Agenda Item E.3.a
Supplemental NMFS Report 2
April 2015

Estimates of Chinook salmon stock composition in bycatch associated with the 2009 and 2010 US West Coast At-Sea Pacific hake fishery

A report to the Northwest Regional Office, NOAA's National Marine Fisheries Service
27 September 2011

Paul Moran and Vanessa Tuttle
Conservation Biology Division
Fishery Resource Analysis and Monitoring Division
Northwest Fisheries Science Center
Seattle, Washington USA

Abstract

This study used genetic mixture analysis to obtain stock composition estimates for Chinook salmon bycatch in the 2009 and 2010 West Coast Pacific hake fishery. We also tested for genotyping efficiency a subsample of a very large historical scale collection. The scales gave excellent results, as good as fin clips. This success opens enormous potential for historical oceanographic genetics. More than 40,000 scale samples taken by NOAA fishery observers since the 1970s can be used to examine stock-specific associations with oceanographic factors spanning ENSO cycles and climatic regimes. In our contemporary collections, Lower Fraser populations were major contributors to Chinook salmon bycatch in 2009 and 2010 (>25% each year) followed by Columbia River stocks in 2009 but shifting south to Klamath, Rogue, and Mid-Oregon coastal stocks in 2010. Several genetic stock groups that include ESA-listed populations showed statistically significant contributions to these bycatch mixtures (95% confidence limits not overlapping zero). In 2009, these included West Cascade spring and fall groups and Spring Cr. Group tules (2.8%, 7.4%, and 10.3%), Snake River falls (3.9%), Hood Canal and North and South Puget Sound stocks (6.2%, 6.2%, and 5.2%). In 2010, genetic stock groups with protected populations included California Coast (2%), West Cascade falls and Spring Cr. Group (3.6% and 4.8%), Hood Canal and North and South Puget Sound (4.9%, 5.2%, and 4.2%). Stratified results, as well as differences among years, underscored the importance of proximity of contributing stocks. Significant temporal differences were also observed in the timing of shifts between northern and southern stocks. These effects were similar in 2009 and 2010 but differed from 2008. The goal of our work is not necessarily to reduce overall Chinook salmon bycatch; the fleet already does a good job of that. Rather, we seek to measure and monitor stock-specific bycatch impacts and to provide information that might help reduce relative impacts on the most sensitive stocks.

Introduction

Pacific hake (*Merluccius productus*), commonly referred to as 'whiting,' is a pelagic fish taken with midwater trawl gear off the West Coast of North America. This fishery produces the largest single-species landings of all fisheries managed under the Groundfish Fishery Management Plan (http://www.nwr.noaa.gov/Groundfish-Halibut/Groundfish-Fishery-Management/Whiting-Management/index.cfm). Despite considerable progress since the 1990s on reducing Chinook salmon bycatch, some level of unintended take continues, and management concern remains, especially for sensitive and ESA-listed stocks.

In this report we describe genetic estimates of Chinook salmon (*Oncorhynchus tshawytscha*) stock composition for fish taken in the 2009 and 2010 U.S. West Coast at-sea Pacific hake fishery. The Pacific hake fishery is comprised of several sectors: the shoreside fleet, catcher processors, and motherships. The samples in this study were collected at-sea from the catcher processors and motherships (including tribal and non-tribal fisheries). Samples from the shoreside sector are not included in this study[1].

Our study sought to provide estimates of overall stock composition for each year as compared to 2008 (Moran et al. 2009) and to explore the spatial and temporal structure of those mixtures. The goal was to support managers in understanding potential impacts on protected and sensitive stocks. More detailed information about the distribution of protected stocks in time and space might allow more efficient harvest of Pacific hake in times and areas that minimize impacts on the most sensitive Chinook salmon populations. This is certainly the explicit goal of genetic mixture analysis applied to harvest management, and DFO's strategy has allowed access to multi-million dollar harvest opportunities that would otherwise have been lost due to precautionary protection of sensitive stocks.

This study supports National Marine Fisheries Service (NOAA-Fisheries) Northwest Region's Bycatch Reduction Plan (FY08 and FY09)[2], which identifies the following action item: "Continue to monitor the bycatch of ESA listed salmonids in the West coast groundfish fishery for compliance with provisions of [the] current biological opinion." It was not clear how these actions would be measured and monitored, nor what milestones would be associated with them. Our analysis provides one measure of stock-specific bycatch and an opportunity to monitor changes in those impacts through time. The NOAA At-Sea Hake Observer Program has collected scale samples from Chinook salmon taken in bycatch since the 1970s. If this material could be used for genetic analysis, it would make available stock composition estimates across considerable time and in different climatic regimes. This information might help understand stock-specific response to climate change. That said, we recognize the challenge in drawing inference from samples that were essentially collected opportunistically and without any explicit experimental design. It could be that any associations between stocks and oceanographic variables are simply obscured by highly variable and perhaps even chaotic systems. Moreover, even if we had a clear understanding of these associations, it's not clear that information could translate to more effective management action. Weak stocks are distributed coast wide. Moving off one stock might simply result in more take of another equally depressed stock. Nevertheless, given DFO and WDFW's success with GSI in terminal harvest management, it seems worth trying to exploit similar methods more broadly, both in directed harvest and in bycatch, to the extent that might be possible.

---

[1] Shoreside samples were collected in the years relevant to this study, and plans are currently underway to conduct genotyping and analysis. Comparisons of 2008 shoreside and at-sea sectors were included in Moran et al. (2009) drawing on independent work of Bellinger et al. (2009). Consideration of shoreside bycatch is essential because it is typically larger there than in the at-sea sectors, often more than double the absolute number of fish http://www.nwr.noaa.gov/Groundfish-Halibut/Groundfish-Fishery-Management/Whiting-Management/prev-summs.cfm.

[2] For the FY09 and FY10 NWR Bycatch Reduction Plan, see www.nmfs.noaa.gov/by_catch/docs/northwest_region_2009_10.pdf

Genetic methods have proven to be powerful partners with traditional tools in fishery research and management. Coded-wire tags (CWTs) provide the current standard for estimating stock composition in Chinook salmon harvest applications, but in bycatch, tag recoveries are limited. Moreover, even in the best case for CWTs, an independent alternative method provides important validation of current models and potential for developing even more robust mixed fishery management.

Allocating mixtures of individuals to source population is now widely used in ecological genetics throughout the world (Manel et al. 2005). These methods originated at NWFSC for fishery applications beginning in the 1970s and 1980s (Milner et al. 1985; Millar 1987; Shaklee et al. 1999). The implementation of coast-wide, internationally-standardized, microsatellite baseline data for Chinook salmon has significantly increased the utility of genetics for a wide range of fishery management applications. Clearly, stock compositions provide just one important element of fishery management, but even if formal time/area consideration is not effective in reducing bycatch of sensitive stocks, it is certainly the case that a better understanding of stock compositions and stock-specific migration patterns will benefit management and conservation, including the measurement and monitoring of bycatch impacts.

Materials and Methods

Sample collection and genotyping

Both contemporary and historical tissue samples were collected by NOAA's At-Sea Hake Observer Program (A-SHOP). Historical samples were taken as scale scrapes and smeared inside scale envelopes. 2009 and 2010 fin clips were collected on board motherships and catcher-processors (tribal and non-tribal sectors) and preserved on slips of paper also placed in scale envelopes (all samples air dried and stored at ambient temperature). Samples taken in 2009 were deposited in the Conservation Biology Division Tissue Archive with the accession number 34592 (N = 390, 184 females and 206 males). 2010 samples were given accession number 34927 (N = 678, 373 females and 305 males). These tissue samples comprised 34% and 48% of total Chinook at-sea bycatch in respective years (14% and 16% of all bycatch, including tribal and non-tribal shoreside). Tissue samples were analyzed for all coded wire tagged fish recovered in both years (40 readable CWTs in 2009 and 48 in 2010). Out of 68 total snouts collected by NOAA A-SHOP observers in 2010, 16 had no wire present, and 2 of those had no CWT code or note recorded. Two more CWTs were noted as unreadable. Finally, one tag was lost before it was read, and another was a blank wire.

Meta data associated with tissue samples (cruise and haul number, length, weight, sex, mark status, etc) were recorded on the scale envelopes and later transcribed for entry into the NorPac database. The historical scale samples tested in this study came from a very large collection of more than 40,000 scales taken since 1976 by NOAA observers. Although the 36 samples analyzed here (33 + 3 coho salmon) were relatively new (2001 – 2005), previous studies have shown that successful genotyping of historical fish scales depends more on the particular paper used for preservation than it does on age, per se (Moran and Baker 2002).

Samples were collected between mid-May and mid-December in both years and ranged in length and weight as follows: **2009** 24 – 104 cm (Mean = 55.21, SD = 12.87), 0.15 - 16.89 kg (Mean = 2.60, SD = 2.41); **2010** 28 - 113 cm (Mean = 61.7, SD = 12.76), 0.26 - 15.85 kg (Mean = 3.56, SD = 2.53). Samples were taken in **2009** between latitude 41.93333 and 48.48333 (Mean = 47.88748, SD = 0.89578) and longitude -125.40000 - -124.38333 (Mean = -124.93389, SD = 0.18403). In **2010** samples were collected between latitude 41.76667 - 48.45000 (Mean = 46.90622, SD = 2.17697) and longitude -125.76667 - 124.38333 (Mean = -125.05400, SD = 0.26157). Fishing depths ranged widely from 75 m to more than 365 m (40 – 200 fathoms). Preliminary analyses did not reveal compelling stock-specific patterns with depth, and we defer further examination of stock-specific depth distribution until more data accumulate across years.

DNA was extracted and purified by using Qiagen® DNeasy™[3] membrane capture. Purified DNA samples were amplified and genotyped for the 13 internationally-standardized GAPS microsatellite loci (Seeb et al. 2007). Genotyping was carried out by using an Applied Biosystems 3100 Genetic Analyzer (specifics available on request).

Analytical methods

We used the Rannala and Mountain (1998) algorithm for genetic mixture analysis as implemented in the ONCOR software package (Kalinowski et al. 2007, with bias correction of Anderson et al. 2008). We estimated stock composition by using fractional allocation, comparing our sample of unknown individuals to the known-origin, reference populations in the GAPS v2.2 baseline. The reporting group structure was agreed on by the GAPS collaborators for previous analysis, and is retained here (Appendix 1) for continuity with previous analyses, e.g., 2008. Additional, newly available baseline samples (version 3) might refine estimates in the lower Columbia River and Puget Sound but would not likely change the principal differences observed here.

We first compared the overall stock compositions of 2009 and 2010 bycatch, irrespective of collection date and location. We estimated 95% confidence intervals around the point estimates in each year (1000 bootstrap replicates, re-sampling both the mixture and the baseline, Kalinowski et al. 2007). Next we stratified our samples to compare a common range of collection dates and areas. Early samples were those taken between 15 May and 15 August and late period from 16 Aug and 31 December. Three spatial strata were based on the INPFC management areas: Vancouver, latitude 48.5000˚ - 47.5000˚; Columbia, 47.4449˚ - 43.0000˚; and Eureka (northern portion), 43.0000˚ - 41.7667˚ (Fig. 1). For both the stratified and overall comparisons, we also tested the overall observed differences in stock composition by using a simulated Fisher's Exact Test of pseudo counts derived from stock proportions and sample size (two or three row-by-44 column contingency test). This is a non-parametric test that is robust to unbalanced sample sizes among classes. Markov-Chain-Monte Carlo sampling was used to obtain probability

---

[3] Reference to trade names does not constitute endorsement or recommendation.

estimates testing for random stock distribution between or among classes (two times or three areas).

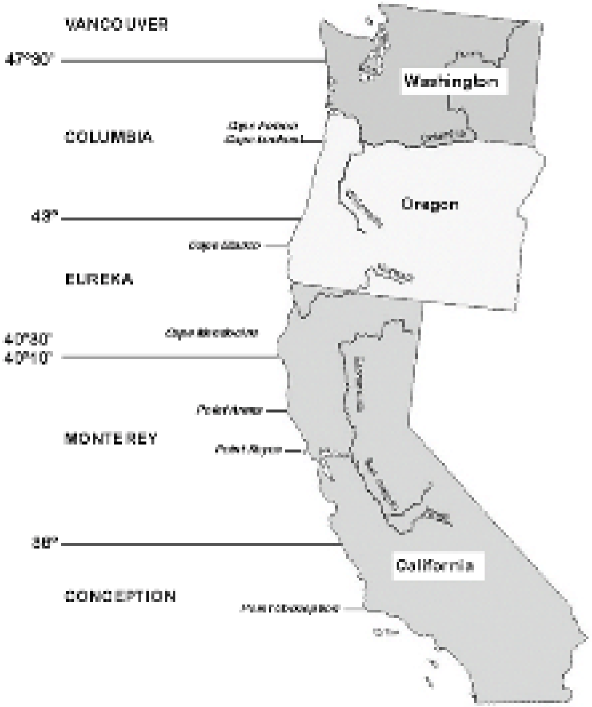

Figure 1. The three spatial strata analyzed here were similar to the INPFC management areas: Vancouver, latitude 48.5000˚ - 47.5000˚; Columbia, 47.4431˚ - 43.1822˚; and Eureka (northern portion), 43.1822˚ - 42.0000˚

Individual assignment (IA) to genetic stock group was used to compare genetic results to CWT records for individual fish (Rannala and Mountain 1998). The distribution of the assignment probabilities for all the mixture samples in the study were examined to provide some context for the assignment probabilities in the CWT results. Individual assignment is less precise and accurate than fractional assignment that models stock compositions directly, irrespective of assignment of individual fish (Manel et al. 2005; Koljonen et al. 2005); nevertheless, it is useful and informative to compare individual genetic assignment results with CWT records.

Results

In general, tissue quality was good and genotyping success was reasonable, however success rates differed slightly (albeit non-significantly) between 2009 and 2010. Overall data density was quite good for 2009 (with only 3.6% missing genotypes). Out of 390 fish, 296 were typed for all 13 loci, and 378 fish were typed for 10 or more loci. No fish from the 2009 collections w`as typed for fewer than five loci. Failed genotypes were uniformly distributed among loci with no obvious problem locus. Results were not as good in 2010 with nearly 11% missing data overall. Only 343 of 678 fish were typed for all 13 loci, but 602 typed for 10 or more. Six fish failed completely for all loci in 2010. *Ogo*2 and *Omm*1080 were the two most difficult loci to amplify consistently in the 2010 analysis. About 1/3 of individuals failed to amplify for each of those loci. *Ogo*4 was the most robust locus with less than 4% missing data.

The 36 scale samples, collected between 2001 and 2005, showed excellent amplification and genotyping efficiency that was at least as good as results obtained from contemporary material (2.6% missing data overall for scales). The only goal in genotyping these test samples was to evaluate their suitability for future studies. Therefore, the test samples were not used in mixture analysis or individual assignment to population of origin.

From the 2009 bycatch samples taken at sea, 14 individuals were removed from analysis because they appeared not to be Chinook salmon (likely coho salmon, *O. kisutch*). Two pairs of duplicate tissue samples were identified in 2010, and one member of each pair was omitted from genetic mixture analysis and stock composition estimates. In both pairs of duplicate multilocus genotypes, members had identical collection site and location but had different sexes, lengths, and weights. The level of variability at these microsatellite markers provides an absolute fingerprint that uniquely identifies every individual fish. Extensive theory and empirical observation indicate that tissue samples that are identical for six or more loci, with no other mismatches, are likely taken from the same fish (data not shown). The samples in question matched perfectly at all 13 loci.

Stock composition estimates

Chinook bycatch in 2009 and 2010 had a more northerly distribution than in 2008 and showed a highly significant difference in stock composition ($P <= 0.000001$). Mid-Oregon and southern-coastal stocks and Central Valley fall run fish all contributed lower proportions in 2009 and 2010. West Cascade (Lower Columbia River) stocks remained relatively constant, but Spring Creek Group tules, Upper Columbia River summer/falls and Snake River falls all showed an increase over 2008. Hood Canal and northern Puget Sound increased markedly in 2009, as did South Thompson. Lower Fraser River showed the most dramatic increase, rising in relative proportion to more than 25%. In 2009 and 2010, lower Fraser River populations contributed far more to bycatch than any other stock group—in fact, more than the next two or three contributors combined (Fig. 2).

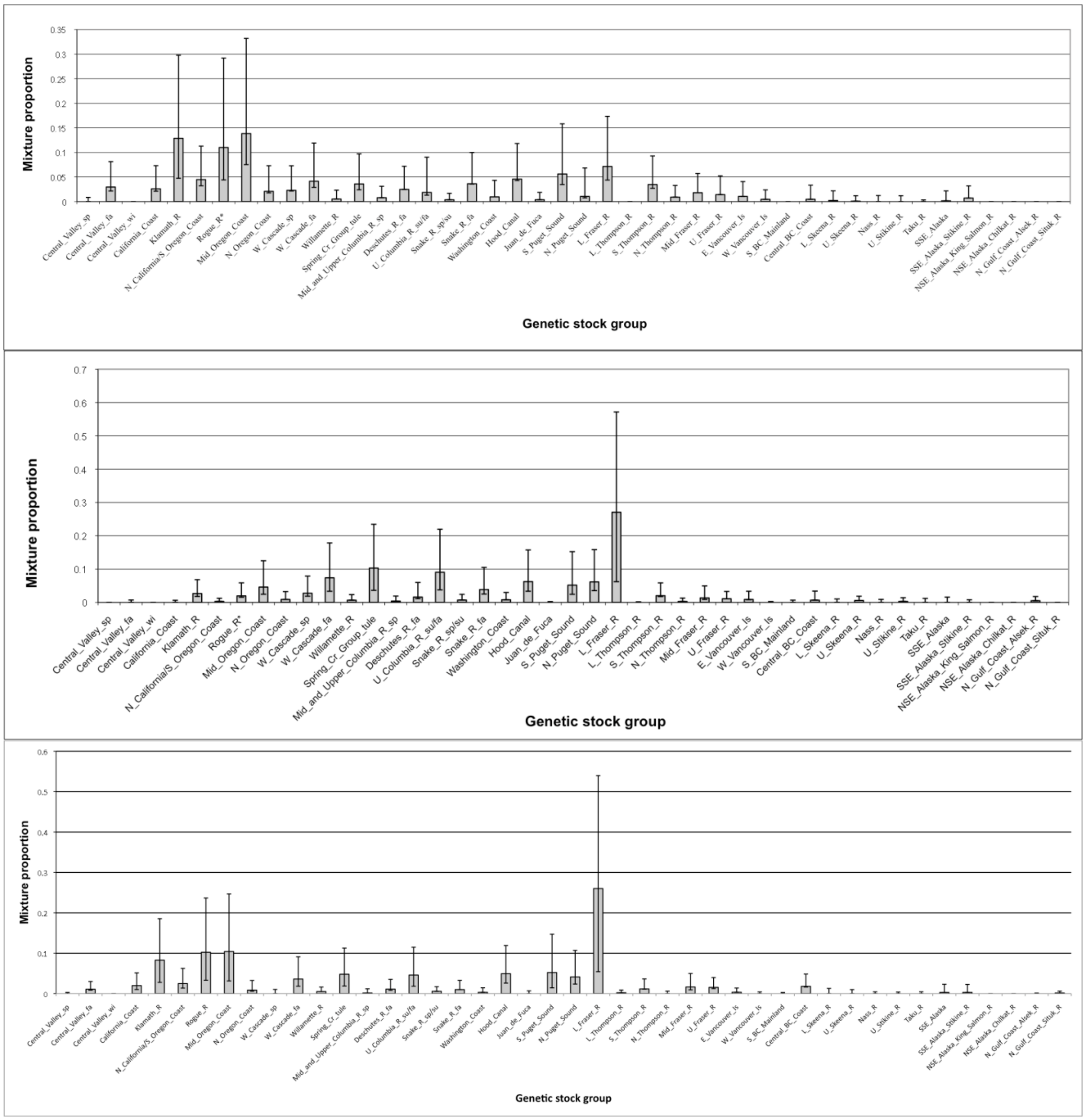

Figure 2. Overall stock composition estimates for Chinook bycatch in the 2008 – 2010 Pacific hake fishery, all areas and times (three panels above ordered by year). To facilitate comparison, all genetic stock groups are included in all plots (even if the estimate was zero in a given year). Stocks are ordered South to North from left to right.

Spatial and temporal stratification of stock composition

In both 2009 and 2010, southern stocks were abundant early in the season between mid May and mid Aug but then declined later as northern stocks increased (Fig. 3). Although the distribution of Columbia River stocks differed slightly between 2009 and 2010, those years were similar and showed a temporal pattern almost opposite that of 2008, when northern stocks were more abundant in the early period and declined later. These temporal differences within years were highly statistically significant in both 2009 and 2010 ($P < 0.000001$).

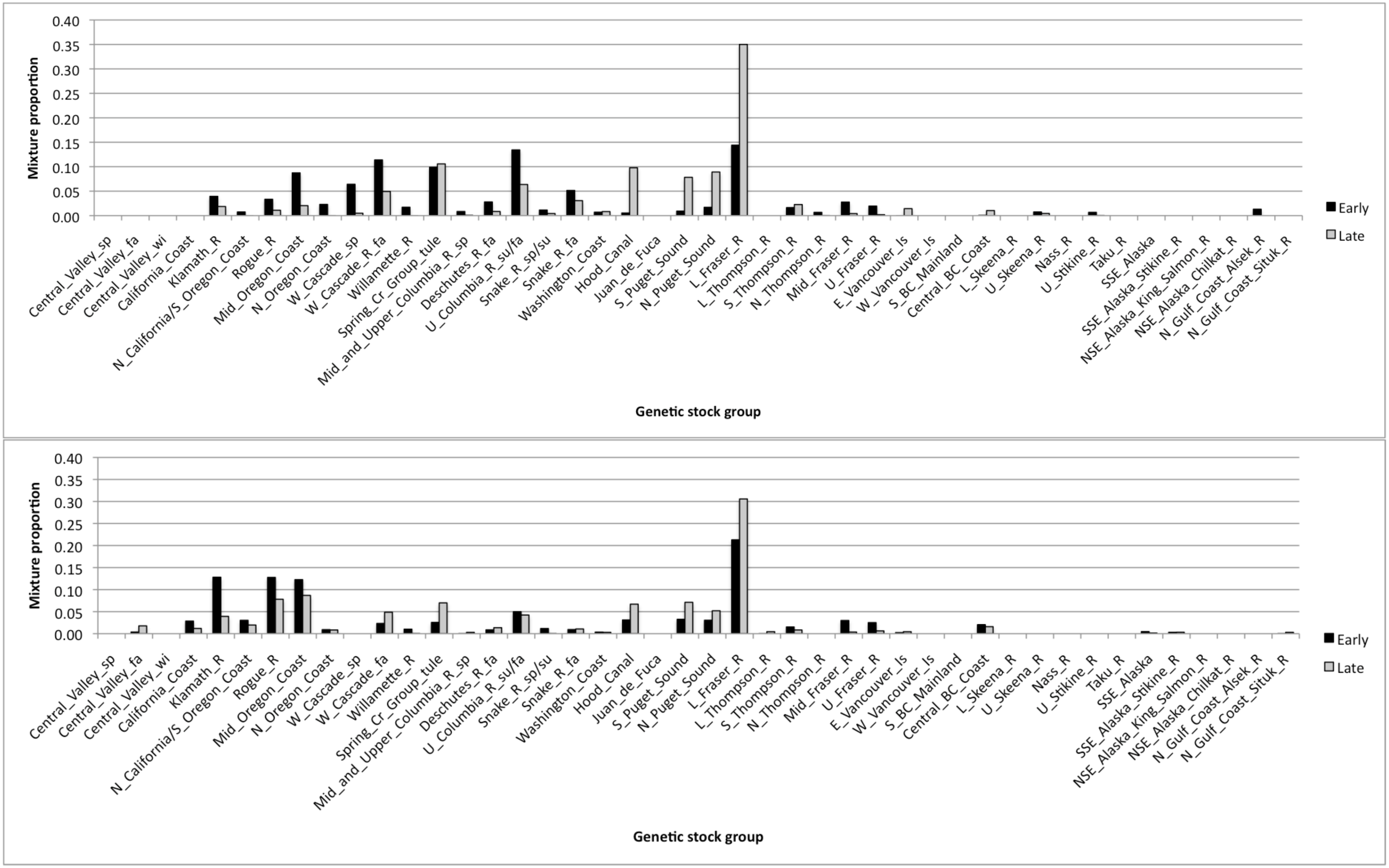

Figure 3. Stock composition of Chinook salmon bycatch from early and late periods in the 2009 (upper) and 2010 (lower) Pacific hake fishery. Early samples were taken between 15 May and 15 August, late period from 16 August to 24 December. The early southern stock abundance and late northern was opposite to that seen in 2008.

Stratification of stock compositions by INPFC area showed similar broad-scale results to 2008. Bycatch in the Eureka Area, the southern-most area sampled here, was dominated by southern stocks, transitioning to Columbia River stocks in the Columbia area (Fig. 4). In the Vancouver Area, the northern-most area, Columbia River stocks remained abundant. Southern stocks were still present, but general stock composition transitioned to Puget Sound and Fraser River stocks. The Lower Fraser genetic stock group contributed more than 30% of the Chinook salmon bycatch in the Vancouver area. Bycatch in the Eureka Area was very small and stock composition was not significantly different from the Columbia Area (N = 7 and 62, respectively, $P = 0.373020$). All other within-year differences between and among areas were highly significant (from $P < 0.000001$ to $P = 0.006$).

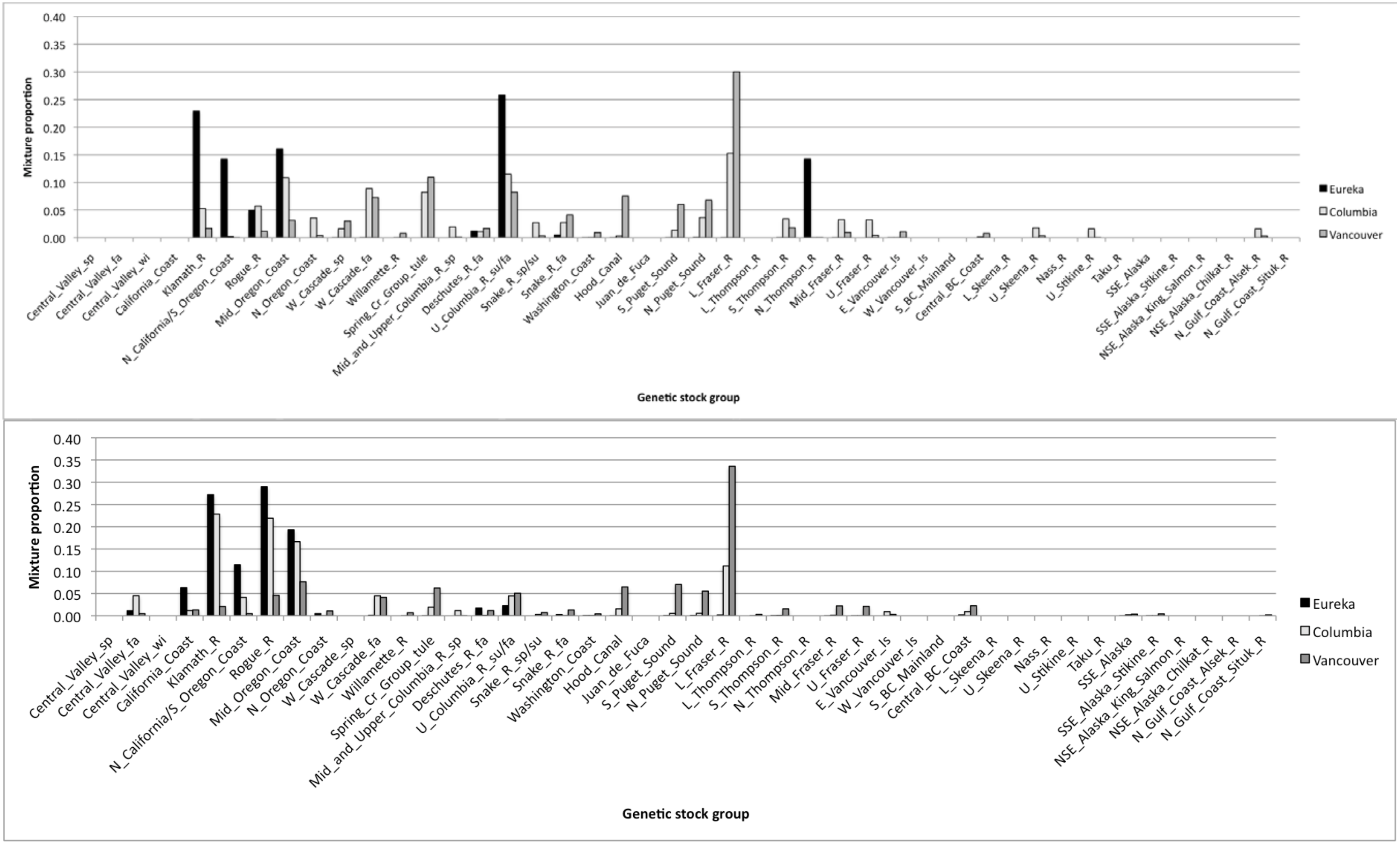

Figure 4. Chinook salmon bycatch stock compositions stratified by area for 2009 (above) and 2010 (below). Three spatial strata were based on the INPFC management areas: Eureka (northern portion), 43.0000˚ - 41.7667˚; Columbia, 47.4449˚ - 43.0000˚; and Vancouver, latitude 48.5000˚ - 47.5000.

ESA-listed stocks in 2009 and 2010 bycatch

Several genetic stock groups that include ESA-listed populations showed statistically significant contributions to these bycatch mixtures (95% confidence limits not overlapping zero). It is important to note that these are conservative estimates for actual impacts on ESA-listed populations. In each case, only a portion of the fish attributed to our genetic stock groups are actually protected by Rule 4.d. take restrictions under the ESA. Despite those caveats, these results are provided to help managers infer potential take on listed populations, not only in the Pacific hake fishery, but in other fisheries that take a wide range of fish sizes. In 2009, these listed stock groups included West Cascade spring and fall groups along with Spring Creek Group tules (2.8%, 7.4%, and 10.3%), Snake River falls (3.9%), Hood Canal (6.2%), and Northern and Southern Puget Sound (6.2% and 5.2%). In 2010, Southern Puget Sound remained constant at 5.2%, but all other listed stocks declined in the fishery relative to unlisted stocks. West Cascade spring-run fish disappeared completely in 2010, and fall-run fish and tules each declined by half to 3.6% and 4.8%. Hood canal and Northern Puget Sound each declined slightly to 4.9% and 4.2% in 2010. Again, these are not ESU impacts, per se. They must instead be view as point estimates for genetic stock groups that contain both listed and unlisted fish. Inference of the former will require additional adjustments that are beyond the scope of this report.

Distribution of P-values for individual assignment

The average assignment probability for individual fish collected in 2009 was 0.91 (standard deviation 0.087, range 0.697 – 1.000, Fig. 5). In 2010, mean assignment probabilities were lower (0.851) than in 2009, likely due to a larger fraction of missing genotypic data. Values ranged from 0.674 – 1.000 with standard deviation 0.091. Although not a statistically significant difference, genotyping success was notably lower in 2010 than in 2009. It is unclear whether the difference in genotyping success was due to sampling conditions (e.g., excessive moisture that delayed tissue desiccation and preservation) or laboratory procedures (e.g., poor reagent-batch quality). Ordinarily, the effect of missing genotypes would be to increase the confidence limits on the stock composition estimates (Fig. 2); however, 2010 sample size was considerably larger than 2009 (678 versus 390), increasing precision on stock composition estimates despite reduced confidence in individual fish assignment.

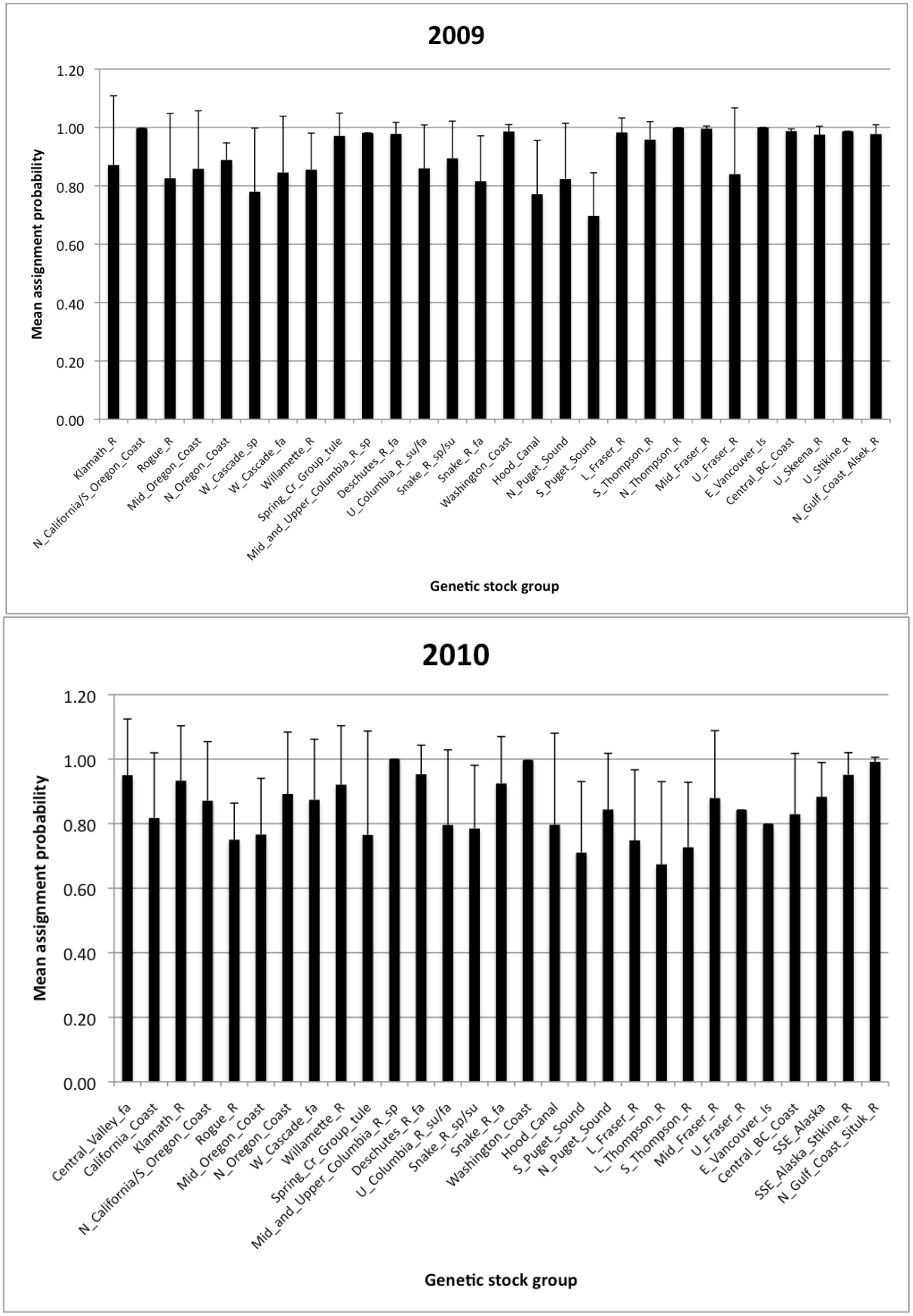

Figure 5. Average individual genetic assignment probabilities by genetic stock group for the Chinook salmon taken as bycatch in US West Coast Pacific hake fisheries in 2009 and 2010. Stock groups are ordered by increasing latitude, but not all groups are included in both plots.

Comparison of genetic assignment and CWTs

Of 40 readable CWTs collected in 2009, 21 matched perfectly for genetic assignment and CWT stock (Appendix 2). Of 16 mismatches, 12 were among genetically similar stocks and were not unexpected (e.g., LYONS FERRY HATCHERY or SNAKE R-LOWR 33.0002 stocks assigned to the genetically similar Upper Columbia River summer/fall stock; or GEORGE ADAMS (PURDY) assigned to South Puget Sound fall). Two more mismatches were unexpected but not impossible. However, two remaining misassignments were completely unexpected and unexplained: 1) Sample number 501922, SNOUT_NUM 3705, tag_code 612513, stock_location_name LYONS FERRY HATCHERY assigned to the Hood Canal genetic stock group. 2) Sample number 502793, SNOUT_NUM 1786 (NOTES "504 949"), tag_code 025650 S-HARRISON R assigned to Mid_Fraser_R. The probability that sample number 502793 arose from the Lower Fraser genetic stock group was very small according to our analysis (P = 0.00024). Extensive leave-one-out, jackknife testing of the baseline samples suggests mis-assignment of Mid-Fraser fish to the Lower Fraser is unlikely. Of 364 fish collected from five Mid-Fraser populations, treated one at a time as unknowns (as were the CWT samples), none assigned to the Lower Fraser. One or both of these tags might have errors associated with them, either related to sample identity (e.g., the note associated with 502793), or to transcription errors uploaded to the RMIS database. Parent-based tagging studies observed a rate of 5% for such errors (CWTs with incorrect origins recorded in RMIS) (E. Anderson, unpubl.[4]). Results were similar in 2010 with excellent concordance between genetic assignment and CWTs, but with some mismatches between genetically similar stocks that might be simple genetic misassignments (e.g., the correct stock is often the second most likely group of origin). Again, however, 3 samples out of 48 had stock assignments that were completely inconsistent with the CWT origin and remain unexplained.

Discussion

Considering three years of bycatch samples, 2008 – 2010, genetic results are consistent with general information from CWTs in that stock compositions are substantially driven by distribution of effort and the areas fished. In 2009, relative to 2008, bycatch shifted to northern stocks, reflecting at least in part, a more northerly distribution of fishing effort (data not shown). In both 2009 and 2010, Lower Fraser River populations became major contributors, jumping from 7.2% in 2008 to more than 25% in both 2009 and 2010. The southern stocks, such as Klamath, Rogue, and Mid-Oregon Coast, which were major contributors in 2008, were replaced in 2009 by Columbia River stocks, West Cascade falls, Spring Creek Group tules, and Upper Columbia summer/falls. The southern stocks were again more abundant in 2010, showing an intermediate distribution relative to 2008 and 2009. Those relationships were consistent with the mean latitudes of bycatch samples take in the 3 consecutive years (45.03, 47.89, and 46.91)—the farther north the fishery, the greater the general impact on northern stocks and vice versa.

---

[4] Presentation at the annual meeting of the American Fisheries Society, Seattle 2011

Although these patterns are clearly influenced by the distribution of fishing effort, it's not the case that impacts could be predicted entirely by distance from the source stocks. It's well known that particular stocks have different migratory routes that put them in specific areas at particular times in their life history (Winans et al. 2001; Weitkamp 2010). For example, Chinook salmon stocks south of Cape Blanco tend to migrate to the south, whereas those to the north of Cape Blanco tend to migrate in a northerly direction (Myers et al. 1998). Indeed, it is this stock-specific migratory behavior and oceanographic preference that we seek to further characterize and eventually exploit to help minimize bycatch impacts on sensitive stocks without limiting harvest.

In addition to stock-specific migratory patterns, our results are probably influenced by demographics. The most dramatic example is evident in the very large number of Lower Fraser fish in recent bycatch. In 2009 there was an especially large return of 3-year-old fish to the Fraser (REF), which undoubtedly contributed to larger stock composition estimates observed in this study in 2009 and 2010.

Variation in stock composition in time and space

The change in stock composition through time between early and late periods was similar in 2009 and 2010 but almost exactly opposite to that seen in 2008. In the early period of 2009 and 2010 (mid-May to mid-August), southern stocks were relatively abundant but were then replaced in the later period by major contributors in the north. This difference in stock timing might be related to the geographic distribution of bycatch in these years. The mean latitudes of sample collections in 2009 and 2010 were around 47 and 48, respectively, whereas 2008 had a more southerly distribution with mean latitude just above 45. The latitudinal effect was more clearly implicated in the area strata where strong apparent association was seen with source population proximity. For example, the Lower Fraser stock group contributed strongly to essentially all time and area strata, except the Eureka Area, in both early and late periods. Eureka is of course the southern most area, whereas the Lower Fraser is the northern most genetic stock group that contributed significantly to our bycatch samples. Clearly, time and area are likely confounded to some unknown degree. Future analyses will examine the interaction of time and area, as well as association of stocks with particular oceanographic conditions (biotic and abiotic).

Genetic assignment and CWT mismatches

It is becoming a familiar pattern when comparing CWTs taken at sea to genetic assignments that most assignments are spot on, and most of the mismatches that do occur are easily explained as normally expected variance associated with the method. However, there are almost always a few samples that have genetic assignments that mismatch the CWT origin and cannot be easily explained as normal errors. We actually have a great deal of experience with genetic assignment of known-origin samples treated as unknowns. The entire baseline of more than 20,000 known-origin individuals has been subjected to extensive leave-one-out jackknife testing. In this procedure, one sample is removed from the baseline, allele frequencies recalculated, and the left-out sample is assigned back to the baseline exactly like an unknown mixture sample or CWT. Leave-one-out misassignment rates and the distribution of those misassignments provide an expectation against which CWT misassignments can be compared. Experience with both bycatch and Chinook salmon harvest shows that about 5% of genetic assignments are fundamentally irreconcilable with the CWT records, e.g., essentially zero probability of a fish with the observed genotype having come from the population of origin recorded in RMIS[5]. This ~5% observation is exactly consistent with known errors in CWT origin recorded in RMIS for ocean-caught fish (E. Anderson, unpubl. results from parent-based tagging). What is needed is a systematic meta-analysis across all available genetic studies that have examined CWT samples. Comparison of those results with fin clips taken from parr at the hatcheries that implant CWTs would allow us to confirm or refute the common observation that mismatch of CWT and genetic origin is more common in fishery samples than in true known-origin fish (i.e., parr sampled at the hatchery).

Genetic stock groups that contain ESA-listed populations

Impacts on ESA-listed stocks always raise concern among fishery managers. Again, we emphasize that the results reported here allow at best a general approximation of those impacts and only with very careful consideration of the relative numbers of listed and unlisted fish in our genetic stock reporting groups.

The proportion of the overall bycatch that came from listed genetic stock groups differed dramatically among years. 2009 had a substantially higher proportion of fish from these groups than were observed in 2008 or 2010 (42% in 2009 compared to 27.5% in 2008 and 24.8% in 2010). This may relate to the latitude at which bycatch was encountered, with 2009 showing the most northerly distribution of the 3 years.

Prudent management and compliance with the Magnuson-Stevens Fishery Conservation and Management Act dictate that management protects the weakest stocks in a mixed fishery. Our stock composition estimates provide some of the only data available to support NOAA’s obligation to measure and monitor bycatch of listed stocks.

Conclusion

Genetic sampling of Chinook salmon bycatch largely confirm and strengthen general knowledge about stock distribution from CWT recoveries and previous genetic studies that used allozymes (Winans et al. 2001). It’s clear that both time and area are important drivers of stock composition in ocean fisheries, whether directed harvest or inadvertent bycatch. Moreover—again consistent with previous studies—stock composition cannot be modeled as a simple diffusion process, with distance from a putative contributor being directly related to stock composition. First, timing plays a role, with different stocks entering different stages of their migration at different ages and at different times of the year (Meyers et al. 1998). Also, different stocks exhibit different migratory pathways (Weitkamp 2010) and probably different predisposition for different oceanographic conditions and prey resources. In the next phase of our work, we will begin to examine these relationships across longer periods of time. We’ll continue our annual analyses of

---

[5] It should be noted that leave-one-out jackknife testing is generally carried out on fish with complete multilocus genotypes, making those results more optimistic than should be expected for normal fishery samples with missing genotypes for some loci. For individual samples, however, the assignment probabilities are robust to missing loci, which are modeled explicitly. Our CWT mismatches are not explained by missing data.

contemporary Chinook salmon bycatch in the Pacific hake fishery, but we'll also analyze samples from the 1980s and 2000s to compare those warm-regime years with the contemporary cool-regime samples. The power of historical data in predictive modeling clearly has its limits. Nevertheless, thousands of historical bycatch samples are now accessible through molecular technology. This new resource, dating back to the 1970s might provide our best hope of understanding how stock composition and ESA impacts might change with climate.

Acknowledgements

This report benefitted from comment by multiple reviewers. We appreciate discussions with Peter Dygert that helped us refine our expectations for the utility of GSI data in the context of the US West Coast Pacific hake fishery. Thanks also to David Teel for discussion of lower Columbia River genetic stock groups. We especially thank the fishers of the hake fleet and observers for NOAA's At-Sea Hake Observer Program who cooperated to collect the tissue samples and associated biological data that allowed this research.

References

Anderson, E.C. R.S. Waples, and S.T. Kalinowski. 2008. An improved method for predicting the accuracy of genetic stock identification. CJFAS 65:1475-1486.

Beacham, T.D., K.L. Jonsen, J. Supernault, M. Wetklo, L. Deng, and N. Varnavskaya. 2006. Pacific Rim population structure of Chinook salmon as determined from microsatellite analysis. Tran. Amer. Fish. Soc. 135:1604–1621.

Bellinger, M.R., M. Banks, and P. Lawson. 2009. Mixed Stock Analysis of Chinook Salmon in Pacific Whiting (Hake) Bycatch Collected Shoreside in Newport, Oregon. *Preliminary Report 5/21/2009*. Project CROOS (Collaborative Research on Oregon Ocean Salmon). www.PacificFishTrax.org & www.projectCROOS.com

Kalinowsi, S. T., K. R. Manlove, and M. L. Taper. 2007. ONCOR A computer program for Genetic Stock Identification. . Department of Ecology, Montana State University, Bozeman MT 59717. Available for download from http://www.montana.edu/kalinowski.

Koljonen, M-L., J.J. Pella, and M. Masuda. 2005. Classical individual assignments versus mixture modeling to estimate stock proportions in Atlantic salmon (*Salmo salar*) catches from DNA microsatellite data. Can. J. Fish. Aquat. Sci. 62: 2143-2158.

Manel, S. O.E. Gaggiotti, and R.S. Waples. 2005. Assignment methods: matching biological questions with appropriate techniques.

Millar, R.B. 1987. Maximum likelihood estimation of mixed stock fishery composition. CJFAS 44:583 – 590.

Milner, G.B., D.J. Teel, F.M. Utter, and G.A. Winans. 1985. A genetic method of stock identification in mixed populations of Pacific salmon, *Oncorhynchus* spp. Marine Fisheries Review 47:1-8.

Moran, P. and J. Baker. 2002. Polymerase chain reaction inhibition in historical fish scale mounting cards. Trans. Amer. Fish. Soc. 131:109-119.

Moran, P., E. Iwamoto, R. Shama, and V. Tuttle. 2009. Chinook salmon bycatch stock composition estimates in the 2008 Pacific hake fishery. A report to the Northwest Regional Office, NOAA Fisheries. Available from Northwest Fisheries Science Center, www.nwfsc.noaa.gov/.

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. U.S. Dept. Commer., NOAA Tech. Memo. NMFS-NWFSC-35, 443 p.

Pella, J., and M. Masuda. 2006. The Gibbs and split–merge sampler for population mixture analysis from genetic data with incomplete baselines. Can. J. Fish. Aquat. Sci. 63: 576–596.

Rannala, B., and Mountain, J.L. 1997. Detecting immigration by using multilocus genotypes. Proc. Natl. Acad. Sci. USA. 94: 9197–9201.

Seeb, L.W., A. Antonovich, M.A. Banks, T.D. Beacham, M.R. Bellinger, S.M. Blankenship, M. Campbell, N.A. Decovich, J.C. Garza, C.M. Guthrie III, T.A. Lundrigen, P. Moran, S.R. Narum, J.J. Stephenson, K.J. Supernault, D.J. Teel, W.D. Templin, J.K. Wenburg, S.F. Young, and C.T. Smith. 2007. Development of a standardized DNA database for Chinook salmon. Fisheries 32:540-552.

Shaklee, J.B., T.D. Beacham, L. Seeb, and B.A. White. 1999. Managing fisheries using genetic data: case studies from four species of Pacific salmon. Fisheries Research 43:45-78.

Teel, D.J., P.A. Crane, C.M. Guthrie III, A.R. Marshall, D.M. VanDoornik, W.D. Templin, N.V. Varnavskaya, and L.W. Seeb. 1999. Comprehensive allozyme databasse discriminates Chinook salmon around the Pacific Rim. (NPAFC document 440) 25p. Alaska Department of Fish and Game, Division of Commercial Fisheries, 333 Raspberry Road, Anchorage, Alaska USA 99518

Weitkamp, L. 2010. Marine distributions of Chinook salmon from the West Coast of North America determined by coded wire tag recoveries. Transactions of the American Fisheries Society 139:147–170.

Winans, G. A., Viele, D., Grover, A., Palmer-Zwahlen, M., Teel, D. J., Van Doornik, D. M. 2001. An Update of Genetic Stock Identification of Chinook Salmon in the Pacific Northwest: Test Fisheries in California. Reviews in Fisheries Science, 9:213-237.

Appendix 1. Genetic stock groups and their representative populations included in GAPS-Chinook version 2.2. Fishery Regulation Assessment Model (FRAM) stocks included for context.

FRAM stock	Genetic stock group	Genetic baseline population
Not included in FRAM	Central_Valley_sp	MillCrsp
Not included in FRAM	Central_Valley_sp	ButteCrSp
Not included in FRAM	Central_Valley_sp	DeerCrsp
Sacramento_Fall	Central_Valley_fa	FeatherHsp
Sacramento_Fall	Central_Valley_fa	StanislausR
Sacramento_Fall	Central_Valley_fa	ButteCrf
Sacramento_Fall	Central_Valley_fa	FeatherHfa
Sacramento_Fall	Central_Valley_fa	BattleCr
Not included in FRAM	Central_Valley_wi	SacramentoH
Not included in FRAM	California_Coast	RussianR
Not included in FRAM	California_Coast	EelR
Not included in FRAM	Klamath_R	TrinityHf
Not included in FRAM	Klamath_R	TrinityHsp
Not included in FRAM	Klamath_R	KlamathRfa
Not included in FRAM	N_California/S_Oregon_Coast	ChetcoR
Not included in FRAM	Rogue_R	ColeRiversH
Not included in FRAM	Rogue_R	ApplegateCr
Not included in FRAM	Mid_Oregon_Coast	SiuslawR
Not included in FRAM	Mid_Oregon_Coast	UmpquaH
Not included in FRAM	Mid_Oregon_Coast	MillicomaR
Not included in FRAM	Mid_Oregon_Coast	CoosH
Not included in FRAM	Mid_Oregon_Coast	SCoosH
Not included in FRAM	Mid_Oregon_Coast	ElkH
Not included in FRAM	Mid_Oregon_Coast	SixesR
Not included in FRAM	Mid_Oregon_Coast	SUmpquaH
Not included in FRAM	Mid_Oregon_Coast	CoquilleR
Oregon_Coast_Fall	N_Oregon_Coast	AlseaR
Oregon_Coast_Fall	N_Oregon_Coast	NehalemR
Oregon_Coast_Fall	N_Oregon_Coast	SiletzR
Oregon_Coast_Fall	N_Oregon_Coast	KilchisR
Oregon_Coast_Fall	N_Oregon_Coast	NecanicumH
Oregon_Coast_Fall	N_Oregon_Coast	NestuccaH
Oregon_Coast_Fall	N_Oregon_Coast	SalmonRf
Oregon_Coast_Fall	N_Oregon_Coast	TraskR
Oregon_Coast_Fall	N_Oregon_Coast	WilsonR
Oregon_Coast_Fall	N_Oregon_Coast	YaquinaR
Cowlitz/Kalama/Lewis_Spring	West_Cascade_sp	CowlitzHsp
Cowlitz/Kalama/Lewis_Spring	West_Cascade_sp	KalamaHsp
Cowlitz/Kalama/Lewis_Spring	West_Cascade_sp	LewisHsp
OR_Tule_&_WA_Tule_&_L_River_Wild_Bright	West_Cascade_fa	SandyR
OR_Tule_&_WA_Tule_&_L_River_Wild_Bright	West_Cascade_fa	CowlitzHfa
OR_Tule_&_WA_Tule_&_L_River_Wild_Bright	West_Cascade_fa	LewisRf
Willamette_Spring	Willamette_R	McKenzieH
Willamette_Spring	Willamette_R	NSantiamH

FRAM stock	Genetic stock group	Genetic baseline population
Bonneville_Pool_Tule	Spring_Cr_Group_tule	SpringCrH
Not included in FRAM	Mid_and_Upper_Columbia_R_sp	UYakimaH
Not included in FRAM	Mid_and_Upper_Columbia_R_sp	WarmSpringsH
Not included in FRAM	Mid_and_Upper_Columbia_R_sp	WenatcheeRsp
Not included in FRAM	Mid_and_Upper_Columbia_R_sp	WenatcheeHsp
Not included in FRAM	Mid_and_Upper_Columbia_R_sp	CarsonH
Not included in FRAM	Mid_and_Upper_Columbia_R_sp	JohnDayR
Upriver_Summer_&_Upriver_Bright_Fall	Deschutes_R_fa	UDeschutesR
Upriver_Summer_&_Upriver_Bright_Fall	Deschutes_R_fa	LDeschutesR
Upriver_Summer_&_Upriver_Bright_Fall	U_Columbia_R_su/fa	MethowR
Upriver_Summer_&_Upriver_Bright_Fall	U_Columbia_R_su/fa	WellsH
Upriver_Summer_&_Upriver_Bright_Fall	U_Columbia_R_su/fa	WenatcheeRsf
Upriver_Summer_&_Upriver_Bright_Fall	U_Columbia_R_su/fa	HanfordReach
Not included in FRAM	Snake_R_sp/su	MinamR
Not included in FRAM	Snake_R_sp/su	RapidRH
Not included in FRAM	Snake_R_sp/su	SeceshR
Not included in FRAM	Snake_R_sp/su	TucannonH
Not included in FRAM	Snake_R_sp/su	TucannonR
Not included in FRAM	Snake_R_sp/su	NewsomeCr
Not included in FRAM	Snake_R_sp/su	WFYankeeFrk
Not included in FRAM	Snake_R_sp/su	EFSalmonR
Not included in FRAM	Snake_R_sp/su	ImnahaR
Snake_R_Fall	Snake_R_fa	LyonsFerryH
WA_Coast	Washington_Coast	QueetsR
WA_Coast	Washington_Coast	SolDucH
WA_Coast	Washington_Coast	ForksCrH
WA_Coast	Washington_Coast	HohR
Not included in FRAM	Washington_Coast	HumptulipsH
WA_Coast	Washington_Coast	MakahH
Hood_Canal_&_Juan_de_Fuca	Hood_Canal	GeorgeAdamsH
Hood_Canal_&_Juan_de_Fuca	Hood_Canal	HammaHammaR
Hood_Canal_&_Juan_de_Fuca	Juan_de_Fuca	ElwhaH
Hood_Canal_&_Juan_de_Fuca	Juan_de_Fuca	ElwhaR
Hood_Canal_&_Juan_de_Fuca	Juan_de_Fuca	DungenessR
South_Puget_Sound	S_Puget_Sound	VoightsH
South_Puget_Sound	S_Puget_Sound	SoosH
South_Puget_Sound	S_Puget_Sound	WhiteH
South_Puget_Sound	S_Puget_Sound	HuppSpH
South_Puget_Sound	S_Puget_Sound	ClearCrH
South_Puget_Sound	S_Puget_Sound	SPrairieCr
Nook/Samish_&_Skagit_&_Stilly/Snohom	N_Puget_Sound	SkagitR
Nook/Samish_&_Skagit_&_Stilly/Snohom	N_Puget_Sound	USkagitR
Nook/Samish_&_Skagit_&_Stilly/Snohom	N_Puget_Sound	USaukR
Nook/Samish_&_Skagit_&_Stilly/Snohom	N_Puget_Sound	LSaukR
Nook/Samish_&_Skagit_&_Stilly/Snohom	N_Puget_Sound	SuiattleR
Nook/Samish_&_Skagit_&_Stilly/Snohom	N_Puget_Sound	MarblemountHsp
Nook/Samish_&_Skagit_&_Stilly/Snohom	N_Puget_Sound	MarblemountHsu
Nook/Samish_&_Skagit_&_Stilly/Snohom	N_Puget_Sound	UCascadeR

FRAM stock	Genetic stock group	Genetic baseline population
Nook/Samish_&_Skagit_&_Stilly/Snohom	N_Puget_Sound	SamishH
Nook/Samish_&_Skagit_&_Stilly/Snohom	N_Puget_Sound	SnoqualmieR
Nook/Samish_&_Skagit_&_Stilly/Snohom	N_Puget_Sound	WallaceH
Nook/Samish_&_Skagit_&_Stilly/Snohom	N_Puget_Sound	SkykomishR
Nook/Samish_&_Skagit_&_Stilly/Snohom	N_Puget_Sound	NFStillaguamH
Nook/Samish_&_Skagit_&_Stilly/Snohom	N_Puget_Sound	NFNooksackH
Fraser_R_Late	L_Fraser_R	BirkenheadH
Fraser_R_Late	L_Fraser_R	WChilliwackH
Fraser_R_Late	L_Fraser_R	MariaSlough
Fraser_R_Early	L_Thompson_R	NicolaH
Fraser_R_Early	L_Thompson_R	SpiusH
Fraser_R_Early	S_Thompson_R	MShuswapH
Fraser_R_Early	S_Thompson_R	LAdamsH
Fraser_R_Early	S_Thompson_R	LThomR
Fraser_R_Early	N_Thompson_R	RaftR
Fraser_R_Early	N_Thompson_R	DeadmanH
Fraser_R_Early	N_Thompson_R	ClearwaterR
Fraser_R_Early	N_Thompson_R	LouisCr
Fraser_R_Early	Mid_Fraser_R	NechakoR
Fraser_R_Early	Mid_Fraser_R	QuesnelR
Fraser_R_Early	Mid_Fraser_R	StuartR
Fraser_R_Early	Mid_Fraser_R	UChilcotinR
Fraser_R_Early	Mid_Fraser_R	ChilkoR
Not included in FRAM	U_Fraser_R	MorkillR
Not included in FRAM	U_Fraser_R	SalmonRsp
Not included in FRAM	U_Fraser_R	SwiftR
Not included in FRAM	U_Fraser_R	TorpyR
Lower_Georgia _Strait	E_Vancouver_Is	BigQualH
Lower_Georgia _Strait	E_Vancouver_Is	QuinsamH
Lower_Georgia _Strait	E_Vancouver_Is	NanaimoHf
Lower_Georgia _Strait	E_Vancouver_Is	PuntledgeHf
Lower_Georgia _Strait	E_Vancouver_Is	CowichanH
West_Coast_Vanc_Island	W_Vancouver_Is	MarbleH
West_Coast_Vanc_Island	W_Vancouver_Is	NitinatH
West_Coast_Vanc_Island	W_Vancouver_Is	RobertsonH
West_Coast_Vanc_Island	W_Vancouver_Is	SaritaH
West_Coast_Vanc_Island	W_Vancouver_Is	TahsisR
West_Coast_Vanc_Island	W_Vancouver_Is	TranquilR
West_Coast_Vanc_Island	W_Vancouver_Is	ConumaH
Lower_Georgia _Strait	S_BC_Mainland	PorteauCoveH
Lower_Georgia _Strait	S_BC_Mainland	KlinakliniR
Not included in FRAM	Central_BC_Coast	WannockH
Not included in FRAM	Central_BC_Coast	AtnarkoH
Not included in FRAM	Central_BC_Coast	KitimatH
Not included in FRAM	L_Skeena_R	EcstallR
Not included in FRAM	L_Skeena_R	LKalumR
Not included in FRAM	U_Skeena_R	BulkleyR
Not included in FRAM	U_Skeena_R	SustutR

FRAM stock	Genetic stock group	Genetic baseline population
Not included in FRAM	U_Skeena_R	BabineH
Not included in FRAM	Nass_R	OwegeeR
Not included in FRAM	Nass_R	DamdochaxR
Not included in FRAM	Nass_R	KincolithR
Not included in FRAM	Nass_R	KwinageeseR
Not included in FRAM	U_Stikine_R	LTahltanR
Not included in FRAM	Taku_R	NakinaR
Not included in FRAM	Taku_R	TatsatuaCr
Not included in FRAM	Taku_R	UNahlinR
Not included in FRAM	Taku_R	KowatuaCr
Not included in FRAM	SSE_Alaska	ChickamWhitH
Not included in FRAM	SSE_Alaska	ChickaminR
Not included in FRAM	SSE_Alaska	ChickaminH
Not included in FRAM	SSE_Alaska	ClearCr
Not included in FRAM	SSE_Alaska	CrippleCr
Not included in FRAM	SSE_Alaska	KetaR
Not included in FRAM	SSE_Alaska	KingCr
Not included in FRAM	SSE_Alaska_Stikine_R	AndrewCr
Not included in FRAM	SSE_Alaska_Stikine_R	AndrewMacH
Not included in FRAM	SSE_Alaska_Stikine_R	AndrewMedH
Not included in FRAM	SSE_Alaska_Stikine_R	AndrewCryH
Not included in FRAM	NSE_Alaska_King_Salmon_R	KingSalmonR
Not included in FRAM	NSE_Alaska_Chilkat_R	TahiniR
Not included in FRAM	NSE_Alaska_Chilkat_R	TahiniMacH
Not included in FRAM	NSE_Alaska_Chilkat_R	BigBoulderCr
Not included in FRAM	N_Gulf_Coast_Alsek_R	KlukshuR
Not included in FRAM	N_Gulf_Coast_Situk_R	SitukR

Appendix 2. Comparison of genetic estimates of origin with coded-wire-tag records[6] for individual Chinook salmon taken as bycatch in the US West Coast at-sea Pacific hake fishery. Gray indicates equivocal genetic assignment (*P* < 0.8), and bold indicates an unreconciled incompatibility (high genetic assignment probability that mismatched the CWT record).

2009

Genetic assignment	*P*	CWT#	Run	CWT stock	Match
L_Fraser_R	1.000	185239	Fall	S-CHILLIWACK R	Yes
L_Fraser_R	1.000	186243	Fall	S-CHILLIWACK R	Yes
Klamath_R	1.000	068809	Fall	TRINITY RIVER	Yes
L_Fraser_R	1.000	186241	Fall	S-CHILLIWACK R	Yes
L_Fraser_R	1.000	185612	Fall	S-HARRISON R	Yes
Mid_Fraser_R	**1.000**	**025650**	**Fall**	**S-HARRISON R**	**No**
L_Fraser_R	1.000	186243	Fall	S-CHILLIWACK R	Yes
Snake_R_fa	1.000	633987	Fall	SNAKE R-LOWR 33.0002	Yes
U_Columbia_R_su/fa	1.000	634182	Summer	METHOW & OKANOGAN	Yes
U_Columbia_R_su/fa	0.999	634092	Fall	SNAKE R-LOWR 33.0002	No
L_Fraser_R	0.997	185612	Fall	S-HARRISON R	Yes
Hood_Canal	0.994	210790	Fall	GROVERS CR 15.0299	No
U_Columbia_R_su/fa	0.991	634184	Summer	WENATCHEE R 45.0030	Yes
Mid_and_Upper_Columbia_R_sp	0.981	094621	Spring	DESCHUTES R	Yes
Snake_R_fa	0.971	634671	Fall	SNAKE R-LOWR 33.0003	Yes
Hood_Canal	0.969	634270	Fall	GEORGE ADAMS (PURDY)	Yes
U_Columbia_R_su/fa	0.969	612511	URB L-Fall	LYONS FERRY HATCHERY	No
Hood_Canal	**0.967**	**612513**	**URB L-Fall**	**LYONS FERRY HATCHERY**	**No**
U_Columbia_R_su/fa	0.965	633987	Fall	SNAKE R-LOWR 33.0002	No
U_Columbia_R_su/fa	0.959	633799	Summer	WELLS HATCHERY	Yes
N_Puget_Sound	0.955	634277	Fall	CLEAR CR 11.0013C	No
U_Columbia_R_su/fa	0.948	633987	Fall	SNAKE R-LOWR 33.0002	No
Mid_Oregon_Coast	0.947	093937	Spring	NESTUCCA R (CEDAR CR	No
Mid_Oregon_Coast	0.927	094643	Fall	ELK R (ELK R HT)	Yes
Deschutes_R_fa	0.919	633987	Fall	SNAKE R-LOWR 33.0002	No
U_Columbia_R_su/fa	0.884	612736	URB L-Fall	LYONS FERRY HATCHERY	No
W_Cascade_fa	0.843	633473	Spring	COWLITZ R 26.0002	No
U_Columbia_R_su/fa	0.828	634671	Fall	SNAKE R-LOWR 33.0002	No
Snake_R_sp/su	0.752	100181	Summer	S FK SALMON	Yes
Snake_R_fa	0.720	633987	Fall	SNAKE R-LOWR 33.0002	Yes
W_Cascade_sp	0.714	633877	Fall	COWLITZ R 26.0002	No
Hood_Canal	0.714	634271	Fall	GEORGE ADAMS (PURDY)	Yes
U_Columbia_R_su/fa	0.697	633987	Fall	SNAKE R-LOWR 33.0002	No

---

[6] Regional Mark Processing Center, http://www.rmpc.org/

2009

Genetic assignment	*P*	CWT#	Run	CWT stock	Match
Snake_R_fa	0.658	634092	Fall	SNAKE R-LOWR 33.0002	Yes
U_Columbia_R_su/fa	0.634	634182	Summer	METHOW & OKANOGAN	Yes
S_Puget_Sound	0.621	634276	Fall	GROVERS CR 15.0299	Yes
S_Puget_Sound	0.611	634270	Fall	GEORGE ADAMS (PURDY)	No
Hood_Canal	0.604	210681	Fall	CLEAR CR 11.0013C	No
Snake_R_fa	0.578	633871	Summer	WELLS HATCHERY	No
W_Cascade_fa	0.554	634092	Fall	SNAKE R-LOWR 33.0002	No

2010

Genetic assignment	*P*	CWT#	Run	CWT stock	Match
Spring_Cr_Group_tule	1.000	094646	URB L-Fall	BIG CR HATCHERY	Yes
L_Fraser_R	1.000	180481	Fall	S-Chilliwack R	Yes
Spring_Cr_Group _tule	1.000	054864	Fall	SPRING CR 29.0159	Yes
L_Fraser_R	1.000	180486	Fall	S-Harrison R	Yes
Klamath_R	1.000	068801	Spring	TRINITY RIVER	Yes
Mid_Oregon_Coast	1.000	094643	Fall	ELK R (ELK R HT)	Yes
Klamath_R	1.000	068820	Fall	TRINITY RIVER	Yes
L_Fraser_R	1.000	186240	Fall	S-Chilliwack R	Yes
Mid_Oregon_Coast	1.000	094516	Fall	COQUILLE R	Yes
Mid_Oregon_Coast	1.000	094643	Fall	ELK R (ELK R HT)	Yes
N_Oregon_Coast	1.000	054379	Fall	NA	N/A
Klamath_R	0.999	065347	Spring	TRINITY RIVER	Yes
Klamath_R	0.999	068810	Spring	TRINITY RIVER	Yes
U_Columbia_R_su/fa	0.998	634182	Summer	METHOW & OKANOGAN	Yes
Klamath_R	0.998	068809	Fall	TRINITY RIVER	Yes
Spring_Cr_Group _tule	0.998	054866	Fall	SPRING CR 29.0159	Yes
Snake_R_sp/su	0.995	094351	Spring	LOSTINE R ENDEMIC	Yes
Klamath_R	0.994	068810	Spring	TRINITY RIVER	Yes
Spring_Cr_Group _tule	0.983	054865	Fall	SPRING CR 29.0159	Yes
Snake_R_fa	0.975	220301	URB L-Fall	LYONS FERRY HATCHERY	Yes
Hood_Canal	0.970	210790	Fall	GROVERS CR 15.0299	No
Snake_R_fa	0.969	633799	Summer	WELLS HATCHERY	No
U_Columbia_R_su/fa	**0.967**	**068616**	**Fall**	**ROWDY CREEK, SMITH R**	**No**
Hood_Canal	0.964	634271	Fall	GEORGE ADAMS (PURDY)	Yes
U_Columbia_R_su/fa	0.962	617218	URB L-Fall	DESCHUTES R	No
Mid_Oregon_Coast	0.961	068618	Fall	ROWDY CREEK, SMITH R	No
S_Puget_Sound	0.953	634298	Fall	BIG SOOS CR 09.0072	Yes
U_Columbia_R_su/fa	0.953	634092	Fall	SNAKE R-LOWR 33.0002	No
Mid_Oregon_Coast	0.939	210734	Fall	QUINAULT R 21.0398	No
W_Cascade_fa	0.933	634996	Fall	LYONS FERRY HATCHERY	No
S_Thompson_R	**0.926**	**185557**	**Fall**	**S-Harrison R**	**No**
Rogue_R	0.907	068616	Fall	ROWDY CREEK, SMITH R	No
N_Puget_Sound	0.893	210777	Summer	SKYKOMISH R 07.0012	Yes
L_Fraser_R	0.887	186242	Fall	S-Chilliwack R	Yes
L_Fraser_R	0.841	180485	Fall	S-Harrison R	Yes
L_Fraser_R	**0.819**	**634092**	**Fall**	**SNAKE R-LOWR 33.0002**	**No**
W_Cascade_fa	0.717	054867	Fall	SPRING CR 29.0159	No
Rogue_R	0.689	090126	URB L-Fall	COLE RIVERS HATCHERY	Yes
N_Puget_Sound	0.681	634272	Fall	SAMISH (FRIDAY CR)	Yes
Snake_R_fa	0.662	612716	URB L-Fall	LYONS FERRY HATCHERY	Yes

2010

Genetic assignment	*P*	CWT#	Run	CWT stock	Match
L_Columbia_R_fa	0.618	634774	Fall	KALAMA R 27.0002	Yes
Hood_Canal	0.609	210824	Fall	CLEAR CR 11.0013C	No
Central_Valley_fa	0.548	068650	Fall	FEATHER R HATCHERY	Yes
U_Columbia_R_su/fa	0.529	634681	Fall	LYONS FERRY HATCHERY	No
U_Columbia_R_su/fa	0.491	634391	Fall	PRIEST RAPIDS (36)	Yes
U_Columbia_R_su/fa	0.454	612755	URB L-Fall	LYONS FERRY HATCHERY	No
U_Columbia_R_su/fa	0.353	612519	URB L-Fall	LYONS FERRY HATCHERY	No
L_Fraser_R	0.260	633466	Fall	DESCHUTES R 13.0028	No