cycles of 95°C for 30 sec., 20

sec. annealing, and 72°C for 30 sec.; a final 72°C extension for 2 minutes. PCR products were visualized by denaturing polyacrylamide gel electrophoresis on automated DNA sequencer (ABI 377, Applied Biosystems Inc.). Microsatellite allele lengths (fragment sizes) were estimated with Genotyper software (Version 2.1, Applied Biosystems Inc.). All genotypes were determined twice independently from the original gel data files and any discrepancies between first and second allele calls were resolved by mutual agreement of two readers. If mutual agreement was not achieved, no genotype was recorded. These discrepancies involved a very small percentage of the genotype dataset.

Genetic Data Analysis

An initial evaluation of differentiation of samples from the same basin in different years (2002 and 2003) was conducted by testing whether F_{ST} , the standardized variance in allele frequencies between the sample years, differed significantly from zero. This analysis used the Θ estimator of Weir and Cockerham (1984) and the permutation algorithm in Genetix (Version 4.05; Belkhir et al. 2004) to assess significance of values. All sample data from the same basin but different collection years that were not significantly differentiated were combined for further analyses. This resulted in combination of all temporal samples except those from the Battle Creek and Upper Sacramento River fall-run populations. The late fall-run populations from Battle Creek in 2003 and the Upper Sacramento River in 2002 were not differentiated, although they were both significantly different from all Battle Creek and Upper Sacramento River fall-run populations. They were combined for further analyses, because of small sample size, although no other populations from different basins were combined, even when they were

not significantly differentiated. In addition, winter-run samples from different years were combined because of small sample sizes and in an attempt to avoid siblings in the data.

To quantify levels of genetic diversity within populations, the observed number of alleles, allelic richness, observed heterozygosity and expected heterozygosity were calculated using FSTAT (Version 2.9.3.2; Goudet 1995) and GENETIX (Version 4.05; Belkhir et al. 2004). Since there was substantial missing data at some loci in some population samples, and to provide estimates of allelic richness based on the same number of sampled individuals (N=19) for all populations, Ar was calculated from only 16 loci in 5 fall-run populations (Table 1), whereas all others were calculated with all 20 loci genotyped in the study. To assess deviations from Hardy-Weinberg equilibrium, Fisher's exact test was used when there were less than four alleles per locus present in a population and when there were more than four alleles the Monte Carlo Markov chain method of Guo and Thompson (1992) was employed to provide an unbiased approximation of Fisher's exact test. The proportion of locus pairs in linkage (gametic phase) disequilibrium was also estimated. These methods were performed as employed in GENEPOP (Version 3.4; Raymond and Rousset 1995). Locus specific estimates of F_{IS} , according to Weir and Cockerham (1984), were calculated using GENETIX (Belkhir et al. 2004). Since a general trend of heterozygote deficiency was observed, we also evaluated whether the same locus consistently exhibited strong deficiencies across all populations using Kendall's concordance (Sokal and Rohlf 2003), to evaluate whether such deviations were due to problems with specific loci, or due to allelic dropout, as is commonly observed with carcass, and other degraded tissue source, samples.

Multi-locus estimates of F_{ST} , using Weir and Cockerham's Θ (1984), were calculated with GENEPOP (Version 3.4; Raymond and Rousset 1995) and statistical significance was assessed by 1000 permutations in GENETIX (Version 4.05; Belkhir et al. 2004). Phylogeographic analysis of population samples was conducted using the PHYLIP software package (Version 3.6; Felsenstein 2004). Two methods were used to build phylogeographic trees. First, a matrix of Cavalli-Sforza and Edwards' (1967) chord distance was calculated using the GENDIST component of the PHYLIP package (Felsenstein 2004). Then, the neighbor-joining algorithm (Saitou and Nei 1987) was used to construct an unrooted phylogeographic tree. Support for individual internal branches of the tree topology was assessed by taking 1000 bootstrap samples of the dataset, constructing a chord distance matrix and neighbor-joining tree for each one, then building a majority-rule consensus tree using the CONSENSE program of the PHYLIP package. Internal branch lengths on the consensus tree are scaled by the number of times that branch was found in the neighbor-joining trees constructed with the bootstrap samples, and is a measure of confidence in that branch. Only bootstrap values above 50% are generally reported. The second method employed is the maximum likelihood method of phylogeographic tree construction (Felsenstein 1981). Consensus trees were also constructed from likelihood trees constructed from 1000 bootstrap replicates.

Individual-based assignment tests were conducted on all population samples using the GeneClass 2 software package (Piry et al. 2004). In an iterative process, each individual is removed from the dataset and then reassigned to a 'most likely' population using the Bayesian allele frequency estimation procedure of Rannala and Mountain (1997). The proportions of individuals correctly assigned to the population of origin is then reported.

Assignment was only conducted for those individuals with data for at least 10 loci. Assignment analyses were performed in two ways, with each population sample separately considered as a source for assigned samples and with all populations for an ESU grouped as a source for assigned individual fish. The nominal “spring-run” from the Feather River Hatchery was excluded from most analyses because previous work has shown that it is genetically a fall-run population (Hedgecock et al. unpublished report).

Analysis of molecular variance (AMOVA; Excoffier et al. 1992) was conducted on the fall-run populations to determine whether there was any detectable geographic population genetic structure and was performed using the software program Arlequin (Excoffier et al. 2005). The population samples were divided into 3 groups by geography. The groups were South (S)-Merced, Toulumne and Stanislaus, Central (C)-Mokelumne, Consumnes and American, and North (N)-Feather, Butte, Deer, Mill, Battle, Upper Sacramento and Clear basins. Four different hypotheses about geographical structure were then evaluated, N+C vs. S, N vs. C+S, N vs. C. vs. S and N vs. S. The genetic variance was then hierarchically partitioned into components of Among Groups, Among Populations within Groups and Within Populations.

Results

Genetic diversity

Two types of genetic diversity measure were evaluated, metrics based on the number of allelic variants and those based upon the proportion of loci with more than one variant on the two chromosomes. Mean allelic richness (A_r), the numbers of alleles observed in a sample while controlling for differences in sample size, for each population sample is shown in Table 1. Mean allelic richness was similar for all populations except the winter-run, which had only about half the diversity of other populations. Aside from the winter-run, there were no clear patterns in genetic diversity, although the three naturally-spawning spring-run population values were among the five lowest. Because of substantially different sample sizes, the observed number of alleles is not as informative as allelic richness. However, the patterns observed were similar to those for allelic richness, with winter-run exhibiting the smallest number, fall-run the highest number and spring-run intermediate values (Table 1). Heterozygosity (H_z), both observed and expected, estimates the frequency with which two different alleles occur at a locus. Observed H_z is simply the proportion of chromosomes observed to have two alleles present within a population, while expected H_z is the proportion expected to have two alleles present in a population at mutation/drift equilibrium and with Hardy Weinberg proportions (Nei 1987). Observed H_z was similar in all populations, varying between 0.650-0.733, for all but the winter-run, which had observed H_z of 0.552. These values are somewhat higher than those in an earlier study of Central Valley Chinook salmon using microsatellite loci (Banks et al. 2000), but similar to those observed in Chinook salmon populations in other microsatellite-based studies (e.g. Beacham et al. 2003).

Evaluation of conformance to the expectations of Hardy-Weinberg equilibrium found that none of the populations were consistent with equilibrium expectations. The amount and direction of deviation from equilibrium is quantified by the parameter F_{IS} (Table 2). Deviations ranged from about 5 – 15%, all in the positive direction, which signifies fewer heterozygotes present than expected. Kendall’s concordance test yielded a coefficient $W = 0.30$, signifying that 70% of the deviation was from sample-related sources. This indicates that allelic dropout and not null alleles or other technical problems caused these slight reductions in the number of observed heterozygotes relative to those expected. The proportion of locus pairs exhibiting linkage disequilibrium is reported in Table 1. The proportion of loci expected to be in linkage disequilibrium by chance alone is 5%. Only three populations had a proportion greater than this, Butte Creek Fall, Klamath River and the nominal “spring-run” from the Feather River Hatchery. When the statistical significance threshold is adjusted for multiple tests, only the Feather River Hatchery “spring-run” population had significant linkage disequilibrium.

Genetic differentiation and phylogeographic analysis

Genetic data were available for two consecutive years (2002 & 2003) for multiple populations and temporal differentiation was evaluated with F_{ST} , the standardized variance in allele frequencies between populations. There was a total of 519 alleles observed at the 20 loci, or 26 alleles/microsatellite locus, and all of the allele frequencies in all of the population samples are found in Appendix A. There were generally few differences between temporal samples from consecutive years as measured by significant F_{ST} values. The only significant values were the Upper Sacramento and Battle Creek fall-

run populations, each of which had significant differentiation between 2002 and 2003 samples. Interestingly, these are also the two locations where the genetically-similar late fall-run salmon also occurs. In addition, the late fall-run population samples from the Upper Sacramento in 2002 and Battle Creek in 2003 were not differentiated, although both late fall-run populations were differentiated from the fall-run populations from both streams in both years (data not shown). Within the Central Valley fall-run, many populations from different locations were not significantly differentiated (Table 3). Feather River Hatchery “spring-run” fish were found to be genetic differentiated from Feather River Hatchery fall-run fish, although just marginally ($F_{ST}=0.0025$), as well from naturally spawning Feather River fall-run fish ($F_{ST}=0.0063$). The largest mean F_{ST} value for a population sample in this study was for Central Valley winter-run. However, F_{ST} values are heavily influenced by effective population size, and the resulting level of genetic diversity, as measured by allelic richness (Pearse et al. in press; Garza et al. submitted). As a result, there is a strong correlation between Ar and a population’s mean pairwise F_{ST} value to all other populations (with an $r^2 > 0.7$ in some datasets), such that populations with lower allelic richness are expected to have higher pairwise F_{ST} values. Central Valley winter-run Chinook salmon have only about half the variation as Central Valley fall-run salmon populations, and much of this differentiation is, therefore, directly due to genetic drift from small effective population size.

We used the genetic data to construct phylogeographic trees, which depict the phylogenetic relationship among the populations from which the data have been collected. We used both the chord distance/neighbor-joining method and maximum likelihood for tree construction. The phylogeographic analyses, which are shown in

Figure 3, generally corroborate the F_{ST} results. There is little genetic differentiation of Central Valley fall-run populations, resulting in a star-like tree topology and no highly significant groupings of internal structure as measured by bootstrap proportions. Nevertheless, the general topology of both the most likely trees and the bootstrap consensus trees from both methods did group together pairs of geographically proximate populations. For example, the Battle Creek 2003 and Deer Creek population samples cluster together with moderate bootstrap support in all analyses, as do the Upper Sacramento 2003 and the late fall-run population samples. In addition, all samples from the northern region of the Central Valley, except for Mill and Butte Creeks, generally cluster together, as do populations from the southern Central Valley and Delta region, although none of these higher-level groupings are with significant bootstrap support. A lack of close clustering relationships was also found between hatchery and naturally-spawned population samples for the three rivers for which both were sampled, the Merced, American and Feather Rivers, although they are all still relatively closely related. However, the Feather River Hatchery fall-run and “spring-run” stocks did cluster together with relatively high bootstrap support, reflecting high gene flow between them. As noted above, the late fall-run component of the ESU is nested within the cluster of fall-run populations, reflecting the lack of genetic distinction of the two temporal runs, either due to recent evolution of the late fall-run (or possibly the fall-run) or past and/or ongoing introgression between the two.

These analyses also find that the three genetically distinct spring-run populations are monophyletic, with the Mill and Deer Creek populations most similar and Butte Creek the most distinct of the three (Figure 3). As noted above, the Feather River Hatchery

“spring-run” is genetically fall-run. Additionally, we find that fall-run and spring-run fish in the same tributary river (Mill, Deer, Butte Creeks) are not closely related and do not appear to interact with each other reproductively any more than with fish from other tributaries (see below). All of the tree analyses also indicate that winter-run is more closely-related to spring-run than to fall-run. Finally, although it is difficult to infer in these unrooted trees, Klamath River Chinook salmon are the outgroup to all Central Valley Chinook salmon, as expected.

Genetic stock identification

Using individual assignment methodology, we evaluated the ability to correctly assign individuals to their ESU and population of origin (Table 4). Since there was a moderate amount of missing data, and only fish with data at 10 microsatellite loci or more were included in this analysis, a total of 2031 fish were used in these analyses. However, for most analyses and unless noted otherwise the Feather River “spring-run” was excluded from consideration, due to uncertainty about its ancestry, leaving 1796 fish for these analyses.

The overall accuracy of assignment to ESU for the dataset was 95.5%. When a 95% probability criterion was applied, the overall assignment accuracy to ESU was 98.5%. Overall assignment accuracy to population of origin for the dataset was very low, 37.2%, primarily because of near random assignment between many fall-run populations that were also not significantly differentiated (accuracy for fall-run only, 24.9%). When a 95% criterion was applied, this accuracy rose to 77.6%, although over 70% of fish remained unassigned. The full assignment matrices are found in Appendix B.

Examination of assignment accuracy for the fall/late fall-run ESU only found 96.5% accuracy for identification of presumptive fall/late-fall ESU fish to ESU of origin (Table 4a). Application of a 95% criterion increased this accuracy to 99.0% (Table 4b). When cross assignment between the genetically similar fall-run and late fall-run phenotypes was considered an error, then assignment accuracy for fall/late fall-run ESU fish decreased to 89.5% overall and to 91.1% for fall-run and 58.6% for late fall-run (Table 4a). Application of a 95% criterion increased this to 96.2% overall and to 97.3% and 64.9% for fall- and late fall-run fish, respectively (Table 4b). Within the fall/late fall-run ESU, assignment accuracy to ESU for individual populations ranged between 100%, for the Merced Hatchery, Butte Creek, Consumnes and American River populations, and 92.1% for the Upper Sacramento 2002 population (Table 4c). When the temporal runs were considered separately, the assignment accuracy ranged between 100% for the Merced Hatchery and 78.7% for the Upper Sacramento population (Table 4c). Application of a 95% criterion increased assignment accuracy to ESU to 100% for all populations except six, both the temporal samples from the Upper Sacramento and Battle Creek, as well as the Feather River Hatchery and Clear Creek population samples, which had accuracy that ranged from 93.2% and 99.2% (Table 4d). Assignment to temporal run using a 95% probability criterion also increased accuracy to above 95% for all population samples except at the two locations where late fall-run is known to occur persistently, the Upper Sacramento River and Battle Creek (Table 4d). Although the Feather River Hatchery “spring-run” was not included in most analyses (see above), in a separate analysis in which it was included (Appendix B), the assignment accuracy to population was 52.8% and this increased to 84.5% when a 95% probability criterion was applied.

There were only two (of 58) confident assignments of Feather River Hatchery “spring-run” populations to naturally spawned spring-run populations (Appendix B).

Assignment accuracy for presumptive spring-run ESU individuals was 88.8% (Table 4a). Since the “spring-run” from the Feather River Hatchery is genetically most similar to fall-run, there are 3 genetically spring-run populations. When these spring-run populations were analyzed separately, assignment accuracy was 79.1% for Deer Creek, 82.9% for Mill Creek and 97.7% for Butte Creek (Table 4c). Application of a 95% criterion increased the overall assignment accuracy for spring-run to 95.3% and the accuracy for individual streams to 84.6% for Deer Creek, 93.0% for Mill Creek and 100% for Butte Creek (Table 4d). Interestingly, there were no misassignments of fall-run fish from the three spring-run streams to the spring-run population occurring in that stream and only two misassignments of spring-run fish from the three spring-run streams to the fall-run population occurring in that stream, and neither of these were supported by the 95% probability criterion (Appendix B).

The Central Valley consists of two main sub-basins, the Sacramento and San Joaquin Rivers, that drain south and north, respectively, and meet in the Bay/Delta area. We divided the fall-run populations into two groups: San Joaquin (Merced, Tuolumne, Stanislaus) and Sacramento/Delta (all others) and evaluated whether fish from these two main sub-basins could be accurately assigned using this dataset. There was limited power to assign fish to the two sub-basins, with 87.9% of Sacramento River fish correctly identified but only 57.3% of San Joaquin River fish properly classified (data not shown). Application of a 95% criterion increased these values to 94.3% and 71.8% for the Sacramento and San Joaquin River sub-basins, respectively (data not shown).

The analysis of molecular variance (AMOVA) evaluation found that the vast majority (>98%) of the genetic variation was between individuals within populations (Table 5), which is the expected pattern for widespread species with substantial gene flow between populations. The proportion of variance between populations within groups was also significantly different from zero in all 4 hypotheses, although the proportion was only about 1%, indicating mild differentiation of populations. The proportion of variance partitioned between groups (N, C, S) was significant only for the N+C vs. S and N vs. C+S hypotheses (Table 5), indicating subtle structure separating northern and southern populations somewhere in the Central Valley Delta region. However, the proportion of variance partitioned at this hierarchical level is very small (<<1%), so this result may be due simply to sampling variance.

Discussion

The population genetic data collected and analyzed in this study offer insight into many aspects of Chinook salmon population structure, from the magnitude of genetic differentiation among Central Valley populations of different run timing, to the evolutionary relationships between geographic regions and ESUs within California's Central Valley. Central Valley Chinook salmon are the object of great interest both scientifically, because they are the southernmost extent Chinook salmon populations and have the greatest range of migratory timing, and from a management perspective, as two of the three ESUs are ESA-protected and the third, fall/late fall-run is the target of large commercial and recreational fisheries. Earlier population genetic work has laid the foundation for an understanding of Central Valley Chinook salmon population structure (Banks et al. 2000; Bartley et al. 1992; Myers et al. 1998; Nielsen et al. 1994). Our study is intended to extend this work through analysis of a larger number of hypervariable genetic markers, thereby providing greater power for use in genetic stock identification and for elucidating several specific questions regarding population structure, and greater coverage of Chinook salmon populations in the Central Valley, particularly the analysis of multiple phenotypic forms (i.e. temporal runs) in the same tributary rivers.

Our study includes data from most Central Valley Chinook salmon populations that are of large size and for over 2600 individual fish. We include all of the four generally recognized phenotypic life history forms present in the Central Valley. We also evaluate fall-run populations in all three of the tributaries where spring-run naturally spawn (Butte, Deer, Mill Creeks) and in the two main locations where late fall-run populations spawn (Upper Sacramento River, Battle Creek). In addition, the 20-locus microsatellite

dataset provides a much greater number of highly variable loci than any previous study of Central Valley-wide population structure and we estimate the frequency of over 500 alleles for our analyses. Such additional statistical power is particularly important when populations are closely related and/or are connected through high rates of migration.

Genetic distances, as measured by F_{ST} , between Central Valley Chinook salmon populations and ESUs are quite small for anadromous fish and are generally smaller than those observed for microsatellite data of other salmonid populations (e.g. Beacham et al., 2003; Garza et al. submitted). For example, mean pairwise F_{ST} between populations of coastal California steelhead and coho salmon are much greater than those between populations of fall-run Chinook salmon and between the 3 populations of spring-run Chinook salmon, and the mean F_{ST} value between ESUs of these two other species are also much larger than between these two ESUs (Garza et al. submitted, unpublished data; Bjorkstedt et al. 2005). Population differentiation is the result of two interacting forces shaping genetic variation: 1) time since population radiation, and 2) the magnitude of subsequent gene flow between distinct populations. It is difficult to disentangle these two issues, since recent divergence with no or limited gene flow and ancient divergence with subsequent gene flow produce similar genetic signatures.

There was a general lack of population structure and divergence between populations observed for Central Valley fall-run Chinook. Nearly 30% (25 of 105) pairwise F_{ST} values between naturally-spawned fall-run populations were not significant, including comparisons between populations at opposite ends of the Central Valley (Merced River and Battle Creek; Table 3). The mean F_{ST} value between naturally-spawned populations was 0.005, or only about one half of one percent of all variation partitioned among

populations within the ESU. The greatest differentiation observed was in Clear Creek, which had a mean pairwise F_{ST} value with other naturally-spawned populations of 0.011, or more than twice that of the mean for all population comparisons. Clear Creek is the only east-flowing Central Valley tributary analyzed in this study, and one of the only such tributaries with Chinook salmon spawning activity, but the cause of this differentiation is unknown. In addition, AMOVA results indicate that the San Joaquin River sub-basin populations are subtly differentiated from fall-run populations further to the north in the Sacramento River sub-basin. However, it is unclear whether this differentiation has biological meaning or is simply the result of sampling variance and the somewhat substantial differentiation of the Merced River Hatchery population.

The general lack of population structure within the widely distributed fall-run, as indicated by the numerous non-significant F_{ST} values and star-like radiation of fall-run population branches on the phylogeographic trees in Figure 3, is likely at least partly due to the practice of trucking juvenile fish to the San Francisco Bay estuary by several Central Valley hatcheries and the consequent migration (straying) upon return. Coded wire tag data indicates that hatchery salmon stray widely throughout the Central Valley (T. McReynolds & R. Benthin, CDFG, pers. comm.). This practice is intended to limit predation on smolts in the Bay/Delta region, but may be limiting opportunities for local adaptation of Chinook salmon within the Central Valley, by increasing gene flow.

We also examined four hatchery stocks by sampling adults from the Merced River Hatchery, Nimbus (American River) Hatchery and the Feather River Hatchery, where we genotyped both fall-run and “spring-run” stocks. Samples from naturally-spawned populations in these three rivers were also examined (Table 1). Naturally spawned fish

were genetically differentiated from the hatchery stocks from the same tributary river in all of the cases, and were not more genetically similar to them than to other fall-run stocks, as measured either by F_{ST} (Table 3) or by clustering on the phylogeographic trees (Figure 3). However, the mean pairwise F_{ST} values for the three hatchery stocks from the American and Feather Rivers ($F_{ST}=0.004-0.007$) were similar to those for other fall-run populations (mean pairwise $F_{ST}=0.005$), indicating that they are not highly divergent from other Central Valley fall-run Chinook salmon.

In contrast, the Merced River Hatchery stock was the most divergent of any of the fall-run population samples examined, with a mean pairwise F_{ST} of 0.028 with the naturally-spawned fall-run populations, which exceeds even the value between spring and fall-run populations (mean pairwise $F_{ST} = 0.021$). This differentiation is found at multiple loci, several of which have alleles present at over 25% frequency in the hatchery stock but are not present in the fish spawned in the Merced River and are nearly absent from the Central Valley, indicating that this divergence is not a technical artifact. The cause of this differentiation is not known, but may be due to past hybridization with a divergent Chinook salmon stock. However, the phylogeographic trees (Figure 3) and the F_{ST} analyses do not indicate a genetic signature of hybridization with fish from any other Central Valley ESU or the Klamath River, as the Merced Hatchery clusters with other fall-run populations in the trees and has even higher F_{ST} values to these other ESUs than to other fall-run populations. It is also possible that there has been strong natural selection acting on this stock and that the genetic markers with substantial frequency differences are in linkage disequilibrium with genes under such selection, although this is unlikely if non-hatchery fish are regularly or occasionally used as hatchery broodstock.

In addition, we found differentiation between population samples of fall-run and late fall-run Chinook salmon from the upper Sacramento Valley. Late fall-run salmon were historically described as a substantially distinct phenotypic variant of Central Valley Chinook salmon (Fisher 1994). However, early genetic work (see Myers et al. 1998) found a lack of genetic differentiation between fall-run and late fall-run fish. When ESUs were designated for Central Valley salmon and considered for ESA listing by the NOAA-led Biological Review Team, the two temporal runs were combined into one ESU and not listed because of the abundance of fall-run salmon. As noted above, when there is a lack of genetic divergence between phenotypically distinct groups or subpopulations, it is hard to disentangle recent gene flow or introgression between populations that were formerly partially or completely isolated and phenotypic divergence in the absence of reproductive isolation. One of the few testable predictions of these two alternative hypotheses is that secondary contact and introgression will generate linkage disequilibrium that may be detectable if not too many generations have elapsed since initial introgression. We found no such linkage disequilibrium in late fall-run populations or the fall-run populations with which they would potentially interbreed (Battle Creek, Upper Sacramento), indicating that this similarity is not due to a recent increase in gene flow between them. In addition, we did find slight but significant differentiation between fall-run and late fall-run populations from Battle Creek and the Upper Sacramento. The late fall-run samples from both sites were combined because of small sample size issues and because they were not significantly differentiated, in spite of the fact that they were from different sites and different years. However, they were significantly differentiated, both separately and combined, from all fall-run populations, including those in the same rivers. Interestingly,

the only temporal samples from the same tributary river in consecutive years that had significant differentiation were the two sites with late fall-run fish present, Battle Creek and the Upper Sacramento. This may be due to the presence of late fall-run fish in some of these population samples.

In contrast to the genetic similarities between Central Valley fall-run Chinook salmon populations, phylogeographic analysis (figure 3) clearly shows that the three naturally-spawning spring-run populations are genetically distinct and monophyletic. Previous work by Banks et al. (2000) with microsatellite allele frequencies also found that these three spring-run populations are distinct, but did not determine whether they were monophyletic. Of the three naturally-spawning spring-run populations, our data found a closer relationship between Mill and Deer Creek than either of them had with Butte Creek. This close relationship is concordant with the finding of Banks et al. (2000), although we did find significant, albeit modest, genetic differentiation between them ($F_{ST} = 0.005$), whereas they found genetic “homogeneity”. We also found the Butte Creek spring-run population to be among the most distinct Chinook salmon populations in the Central Valley. We therefore confirm the earlier finding of two major spring-run Chinook salmon lineages, the first Butte Creek and the second the Deer Creek/Mill Creek complex. In addition, there are multiple tributary rivers (e.g. Clear, Antelope, Cottonwood, and Big Chico Creeks) where small numbers of fish generally return earlier than fall-run fish and are suspected to be spring-run. We were not able to analyze any of these groups in this study, but future investigation should attempt to evaluate whether these are genetically spring-run fish and, if so, whether they pertain to one of the two known spring run lineages or are remnants of others, since the spring run is believed to

have been widespread and abundant before the 20th century wave of extirpation (Lindley et al. 2004).

Evaluation of the Feather River Hatchery “spring-run” found that it is genetically most similar to the Feather River Hatchery fall-run stock, as indicated both by clustering on the phylogeographic trees and by comparison of F_{ST} values, and is nested within the fall-run group of populations in all analyses. F_{ST} values between the Feather River Hatchery “spring-run” and naturally-spawned spring-run are in the low end of the range of values for fall-run populations to spring-run populations, but not the lowest. In addition, they are the essentially the same as those of Feather River Hatchery fall-run to spring-run populations. This demonstrates convincingly that the Feather River Hatchery “spring-run” stock is dominated by fall-run ancestry. However, we also found very slight, but significant, differentiation between the two Feather River Hatchery stocks, which is concordant with the results of Hedgecock et al. (unpublished study) on these stocks. In addition, we found a strong signal of linkage (gametic phase) disequilibrium, absent in all other population samples, in the Feather River Hatchery “spring-run” stock (Table 1). We interpret this as evidence that the FRH "spring" run retains remnants of the phenotype and ancestry of the Feather River spring-run that existed prior to the dam and hatchery, (as opposed to representing a hatchery selection-created and maintained phenotypic variant), but that has been heavily introgressed by fall-run fish through some combination of hatchery practices and natural hybridization, induced by habitat concentration due to lack of access to spring-run habitat above the dam. This suggests that it may be possible to preserve some additional component of the ancestral Central Valley spring-run genomic variation through careful management of this stock that can contribute to the

recovery of the ESA-listed Central Valley spring-run ESU, although it will not be possible to reconstitute a “pure” spring-run stock from these fish. We are planning experiments with pedigree reconstruction, haplotype evaluation, and linkage mapping to elucidate the genetic basis of phenotypic variation at the Feather River Hatchery, so as to facilitate the preservation and propagation of this spring-run-like stock, possibly through the application of marker assisted-selection.

We found winter-run Chinook salmon to be the most divergent population in our study, with F_{ST} values exceeding even those to Klamath River Chinook salmon. In fact, in a range-wide evaluation of Chinook salmon population structure (GAPS Consortium, unpublished data), Central Valley winter-run had the longest branch length (greatest divergence) of any of the 100+ populations in the study. However, F_{ST} values are strongly negatively correlated with allelic diversity (and therefore effective population size), as genetic drift can remove shared alleles and change allele frequencies quickly and dramatically during population bottlenecks and other reductions in effective size. The winter-run population has about one half the allelic diversity of other Central Valley Chinook salmon populations, and the population/ESU is known to have gone through a severe reduction in size in the early 1990s, when the number of returning adults reached a nadir of less than 200 fish. Most of this divergence is therefore due to extreme genetic drift and not extended evolution in isolation. This is reinforced by the finding in the range-wide study that winter-run cluster very closely with other Central Valley Chinook salmon populations and our finding that the winter-run genetic distance (F_{ST}) to the Klamath River outgroup is greater than to any Central Valley population (Table 3).

The three Central Valley Chinook salmon ESUs could either have separated at roughly the same time, or two of the three ESUs could be more closely related to each other, having diverged after the other group began the process of reproductive isolation. In our data, we find an unambiguous signal of closer ancestry between winter-run and spring-run than either group with the fall/late fall-run ESU (Figure 3). Hedgecock et al. (unpublished manuscript) reported hybridization of winter-run with spring-run fish at Coleman National Fish Hatchery in the early 1990s, but the data in that study (one microsatellite locus) could not distinguish between spring-run and fall-run fish. Subsequent efforts appear to have confirmed that these fish were Butte Creek spring-run (D. Hedgecock, pers. comm.). If this is indeed the case, then this hybridization might explain the clustering of winter-run and spring-run and would leave unanswered the question of whether winter-run evolved from spring-run, fall-run, or the common ancestor of the two ESUs. Extensive haplotype data that we have begun to collect should be able to resolve this question.

Aside from elucidation of population structure, one of the primary uses of such genetic datasets is for genetic stock identification (GSI), the classification of an individual to its population of origin. GSI is useful for estimation of stock composition of ocean or inland fisheries, ecological investigation of migration and life history, and for forensic investigations. Our data have substantial power for GSI with more than 95% of the fish accurately assigned to ESU of origin. Applying a 95% probability criterion brought assignment accuracy to nearly 99%. There was a bit more power for assignment to ESU for the fall/late fall-run (96.5%) than for the spring-run ESU (88.8%), although application of a 95% criterion brought both accuracy proportions above 95% (99.0% and

95.3% for fall/late fall-run and spring-run, respectively). The accuracy of assignment to ESU was high for all individual fall/late fall-run populations (92.1-100%), but a bit lower for spring-run populations (79.1-97.7%). Butte Creek spring-run fish were assigned with 100% accuracy when a 95% probability criterion was applied and Deer/Mill Creek fish were assigned with about 90% accuracy. Winter-run was identified with 100% accuracy either with or without a probability criterion, due to its drift-induced genetic divergence.

Assignment to populations within ESUs was considerably less powerful, particularly within the fall/late fall-run ESU, where accuracy was around 25%. This is not surprising given the broad lack of differentiation of fall-run populations. Application of the probability criterion increased accuracy to over 50%, but at a cost of leaving nearly 3/4 of the fish unassigned. Identification of late fall-run fish from this ESU to temporal run was also more difficult, with accuracy of 58.6%, which is only marginally better than random (50%). Application of the probability criterion increased this marginally to 65%, but this low accuracy is concordant with the very low level of genetic differentiation between the late fall-run and fall-run populations from the upper Sacramento River sub-basin.

Assignment of spring-run fish to population of origin was considerably more accurate, with 83.6% of fish correctly assigned to ESU also correctly assigned to population of origin. When the 95% probability criterion was applied, this rose to 97.3%, but only 54% of fish were assigned. Nearly all of the cross assignments were between Mill and Deer Ck, which is not surprising given the repeated finding (this study, Banks et al. 2000) of a close genetic relationship between spring-run populations in these two tributaries, which is presumably mediated by high contemporary gene flow. Nevertheless, the ability to assign fish to one of these two natal sites at accuracy that is considerably

greater than random (50%) contrasts with the conclusion of Banks et al. (2000) of genetic “homogeneity” of spring-run in these two streams. However, it is possible that some of this assignment power is due to cohort effects, or the presence of siblings in the baseline sample, which causes kin structure correlations that would not be present when assigning fish from other cohorts using this baseline. Evaluation of this possibility using samples from other cohorts should help to determine the extent to which kin structure contributes to this statistical power. Interestingly, we found no signal of hybridization between spring-run and fall-run in Butte, Mill and/or Deer Creeks, either in analyses of genetic distance (F_{ST}) or individual assignments. While occasional hybridization may occur, it does not appear to happen with a frequency that threatens the continued integrity of the two life history types in these three streams.

Overall, the dataset presented here provides considerable power for GSI, with nearly all samples assigned correctly to ESU, even without application of a probability criterion (which results in many fish not being assigned), and many to population as well. In particular, winter-run salmon are always correctly identified, as are Butte Creek spring-run. In addition, there is a possibility that some of the cross assignments are due to misclassification of fish in the baseline population sampling (e.g. fall-run fish classified upon field sampling as spring-run), as these samples were almost all collected from carcasses. Since the spring-run phenotype is not just a difference in timing of freshwater entry, but a suite of correlated phenotypic traits, and there is some overlap in temporal and spatial distribution of spring-run and fall-run fish, it is possible that this is a partial explanation for the less than perfect assignment accuracy that we achieve with GSI. It is also possible that it is due to gene flow/hybridization between the two runs, in which case

further increases in accuracy through application of more genetic data is unlikely to be successful and these results may then represent the limits of traditional, allele frequency-based genetic identification methods. Further refinement in accuracy will require parentage-based tagging (Garza and Anderson, in prep., see section on full parental genotyping in Hankin et al. 2005), which is not dependent upon genetic differentiation between stocks and has essentially unlimited power to assign individuals to population of origin with a sufficient sampling scheme (Anderson and Garza 2006). We are currently developing the molecular genetic and analytical tools necessary for application of this method and hope to begin applying them in the near future at the Feather River Hatchery and then eventually at all Chinook salmon hatcheries in California. This will be part of an integrated, life-cycle monitoring program that will rely on a shared database of genotypes from salmon bred at hatcheries, captured in ocean fisheries, sampled at weirs and fish ladders in the Central Valley, sampled in the Bay Delta region and recovered from carcasses collections. Such an integrated genetic monitoring system will provide unprecedented insight into everything from the genetic basis of age at maturation and run timing, to detailed information about the harvest of Central Valley fish throughout the northeastern Pacific region, since California Chinook salmon can constitute up to 20% of the catch in the Canadian troll fishery, according to GSI estimates from the Department of Fisheries and Oceans genetics lab in Nanaimo, British Columbia (Terry Beacham and Ruth Withler, pers. comm.).

The utility of GSI methods in many ecological and management-related investigations depends upon the genetic dataset, commonly referred to as a baseline, and the populations that it includes. Because of the broad geographic distribution of Central

Valley Chinook salmon in the ocean and its importance in fishery catches, we helped initiate and establish a consortium of federal, state and tribal laboratories from throughout western North America to create a standardized, range-wide, baseline genetic dataset of Chinook salmon populations. This group is referred to as the Genetic Analysis of Pacific Salmonids (GAPS) consortium and the 9 original cooperating laboratories have now created a huge, standardized, baseline dataset that includes data from nearly 200 Chinook salmon populations from Russia to the Central Valley and genotypes from nearly 20,000 fish at 13 microsatellite marker loci. The GAPS dataset is an enormously powerful genetic tool that is now being used to evaluate stock composition of commercial and recreational fisheries in California.

However, one of the consequences of the GAPS standardization and database construction process is that the 13 microsatellite markers that were chosen were ones that could be reliably analyzed in all of the participating labs. The GAPS process occurred concurrent with the work in this study and through careful coordination and integration of the GAPS effort (and at a non-trivial expense in staff time and supply costs) with our more detailed effort in the Central Valley, we were able to include 7 of the 13 GAPS microsatellite loci in the markers for this study. While the GAPS baseline dataset is very powerful for identifying divergent stocks of Chinook salmon, it lacks power for distinguishing fish from the closely related Central Valley stocks and we will add additional genetic markers to this dataset in the future. Future efforts will focus on single nucleotide polymorphisms (SNP) because of the prospect of low cost, high throughput genotyping and the ease of inter-laboratory standardization. The GAPS standardization process cost well over \$1 million in direct costs alone, so this is a strong incentive to use

SNP markers. We are currently developing and evaluating SNP markers in our laboratory for this purpose and have completed genotyping a subset of the samples described here with 22 SNP loci to augment the baseline database.

We also analyzed a gene of the major histocompatibility complex (MHC), Class 1 DRB, as part of this study, but technical difficulties related to tissue quality precluded its easy analysis. We could therefore not provide comparable data to analyze jointly with the microsatellite data here. Efforts to obtain informative data from MHC genes is ongoing and will be described in a future report.

Evolutionary Significant Unit (ESU) designations for Chinook salmon were determined by a combination of phenotypic, genetic and ecological data (Myers et al. 1998). Our finding on genetic population structure support these and are consistent with these ESU designations, possibly with the exception of the Feather River “spring-run”, which has predominately fall-run genotypes, although some spring-run ancestry appears to persist. In spite of the signal of high recent gene flow between the late fall-run and fall-run populations, there was a significant signal of differentiation between them, although not at the same scale as genetic differentiation between ESUs. This supports the importance of considering the late fall-run phenotype as a heritable component of diversity in the ESU, which is one of the four key parameters influencing viability of salmonid populations (McElhany et al. 2000).

Our results are concordant with the findings with upper Columbia River and Snake River Chinook, where genetic data supports classifying spring and fall ecotypes as different lineages (Myers et al. 1998; Brannon et al. 2004), but the question of whether the Central Valley Chinook salmon populations are all monophyletic remains open.

Acknowledgements

Celeste Gallardo, Amy Bouck, and Cheryl Dean provided invaluable laboratory assistance. Randy Benthin, Alice Low, Rich Dixon and Jennifer Navicky (California Department of Fish and Game) coordinated sample collection and cataloguing. Randy Brown (CalFed & California Department of Water Resources-deceased) and Gonzalo Castillo (US Fish & Wildlife Service) provided insightful discussion and advice. Funding for this project was received from the US Fish & Wildlife Service's Anadromous Fisheries Restoration Project, the California Department of Fish and Game and the National Oceanic and Atmospheric Administration's Southwest Fisheries Science Center.

References Cited

- Anderson, E.C., and J.C. Garza. 2006. The power of single nucleotide polymorphisms for large scale parentage analysis. *Genetics* 172: 2567-2582.
- Banks, M. A., M. S. Blouin, B. A. Baldwin, V. K. Rashbrook, H. A. Fitzgerald, S. M. Blankenship, and D. Hedgecock. 1999. Isolation and inheritance of novel microsatellites in chinook salmon (*Oncorhynchus tshawytscha*). *Journal of Heredity* 90:281-288.
- Banks, M. A., V. K. Rashbrook, M. J. Calavetta, C. A. Dean, and D. Hedgecock. 2000. Analysis of microsatellite DNA resolves genetic structure and diversity of chinook salmon (*Oncorhynchus tshawytscha*) in California's Central Valley. *Canadian Journal of Fisheries and Aquatic Sciences* 57:915-927.
- Bartley, D., B. Bentley, J. Brodziak, R. Gomulkiewicz, M. Mangel, and G. A. E. Gall. 1992. Geographic variation in population genetic structure of chinook salmon from California and Oregon. *Fishery Bulletin* 90:77-100.
- Beacham, T. D., K. J. Supernault, M. Wetklo, B. Deagle, K. Labaree, J. R. Irvine, J. R. Candy, K. M. Miller, R. J. Nelson, and R. E. Withler. 2003. The geographic basis for population structure in Fraser River chinook salmon (*Oncorhynchus tshawytscha*). *Fishery Bulletin* 101:229-242.
- Beacham, T. D., R. E. Withler, and T. A. Stevens. 1996. Stock identification of chinook salmon (*Oncorhynchus tshawytscha*) using minisatellite DNA variation. *Canadian Journal of Fisheries and Aquatic Sciences* 53:380-394.
- Belkhir K., B. P., Chikhi L., Raufaste N., and Bonhomme F. 2001. 1996-2001 GENETIX 4.02, logiciel sous Windows™ pour la génétique des populations. Laboratoire Génome, Populations, Interactions, CNRS UMR 5000, Université de Montpellier II, Montpellier (France).
- Bjorkstedt, E.B., B. Spence, J.C. Garza, D. Hankin, D. Fuller, W. Jones, J. Smith, and R. Macedo. 2005. An analysis of historical population structure for Evolutionarily Significant Units of Chinook salmon, coho salmon, and steelhead in the North-Central California Coast Recovery Domain. NOAA Technical Memorandum NMFS-SWFSC-382.

- Bowcock, A. M., A. Ruiz-Linares, J. Tomfohrde, E. Minch, J. R. Kidd, and L. L. Cavalli-Sforza. 1994. High resolution of human evolutionary trees with polymorphic microsatellites. *Nature* **368**:455-457.
- Brannon, E. L., M. S. Powell, T. P. Quinn, and A. Talbot. 2004. Population structure of Columbia River Basin chinook salmon and steelhead trout. *Reviews in Fisheries Science* **12**:99-232.
- Cairney, M., J. B. Taggart, and B. Hoyheim. 2000. Characterization of microsatellite and minisatellite loci in Atlantic salmon (*Salmo salar*) and cross-species amplification in other salmonids. *Molecular Ecology* **9**:2175-2178.
- Cavalli-Sforza, L. L., and A. W. F. Edwards. 1967. Phylogenetic analysis: models and estimation procedures. *Evolution* **32**:550-570.
- Excoffier, L., P. Smouse, and J.M. Quattro (1992) Analysis of molecular variance inferred from metric distances among DNA haplotypes: Application to human mitochondrial DNA restriction data. *Genetics* **131**:479-491.
- Excoffier, L., G. Laval, and S. Schneider. 2005. Arlequin version 3.0: An integrated software package for population genetics data analysis. *Evolutionary Bioinformatics Online* **1**:47-50.
- Felsenstein, J. 1981. Evolutionary trees from DNA sequences: a maximum likelihood approach. *Journal of Molecular Evolution* **17**:368-376
- Felsenstein, J. 2004. PHYLIP (Phylogeny Inference Package), Department of Genome Sciences, University of Washington, Seattle.
- Fisher, F. 1994 Past and present status of Central Valley chinook salmon. *Conservation Biology* **8**:870-873.
- Goudet, J. 1995. FSTAT (Version 1.2): A computer program to calculate F-statistics. *Journal of Heredity* **86**:485-486.
- Greig, C., D. P. Jacobson, and M. A. Banks. 2003. New tetranucleotide microsatellites for fine-scale discrimination among endangered chinook salmon (*Oncorhynchus tshawytscha*). *Molecular Ecology Notes* **3**:376-379.
- Guo, S.W., and E.A. Thompson. 1992. Performing the exact test of Hardy-Weinberg proportion for multiple alleles. *Biometrics* **48**:361-72.

- Hankin, D.G., J.H. Clark, R.B. Deriso, J.C. Garza, G.S. Morishima, B.E. Riddell, C. Schwarz, and J.B. Scott. 2005. Report of the expert panel on the future of the coded wire tag recovery program for Pacific salmon. Final Report to the Pacific Salmon Commission. Available at: www.psc.org/info_codedwiretagreview.htm
- Healey, M. 1994. Variation in the life history characteristics of chinook salmon and its relevance to conservation of the Sacramento winter-run of chinook salmon. *Conservation Biology* **8**:876-877.
- Healey, M. 1991. The life history of Chinook salmon. Pp. 39-52 in C. Groot, and L. Margolis, eds. *Pacific Salmon Life Histories*. University of British Columbia, Vancouver, B.C.
- Kim, J. E., R. E. Withler, C. Ritland, and K. M. Cheng. 2004. Genetic variation within and between domesticated chinook salmon, *Oncorhynchus tshawytscha*, strains and their progenitor populations. *Environmental Biology of Fishes* **69**:371-378.
- Kim, T. J., K. M. Parker, and P. W. Hedrick. 1999. Major histocompatibility complex differentiation in Sacramento River chinook salmon. *Genetics* **151**:1115-1122.
- Lindley, S.T., R. Schick, B.P. May, J.J. Anderson, S. Greene, C. Hanson, A. Low, D. McEwan, R.B. MacFarlane, C. Swanson, and J.G. Williams. 2004. Population structure of threatened and endangered chinook salmon ESUs in California's Central Valley basin. NOAA Technical Memorandum NMFS-SWFSC-360.
- McElhany, P., M.H. Ruckelshaus, M.J. Ford, T.C. Wainwright, and E.P. Bjorkstedt. 2000. Viable salmonid populations and the recovery of evolutionarily significant units. NOAA Technical Memorandum NMFS-NWFSC-42
- Morris, D. B., K. R. Richard, and J. M. Wright. 1996. Microsatellites from rainbow trout (*Oncorhynchus mykiss*) and their use for genetic study of salmonids. *Canadian Journal of Fisheries & Aquatic Sciences* **53**:120-126.
- Myers, J. M., R.G. Kope, G.J. Bryant, D. Teel, L.J., Lierheimer, T.C. Wainwright, W.S. Grand, F.W. Waknitz, K. Neely, S.T. Lindley, and R. S. Waples. 1998. Status review of chinook salmon from Washington, Idaho, Oregon, and California. NOAA Technical Memorandum NMFS-NWFSC-35.
- Nei, M. (1987) *Molecular Evolutionary Genetics*. Columbia University Press, New York, New York.

- Nelson, R. J., and T. D. Beacham. 1999. Isolation and cross species amplification of microsatellite loci useful for study of Pacific salmon. *Animal Genetics* **30**:228-229.
- Nielsen, J., D. Tupper, and W. Thomas. 1994. Mitochondrial DNA polymorphism in unique runs of chinook salmon (*Oncorhynchus tshawytscha*) from the Sacramento San Joaquin river basin. *Conservation Biology* **8**:882-884.
- Nielsen, R., and J. Wakeley. 2001. Distinguishing migration from isolation. A Markov chain Monte Carlo approach. *Genetics* **158**:885-896.
- Oconnell, M., R. G. Danzmann, J. M. Cornuet, J. M. Wright, and M. M. Ferguson. 1997. Differentiation of rainbow trout (*Oncorhynchus mykiss*) populations in Lake Ontario and the evaluation of the stepwise mutation and infinite allele mutation models using microsatellite variability. *Canadian Journal of Fisheries & Aquatic Sciences* **54**:1391-1399.
- Olsen, J. B., P. Bentzen, and J. S. Seeb. 1998. Characterization of seven microsatellite loci derived from pink salmon. *Molecular Ecology* **7**:1087-1089.
- Oreilly, P. T., L. C. Hamilton, S. K. McConnell, and J. M. Wright. 1996. Rapid analysis of genetic variation in Atlantic salmon (*Salmo salar*) by PCR multiplexing of dinucleotide and tetranucleotide microsatellites. *Canadian Journal of Fisheries and Aquatic Sciences* **53**:2292-2298.
- Piry, S., A. Alapetite, J. M. Cornuet, D. Paetkau, L. Baudouin, and A. Estoup. 2004. GENECLASS2: A software for genetic assignment and first-generation migrant detection. *Journal of Heredity* **95**:536-539.
- Rannala, B., and J. L. Mountain. 1997. Detecting immigration by using multilocus genotypes. *Proceedings of the National Academy of Sciences of the United States of America* **94**:9197-9201.
- Raymond, M., and F. Rousset. 1995. Genepop (Version-1.2) - Population genetics software for exact tests and ecumenicism. *Journal of Heredity* **86**:248-249.
- Rexroad, C. E., R. L. Coleman, A. M. Martin, W. K. Hershberger, and J. Killefer. 2001. Thirty-five polymorphic microsatellite markers for rainbow trout (*Oncorhynchus mykiss*). *Animal Genetics* **32**:317-319.

- Saitou, N. and M. Nei 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution* 4:406-425.
- Sokal, R. R., and F. J. Rohlf. 2003. *Biometry*. W. H. Freeman and Company, New York.
- Utter, F., G. Milner, G. Stahl, and D. Teel. 1989. Genetic population structure of Chinook salmon, *Oncorhynchus tshawytscha*, in the Pacific Northwest. *Fishery Bulletin* 87:239-264.
- Waples, R. S., D. J. Teel, J. M. Myers, and A. R. Marshall. 2004. Life-history divergence in Chinook salmon: Historic contingency and parallel evolution. *Evolution* 58:386-403.
- Weir, B. S., and C. C. Cockerham. 1984. Estimating F-Statistics for the analysis of population structure. *Evolution* 38:1358-1370.
- Williamson, K., J. Cordes, and B. May. 2002 Characterization of microsatellite loci in chinook salmon (*Oncorhynchus tshawytscha*) and cross-species amplification in other salmonids. *Molecular Ecology Notes* 2:17-19.
- Winans, G. A. 1989. Genetic variability in chinook salmon stocks from the Columbia River Basin. *North American Journal of Fishery Management* 9:47-52.

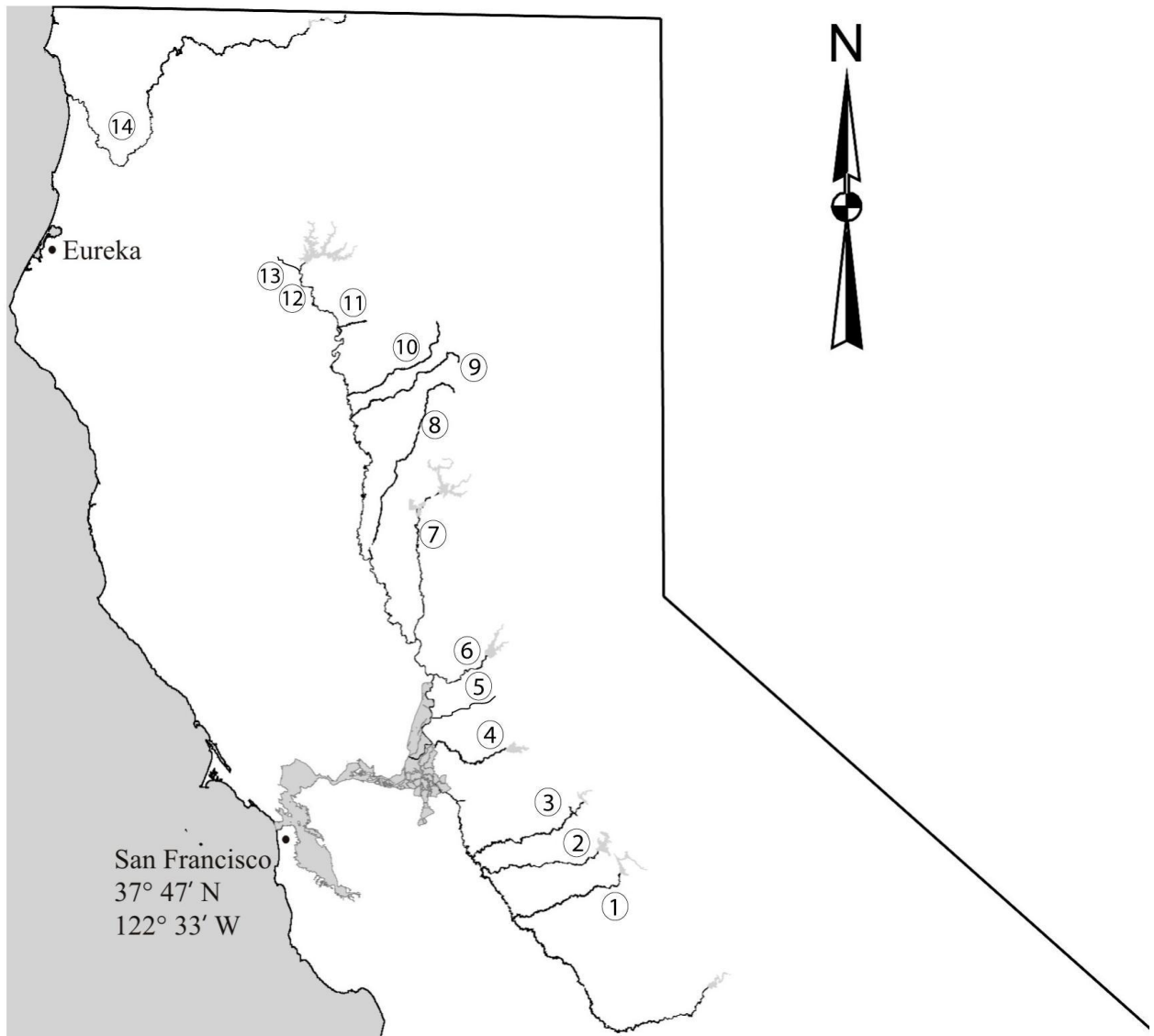


Figure 1. Partial map of California identifying general sampling locations. Numbers for specific locations indicate: (1) Merced River, (2) Tuolumne River, (3) Stanislaus River, (4) Mokelumne River, (5) Consumes River, (6) American River, (7) Feather River, (8) Butte Creek, (9) Deer Creek, (10) Mill Creek, (11) Battle Creek, (12) Upper Sacramento River, (13) Clear Creek, and (14) Klamath River.

Figure 2

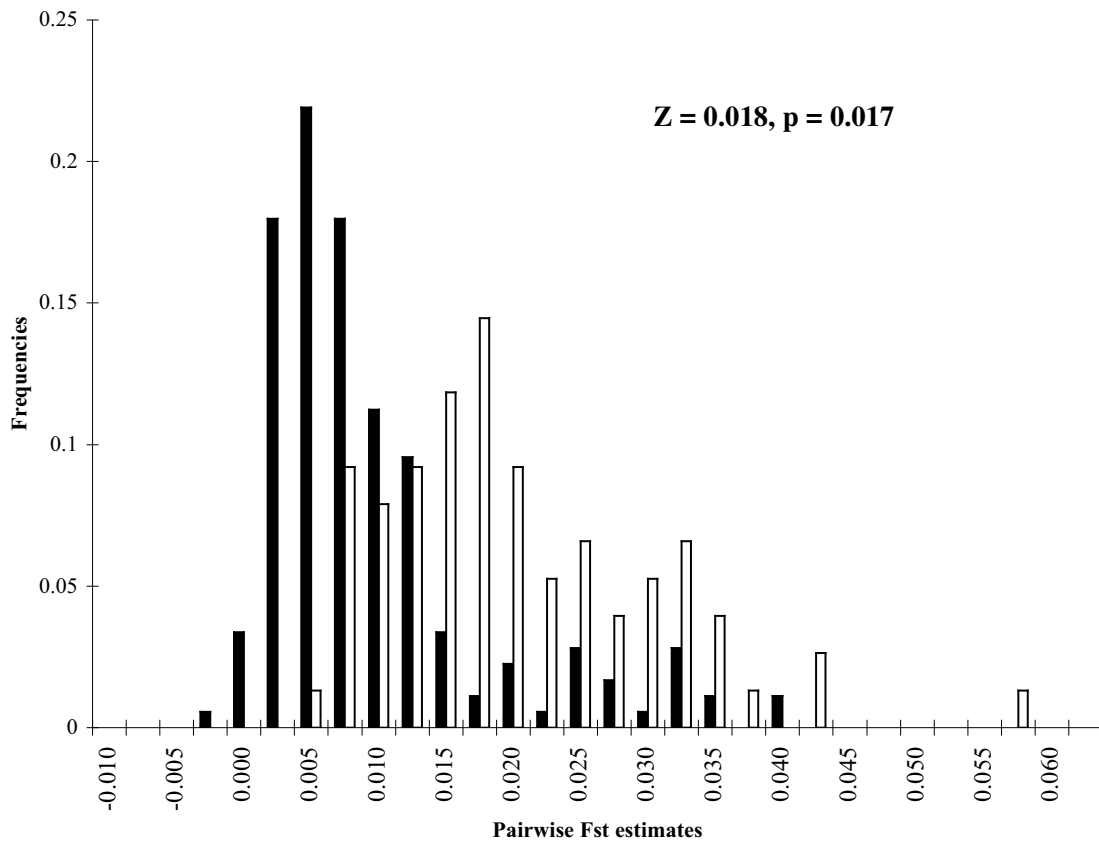


Figure 2 : Relative frequencies of pairwise F_{ST} estimates within ESUs (black) and between ESUs (white). Result of the Mantel test is given.

Figure 3a: Chord distance/neighbor joining

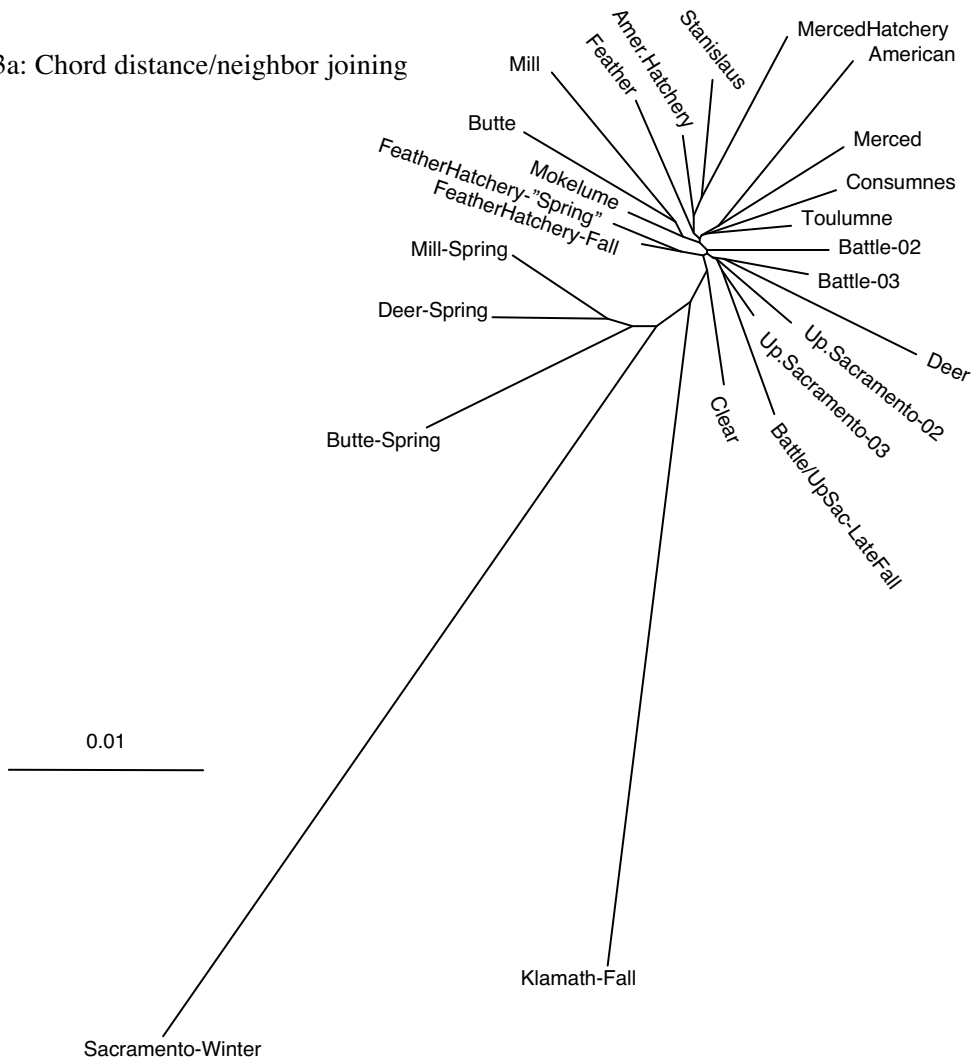


Figure 3b: Chord distance/neighbor joining bootstrap consensus

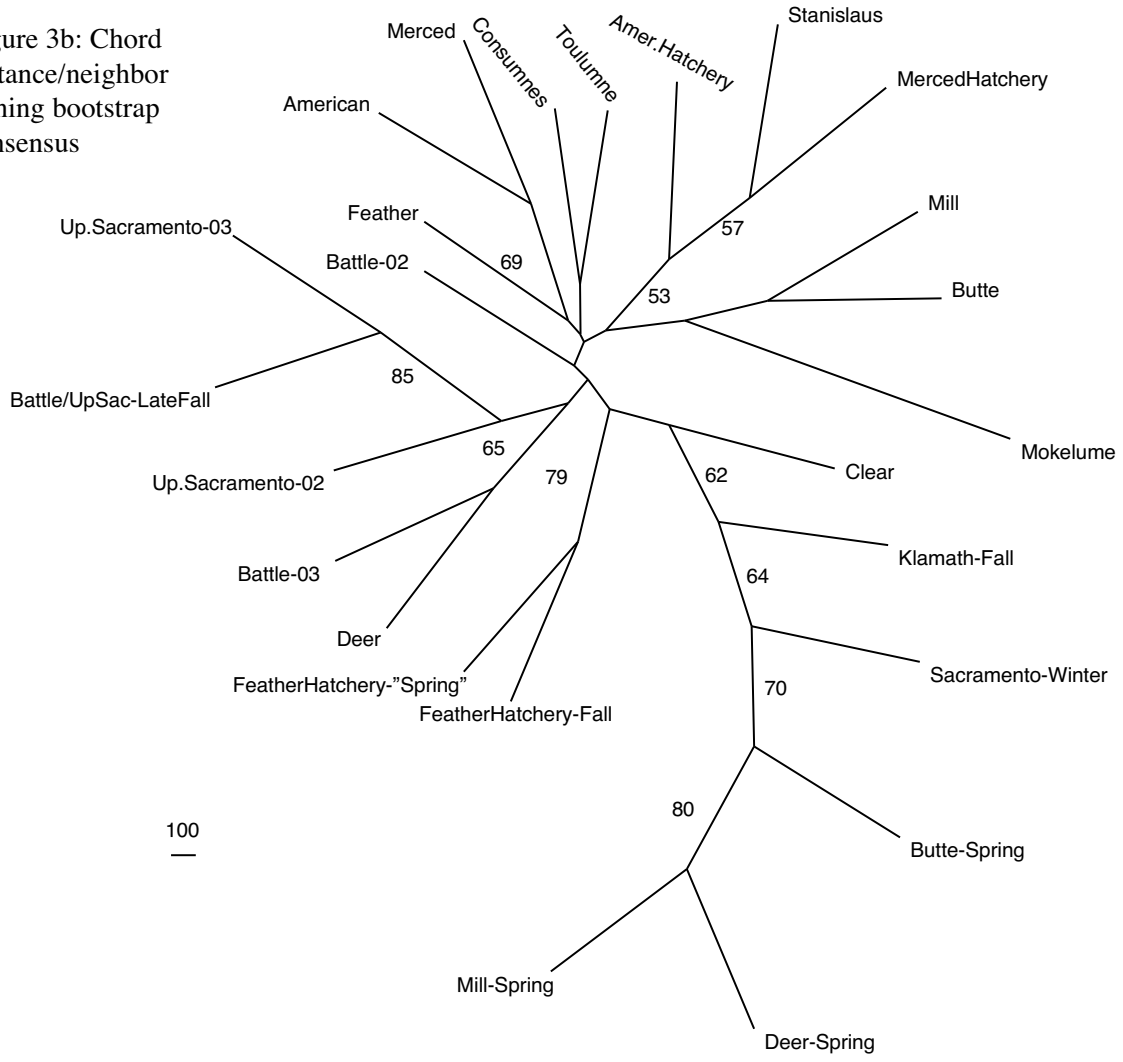


Figure 3c: Maximum Likelihood

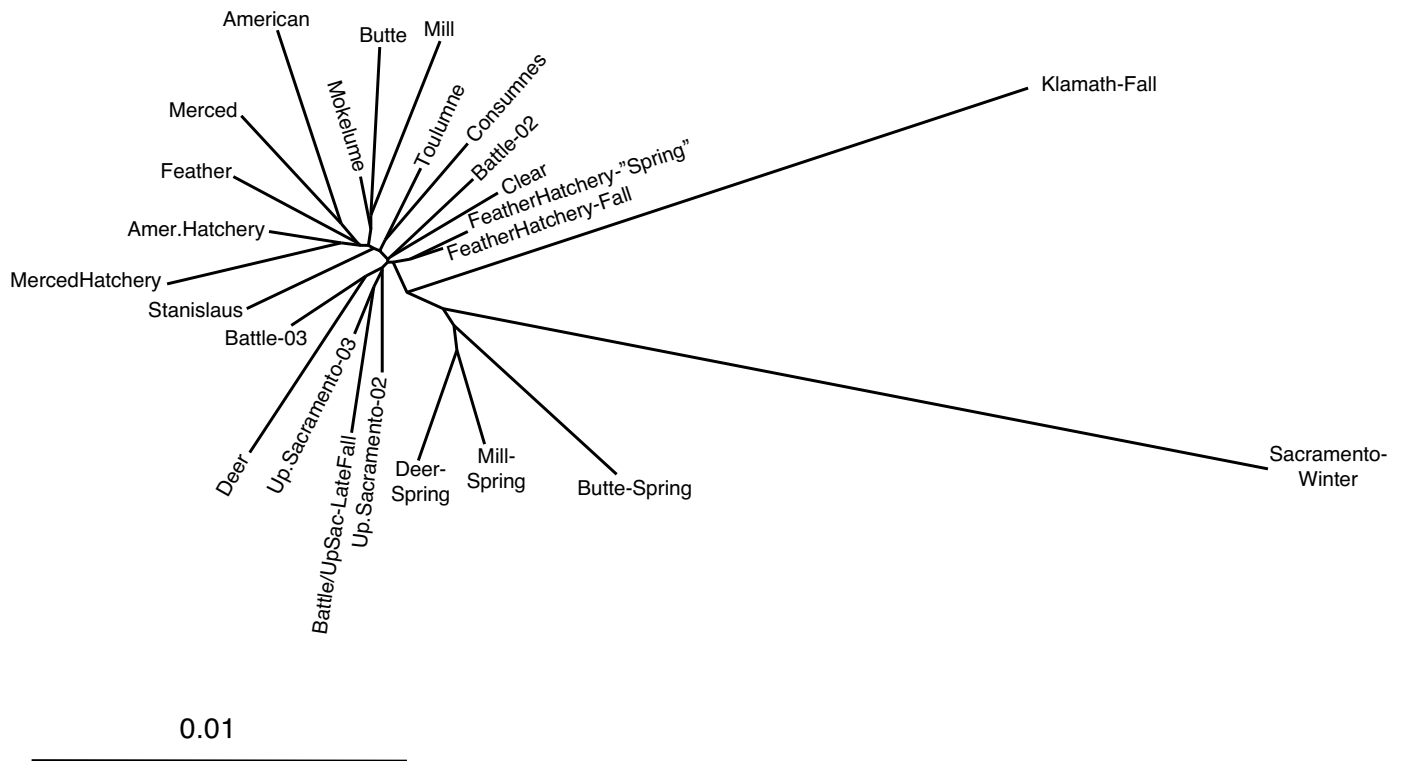


Figure 3d: Maximum Likelihood Bootstrap Consensus

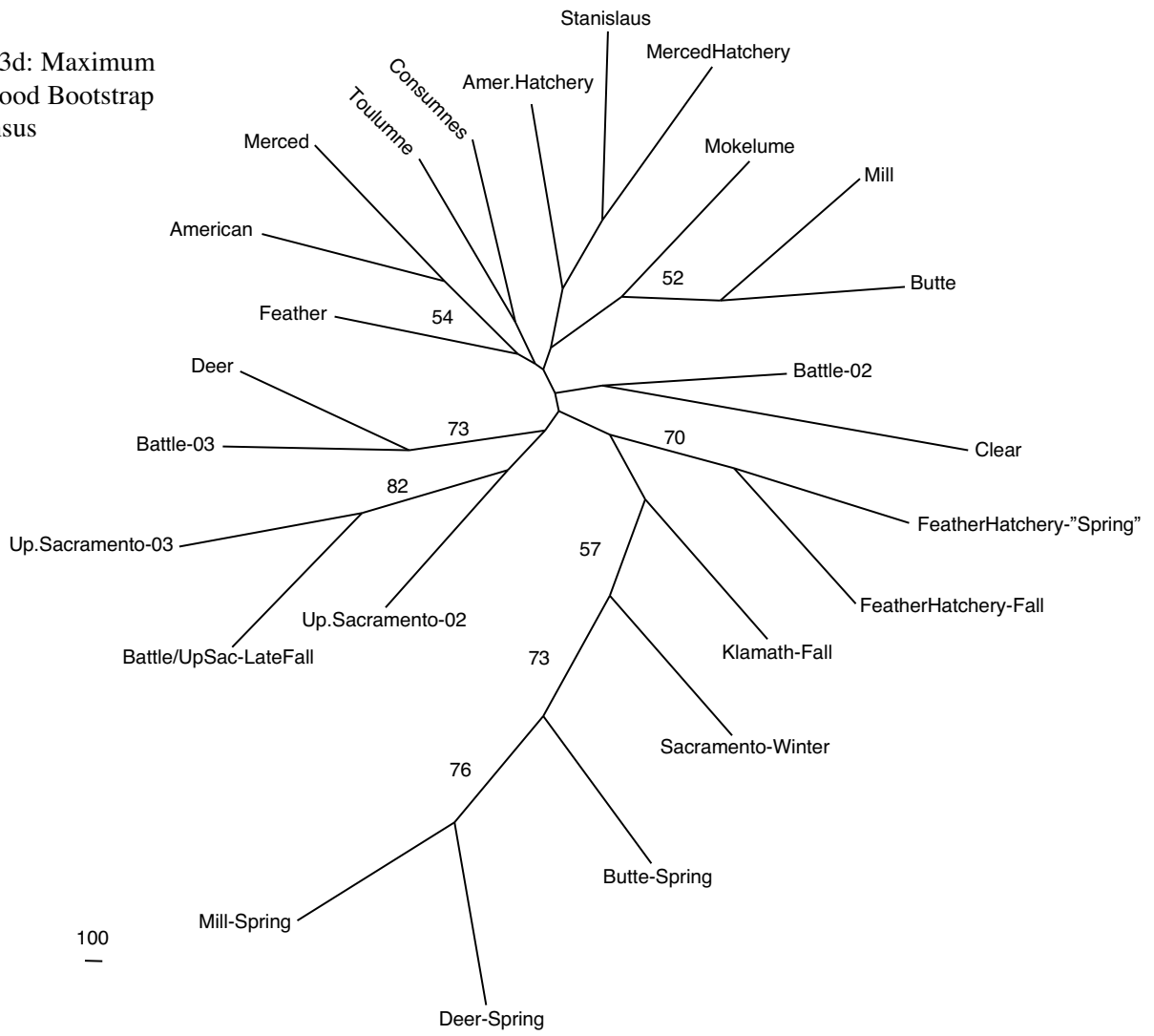


Table 1: Summary statistics for Chinook salmon population samples studied here. LD is the proportion of locus pairs in linkage disequilibrium. Ar is allelic richness. * values estimated with only 16 loci.

Population location	Run timing	Year	Sample size	Unb. Hz	Obs. Hz	LD	Ar	No. Alleles
Merced	Fall	2002	57	0.7818	0.6516	0.0	11.57*	14.3
Merced-Hatchery	Fall	2002	89	0.7953	0.6635	3.0	11.05	16.3
Toulumne	Fall	2002	75	0.7716	0.7193	2.0	11.58	16.4
Stanislaus	Fall	2002	91	0.8019	0.7328	3.0	11.85	17.0
Mokelumne	Fall	2002-03	108	0.7865	0.7245	2.0	12.32	17.9
Consumnes	Fall	2003	58	0.7631	0.7143	1.0	11.12	14.8
American	Fall	2002	53	0.7665	0.6496	1.0	10.28*	12.4
American-Hatchery	Fall	2002	100	0.7944	0.7273	1.0	11.79	17.8
Feather	Fall	2002	69	0.7775	0.6733	3.0	11.89	15.4
Feather-Hatchery	Fall	2002-03	167	0.7897	0.7314	0.0	12.33	18.6
Feather-Hatchery	"Spring"	2003	276	0.7764	0.7279	21.0	11.25	18.7
Butte	Fall	2002	100	0.7570	0.6684	6.0	11.17*	15.3
Butte	Spring	2002-03	196	0.7407	0.6639	2.0	9.76	14.7
Deer	Fall	2002-03	48	0.7755	0.6763	0.0	10.67*	12.8
Deer	Spring	2002-03	110	0.7663	0.6833	0.0	10.85	15.0
Mill	Fall	2002	79	0.7709	0.6931	1.0	10.55*	13.9
Mill	Spring	2002-03	101	0.7709	0.7166	2.0	11.09	14.8
Battle	Fall	2002	100	0.7956	0.7023	0.0	11.60	16.1
Battle	Fall	2003	95	0.7665	0.7020	0.0	11.37	15.9
Battle/Sacramento	Late Fall	2002-03	83	0.7569	0.7170	2.0	11.12	14.5
Upper Sacramento	Fall	2002	100	0.7732	0.7208	3.0	11.69	16.4
Upper Sacramento	Fall	2003	110	0.7645	0.7297	2.0	11.46	17.0
Upper Sacramento	Winter	1995-2003	99	0.5889	0.5519	2.0	6.46	9.1
Clear	Fall	2002-03	189	0.7629	0.6740	3.0	11.54	17.6
Klamath	Fall	2003	60	0.7490	0.6937	10.0	10.20	13.7

Table 2: Microsatellite locus and PCR primer summary. Forward and reverse primers used for PCR are listed. In some cases, the primers have been modified from the original citation. The allele range reported is that observed in this study. F_{IS} is the proportion of pairwise tests (across 25 population samples) that were significant at 0.01.

Locus	Primer	Primer Sequence (5' to 3')	Allele Range	F_{IS}	Citation
<i>Ogo 2</i>	F	ACA TCG CAC ACC ATA AGC AT	211-259	0.04	Olsen et al. 1998
	R	GTT TCT TCG ACT GTT TCC TCT GTG TTG AG			
<i>Ogo 4</i>	F	GTC GTC ACT GGC ATC AGC TA	134-174	0.24	Olsen et al. 1998
	R	GAG TGG AGA TGC AGC CAA AG			
<i>Oke 4</i>	F	AGG CCC AAA GTC TGT AGT GAA GG	241-255	0.00	Buchholz USFWS 99-1
	R	GAT GAA TCG AGA GAA TAG GGA CTG AAT			
<i>Omm 1032</i>	F	GCG AGG AAG AGA AAG TAG TAG	182-216	1.00	Rexroad et al. 2001
	R	CCC ATC TTC TCT CTG ATT ATG			
<i>Omm 1080</i>	F	GAG ACT GAC ACG GGT ATT GA	174-382	0.24	Rexroad et al. 2001
	R	GTT ATG TTG TCA TGC CTA GGG			
<i>Omy 77</i>	F	CGT TCT CTA CTG AGT CAT	124-146	0.20	Morris et al. 1996
	R	GTC TTT AAG GCT TCA CTG CA			
<i>Omy 325</i>	F	TGTGAGACTGTCAGATTTTGC	82-108	1.00	O'Connell et al. 1997
	R	CGGAGTCCGTATCCTTCCC			
<i>Ots M2</i>	F	ACA CCT CAC ACT TAG A	132-172	0.04	Banks et al. 1999
	R	CAG TGT GAA GGA TAT TAA A			
<i>Ots 4</i>	F	GAA CCC AGA GCA CAG CAC AA	133-161	0.12	Banks et al. 1999
	R	GGA GGA CAC ATT TCA GCA G			
<i>Ots M9</i>	F	ATC AGG GAA AGC TTT GGA GA	100-110	0.16	Banks et al. 1999
	R	CCC TCT GTT CAC AGC TAG CA			
<i>Ots 201b</i>	F	CAG GGC GTG ACA ATT ATG C	139-311	0.12	M. Banks unpublished
	R	TGG ACA TCT GTG CGT TGC			
<i>Ots 211</i>	F	TAGGTTACTGCTTCCGTCAATG	193-297	0.04	Greig et al. 2003
	R	GAGAGGTGGTAGGATTTGCAG			

Table 2 cont.: Microsatellite locus and PCR primer summary continued.

Locus	Primer	Primer Sequence (5' to 3')	Allele Range	F _{IS}	Citation
<i>Ots</i> 213	F	CCCTACTCATGTCTCTATTTGGTG	204-348	0.16	Greig et al. 2003
	R	AGCCAAGGCATTTCTAAGTGAC			
<i>Ots</i> G78b	F	GTC CCT TGA ATT GAA TTG ATT AGA	200-384	0.88	Williamson et al. 2002
	R	CAG CCT ACT GCA GTT CAA TAG ACT			
<i>Ots</i> G83b	F	TAG CCC TGC ACT AAA ATA CAG TTC	149-333	0.16	Williamson et al. 2002
	R	CAT TAA TCT AGG CTT GTC AGC AGT			
<i>Ots</i> G249	F	TTC TCA GAG GGT AAA ATC TCA GTA AG	136-316	0.32	Williamson et al. 2002
	R	GTA CAA CCC CTC TCA CCT ACC C			
<i>Ots</i> G311	F	TGC GGT GCT CAA AGT GAT CTC AGT CA	251-427	0.64	Williamson et al. 2002
	R	TCC ATC CCT CCC CCA TCC ATT GT			
<i>Ots</i> G432	F	TGA AAA GTA GGG GAA ACA CAT ACG	107-211	0.20	Williamson et al. 2002
	R	TAA AGC CCA TTG AAT TGA ATA GAA			
<i>Ssa</i> 85	F	AGG TGG GTC CTC CAA GCT AC	118-172	0.12	O'Reilly et al. 1996
	R	ACC CGC TCC TCA CTT AAT C			
<i>Ssa</i> 408	F	AATGGATTACGGGTACGTTAGACA	183-275	0.04	Cairney et al. 2000
	R	CTCTGTGCAGGTTCTTCATCTGT			

Table 4: Individual assignments to ESU/temporal run using a pooled baseline for each group. Feather River "spring" run fish excluded.

4a. All fish assigned to most likely group. Overall accuracy = 96.5%

	Fall	Latefall	Spring	Winter	Klamath	Accuracy
Fall	1203	69	46	0	2	91.1
Latefall	29	41	0	0	0	58.6
Spring	26	5	246	0	0	88.8
Winter	0	0	0	73	0	100.0
Klamath	0	0	1	0	55	98.2

4b. Confident assignments using 95% probability criterion. Overall accuracy = 99.0%

	Fall	Latefall	Spring	Winter	Klamath	Accuracy
Fall	1015	17	9	0	2	97.3
Latefall	13	24	0	0	0	64.9
Spring	10	0	202	0	0	95.3
Winter	0	0	0	73	0	100.0
Klamath	0	0	0	0	54	100.0

Table 4 cont.: Individual assignments to ESU/temporal run using a pooled baseline for each group.
Feather River "spring" run fish excluded.

4c. All fish assigned to most likely group.

Assigned samples		Assignment results				Klamath	Percent accuracy	
		Fall	Latefall	Spring	Winter		To Run	To ESU
Fall	Total	1203	69	46	0	2	91.1	96.4
	Merced	37	0	2	0	0	94.9	94.9
	Merced-Hatchery	89	0	0	0	0	100.0	100.0
	Toulumne	65	2	1	0	0	95.6	98.5
	Stanislaus	72	5	3	0	0	90.0	96.3
	Mokelumne	99	5	2	0	0	93.4	98.1
	Consumnes	53	4	0	0	0	93.0	100.0
	American	24	4	0	0	0	85.7	100.0
	American-Hatchery	84	3	1	0	0	95.5	98.9
	Feather	44	2	2	0	0	91.7	95.8
	Feather-Hatchery	146	6	12	0	0	89.0	92.7
	Butte	64	2	0	0	0	97.0	100.0
	Deer	30	2	1	0	0	90.9	97.0
	Mill	46	3	3	0	0	88.5	94.2
	Battle02	62	2	4	0	0	91.2	94.1
	Battle03	58	7	2	0	2	84.1	94.2
	Up. Sacramento02	50	7	4	0	0	82.0	93.4
	Up. Sacramento03	70	12	7	0	0	78.7	92.1
	Clear	110	3	2	0	0	95.7	98.3
	Latefall	29	41	0	0	0		58.6
Spring	Total	26	5	246	0	0		98.2
	Butte	2	1	125	0	0		97.7
	Deer	14	0	53	0	0		79.1
	Mill	10	4	68	0	0		82.9
Winter		0	0	0	73	0		100.0
Klamath		0	0	1	0	55		98.2

Table 4 cont.: Individual assignments to ESU/temporal run using a pooled baseline for each group. Feather River "spring" run fish excluded.

4d. Confident assignments using 95% probability criterion.

Assigned samples		Assignment results				Klamath	Percent accuracy	
		Fall	Latefall	Spring	Winter		To Run	To ESU
Fall	Total	1015	17	9	0	2	97.3	98.9
	Merced	31	0	0	0	0	100.0	100.0
	Merced-Hatchery	86	0	0	0	0	100.0	100.0
	Toulumne	51	0	0	0	0	100.0	100.0
	Stanislaus	61	0	0	0	0	100.0	100.0
	Mokelumne	90	1	0	0	0	98.9	100.0
	Consumnes	46	1	0	0	0	97.9	100.0
	American	21	0	0	0	0	100.0	100.0
	American-Hatchery	71	1	0	0	0	98.6	100.0
	Feather	36	0	0	0	0	100.0	100.0
	Feather-Hatchery	130	2	1	0	0	97.7	99.2
	Butte	53	0	0	0	0	100.0	100.0
	Deer	22	0	0	0	0	100.0	100.0
	Mill	38	1	0	0	0	97.4	100.0
	Battle02	53	1	1	0	0	96.4	98.2
	Battle03	46	2	0	0	2	92.0	96.0
	Up. Sacramento02	36	3	2	0	0	87.8	95.1
	Up. Sacramento03	51	4	4	0	0	86.4	93.2
	Clear	93	1	1	0	0	97.9	98.9
	Latefall	13	24	0	0	0		64.9
Spring	Total	10	0	202	0	0		95.3
	Butte	0	0	116	0	0		100.0
	Deer	6	0	33	0	0		84.6
	Mill	4	0	53	0	0		93.0
Winter		0	0	0	73	0		100.0
Klamath		0	0	0	0	54		100.0

Table 5: AMOVA results from different hypotheses. “S” is composed of tributary rivers 1 to 3 (see Table 1), “C” by rivers 4 to 6 and “N” by rivers 7 to 13. Nb is the number of groups. Var is the variance partitioned to that level and % is the proportion of the total variance that it represents. Results significantly different than zero are indicated by * ($p < 0.05$) and *** ($p < 0.001$).

Grouping Description	Nb	Among Groups			Among Populations within Groups			Within populations		
		Var	%	FCT	Var	%	FST	Var	%	FSC
N+C/S	2	0.0257	0.3257	0.0033*	0.0736	0.9330	0.0126***	7.7900	98.7413	0.0094***
N/C+S	2	0.0117	0.1489	0.0015*	0.0772	0.9794	0.0113***	7.7900	98.8717	0.0098***
N/C/S	3	0.0152	0.1935	0.0019	0.0737	0.9352	0.0113***	7.7900	98;8714	0.0094***
N/S	2	0.0284	0.3600	0.0036	0.0830	1.0502	0.0141***	7.7823	98.5900	0.0105***

Appendix A: Allele frequencies for all populations by locus

Locus

Locus	Merced	Merced-Hatchery	Toulumne	Stanislaus	Mokelumne	Consumnes	American	American-Hatchery	Feather	Feather-Hatchery	Feather HatcherySp	Butte	Butte-Spring	Deer	Deer-Spring	Mill	Mill-Spring	Battle02	Battle03	Battle/SacramentoLF	Up. Sacramento02	Up. Sacramento03	Up. Sacramento Winter	Clear	Klamath
Ogo 2																									
211																									0.89
213																						0.51		0.32	
215		0.68																							
217	1.22	1.37	0.72	1.95	0.86	0.86	1.92	1.85	1.14	1.57	0.97	0.56			0.61	1.79	1.54	1.52	0.64	0.65	0.65	0.51	19.64		4.46
219																									
221		1.37																							1.27
223	15.85	23.29	8.70	9.74	10.34	6.90	15.38	11.73	10.23	13.52	11.87	13.48	7.50	6.56	11.59	14.29	16.15	11.36	14.10	12.99	11.04	9.09	1.79	12.97	66.96
225	50.00	32.19	41.30	42.86	41.38	42.24	46.15	45.06	43.18	42.14	48.83	38.76	73.57	59.84	54.27	41.07	43.08	46.97	48.08	48.05	53.25	54.04	39.88	45.89	10.71
227	8.54	13.70	13.04	14.29	19.83	18.97	13.46	18.52	17.05	18.55	18.48	21.35	2.14	6.56	5.49	16.07	15.38	16.67	16.03	11.04	12.99	12.63		17.41	3.57
229	15.85	11.64	21.01	17.53	12.07	12.93	13.46	12.96	7.95	15.41	11.67	14.61	12.14	9.84	12.20	12.50	10.77	13.64	10.26	10.39	9.74	12.12		14.87	2.68
231	2.44	6.16	7.25	5.19	7.76	10.34		4.32	6.82	3.46	1.95	3.37		7.38	1.83	5.36	4.62	3.79	7.69	7.79	5.19	3.54	2.38	3.48	9.82
233							1.92								0.61	1.79									0.89
235		0.68	1.45	0.65	0.86	0.86	5.77	1.23	2.27	1.26	1.56	1.69	1.07	6.56	4.88	1.79	1.54	1.52		3.90	1.30	1.01	0.60	0.95	
237		0.68	0.72		0.86			0.62								1.79		1.52				2.02	34.52		
239																							0.60		
241		1.37																							
243	2.44	4.79	2.90	5.19	4.31	2.59		2.47	5.68	2.52	1.75	3.93		0.82	1.83	1.79	4.62		1.92	4.55	3.90	3.03		0.63	
245		1.37	2.17	0.65	0.86	1.72			3.41	0.31	0.39	1.69	0.36	1.64	0.61			1.52	1.28		0.51			1.27	
247		0.68																							
249									1.14																
251																									0.32

266	1.25	2.54	2.99	1.88	2.00			4.67	1.92	2.27	4.07	1.32	7.89	12.24	6.67	11.11	3.41	2.24	2.34	8.57	3.33	5.98	0.60	3.21	1.56	
270	6.25	4.24	2.99	6.88	8.00	5.45		2.67	1.92	6.49	11.79	5.26	0.88	2.04	8.00	5.56	6.82	5.97	7.81	5.00	8.33	4.89	9.04	6.42	12.50	
274	1.25	2.54	5.97	5.63	4.00	5.45	7.41	6.67	6.73	7.14	4.07	5.26	5.70	5.10	2.67	3.70	2.27	3.73	3.13	5.71	5.00	4.35	4.82	3.21	1.56	
278	3.75	5.93	4.48	3.75	3.00	6.36	11.11	4.67	2.88	6.82	12.80	3.95		14.29	10.67	5.56	4.55	2.99	3.13	2.14		5.43	1.20	3.21		
282	6.25	4.24	2.99	5.00	4.00	0.91	1.85	4.67	2.88	4.87	5.08	1.32	3.51	4.08	10.00	5.56	4.55	8.96	1.56	2.86	5.83	3.80		6.88	9.38	
286	8.75	5.08	8.21	7.50	5.00	7.27	3.70	7.33	1.92	3.57	5.28		3.95	11.22	5.33	5.56	9.09	6.72	5.47	2.86	3.33	2.17	7.23	5.50	6.25	
290	5.00	5.08	2.99	5.00	3.50	4.55	1.85	4.00	0.96	4.22	8.13	1.32	2.63	4.08	6.00	3.70	3.41	5.22	3.91	1.43	4.17	8.15	24.70	5.05	3.13	
294	1.25	4.24	8.96	6.25	7.00	6.36	7.41	6.00	1.92	8.77	3.05	1.32	7.02	6.12	3.33			2.27	5.22	0.78	18.57	5.00	8.70	16.27	4.13	
298	8.75	5.08	3.73	3.13	4.00	7.27	11.11	4.67	2.88	7.79	4.88	5.26	2.19	4.08	2.00	1.85	7.95	5.22	6.25	7.86	9.17	4.35	1.81	4.59	7.81	
302		1.69	5.97	1.88	7.00	3.64		3.33	1.92	3.90	2.85	1.32	5.26	1.02		3.70		2.99	3.91	3.57	5.00	3.80	1.81	3.21	1.56	
306	5.00	5.93	7.46	2.50	9.00	4.55	11.11	7.33	4.81	6.17	2.24	1.32	3.95	2.04	0.67	5.56	9.09	3.73	7.81	0.71	7.50	3.26	16.87	5.05	3.13	
310	5.00	5.08	3.73	4.38	4.50	3.64	7.41	5.33	4.81	2.27	4.67	6.58	3.51		5.33	1.85	2.27	4.48	5.47	0.71	5.00	5.43	9.04	3.21		
314	5.00	2.54	2.24	1.88	6.00	3.64	1.85	4.00	6.73	3.25	3.05	2.63		2.04	4.00	1.85	5.68	3.73	4.69		2.50	4.35	1.20	5.05	1.56	
318	1.25	1.69	2.24	3.75	1.00	0.91	1.85	3.33	1.92	1.95	2.44		3.07	5.10	5.33	5.56	2.27	2.24	1.56	2.86	0.83	2.17	2.41	3.21	1.56	
322	3.75	1.69	3.73	1.88	0.50	0.91		1.33	5.77	2.60	1.83	2.63				1.85	1.14	3.73	1.56	0.71	2.50	2.17		3.67		
326			0.75	1.25	1.00			1.33		0.97			0.44	1.02				0.75	0.78	1.43	0.83	0.54			0.92	
330	1.25	0.85	1.49	2.50	2.00	0.91		1.33	0.96	0.65	0.41			2.04		1.85	1.14	1.49	3.91		2.50	1.09		0.92	1.56	
334	1.25	3.39	2.24	1.25	2.00	0.91	1.85	2.67	1.92	0.65	2.85		1.75	7.14	10.67	1.85	2.27	2.24	3.13		2.50	1.63		2.75		
338	1.25	2.54	2.24	3.75	2.00	2.73	1.85		2.88	1.62	1.42		9.21	1.02	1.33		1.14	0.75			0.83	1.09		2.29		
342		0.85	0.75	2.50	0.50			0.67	1.92	1.30	0.20			1.02		1.85			1.56			0.54				
346	1.25	1.69		0.63	0.50			0.67	0.96	0.32	0.41	2.63	0.44			1.85					1.43	0.83				
350					0.50					0.32	0.41								0.78	2.14	1.67	2.72		0.92		
354					0.50	0.91		0.67		0.65	0.41							0.75		0.71				0.46		
358					0.50					0.32			3.95		1.33							1.67	0.54			
362	1.25			0.63									0.44													
366													0.44													
374													0.88													
378		0.85		0.63		1.82		0.67																		
382					0.50																					

Ots 4	Merced	Merced-Hatchery	Toulumne	Stanislaus	Mokelumne	Consumnes	American	American-Hatchery	Feather	Feather-Hatchery	Feather HatcherySp	Butte	Butte-Spring	Deer	Deer-Spring	Mill	Mill-Spring	Battle02	Battle03	Battle/SacramentoLF	Up. Sacramento02	Up. Sacramento03	Up. Sacramento Winter	Clear	Klamath	
133													7.87	0.67	1.25											
141				0.68							0.21		0.39		0.63											
143	1.47	0.60	2.42	2.05	2.88	3.77	2.00	2.47	2.33	6.98	1.89	5.15	20.87	7.33	9.38	3.70	2.88	3.33	4.39	2.42	5.45	7.53		2.27		
145		4.22	0.81	3.42	5.29	1.89	4.00	2.47	3.49	1.55	1.26	4.41	2.76	10.00	11.88	5.56	2.88		1.75	5.65	1.82	1.37			4.00	
147	44.12	34.34	48.39	47.95	43.27	44.34	34.00	41.36	50.00	44.96	49.58	48.53	28.74	30.00	30.00	44.44	43.27	40.00	37.72	43.55	40.91	39.04	0.75	50.76	65.00	
149	22.06	11.45	12.90	10.96	16.83	17.92	22.00	14.20	10.47	20.93	23.74	7.35	21.26	25.33	26.88	12.96	20.19	24.17	21.93	21.77	23.64	17.12	41.04	12.12	3.00	
151	13.24	3.61	10.48	13.01	7.69	7.55	4.00	11.11	10.47	5.43	4.83	8.09	5.91	8.00	10.00	14.81	6.73	9.17	8.77	7.26	5.45	8.22	23.88	12.88	5.00	
153	17.65	8.43	23.39	16.44	24.04	23.58	34.00	25.31	23.26	19.77	18.49	26.47	12.20	18.67	10.00	18.52	23.08	23.33	25.44	19.35	22.73	26.03	34.33	21.97	13.00	
155	1.47	1.20	1.61	2.74		0.94		1.85		0.39						0.96						0.68			9.00	
157		4.82		1.37				0.62																	1.00	
159		28.92						0.62																		
161		2.41		1.37																						

Ots G249	Merced	Merced-Hatchery	Toulumne	Stanislaus	Mokelumne	Consumnes	American	American-Hatchery	Feather	Feather-Hatchery	Feather HatcherySp	Butte	Butte-Spring	Deer	Deer-Spring	Mill	Mill-Spring	Battle02	Battle03	Battle/SacramentoLF	Up. Sacramento02	Up. Sacramento03	Up. Sacramento Winter	Clear	Klamath
136													0.37												
144																									0.44
160	1.19	4.76			1.92	0.89	1.43	0.56		0.96		1.41	0.74	3.80	1.90	2.86		1.49	1.49		3.28	1.10			0.88
164	3.57		0.77		0.96	0.89	5.71	2.78	0.91	3.85	0.21	3.52	0.37	0.63				2.00	4.48	1.49	0.72	3.85			3.51

168	1.19	3.08		5.29	11.61	4.29	8.33	6.36	2.24	1.26	6.34		3.80	1.27	5.71	2.00	4.48	2.24	2.90	3.28	7.14		4.82			
172	4.76	2.31		4.81	2.68	4.29	1.67	6.36	2.88	3.57	7.04	3.31	8.23	2.53	2.86	4.00	1.49	2.99	1.45	0.82	3.30		3.51			
176		0.79		2.78	1.44		1.43	1.67	0.91				0.70	1.27	1.27		1.00	0.75	0.75	0.72		0.76	0.88	2.44		
180	1.19	1.59	1.54	7.64	0.96	0.89		1.11		0.64	0.21	1.41			1.43	2.00		0.75	1.45				0.44			
184			3.85	0.96	0.89		1.11					0.70		0.63		4.00	1.49	0.75	1.45	0.82	1.65		2.19			
188	2.38		4.62	3.85	0.89	1.43	1.11	0.91	2.88	1.05	2.82	0.37		1.27	1.43	4.00	2.24	0.75	1.45	0.82	2.75		1.75	1.22		
192	2.38		4.62	1.39	0.96	1.79		5.00		0.96	1.05	0.70	4.41	1.27	0.63	1.43		2.24	5.97		0.82		3.07	1.22		
196	2.38	5.56	3.08		1.44		4.29	3.33	3.64	1.60	1.89	2.11	4.78		3.16	1.43	1.00	0.75	2.24	3.62	0.82	2.20		3.07		
200	3.57	4.76	3.85	6.25	4.33	6.25	4.29	6.11	5.45	2.88	1.68	2.82	19.85	5.06	0.63	5.71	1.00	2.99	4.48	10.14	4.92	7.14		1.75		
204		5.56		5.56	1.92	1.79			0.91	0.96	1.26	0.70	2.57	5.06	1.90						0.82	1.10		4.88		
208		1.59	1.54		1.92	1.79		1.67	0.91	2.24	3.57	0.70	2.21	1.90	4.43	1.43	2.00		2.24	2.17		0.55	3.79	3.07	2.44	
212	3.57	2.38	6.15	2.78	5.77	1.79	5.71	2.22	7.27	4.17	5.04	6.34	6.62		3.16	5.71	6.00	5.22	8.21	1.45	6.56	1.65		5.70		
216	7.14	6.35	3.85	4.17	8.17	7.14	12.86	9.44	5.45	3.53	5.04	4.23	0.74	1.90	1.27	8.57	9.00	4.48	10.45	5.07	4.10	5.49	0.76	6.58		
220	4.76	2.38	3.08	3.47	5.77	1.79	1.43	1.67	8.18	6.41	7.77	4.23	11.40	6.96	9.49	5.71	3.00	7.46	2.24	10.87	4.10	7.14	0.76	5.70	8.54	
224	2.38		2.31	5.56	2.88	1.79	5.71	3.33	0.91	3.21	2.94	1.41	1.84	13.92	5.70	2.86	5.00	5.97	0.75	2.17	4.92	4.40	18.18	3.51	6.10	
228	3.57	7.94	3.85	2.78	2.88	6.25	4.29	1.67	1.82	2.56	1.47	2.82	1.47	2.53	3.80			1.49	2.99	2.90	3.28	2.20	0.76	2.63	3.66	
232	5.95	1.59	3.08	2.08	3.85	4.46	4.29	3.89	4.55	4.49	5.04	3.52	0.37	8.86	6.33		6.00	2.24	2.24	4.35	5.74	3.85		5.26	10.98	
236	2.38	3.97	3.08	0.69	2.88	2.68	1.43	3.33	3.64	3.53	3.15	3.52		2.53	3.16	2.86	1.00	3.73	4.48	7.97	4.10	2.75		3.51	15.85	
240	2.38		2.31	1.39	3.37	1.79		3.33	5.45	5.77	3.99	5.63	3.31	1.27	5.06	10.00		3.73	5.97	5.07	4.92	4.40	26.52	3.07	7.32	
244		4.76	3.08	3.47	3.37	4.46	10.00	5.00	2.73	3.53	5.46	4.93	0.37	5.06	4.43	2.86	5.00	2.24	2.99	1.45	7.38	3.85	0.76	3.51	2.44	
248	5.95	7.94	3.85	4.17	3.85	1.79	4.29	3.89	3.64	2.88	2.52	2.11	1.84	3.16	6.96	4.29	1.00	2.99	1.49	6.52	2.46	3.85		5.70	1.22	
252	5.95	2.38	3.85	1.39	5.29	5.36	7.14	6.11	6.36	7.05	6.72	4.93	4.78	1.90	5.06	8.57	12.00	11.94	7.46	5.07	4.92	7.69	6.82	7.89	8.54	
256	9.52	3.97	8.46	2.78	4.81	4.46	1.43	3.89	6.36	5.45	5.25	6.34	2.21	4.43	5.70	2.86	11.00	6.72	6.72	5.80	6.56	7.14	3.03	4.82	4.88	
260	4.76	5.56	6.15	4.86	3.37	4.46		2.78	3.64	4.81	7.35	2.11	0.37	7.59	3.16	2.86	3.00	2.24	3.73	2.17	3.28	3.30		3.95	2.44	
264	5.95	5.56	6.15	0.69	2.88	5.36	5.71	3.89	2.73	5.45	8.40	4.23	7.35	3.80	7.59	4.29	2.00	3.73	0.75	2.90	1.64	0.55	0.76	2.19	3.66	
268	3.57	2.38	0.77	3.47	2.88	5.36	2.86	1.11	1.82	4.17	5.88	3.52	2.57	0.63	3.16	2.86	2.00	2.99			3.28	2.75	13.64	2.63	3.66	
272	1.19	3.17	2.31	4.86	3.37	1.79	2.86	5.56	2.73	2.24	1.26	1.41	1.84				1.43	1.00	1.49	1.49	2.90	2.46	1.10	2.27	0.88	2.44
276	3.57	1.59	3.08	5.56	1.92	2.68	2.86	1.67	0.91	2.56	4.20	1.41	9.93	1.90	4.43		1.00	2.24	2.24	4.35	6.56	4.95	0.76	2.19	1.22	
280	4.76		1.54	2.08	0.48	3.57		1.11	3.64	1.28	0.63		1.10	1.90		5.71	1.00	1.49	3.73		2.46	1.10		1.22		
284		2.38	1.54	7.64		0.89		0.56	0.91	1.92	1.05	2.82	1.84		0.63	2.86	1.00	1.49	2.24		0.55			1.22		
288		1.59		4.17	0.48			1.11		0.64		1.41	1.10		0.63	1.43	1.00	1.49	0.75	0.72	0.82	0.55	2.27			
292		1.59		1.39		0.89				1.28	0.42				0.63		1.00	1.49	0.75	0.72	2.46		0.76			
296		3.17	1.54	1.39	0.48				0.91		0.21	0.70		0.63			1.00	0.75			0.82		3.03	0.44	2.44	

86	28.89	30.12	27.34	29.52	25.25	24.44	42.50	23.26	18.87	19.13	20.25	23.81	15.58	21.25	31.54	23.53	20.18	20.95	25.66	30.91	15.97	21.51	8.54	19.90	26.79
88	55.56	61.45	59.38	59.64	64.14	71.11	55.00	68.02	66.04	66.11	68.10	67.26	75.00	64.38	58.46	72.06	74.56	65.54	68.42	67.27	76.39	75.00	91.46	77.67	25.89
90	3.33	1.81	0.78	2.41	7.07	1.11		1.16	3.77	5.70	2.45	1.79	2.17	7.50	6.15		0.88	10.14	1.32		0.69				
92				1.81						0.67	0.31	0.60			0.77										2.68
94	5.56	3.01	2.34	2.41	0.51			2.33	2.83	1.68	3.99	2.38	3.62	3.75	0.77			1.35	1.97		3.47	1.16			
96		1.20	3.13	0.60	1.01			1.16	0.94	1.01	2.15	0.60	2.90		1.54		0.88		1.32	0.91		1.16			41.96
98	5.56	0.60	3.13	1.20	1.52	3.33	2.50	1.74	4.72	1.68	1.53	1.79	0.36	3.13	0.77		0.88	2.03	0.66			0.58		0.49	
100	1.11		1.56					0.58					0.36			1.47	0.88				0.69				2.68
102			1.56	0.60						4.03	0.31	0.60				2.94	0.88		0.66		1.39			0.97	
104								0.58				0.61													
106								0.58																	
108													1.19												

Omy 77	Merced	Merced-Hatchery	Toulumne	Stanislaus	Mokelumne	Consumnes	American	American-Hatchery	Feather	Feather-Hatchery	Feather HatcherySp	Butte	Butte-Spring	Deer	Deer-Spring	Mill	Mill-Spring	Battle02	Battle03	Battle/SacramentoLF	Up. Sacramento02	Up. Sacramento03	Up. SacramentoWinter	Clear	Klamath
124		2.25	4.55	1.22	4.08	4.17			3.23	3.21	4.55		3.21	2.56		12.50	2.08	3.95	1.92		1.79	2.82		2.54	1.89
128		0.56		3.66	0.51			4.93											0.96						
130	3.57	58.43	3.64	18.90	8.67	2.08	4.35	16.20	3.23	6.73	2.38		0.92		3.23		10.42	9.21	2.88	9.21		4.23	0.93	3.39	2.83
132	82.14	32.58	89.09	70.73	79.08	88.54	86.96	69.72	77.42	79.81	84.20	####	81.65	83.33	91.94	75.00	81.25	57.89	89.42	84.21	87.50	84.51	99.07	86.44	93.40
134	7.14	2.25		2.44	5.61	4.17	2.17	7.04	4.84	8.65	6.49		4.59	10.26	1.61	12.50	4.17	18.42	3.85	6.58	6.25	7.75		5.08	
136	7.14	3.37	0.91	3.05	2.04	1.04	6.52	2.11	11.29	1.60	2.38		9.63	3.85	3.23		2.08	10.53	0.96		3.57	0.70		2.54	1.89
144			1.82																						
146		0.56																			0.89				

Ots G83b	Merced	Merced-Hatchery	Toulumne	Stanislaus	Mokelumne	Consumnes	American	American-Hatchery	Feather	Feather-Hatchery	Feather HatcherySp	Butte	Butte-Spring	Deer	Deer-Spring	Mill	Mill-Spring	Battle02	Battle03	Battle/SacramentoLF	Up. Sacramento02	Up. Sacramento03	Up. Sacramento Winter	Clear	Klamath	
149					0.51							0.72														
153	4.29	1.37	3.79	2.47	1.01	1.82		1.67	3.13	1.27	0.90	4.35			0.72	8.82	2.04		3.03	4.48	2.46	1.09		3.21	0.91	
157	1.43	0.68	0.76	3.09	3.54	0.91	1.79	3.33	2.08	0.64	0.45	2.90			0.72	8.82	2.04	2.90	1.52	0.75	1.64	0.54		3.21		
161	2.86	0.68	1.52	3.70	1.01	3.64		1.67	4.17	1.91	0.23	2.17		0.89		2.94	1.02	2.17	0.76	1.49	3.28	1.09	0.71	0.92	1.82	
165	4.29	2.05	3.79	6.17	1.52	6.36	1.79	1.67	1.04	3.18	4.07	1.45		0.89	2.17	2.94	2.04	1.45	2.27	1.49	1.64	2.72		3.21	3.64	
169	8.57	0.68	0.76	1.85	0.51	0.91	3.57	1.67	4.17	1.27	0.90	1.45	0.43		0.72				5.07	1.52		0.82	1.09		1.38	3.64
173			1.52		1.01	1.82		1.11		0.32	0.68	1.45	0.86	6.25	2.17	2.94	2.04		0.76		0.82	0.54		1.83	6.36	
177	2.86	9.59	3.79	6.17	5.05	2.73	3.57	2.78	6.25	2.87	1.13	2.90			0.72	2.94	3.06	1.45	0.76	2.24	4.92	4.35		1.83	1.82	
181	1.43	0.68	3.79	6.17	3.03	10.91	7.14	1.67	4.17	5.73	4.07	2.90	0.86	3.57	2.90	2.94	5.10	2.90	3.79	1.49	4.10	3.80	4.29	5.96	16.36	
185	4.29	8.90	9.09	4.32	6.57	2.73	5.36	5.00	4.17	6.69	3.17	7.25	7.33	8.04	2.90		7.14	5.07	6.06	2.99	4.92	3.80	0.71	2.75	10.00	
189		4.79	5.30	5.56	3.03	4.55		5.56	6.25	5.10	4.75	5.80	1.72	5.36	1.45	2.94	6.12	4.35	3.79	1.49	2.46	4.89	10.71	3.67	20.91	
193	12.86	2.74	4.55	6.79	7.58	5.45	7.14	11.67	6.25	7.32	5.20	9.42	12.93	1.79	7.25	14.71	3.06	9.42	9.85	8.96	6.56	10.33	29.29	7.34	2.73	
197	2.86	6.85	4.55	8.02	5.56	6.36	7.14	4.44	2.08	7.64	6.11	2.17	14.66	15.18	10.87		12.24	8.70	5.30	9.70	6.56	6.52	5.71	5.50	1.82	
201	7.14	13.01	4.55	8.64	7.58	6.36	5.36	3.89	8.33	5.73	7.92	9.42	5.60	10.71	5.80	11.76	7.14	5.07	9.85	2.99	4.10	4.89	20.71	4.59	3.64	
205	10.00	4.79	11.36	8.02	11.11	7.27	7.14	7.22	5.21	5.73	9.05	10.87	1.29	10.71	21.01	2.94	9.18	7.97	6.06	12.69	7.38	13.04	14.29	12.84	4.55	
209	2.86	4.79	4.55	6.17	5.05	8.18	8.93	3.89	6.25	6.37	8.37	4.35	11.64	5.36	13.77	8.82	6.12	7.97	5.30	6.72	7.38	3.26	0.71	5.96	3.64	
213	4.29	9.59	6.06	6.79	10.10	3.64	5.36	8.89	3.13	9.24	8.37	5.80	8.19	9.82	8.70	8.82	10.20	9.42	11.36	3.73	3.28	10.87	2.14	6.88	4.55	
217	5.71	8.22	3.79	2.47	5.05	5.45	5.36	6.67	5.21	8.28	7.24	2.90	6.47	3.57	3.62	2.94	5.10	5.80	3.79	2.24	5.74	5.43	0.71	7.80		
221	5.71	4.11	5.30	2.47	3.03	5.45	5.36	4.44	6.25	4.78	2.49	2.17	5.60	8.04	5.07	2.94	2.04	4.35	6.82	2.24	4.92	2.17	4.29	3.67		
225	4.29	2.05	3.79	0.62	2.53	2.73	10.71	5.00	5.21	1.59	3.17	6.52	2.16	1.79	1.45	5.88	4.08	7.25	1.52	9.70	4.92	2.17	2.86	5.05	0.91	
229	1.43	4.79	2.27	2.47	4.04	3.64	3.57	4.44	4.17	2.55	5.43	3.62	1.72	0.89	1.45		3.06	1.45	3.79	6.72	8.20	7.07		2.75		
233	2.86	2.74	1.52	0.62	1.52			1.67	5.21	1.91	2.04	1.45	2.59	1.79			1.02	2.90	2.27	3.73	4.92			0.92	1.82	
237	2.86	1.37	2.27	0.62	2.53	2.73	7.14	2.22	1.04	2.87	5.88	2.17	1.72			2.94	2.04		3.03	8.21	0.82	1.63		3.67	0.91	
241	2.86	2.05	1.52	1.85	0.51	0.91	1.79	0.56		1.27	0.90	1.45	0.43				2.04		2.99	1.64	2.17			0.46	2.73	
243																							1.43			

245	2.86	2.74	2.27	1.23	1.52		1.79	1.11	2.08	0.32	2.49	1.45	1.29	0.89	1.45		2.17	1.52	0.82	1.09	0.71	0.92	1.82		
249			0.76		1.52			0.56	1.04	1.59	2.26	1.45					0.72		1.64	1.09			2.73		
253						0.91					0.45	0.72	2.59				0.76		0.82		0.71				
257										0.32	0.90														
261								0.56					6.47		3.62					0.54					
265			0.76					0.56					2.59										0.91		
269			2.27		0.51			1.11	3.13	1.27						1.02	0.76	0.75		1.09		0.46	1.82		
273								1.11		0.32				0.89	0.72	1.02						0.46			
277				1.85	0.51			0.56											0.82						
281	1.43	0.68								0.32	0.68														
285										0.32								0.75							
289												0.72													
293				0.62	0.51			1.11			0.23								0.82						
297			0.76		1.01	0.91		1.11								0.72	0.75	0.82							
301			1.52	0.62		2.73		0.56				0.43			2.94					0.54					
305			0.76		0.51					0.32	0.23		0.43			0.72		0.82				0.46			
309			0.76	0.62	1.01	0.91		0.56						0.89			0.76		0.82	0.54		0.46			
313										0.32				1.79	0.72		1.52	0.75		1.09					
317										0.32	0.23			0.89			1.52		0.54						
321																						0.46			
329																						0.46			
333										0.32												0.92			
Ots M2	Merced	Merced-Hatchery	Toulumne	Stanislaus	Mokelumne	Consumnes	American	American-Hatchery	Feather	Feather-Hatchery	Feather HatcherySp	Butte	Butte-Spring	Deer	Deer-Spring	Mill	Mill-Spring	Battle02	Battle03	Battle/SacramentoLF	Up. Sacramento02	Up. Sacramento03	Up. SacramentoWinter	Clear	Klamath
132	2.38	5.63	0.76	2.87	1.90			0.59		2.83	10.26	2.44	9.80	5.19	7.83	1.43	5.00	2.98	0.64	1.41	3.73	4.30	80.98	2.94	
136	34.52	28.17	29.55	29.89	24.76	23.68	39.58	28.24	34.91	33.96	29.04	32.32	34.80	47.40	38.55	34.29	28.57	27.98	32.05	28.17	23.88	26.34	11.41	32.03	8.93

138		0.70	0.76	0.57	0.95			3.53		0.94	0.66	1.83	0.34	0.65		2.86	2.14	1.19	1.28		0.75			0.65	12.50
140	5.95	6.34	2.27	1.15	3.81	5.26		3.53	5.66	2.52	6.55	2.44	3.04	5.19	2.41	1.43	4.29	7.14	3.21	3.52	5.22	4.30		4.25	35.71
142				0.57														0.71							
146	3.57	2.11	6.82	4.60	2.38	1.75	4.17	4.12	4.72	8.18	6.77	1.83	7.77	0.65	0.60	8.57	2.86	5.36	4.49	1.41	9.70	3.23			
148	2.38	5.63	3.79	4.02	3.33	3.51	6.25	2.94	1.89	2.52	1.97	1.83	0.68	1.95	3.01		1.43	2.98	3.21	4.93	5.22	2.69	0.54	4.25	
150	2.38	2.11	10.61	8.62	10.00	4.39	6.25	6.47	9.43	5.35	6.33	10.37	4.05	5.19	6.02	11.43	5.71	8.33	8.33	7.75	7.46	10.22		3.27	23.21
152	30.95	34.51	32.58	25.86	31.43	38.60	29.17	31.18	31.13	26.73	27.51	25.61	25.34	23.38	28.31	28.57	37.14	23.21	28.21	29.58	28.36	30.65		7.19	16.96
154			0.76	2.30	0.48				0.94			3.05	1.01					5.95	0.64			0.54	4.35	28.10	
156		0.70		0.57	0.48				0.94									0.60							0.65
158													0.34	0.65	1.81										2.68
160						0.88				0.63		0.61					0.71	1.79	0.64		0.75			0.98	
162	14.29	7.04	6.06	10.92	14.29	12.28	10.42	9.41	5.66	8.81	3.71	6.71	0.68	1.30	0.60	7.14	6.43	4.76	8.33	7.04	9.70	7.53	1.09	6.21	
164			0.76																						
166	2.38	2.82	1.52	4.60	0.95	1.75		2.35	1.89	3.14	1.31	3.05	2.36	1.95	1.81	1.43	2.86	2.98	1.92	4.93	1.49	2.69		3.59	
168	1.19	4.23	3.79	3.45	5.24	7.89	4.17	7.65	2.83	4.40	5.90	7.93	9.80	5.84	8.43	2.86	2.14	4.76	7.05	11.27	2.99	7.53	1.63	5.23	
170														0.65	0.60						0.75			0.33	
172																								0.33	

Ssa 408	Merced	Merced-Hatchery	Toulumne	Stanislaus	Mokelumne	Consumnes	American	American-Hatchery	Feather	Feather-Hatchery	Feather HatcherySp	Butte	Butte-Spring	Deer	Deer-Spring	Mill	Mill-Spring	Battle02	Battle03	Battle/SacramentoLF	Up. Sacramento02	Up. Sacramento03	Up. SacramentoWinter	Clear	Klamath
183			2.08							0.86	0.31		1.11						2.88						39.81
187	10.00	12.07	14.29	4.17	6.10	3.70	6.67	7.14	5.26	8.19	7.76	8.33	4.44	8.11	5.88		5.77	11.54	9.62	4.29	8.75	12.28	3.95	13.89	7.41
191		1.72		2.08	1.22				2.63		0.93		1.11				1.92	1.28	1.92			2.63	47.37	1.39	
195		5.17	4.76	10.42	4.27	5.56		6.12	5.26	3.45	1.55		1.67		2.94		5.77	3.85	1.92	5.71	6.25	4.39		5.56	
199	10.00	27.59	11.90	16.67	14.02	20.37	13.33	16.33	15.79	15.09	17.39	29.17	16.67	21.62	11.76	7.14	5.77	14.10	9.62	30.00	16.25	14.91	2.63	8.33	
203		5.17	1.19	12.50	5.49	1.85	6.67	3.06	10.53	3.88	4.66		13.33	4.05	13.24		1.92	7.69	0.96	1.43	3.75	4.39		1.39	
207		1.72	1.19		4.88	5.56	3.33	3.06	5.26	3.88	0.62			2.70	2.94		1.92	2.56		10.00	2.50		1.32		0.93

211			1.19		1.22					5.26	1.72	3.42			5.41	10.29		1.92		2.88	5.71		0.88		1.39	14.81
215	10.00	13.79	2.38	4.17	7.32	3.70	3.33	9.18	7.89	9.91	9.63	8.33	2.78	4.05	8.82	14.29	7.69	6.41	5.77	4.29	6.25	4.39		9.72	10.19	
219		12.07	14.29	8.33	10.98	3.70	13.33	14.29	7.89	12.50	14.91	8.33	6.11	4.05	4.41	7.14	11.54	17.95	12.50	12.86	12.50	9.65		11.11	3.70	
223			4.76	8.33	1.22	11.11	10.00	2.04		2.59	4.04	4.17	3.33	8.11	16.18		5.77	3.85	3.85		2.50	5.26	2.63	5.56	1.85	
227			2.38		1.22			1.02		2.16	1.24	4.17		5.41	1.47		5.77	2.56	0.96	2.86	3.75	3.51		1.39	3.70	
231	10.00	1.72	4.76	2.08	10.98	9.26	6.67	11.22		4.74	9.01	4.17	5.00		1.47	7.14	5.77	8.97	11.54	5.71	10.00	7.89		4.17	1.85	
235	30.00	8.62	17.86	8.33	12.80	14.81	23.33	14.29	18.42	11.21	9.63	8.33	1.67	10.81	1.47	21.43	15.38	7.69	10.58	11.43	6.25	9.65		12.50	6.48	
239	10.00	6.90	7.14	8.33	5.49	3.70	3.33	4.08	2.63	5.60	6.52	4.17	2.78	8.11	1.47	7.14	5.77		5.77	2.86	10.00	2.63	1.32	5.56	1.85	
243			8.33	4.17	7.93	7.41	3.33	5.10	7.89	6.90	4.35		9.44	13.51	4.41	21.43	3.85	2.56	7.69	2.86	2.50	6.14	5.26	5.56	2.78	
247	20.00	3.45	2.38	6.25	3.66	3.70	6.67	3.06	5.26	4.74	3.73	20.83	27.22	2.70	8.82	7.14	11.54	7.69	10.58		7.50	9.65	34.21	5.56	1.85	
251				2.08	1.22	5.56				1.29	0.31		3.33	1.35	4.41	7.14	1.92		0.96		1.25	1.75	1.32	2.78	2.78	
255			1.19								0.86								1.28						4.17	
275											0.43															

Ogo 4	Merced	Merced-Hatchery	Toulumne	Stanislaus	Mokelumne	Consumnes	American	American-Hatchery	Feather	Feather-Hatchery	Feather HatcherySp	Butte	Butte-Spring	Deer	Deer-Spring	Mill	Mill-Spring	Battle02	Battle03	Battle/SacramentoLF	Up. Sacramento02	Up. Sacramento03	Up. SacramentoWinter	Clear	Klamath
134		28.65			2.02			4.55	2.83	4.19	0.28	1.69		0.52										0.32	13.64
136	28.21	2.25	28.57	21.15	22.22	20.75	23.26	15.91	16.04	20.65	22.32	21.35	7.67	15.10	17.37	21.79	18.49	19.89	24.05	18.18	30.00	19.71	12.89	20.83	21.82
138	1.28	4.49			0.51		1.16	3.41						0.52			0.68		0.63						1.82
140	57.69	58.43	60.00	58.97	55.56	64.15	51.16	46.59	58.49	55.81	52.82	64.04	61.35	53.13	55.26	69.23	70.55	69.32	63.29	72.08	57.50	65.87	42.78	63.78	40.91
142	7.69	3.93	4.29	5.77	5.56	2.83	16.28	21.59	13.21	7.42	17.80	3.37	17.48	21.35	17.89	2.56	3.42	6.82	6.96	2.60	5.00	8.17	43.30	6.09	9.09
144														1.56											
146														0.52											
148			0.71				1.16			1.61															
154		0.56	1.43	0.64	1.01	1.89				0.65	3.95		11.35	1.04	1.05				0.63		1.88	2.40		0.64	
156							1.16										1.28		0.57						0.32
158				0.64								0.31													

Omm 1032	Merced	Merced-Hatchery	Toulumne	Stanislaus	Mokelumne	Consumnes	American	American-Hatchery	Feather	Feather-Hatchery	Feather HatcherySp	Butte	Butte-Spring	Deer	Deer-Spring	Mill	Mill-Spring	Battle02	Battle03	Battle/SacramentoLF	Up. Sacramento02	Up. Sacramento03	Up. SacramentoWinter	Clear	Klamath
160			0.71	0.64	1.01					0.32		0.56			1.58								0.48	0.32	0.91
162		0.56	2.86	7.69	3.54	4.72		1.70	2.83	3.87	1.69	2.81	1.84	4.69	6.84	1.28	2.74	2.27	1.90	6.49	2.50	1.92	1.03	3.85	3.64
164	2.56	0.56			0.51		3.49	1.70	3.77	0.65		0.56		0.52		2.56									0.32
166	2.56		1.43	4.49	5.05	5.66		3.98	2.83	3.87	1.13	5.62					3.42	1.14	2.53	0.65	3.13	1.44		3.53	5.45
168					3.03		2.33	0.57		0.97						1.28	0.68								2.73
170		0.56																							
174														0.52											
182										0.62															
186				0.55						0.21				0.61											0.96
188			2.20	1.47						0.63				3.05	1.15				1.49						14.42
190	2.94	7.87	8.46	10.44	9.80	3.70	4.41	10.12	4.72	8.23	3.73	2.90	7.31	17.68	9.20	10.81	2.73	3.33	9.70	8.11	4.00	10.53	8.78	4.29	29.81
192	50.00	50.00	52.31	41.21	53.43	49.07	52.94	60.71	45.28	48.73	55.60	44.93	63.46	53.05	59.77	45.95	45.45	36.67	53.73	50.68	44.67	50.53	85.81	51.43	45.19
194	10.29	9.55	6.92	14.84	10.78	12.04	5.88	2.98	9.43	9.49	8.09	6.52	3.08	5.49	5.17	9.46	7.27	10.67	7.46	6.76	7.33	10.00	1.35	5.36	
196	33.82	29.21	29.23	22.53	22.06	35.19	33.82	24.40	36.79	26.90	25.73	40.58	16.54	18.90	22.99	33.78	44.55	46.67	26.12	33.78	41.33	26.84	4.05	34.29	
198	2.94	3.37	3.08	7.14	2.45		2.94	1.79	1.89	5.06	4.98	4.35	2.31					2.67	0.75		0.67			4.64	3.85
200				1.10					1.89	0.95	1.04		7.31	1.22	1.15					0.68		2.11			1.92
206																									2.88
210												0.72													
212																									
214																				0.75		1.33			0.96
216																									

Ots 211	Merced	Merced-Hatchery	Toulumne	Stanislaus	Mokelumne	Consumnes	American	American-Hatchery	Feather	Feather-Hatchery	Feather HatcherySp	Butte	Butte-Spring	Deer	Deer-Spring	Mill	Mill-Spring	Battle02	Battle03	Battle/SacramentoLF	Up. Sacramento02	Up. Sacramento03	Up. Sacramento Winter	Clear	Klamath
193														0.96											
197	1.72	2.35	3.85	1.47	3.73	4.08	6.82	1.27	2.38	1.85	1.42		2.40	8.65	3.77	3.33		3.77	2.44		3.13		4.11	2.04	
201	3.45	1.76	0.77	1.47	1.49	2.04	2.27	1.27		1.85	2.84		2.80	0.96		6.67	4.55	5.66	2.44		5.21	1.47			
205	5.17	4.71	3.08	1.47	4.48	9.18	6.82	1.27		1.85	2.13	2.63		0.96	0.94	3.33	4.55	8.49	4.88	9.72	5.21	2.94		1.02	
209		3.53	0.77	0.74	0.75		2.27		2.38	1.85				1.92	1.89		2.27				1.04		17.12		
213	6.90	3.53	3.85	3.68	4.48	3.06		1.90	5.95	7.41	5.32	5.26	11.20	17.31	16.04	3.33		7.55	4.88	1.39	4.17	8.82	73.97	8.16	1.39
217		1.76	0.77	1.47	1.49	1.02	2.27	2.53	1.19	2.31	0.71	2.63	3.60		0.94		6.82	3.77	2.44	2.78	4.17	0.74	0.68	1.02	2.78
221	6.90	7.65	6.92	8.82	14.18	4.08	9.09	6.33	7.14	6.48	7.09	13.16	0.80	2.88	1.89		9.09	9.43	3.66	5.56	4.17	8.09		6.12	2.78
225	6.90	4.71	3.85	4.41	5.22	12.24	2.27	5.70	5.95	3.24	3.90	2.63	6.40	3.85	0.94	3.33	2.27	1.89	1.22	2.78	3.13	4.41		5.10	15.28
229	8.62	2.94	6.15	6.62	4.48	9.18	11.36	5.70	1.19	4.17	2.13	7.89	0.80	0.96		3.33	2.27	2.83	6.10	2.78	3.13	2.94		7.14	22.22
233	1.72	8.82	6.15	3.68	9.70	8.16	2.27	5.06	2.38	5.09	4.96	5.26	1.20	8.65	7.55	16.67		3.77	3.66	2.78	3.13	6.62		7.14	6.94
237		0.59						1.27		1.39	1.42			0.96								0.74		1.02	
241	5.17	7.65	7.69	5.15	7.46	8.16	9.09	6.96	7.14	6.48	9.57	5.26	12.80	1.92	3.77		9.09	6.60	6.10	4.17	6.25	4.41		4.08	
245	13.79	14.71	23.85	16.18	13.43	10.20	11.36	11.39	20.24	17.13	11.35	13.16	7.20	3.85	4.72	6.67	15.91	9.43	14.63	40.28	17.71	19.12		14.29	9.72
249	12.07	5.88	3.85	8.82	7.46	6.12	4.55	8.86	9.52	5.56	6.74	10.53	1.60	8.65	5.66	3.33	9.09	2.83	6.10	2.78	7.29	5.15		6.12	6.94
253	5.17	4.12	2.31	3.68	2.99	3.06	2.27	1.90	1.19	5.56	5.32	2.63				10.00	9.09	1.89	3.66	4.17	3.13	2.94		5.10	1.39
257	5.17	0.59	3.85	3.68	2.24		4.55	1.27	1.19	4.17	1.77	2.63	5.20	3.85	2.83			1.89	4.88	4.17	2.08	3.68		3.06	
261	1.72	1.76	0.77	3.68		2.04		2.53	2.38	1.85	1.06		0.40	3.85	2.83	10.00	2.27	0.94	1.22		1.04	1.47			2.78
265	1.72	5.29	3.85	2.94	3.73	2.04	2.27	6.33	5.95	3.24	3.90	5.26	12.00	0.96	6.60	6.67	2.27	6.60	13.41	5.56	1.04	5.15		4.08	2.78
269	1.72	4.12	2.31	5.15	0.75	1.02		6.33	5.95	5.09	8.51	10.53	7.60	7.69	15.09	3.33	9.09	1.89	2.44	1.39	9.38	5.15	2.74	5.10	4.17
273	6.90	6.47	10.77	4.41	6.72	7.14	11.36	10.13	7.14	3.70	10.64	7.89	7.20	1.92	5.66	3.33	6.82	8.49	3.66	4.17	7.29	8.09		11.22	6.94
277	3.45	4.71		5.88	4.48	6.12	9.09	6.33	3.57	7.41	5.67		4.00	9.62	6.60	10.00	4.55	6.60	8.54	1.39	6.25	5.15		6.12	2.78
281		1.76	3.08	3.68		1.02		4.43	1.19	1.39	1.77			4.81	5.66			3.77	3.66	1.39	1.04	2.21	1.37	2.04	
285		0.59	0.77	0.74				1.27	3.57	0.46	1.77		1.20	0.96		6.67		1.89		2.78	1.04	0.74			4.17
289	1.72		0.77	1.47	0.75				2.38				11.20	2.88	4.72										4.17

Ots	213	204	220	224	228	232	236	240	244	248	252	256	260	264	268	272	276	280	284	288	292	296	300		
	Merced	Merced-Hatchery	Toulumne	Stanislaus	Mokelumne	Consumnes	American	American-Hatchery	Feather	Feather-Hatchery	Feather HatcherySp	Butte	Butte-Spring	Deer	Deer-Spring	Mill	Mill-Spring	Battle02	Battle03	Battle/SacramentoLF	Up. Sacramento02	Up. Sacramento03	Up. SacramentoWinter	Clear	Klamath
293													0.40	0.96	1.89										1.39
297			0.74						0.46		2.63														1.39
204																									0.98
220	2.94	1.70		2.63	1.92	1.47	2.17	2.03	1.32	0.78	0.69	1.09		2.13		1.67	7.69	2.05	1.09	0.91		0.68		1.32	
224	4.41	0.57		0.66	0.64	1.47	2.17	2.03									1.92	0.68			1.72	0.68	1.35	1.32	
228				0.66	1.28		4.35	0.68			1.04	2.17	0.78					0.68				0.68		1.32	
232	7.35	3.41	4.35	5.26	3.85	4.41	13.04	10.81	2.63	5.47	7.64	5.43		1.06		10.00	3.85	8.90	5.43	9.09	13.79	8.11	54.73	9.21	0.98
236	2.94	1.14	4.35	4.61	1.28	2.94		0.68	2.63	4.30	3.47	5.43		4.26	2.59		1.92	2.05				2.03	0.68	4.61	8.82
240	5.88	4.55	7.97	5.26	3.21	11.76	4.35	2.70	10.53	8.20	4.86	4.35			1.72	6.67	1.92	4.79	4.35	5.45	6.90	6.08		7.89	5.88
244		1.70		0.64				1.35	1.32	1.95	2.43		1.56	8.51	6.03	1.67		3.42	4.35	2.73	1.72	4.05	15.54	1.97	1.96
248	1.47	2.84	4.35	3.95	3.21	1.47		2.70	3.95	1.95	3.82	5.43		1.06		1.67	5.77	4.11	3.26	3.64	3.45	1.35	0.68	0.66	1.96
252		2.27	2.17	0.66	0.64		2.17	0.68	2.63			6.52						2.05	2.17	1.82	3.45	1.35		3.95	0.98
256	5.88	5.68	2.90	1.32	1.28	5.88	2.17	2.70		2.34	2.43	2.17	0.78	5.32	1.72						1.72	3.38	0.68	1.32	
260	4.41	6.82	7.25	2.63	7.05	10.29	2.17	3.38	5.26	3.91	3.47	8.70	3.13	1.06	10.34	5.00	5.77	4.11	4.35	2.73	6.90	0.68	8.78	4.61	0.98
264	7.35	5.68	11.59	8.55	14.74	14.71	6.52	5.41	9.21	9.38	7.64	6.52	8.59	7.45	6.90	5.00	7.69	4.79	5.43	9.09	13.79	10.14		8.55	7.84
268	2.94	5.68	2.90	3.95	4.49	1.47	8.70	4.73	3.95	4.30	2.43	2.17	14.06	2.13	2.59	3.33	5.77	1.37	4.35	2.73	3.45	2.03		3.95	12.75
272	1.47	2.27	3.62	1.97	2.56	2.94		0.68	1.32	3.13	1.74		5.47	3.19	0.86	3.33	3.85	2.05		3.64	1.72	2.70		5.92	13.73
276	4.41	5.68	6.52	0.66	4.49	2.94	6.52	10.14	11.84	5.08	4.51	6.52	6.25	6.38	3.45	1.67	3.85	5.48	5.43	10.91	6.90	5.41	2.70	3.29	9.80
280	4.41	1.14	2.90	7.24	5.13		4.35	2.70	1.32	7.03	8.33	4.35		2.13	0.86	6.67	9.62	2.74	2.17	2.73	3.45	4.73		3.29	5.88
284	2.94	2.27	2.17	2.63	0.64	2.94	2.17	2.03	1.32	2.73	4.51	2.17				3.33		2.74	4.35	4.55		4.73	0.68	1.97	5.88
288	2.94	2.27	2.90	5.92	4.49	1.47	8.70	1.35	2.63	2.34	6.94	2.17	3.91	5.32	11.21	1.67	1.92	5.48	2.17	4.55		2.70	0.68	1.97	
292		1.70	1.45	2.63	3.85	2.94			2.63	1.17	3.13	4.35	3.13	5.32	6.03	1.67	1.92	3.42	3.26	2.73	5.17	1.35		4.61	9.80
296	13.24	4.55	6.52	2.63	6.41	1.47	10.87	6.76	3.95	5.47	2.08	5.43	7.81	10.64	12.07	8.33	5.77	6.16		7.27	1.72	4.73		2.63	2.94
300	2.94	4.55	2.90	4.61	5.77	2.94	2.17	4.73	2.63	7.42	5.90		15.63	6.38	6.03	6.67	5.77	6.85	10.87	5.45	6.90	4.73		5.26	6.86

304	8.82	3.98	3.62	9.21	3.85	13.24		8.11		3.91	2.08	5.43	6.25	3.19	6.03	6.67	5.77	2.74	3.26	2.73	5.17	5.41		4.61	0.98
308	1.47	4.55	0.72	2.63	3.21	1.47	2.17	1.35	6.58	1.95	2.08	1.09	9.38	3.19	1.72	6.67	7.69	2.74	7.61	2.73		2.03	6.76	3.95	
312	5.88	12.50	4.35	10.53	7.05	1.47	6.52	5.41	11.84	7.81	6.25	8.70	1.56	6.38	3.45	13.33	3.85	7.53	11.96	8.18	3.45	6.08	0.68	4.61	
316	2.94	2.27	4.35	1.97	1.28	2.94	4.35	4.73	3.95	2.34	2.78	2.17	2.34	1.06	2.59	1.67	1.92	5.48	6.52		1.72	4.05		3.29	
320	2.94				0.64				1.32	0.39	1.39		1.56		4.31		3.85	0.68		0.91		0.68		1.32	
324		5.11	4.35	2.63	3.21	7.35	4.35	7.43	2.63	2.34		2.17	4.69	2.13			1.92	1.37	2.17	4.55	3.45	2.70	1.35	1.32	
328		2.84	2.90	0.66	0.64			2.03	1.32	1.56	0.69	2.17	1.56	1.06	5.17	1.67		1.37	1.09		1.72	0.68	0.68		
332			0.72	1.32	0.64			1.35				1.74	2.17	1.56	5.32	1.72		0.68	1.09			0.68		0.98	
336		2.27	1.45	1.97	1.92			0.68		2.73	5.21	1.09		2.13	2.59	1.67		3.42	3.26	0.91	1.72	3.38	3.38	1.32	
340			0.72	0.66																		1.35	0.68		
344									1.32		0.69			3.19								0.68			
348								0.68																	

Ssa 85	Merced	Merced-Hatchery	Toulumne	Stanislaus	Mokelumne	Consumnes	American	American-Hatchery	Feather	Feather-Hatchery	Feather HatcherySp	Butte	Butte-Spring	Deer	Deer-Spring	Mill	Mill-Spring	Battle02	Battle03	Battle/SacramentoLF	Up. Sacramento02	Up. Sacramento03	Up. SacramentoWinter	Clear	Klamath
118	1.22	2.25		0.57	9.77							25.56				1.79	22.73	0.68							
120	21.95	26.97	34.09	27.01	25.29	19.61	26.67	18.97	26.09	27.73	24.14	6.67	20.00	29.89	16.03	42.86	20.91	39.04	38.96	23.19	20.00	28.49			
122	7.32	8.43	13.64	10.92	5.17	9.80	3.33	5.75	8.70	13.28	16.16	9.44	19.26	17.82	17.95	8.93	8.18	7.53	8.44	8.70	13.33	8.06		0.72	6.38
124	12.20	9.55	6.06	8.05	13.22	5.88	1.67	10.34	8.70	10.16	9.48	20.56	10.74	10.92	21.79	5.36	17.27	4.11	4.55	4.35	5.56	5.38	3.53	31.65	12.77
126	13.41	17.98	15.15	18.39	14.94	15.69	25.00	21.26	19.57	12.50	19.18	8.33	14.81	13.22	8.97	14.29	10.00	11.64	21.43	20.29	22.22	12.90	82.35	11.15	18.09
128	13.41	8.43	6.82	6.90	4.02	15.69	8.33	5.17	7.61	10.16	9.70	2.22	7.41	5.75	10.90	14.29		8.22	6.49	7.25	5.56	10.22	0.59	8.99	31.91
130	10.98	4.49	10.61	6.32	8.62	0.98	11.67	10.92	8.70	2.73	1.08	7.78	7.78	1.72	1.92	3.57	10.91	13.01	1.30	1.45		0.54	0.59	16.91	2.13
132	7.32	7.30	6.82	6.32	6.32	11.76	5.00	9.20	6.52	7.42	6.25	5.56	11.85	5.75	9.62	3.57	5.45	4.79	7.79	4.35	8.89	9.68		4.68	5.32
134	3.66	8.43	0.76	6.32	4.60	5.88	1.67	6.90	4.35	5.08	3.45	3.89	0.74	5.17	1.92	1.79		2.05	1.30	10.14	8.89	5.91	0.59	1.44	
136	1.22	3.37	2.27	1.72	1.72	5.88	3.33	0.57	3.26	5.86	3.23	1.67	2.22	5.75	1.28	3.57	0.91	2.05	3.25	8.70	5.56	8.06	2.94	8.63	1.06
138		1.69		2.87		0.98		2.30		0.39	0.43			0.57					1.30	3.62	1.11	3.23	0.59	7.19	
140	1.22													1.15			0.91							2.52	1.06

195	1.96	3.37	3.79	4.86	2.83	0.89	3.57	4.30	5.08	5.19	4.17		31.05	8.93	6.52	4.76	4.69	7.32	8.86	0.72	8.47	3.53	24.70	3.75	0.91
199	12.75	8.43	6.06	6.25	5.66	8.93	4.76	10.22	2.54	2.27	3.27	6.25	3.59	1.79	1.09	4.76	6.25	7.32	5.70	10.14	4.24	12.94	22.29	7.19	0.91
203	0.98	2.25		1.39	4.25	4.46	4.76	2.15	2.54	1.62	2.08	4.17				5.95	7.03	4.88	1.90	2.90	5.08	1.18	0.60	2.81	
207	1.96	1.69	5.30		2.83	2.68	1.19	0.54	5.08	0.65	0.89	2.08	1.96	4.17	2.17	1.19	3.13	3.05	1.27	4.35	0.85	1.18		5.00	
211	4.90	5.06	9.09	9.03	8.96	8.93	11.90	8.06	7.63	6.49	6.55	6.25	1.96	3.57	2.17	9.52	7.81	2.44	6.33	5.80	3.39	6.47	1.81	5.00	8.18
215	2.94	5.62	2.27	6.25	2.83		4.76	5.91	4.24	3.25	1.49	8.33	2.61	5.36	7.61	2.38	0.78	2.44	6.96	2.90	5.93	2.94	2.41	3.75	0.91
219	10.78	13.48	15.91	18.75	13.68	19.64	14.29	14.52	7.63	14.94	9.23	8.33	16.34	10.71	12.50	15.48	13.28	19.51	16.46	11.59	19.49	15.29		14.38	1.82
223	0.98	3.93	1.52	2.78	2.83	0.89	1.19	4.30	2.54	1.95	5.95	4.17	0.65	1.19		1.19		1.22	0.63	2.90	2.54	1.76		3.44	16.36
227	1.96		1.52	1.39	0.47	2.68	1.19	0.54	1.69	3.57	1.49	2.08						0.61	0.63	1.45				0.94	2.73
231	0.98	1.12	3.79	1.39	1.89	1.79	1.19	1.61	3.39	2.27	2.68	4.17				1.19	1.56	0.61		0.72	1.69	0.59		1.88	1.82
235		0.56				0.89					0.32			1.19							0.85			0.31	0.91
239					0.47		1.19				0.65		0.65	4.76	4.89	1.19					0.85		0.60	0.31	4.55
243	0.98	1.69	2.27	2.78	2.36	0.89	4.76	2.15	1.69	1.30	0.30	4.17	0.98	1.19	1.63		1.56	1.22	0.63	4.35	1.69	0.59		0.31	1.82
247		1.12	2.27	0.69	3.30	0.89	1.19	2.69	0.85	0.65					0.54	2.38	3.13	3.05	3.16	2.17	1.69	2.35		1.88	6.36
251		1.12		2.08	0.47			1.61		0.65	0.30	4.17	0.33												0.31
255										0.85	0.32														
259	0.98				0.94			2.15			0.60			2.38	2.72		0.78			0.72	0.85	0.59		0.31	
263				0.69							0.60					2.38		0.61	1.90			1.18			
275	0.98										0.30											0.59		0.31	
279								0.54		0.65					0.54	1.19		0.61	0.63					0.94	
291			0.76		0.47																	0.85			
295				0.69				0.54																	
307																						0.85			
311													2.08												

OtsG311	Merced	Merced-Hatchery	Toulumne	Stanislaus	Mokelumne	Consumnes	American	American-Hatchery	Feather	Feather-Hatchery	Feather HatcherySp	Butte	Butte-Spring	Deer	Deer-Spring	Mill	Mill-Spring	Battle02	Battle03	Battle/SacramentoLF	Up. Sacramento02	Up. Sacramento03	Up. Sacramento Winter	Clear	Klamath
251											0.24	0.88													
255		1.19			0.70	0.89			1.39	1.28	0.73	0.88		1.04				4.88			0.88	1.43		0.72	2.27
259	8.93	1.19	2.73	6.72	2.82	1.79	3.85	4.38	2.78	0.96	0.24		15.22	4.17	10.16				0.75	1.85		2.86		1.45	5.68
263		1.79	0.91	2.24	1.41				1.39		0.24	1.75	0.72	5.21	4.69			4.88	2.99		0.88		2.13	2.17	1.14
267	1.79	1.79	0.91	4.48	2.82	2.68				3.53	1.46			3.13	0.78		5.00	3.66	3.73	0.93	0.88	1.43		1.45	2.27
271	3.57	3.57			2.11	0.89	1.92	2.50	1.39		3.40	1.75			1.56		5.00	1.22	2.99	3.70				0.72	1.14
275	1.79	2.38	7.27	0.75	6.34	3.57	1.92	2.50		2.24	2.43	2.63	4.35	6.25	4.69	3.57		1.22	3.73	8.33	2.63	5.00	4.26	0.72	2.27
279		0.60	3.64	2.99	2.11	1.79		1.88	1.39	3.53	2.18	1.75	0.72		3.13		10.00		2.24	0.93	2.63	2.14	1.06	0.72	4.55
283	1.79	2.38	3.64		2.82	3.57	5.77	1.25	6.94	2.88	0.97	2.63		2.08	3.91		5.00	1.22	2.24	3.70	1.75	2.14		1.45	7.95
287	10.71	2.98	5.45	3.73	3.52	0.89	1.92	1.88		3.85	4.37	0.88	0.72		0.78			2.44	2.24	1.85	2.63	2.14	4.26	2.17	10.23
291	3.57	2.98	1.82	3.73	4.93	0.89		1.25	1.39	6.09	5.10	4.39	5.07	3.13	6.25	3.57	5.00	4.88	4.48	3.70	2.63	3.57		3.62	15.91
295	7.14	1.79	2.73	2.99	4.23	0.89	5.77	3.75	2.78	2.24	1.70	0.88	7.97	4.17	3.91	7.14	5.00		6.72	6.48	2.63	1.43		4.35	6.82
299	1.79	6.55	3.64	5.97	5.63	8.04	3.85	7.50	4.17	5.13	6.55	5.26	18.12	5.21	7.03	14.29		12.20	8.21	5.56	7.02	9.29		10.14	3.41
303	7.14	5.95	10.00	4.48	4.93	9.82	1.92	8.75	9.72	5.77	8.74	7.02	13.04	11.46	10.94	7.14	5.00	8.54	5.97	6.48	8.77	7.86	2.13	8.70	1.14
307	3.57	7.14	5.45	10.45	4.93	1.79	3.85	11.25	8.33	5.45	4.61	9.65		6.25	3.13	10.71	10.00	3.66	2.99	3.70	7.89	7.14		5.80	3.41
311	3.57	7.14	3.64	2.99	2.11	8.04	15.38	3.13	4.17	6.73	8.25	2.63	4.35	2.08	4.69			6.10	5.22	3.70	4.39		2.13	9.42	
315	3.57	4.76	8.18	8.96	5.63	3.57	5.77	4.38	9.72	4.49	4.13	7.89	2.17					4.88	2.99	0.93	0.88	5.71		2.90	
319	1.79	2.38	5.45	3.73	3.52	5.36	9.62	4.38	2.78	5.45	5.34	4.39	3.62	7.29	5.47	3.57		1.22	7.46	7.41	3.51	5.00		5.07	1.14
323		2.98	2.73	3.73	2.82	3.57	5.77	4.38	4.17	2.24	1.70	4.39	2.90	3.13	1.56	7.14		3.66	4.48	12.04	7.02	9.29	3.19	5.80	1.14
327	1.79	4.76	2.73	0.75	3.52	3.57	1.92	1.25	1.39	4.49	5.10	0.88	0.72	4.17	0.78	3.57	5.00	1.22	1.49	3.70	4.39	10.00	8.51	7.25	1.14
331	8.93	5.95	3.64	5.97	4.93	6.25	1.92	7.50	8.33	3.21	5.10	9.65	3.62	3.13		3.57		7.32	2.99	5.56	3.51	2.86	4.26	7.25	
335	7.14	16.07	4.55	4.48	11.27	3.57	11.54	3.75	5.56	7.69	5.34	5.26	0.72	3.13	2.34	14.29	5.00	2.44	1.49	2.78	7.89	2.86		2.90	
339	1.79	2.98	1.82	4.48	4.23	8.04	3.85	2.50	1.39	4.81	3.40	4.39	0.72	2.08	2.34	3.57	5.00	4.88	2.99	0.93	7.02	2.14		3.62	
343	8.93	1.79	5.45	5.97	2.11	5.36	1.92	5.63	4.17	2.24	1.70	2.63	7.25	6.25	0.78	7.14	5.00	3.66	5.97	1.85	9.65	4.29	14.89	1.45	
347	1.79	1.79	3.64	6.72	3.52	6.25	7.69	3.75		4.81	1.46	7.02		1.04	3.13		5.00	6.10	2.24	4.63	0.88	3.57	3.19	1.45	2.27

351		1.19			0.70	1.79	1.92	1.25	4.17	2.88	8.74	0.88	1.45	2.08	8.59			3.73	2.78	3.51	1.43	31.91	0.72		
355	3.57		0.91	2.24	1.41	4.46		1.88	1.39	1.28	0.97	0.88	0.72	2.08	3.91	3.57		1.49	0.93		2.14	13.83	1.45		
359	1.79	0.60	0.91		1.41			1.88			0.24	4.39		4.17			15.00	1.22	2.24	0.93		1.43	0.72	1.14	
363		2.98			0.70		1.92	3.13		1.60	0.97	1.75	2.17	3.13	1.56		10.00	2.44	0.75		2.63	0.71	1.45	3.41	
367		0.60	0.91	1.49	0.70	0.89		0.63	2.78		0.97	1.75	3.62	1.04	2.34	7.14		1.22	2.24	0.93		0.71	2.13	1.45	
371		1.19				0.89		0.63	1.39	0.96					1.04			1.22							
375		0.60	3.64		1.41	0.89		0.63	1.39	0.64	1.21							1.22	0.75		0.88	0.71		1.45	5.68
379	1.79		1.82		0.70			0.63	1.39	1.28	0.24				2.08	1.56						0.71		0.72	1.14
383								1.25		1.28		0.88								0.93	1.75				1.14
387			1.82						2.78										0.75	1.85			2.13		1.14
391	1.79																	1.22							1.14
395												0.49									0.88			0.72	
399											0.64	1.21						1.22	1.49	0.93					1.14
403									1.39	0.32	0.24														2.27
407								0.63																	
411												0.24													
415																									3.41
419																									1.14
423																									2.27
427																									1.14

OtsG432	Merced	Merced-Hatchery	Toulumne	Stanislaus	Mokelumne	Consumnes	American	American-Hatchery	Feather	Feather-Hatchery	Feather HatcherySp	Butte	Butte-Spring	Deer	Deer-Spring	Mill	Mill-Spring	Battle02	Battle03	Battle/SacramentoLF	Up. Sacramento02	Up. Sacramento03	Up. SacramentoWinter	Clear	Klamath
107																		3.38							1.02
111		3.16	1.52	5.13	0.48	1.82		1.67	2.59	1.85	0.83	1.69			2.35		1.00	0.68	4.03	2.24	1.35	1.69		1.56	1.02
115	2.08	1.90	2.27	3.21	0.95	0.91	5.95	0.56		0.93	2.90	1.69	0.66	5.95	2.35	1.28	2.00	1.35	2.42	5.97	2.70	2.25		1.56	38.78
119		0.63																						0.78	3.06

123	15.63	14.56	9.09	12.18	10.95	10.00	4.76	10.56	15.52	13.89	20.12	9.55	11.84	10.12	12.94	12.82	13.00	10.81	11.29	8.21	10.81	10.67	0.76	12.11	
127	35.42	26.58	34.09	40.38	30.95	37.27	32.14	27.22	29.31	33.33	32.16	34.83	35.86	45.83	36.47	34.62	28.00	30.41	35.48	22.39	32.43	31.46	59.09	37.50	8.16
131	4.17	3.16	3.79	1.92	5.24	0.91	5.95	3.33	7.76	5.56	4.15	2.81	5.26	1.19	1.76	2.56		4.73	1.61		3.38	2.81		3.52	
135	7.29	17.72	13.64	18.59	17.62	12.73	23.81	18.33	16.38	10.49	9.13	19.66	6.91	3.57	4.71	8.97	13.00	16.89	13.71	8.21	10.14	12.92		11.33	
139	3.13	3.80	2.27	1.28	4.29	4.55	2.38	4.44	1.72	2.16	2.07	2.25	3.95	1.19	0.59	5.13	9.00	1.35	0.81	8.96	2.70	3.93	1.95	1.02	
143										0.31									1.61			0.56		7.14	
147	7.29	9.49	14.39	7.05	5.24	7.27	3.57	10.00	6.03	7.41	1.24	5.62	1.97	8.33	5.88	2.56	8.00	7.43	10.48	7.46	6.08	7.30	2.27	7.03	12.24
151	5.21	3.16	4.55	3.21	2.86	5.45	2.38	6.11	6.90	4.63	3.53	3.37	3.29	1.19	4.12	6.41	6.00	4.05	6.45	7.46	5.41	6.74	12.12	4.30	1.02
155	3.13	5.70	2.27		2.38	6.36	3.57	5.00	2.59	1.54	1.66	3.37		3.57	1.76	2.56	4.00	4.05	0.81		4.73	3.37	10.61	1.56	2.04
159	2.08	1.27	3.03	1.92	2.38	3.64	1.19	1.67	0.86	0.31	1.87	2.81	0.66	1.79		1.28	2.00	0.68	0.81		1.35		0.39	16.33	
163	1.04			0.64	0.48			0.56		0.62	0.41		7.57	1.79	4.71			1.35			0.68		1.17	2.04	
167	1.04			0.64				0.56		1.85	1.45		3.62	3.57	10.59	1.28		0.68		2.24	1.35	0.56		1.56	2.04
171	3.13	1.90	1.52	1.28	2.86	0.91	5.95	3.33	3.45	2.78	2.28	1.69	0.33	1.19	1.76	1.28	1.00	1.35	0.81	1.49	1.35	2.25	0.76	3.52	2.04
175	1.04	1.27	1.52	0.64	3.33	0.91		1.11	4.31	0.31	2.28	0.56	2.96	0.60	2.35	1.28	4.00	1.35		2.24	0.68	2.25	0.76	1.56	1.02
179	3.13	3.16	2.27	0.64	3.81	2.73	1.19	2.22	1.72	3.09	6.02	3.93	12.83	8.93	5.29	10.26	7.00	4.05	3.23	2.24	4.73	1.69	0.76	3.13	1.02
183	4.17	2.53	3.79	1.28	3.33	2.73	4.76		0.86	4.01	3.94	2.25	0.33	1.19		3.85	2.00	3.38	2.42	8.21	6.76	4.49	12.88	1.95	
187	1.04				1.43	0.91	2.38	3.33		1.85	0.83	1.12	0.33		2.35	1.28		2.03	2.42	1.49	1.35	0.56		1.56	
191					0.48					0.62	0.21	1.12								2.99	0.68	1.69		1.17	
195						0.91				0.93	0.83	0.56	0.33							2.99		1.12			
199					0.48					0.93	1.24	1.12	0.66			2.56			1.61	2.99	1.35	1.12		0.78	
207											0.21		0.66								2.24				
211					0.48					0.62	0.62												0.56		

OtsG78b

200
204

Merced	6.06	4.67	0.83	2.54																					
Merced-Hatchery		0.67																							
Toulumne																									
Stanislaus																									
Mokelumne					0.81																				
Consumnes																									
American																									
American-Hatchery										2.38	2.50	1.43	0.81	5.00											
Feather										0.60	1.25														
Feather-Hatchery																									
Feather HatcherySp																									
Butte																									
Butte-Spring																									
Deer																									
Deer-Spring																									
Mill																									
Mill-Spring																									
Battle02																									
Battle03																									
Battle/SacramentoLF																									
Up. Sacramento02																									
Up. Sacramento03																									
Up. SacramentoWinter																									
Clear																									
Klamath																									

208	1.52	0.67		0.85	0.81			2.38	2.50					1.61				0.81		2.44					
212	1.52			2.54				0.60	1.25		1.34		7.03	0.98	1.49					2.44					
216	3.03	8.67	2.50	5.93	4.03		4.17	2.98	1.25	2.50	3.23	1.67		1.49	3.23	16.67		2.94	5.10	3.70	4.03	8.70	7.41	1.22	
220	1.52	2.00	0.83	5.08	1.61			4.17	2.50	2.50	3.23	1.67						1.52	4.41		0.93	0.81		0.62	
224		1.33						1.19		0.36	0.27	1.67		1.96				1.47	1.02					1.22	
228	1.52	2.67		0.85						1.79	1.88					1.61		0.76							
232			0.83						1.25	0.36	4.03							0.76							
236	3.03	1.33			1.61	1.43	2.08	1.79	3.75	0.36	2.96		0.78					1.47	2.04	0.93	3.23		2.47	9.76	
240	4.55	2.67	2.50		0.81	2.86	2.08	2.98		2.14	2.96	1.67	2.34				3.33	3.03		0.93	0.81		4.32	3.66	
244	3.03		1.67	5.08	4.84	2.86		2.38	5.00	1.43	1.34	8.33	2.34	3.92	2.99		3.33	1.52	1.47		2.78	0.81		2.44	
248	1.52	2.00	2.50			7.14	2.08	0.60	2.50	3.57	1.08		3.13	0.98		1.61		3.03	1.47	2.04	0.93		1.85	8.54	
252	1.52	5.33	0.83	3.39	1.61		2.08	1.79	5.00	5.71	9.41	1.67		3.92	5.97	6.45	3.33	3.03	7.35	8.16	3.70	9.68	2.17	3.70	10.98
256	6.06	4.00	6.67	0.85	7.26		6.25	5.36	3.75	2.86	1.34	8.33	3.13	3.92	8.21	9.68	3.33	1.52	5.88	1.02	7.41	4.84		8.64	4.88
260	1.52	4.67		4.24	4.03	4.29		5.36	1.25	7.14	3.23	3.33		0.98	2.24	1.61		1.52			3.70	4.84		3.70	4.88
264	1.52	2.00	6.67	1.69	0.81		10.42	4.17	1.25	2.14	2.96	1.67	0.78	5.88	7.46	6.45		3.79		2.04	3.70	4.84		2.47	21.95
268			2.50	5.08	3.23	5.71		2.98	1.25	1.43	2.42	6.67	3.13	3.92	0.75	3.23		3.79	2.94	10.20	3.70	3.23		3.70	7.32
272	1.52	2.67	1.67	1.69	0.81	2.86	2.08	0.60	6.25	1.79	1.88	1.67		1.96		1.61	3.33	3.79			2.78	1.61		2.47	2.44
276	9.09	4.67	5.00	5.08	2.42	10.00	8.33	5.36	7.50	4.29	3.23	3.33	2.34	5.88	5.97	4.84	3.33	4.55	4.41	3.06	0.93	4.03		6.79	1.22
280	9.09	4.67	3.33	4.24	4.03	1.43		2.38	2.50	6.07	0.81	5.00	3.91	3.92	4.48	3.23	3.33	8.33	4.41	11.22	6.48	4.03	2.17	4.94	
284	1.52	6.67	5.83	5.08	4.03	5.71	8.33	4.76		3.93	2.96	3.33	0.78	7.84	5.22	6.45	3.33	3.79	10.29	4.08	0.93	4.84		7.41	2.44
288	7.58	3.33	4.17	6.78	7.26	2.86	8.33	4.76	7.50	5.71	5.91		8.59	3.92	11.19	8.06	6.67	11.36	4.41	2.04	7.41	4.03		4.94	1.22
292	3.03	8.00	9.17	0.85	5.65	4.29	8.33	2.98	2.50	3.21	3.23	13.33	3.13	1.96	2.24	1.61	6.67	3.03	7.35	1.02	0.93	4.03	2.17	5.56	1.22
296	12.12	5.33	5.83	7.63	8.06	8.57	4.17	5.95	6.25	4.64	4.03	8.33	17.97	12.75	11.19	6.45	10.00	10.61	5.88	7.14	13.89	7.26		3.70	
300	7.58	8.67	11.67	6.78	4.84	4.29	4.17	8.93	8.75	7.86	5.65	3.33	13.28	7.84	8.21	4.84	3.33	11.36	8.82	11.22	2.78	10.48	4.35	7.41	
304	3.03	2.00	5.00	4.24	6.45	10.00	6.25	5.36	2.50	4.29	2.69	1.67	1.56	6.86	0.75	4.84	3.33	2.27	7.35	11.22	7.41	1.61	8.70	3.09	7.32
308	1.52	4.67	4.17	4.24	3.23	5.71		5.95	2.50	1.07	0.27	5.00	0.78		1.49	8.06	6.67	6.06	5.88	3.06	7.41	4.03	17.39	1.85	
312		3.33	3.33	4.24	2.42	4.29	4.17	0.60	3.75	1.43	3.49		3.13		0.75	3.23			4.41	6.12	2.78	4.03		1.85	1.22
316	1.52	2.67	2.50	3.39	4.84	7.14		2.98	2.50	4.29	2.96	3.33	1.56	2.94	2.99	3.23		2.27		1.02	4.63	3.23	2.17	1.85	
320	1.52	0.67	1.67	0.85	4.03	1.43		1.79	3.75	1.43	0.81							0.75		1.02	1.85	0.81	4.35	1.85	
324			0.83		1.61			1.19		1.43	4.57			2.94	0.75					2.04		0.81	2.17	1.85	
328			3.33		1.61	1.43			1.25	1.79	1.34	1.67						0.76						4.35	
332			0.83		3.23	2.86	8.33	0.60	1.25	0.71	1.61	5.00	1.56	0.98	0.75		3.33	2.27		1.02	0.93	1.61	15.22	1.23	1.22
336			1.67		1.61	1.43	2.08	1.19	2.50	2.14	0.81			2.94	0.75	1.61					1.85		4.35	0.62	

Appendix B: Full matrices of individual assignments. The diagonal are correct assignments. Columns are all fish assigned to that population. Rows are inferred assignment origin for all fish from that population.

a. All fish assigned to most likely population. No Feather River Hatchery "spring-run"

	Merced	Merced-Hatchery	Toulumne	Stanislaus	Mokelumne	Consumnes	American	American-Hatchery	Feather	Feather-Hatchery	Butte-Fall	Deer-Fall	Mill-Fall	Clear	Battle02	Battle03	Up. Sacramento02	Up. Sacramento03	Battle/SacramentoLF	Butte-Spring	Deer-Spring	Mill-Spring	Up. Sacramento-Winter	Klamath
Merced	1	1	5	2	1	2	3	5	4	2	1	1	1	1	3	1	3	2	0	0	0	0	0	0
Merced-Hatchery	1	61	2	0	4	0	0	9	3	3	0	0	1	0	2	0	2	1	0	0	0	0	0	0
Toulumne	3	1	9	3	15	2	1	4	4	3	1	0	1	3	2	7	4	3	0	1	1	0	0	0
Stanislaus	1	4	7	24	5	2	0	4	1	6	2	1	2	0	3	4	4	7	1	1	0	1	0	0
Mokelumne	5	0	6	4	17	5	2	9	2	8	8	1	3	3	4	8	7	10	3	0	1	0	0	0
Consumnes	1	0	5	3	7	10	0	5	1	6	1	1	0	2	1	1	4	7	2	0	0	0	0	0
American	0	1	0	0	6	1	3	4	1	3	1	1	0	0	3	1	2	0	1	0	0	0	0	0
American-Hatchery	3	5	4	4	14	2	2	15	2	6	1	2	3	4	2	5	3	7	3	1	0	0	0	0
Feather	0	1	6	1	7	3	0	6	5	5	3	1	2	0	4	0	0	2	1	1	0	0	0	0
Feather-Hatchery	7	3	13	4	11	4	0	6	5	51	1	1	2	5	4	10	13	15	5	2	0	2	0	0
Butte-Fall	1	2	3	1	14	3	1	3	4	1	15	0	4	4	6	2	1	0	0	0	0	1	0	0
Deer-Fall	0	2	0	0	0	0	0	5	2	5	1	3	0	1	3	6	1	3	1	0	0	0	0	0
Mill-Fall	5	1	2	2	9	0	1	1	2	1	5	4	3	2	5	3	1	3	1	1	0	0	0	0
Clear	3	0	4	0	6	1	2	3	6	2	3	1	2	63	5	2	2	7	2	0	0	1	0	0
Battle02	1	1	4	2	6	0	2	4	4	10	0	2	0	2	14	2	7	5	0	0	1	1	0	0
Battle03	1	0	4	4	6	1	2	2	1	5	2	6	1	0	5	14	3	5	2	0	1	2	0	2
Up. Sacramento02	3	0	3	0	5	3	1	3	1	9	2	1	0	1	5	4	5	5	5	2	2	1	0	0
Up. Sacramento03	0	0	6	1	3	3	0	6	0	12	1	0	3	6	4	8	8	16	9	1	1	1	0	0
Battle/SacramentoLF	0	1	4	0	4	1	2	2	2	6	0	0	0	1	2	1	4	12	28	0	0	0	0	0
Butte-Spring	0	0	1	1	0	0	0	0	0	2	0	1	0	0	1	3	1	0	0	115	1	2	0	0
Deer-Spring	1	0	3	3	1	0	1	1	2	4	0	1	0	1	1	3	1	2	0	0	23	19	0	0
Mill-Spring	3	0	1	2	1	0	1	0	0	1	1	3	1	2	2	2	1	1	0	4	10	46	0	0
Up. Sacramento-Winter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73	0
Klamath	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	55

b. Confident assignments using 95% probability criterion. No Feather River Hatchery "spring-run"

	Merced	Merced-Hatchery	Toulumne	Stanislaus	Mokelumne	Consumnes	American	American-Hatchery	Feather	Feather-Hatchery	Butte-Fall	Deer-Fall	Mill-Fall	Clear	Battle02	Battle03	Up. Sacramento02	Up. Sacramento03	Battle/SacramentoLF	Butte-Spring	Deer-Spring	Mill-Spring	Up. Sacramento-Winter	Klamath
Merced	0	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Merced-Hatchery	0	45	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Toulumne	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Stanislaus	1	2	1	10	2	1	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mokelumne	1	0	0	0	0	0	0	0	1	0	2	0	1	0	0	1	1	1	0	0	0	0	0	0
Consumnes	0	0	0	0	0	2	0	0	0	2	0	0	0	0	0	1	0	2	0	0	0	0	0	0
American	0	0	0	0	1	1	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
American-Hatchery	1	0	0	1	4	1	0	5	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
Feather	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Feather-Hatchery	1	1	2	0	1	0	0	0	2	13	0	0	0	0	1	1	0	2	1	0	0	0	0	0
Butte-Fall	0	0	0	1	2	0	0	0	1	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Deer-Fall	0	0	0	0	0	0	0	0	1	0	1	0	1	0	0	1	0	0	0	0	0	0	0	0
Mill-Fall	0	0	0	1	1	0	0	0	0	1	1	0	0	0	0	0	2	0	0	0	0	0	0	0
Clear	1	0	1	0	1	0	0	1	0	1	0	0	1	26	2	0	0	0	0	0	0	0	0	0
Battle02	0	0	0	1	0	0	1	0	0	0	0	0	0	1	5	0	1	0	0	0	0	0	0	0
Battle03	0	0	0	1	0	0	1	0	0	0	1	1	0	0	0	2	0	0	0	0	0	0	0	2
Up. Sacramento02	0	0	0	0	2	0	0	0	0	1	0	0	0	0	1	0	0	1	3	2	0	0	0	0
Up. Sacramento03	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	2	0	1	2	0	0	1	0	0
Battle/SacramentoLF	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	12	0	0	0	0	0
Butte-Spring	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	100	0	0	0	0
Deer-Spring	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	14	1	0	0
Mill-Spring	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	2	31	0	0
Up. Sacramento-Winter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73	0
Klamath	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	54

c. All fish assigned to most likely population. Includes Feather River Hatchery "spring-run".

	Merced	Merced-Hatchery	Toulumne	Stanislaus	Mokelumne	Consumnes	American	American-Hatchery	Feather	Feather-Hatchery	Butte-Fall	Deer-Fall	Mill-Fall	Clear	Battle02	Battle03	Up. Sacramento02	Up. Sacramento03	Feather-HatcherySp	Battle/SacramentoLF	Butte-Spring	Deer-Spring	Mill-Spring	Up. Sacramento-Winter	Klamath
Merced	1	1	5	2	1	2	3	5	4	2	1	1	1	1	3	1	3	1	1	0	0	0	0	0	0
Merced-Hatchery	1	61	2	0	4	0	0	9	3	3	0	0	1	0	2	0	2	1	0	0	0	0	0	0	0
Toulumne	3	1	9	3	14	2	1	4	4	3	1	0	1	3	2	7	3	2	4	0	1	0	0	0	0
Stanislaus	1	4	7	23	5	2	0	4	1	6	2	1	2	0	3	4	4	6	2	1	1	0	1	0	0
Mokelumne	5	0	6	3	17	4	2	9	2	8	8	1	3	3	4	8	6	10	3	3	0	1	0	0	0
Consumnes	1	0	5	3	6	10	0	5	1	6	1	1	0	2	1	1	4	7	1	2	0	0	0	0	0
American	0	1	0	0	6	1	3	3	1	0	1	1	0	0	3	1	2	0	4	1	0	0	0	0	0
American-Hatchery	3	5	4	4	13	2	2	15	2	6	1	2	3	4	1	5	3	7	2	3	1	0	0	0	0
Feather	0	1	6	1	7	3	0	6	3	4	3	1	1	0	4	0	0	2	4	1	1	0	0	0	0
Feather-Hatchery	7	3	13	4	11	4	0	6	5	42	0	1	1	4	3	9	10	11	22	5	2	0	1	0	0
Butte-Fall	1	2	3	1	14	3	1	3	4	1	15	0	4	4	5	2	1	0	1	0	0	0	1	0	0
Deer-Fall	0	2	0	0	0	0	0	5	2	4	1	3	0	1	3	6	1	2	2	1	0	0	0	0	0
Mill-Fall	5	1	2	2	8	0	1	1	2	1	5	4	3	2	4	3	1	3	2	1	1	0	0	0	0
Clear	3	0	4	0	6	1	2	3	6	1	3	1	2	62	5	2	2	7	3	1	0	0	1	0	0
Battle02	1	1	4	2	6	0	2	4	4	9	0	2	0	1	14	2	7	5	2	0	0	1	1	0	0
Battle03	1	0	4	4	6	1	2	2	1	5	2	6	1	0	5	14	2	5	1	2	0	1	2	0	2
Up. Sacramento02	2	0	3	0	5	3	1	3	1	8	1	1	0	1	5	3	5	5	5	5	2	2	0	0	0
Up. Sacramento03	0	0	6	1	2	3	0	6	0	6	1	0	3	5	4	8	7	15	10	9	1	1	1	0	0
Feather-HatcherySp	1	0	6	3	8	5	1	4	5	29	0	1	2	5	7	6	6	16	124	1	0	2	3	0	0
Battle/SacramentoLF	0	1	4	0	4	1	2	2	2	5	0	0	0	1	2	1	4	11	2	28	0	0	0	0	0
Butte-Spring	0	0	1	1	0	0	0	0	0	2	0	1	0	0	1	3	1	0	2	0	113	1	2	0	0
Deer-Spring	1	0	3	1	1	0	1	1	2	3	0	1	0	1	1	2	1	2	4	0	0	23	19	0	0
Mill-Spring	3	0	1	1	1	0	1	0	0	1	0	3	1	2	2	2	1	1	3	0	4	10	45	0	0
Up. Sac-Winter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73	0
Klamath	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	55

d. Confident assignments using 95% probability criterion. Includes Feather River Hatchery "spring-run"

	Merced	Merced-Hatchery	Toulumne	Stanislaus	Mokelumne	Consumnes	American	American-Hatchery	Feather	Feather-Hatchery	Butte-Fall	Deer-Fall	Mill-Fall	Clear	Battle02	Battle03	Up. Sacramento02	Up. Sacramento03	Feather-HatcherySp	Battle/SacramentoLF	Butte-Spring	Deer-Spring	Mill-Spring	Up. Sacramento-Winter	Klamath
Merced	0	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Merced-Hatchery	0	44	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Toulumne	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Stanislaus	1	2	1	10	2	1	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mokelumne	1	0	0	0	0	0	0	0	1	0	2	0	1	0	0	1	1	1	1	0	0	0	0	0	0
Consumnes	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0
American	0	0	0	0	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
American-Hatchery	1	0	0	1	4	1	0	5	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Feather	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Feather-Hatchery	0	1	2	0	1	0	0	0	2	6	0	0	0	0	1	1	0	2	4	1	0	0	0	0	0
Butte-Fall	0	0	0	1	2	0	0	0	1	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Deer-Fall	0	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Mill-Fall	0	0	0	1	1	0	0	0	0	0	1	1	0	0	0	0	0	2	0	0	0	0	0	0	0
Clear	1	0	1	0	1	0	1	0	1	0	0	0	1	25	2	0	0	0	0	0	0	0	0	0	0
Battle02	0	0	0	1	0	0	1	0	0	0	0	0	0	0	5	0	1	0	0	0	0	0	0	0	0
Battle03	0	0	0	1	0	0	1	0	0	0	1	0	0	0	0	2	0	0	0	0	0	0	0	0	2
Up. Sacramento02	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	3	2	0	0	0	0
Up. Sacramento03	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	2	0	1	1	1	0	0	1	0	0
Feather-HatcherySp	0	0	0	0	0	1	0	0	0	4	0	0	0	0	0	0	0	2	49	0	0	1	1	0	0
Battle/SacramentoLF	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	12	0	0	0	0	0
Butte-Spring	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	99	0	0	0	0
Deer-Spring	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	14	1	0	0
Mill-Spring	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	2	29	0	0
Up. Sac-Winter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73	0
Klamath	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	54