

Genetic Analysis of Juvenile Chinook Salmon at Tidal Freshwater Monitoring Sites in the Vicinity of the Sandy River Delta, Lower Columbia River, 2007

The information in the following pages is provided by NWFSC geneticists to PNNL scientists for inclusion in the Tidal Freshwater Monitoring study's March 2008 annual research report to the Bonneville Power Administration. The citation for the full report is as follows.

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Methods

Tissue Collection. Fin clips on sub-samples of salmon (~15 per sample site per trip) were preserved in ethanol for genetic mixture analysis. A total of 121 clips were sent the NMFS laboratory for genetic analysis as part of the 2007 Tidal Freshwater Monitoring Study.

Processing and Analysis. We used standard methods of genetic stock identification and individual assignment (recently reviewed by Manel et al. 2005). Chinook salmon were genotyped using the methods described in Van Doornik et al. (2007). Data were collected for 13 microsatellite loci that have recently been standardized among several west coast genetics laboratories (Seeb et al. 2007). Genetic mixture analysis and the relative probability of stock origin of each sample were estimated using the genetic stock identification computer program ONCOR (Kalinowski et al. 2007). Population baseline data were from the multi-laboratory standardized Chinook salmon genetic database described by Seeb et al. (2007). Mixture proportions and assignments probabilities for individual baseline populations were summed to nine Columbia River Basin stock groups (Table 1). Confidence intervals of the mixture proportions were estimated using ONCOR by re-sampling mixture and baseline data 100 times.

Results

Genotypic data were collected for 108 Chinook salmon and used in the genetic stock identification analysis. Results of the mixture analysis are presented in Table 1. Percentage estimates for four genetic stock groups (West Cascade Tributary Fall, Willamette River Spring, Deschutes River Fall, and Upper Columbia River Summer/Fall) ranged from 11% to 43%, all with non-zero lower 95% confidence intervals. Small contributions were also estimated for the West Cascade Tributary Spring (3%) and Snake River Fall (6%) stock groups. Results of individual fish probability assignments were summed by collection date (Figure 1) and site (Figure 2). Assignment probabilities for the most likely stock group for each individual ranged from 0.51 to 1.00 with approximately 60% of the assignments greater than 0.90 (data not shown). Nearly all of the low probability assignments were fish with assignments split between the Deschutes River Fall and Upper Columbia River Summer/Fall groups.

Table 1. Estimated percentage genetic stock group composition and 95% confidence intervals of 108 juvenile Chinook salmon sampled in the study area from June through December 2007.

<i>Genetic Stock Group and Baseline Populations</i>	<i>Estimated Contribution</i>	<i>95% Confidence Interval</i>
West Cascade Tributary Fall	23%	10% - 28%
Cowlitz Hatchery		
Lewis River		
Sandy River		
West Cascade Tributary Spring	3%	0% - 10%
Cowlitz Hatchery		
Kalama Hatchery		
Lewis Hatchery		
Willamette River Spring	15%	7% - 21%
Mckenzie Hatchery and River		
North Santiam Hatchery and River		
North Fork Clackamas River		
Spring Creek Group Tule Fall	0%	0% - 5%
Spring Creek Hatchery		
Big Creek Hatchery		
Elochoman River		
Willamette River		
Deschutes River Fall	11%	1% - 19%
Lower Deschutes River		
Upper Deschutes River		
Upper Columbia River Summer/Fall	43%	33% - 56%
Handford Reach		
Methow River		
Wells Hatchery		
Wenatchee River		
Mid and Upper Columbia River Spring	0%	0% - 0%
Carson Hatchery		
John Day River		
Upper Yakima River		
Warm Springs Hatchery		
Wenatchee Hatchery and River		
Snake River Fall	6%	0% - 15%
Lyons Ferry Hatchery		
Snake River Spring	0%	0% - 2%
Imnaha River		
Minam River		
Rapid River Hatchery		
Secech River		
Tucannon Hatchery and River		
Newsome Creek		
West Fork Yankee Creek		

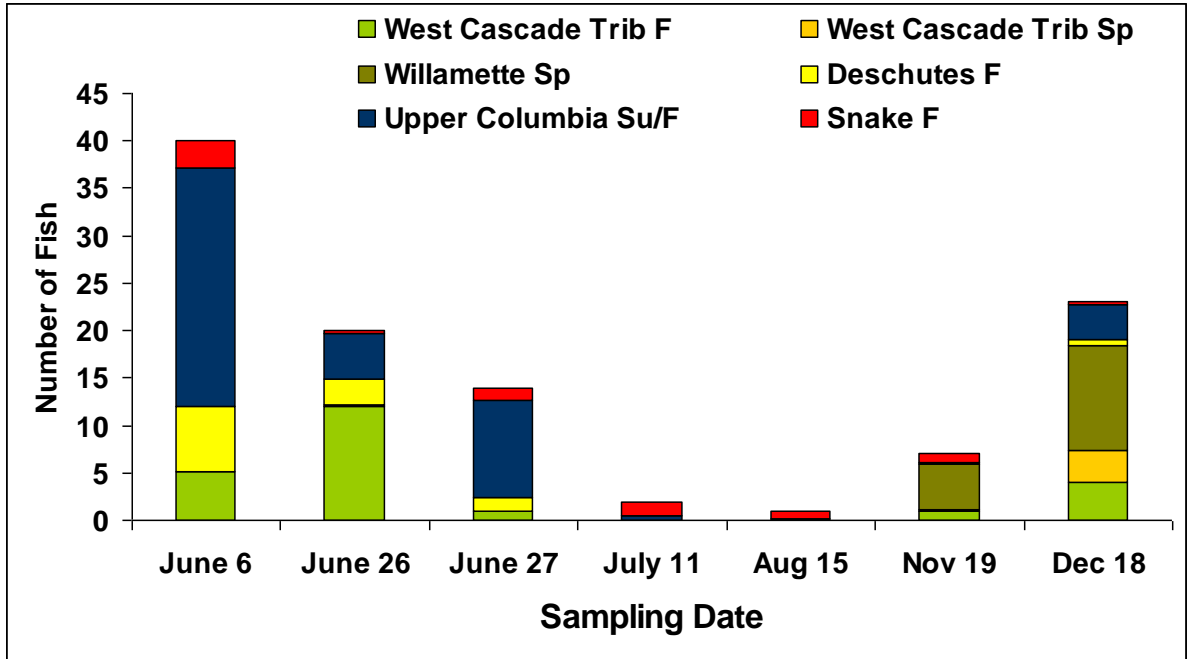


Figure 1. Sums of fractional genetic assignments of individual Chinook salmon by collection date. Fractions for the Spring Creek Group Tule Falls, Mid and Upper Columbia Springs, and Snake Springs totaled to 0.25 and are not shown. F=fall run, Su=summer run, Sp=spring run.

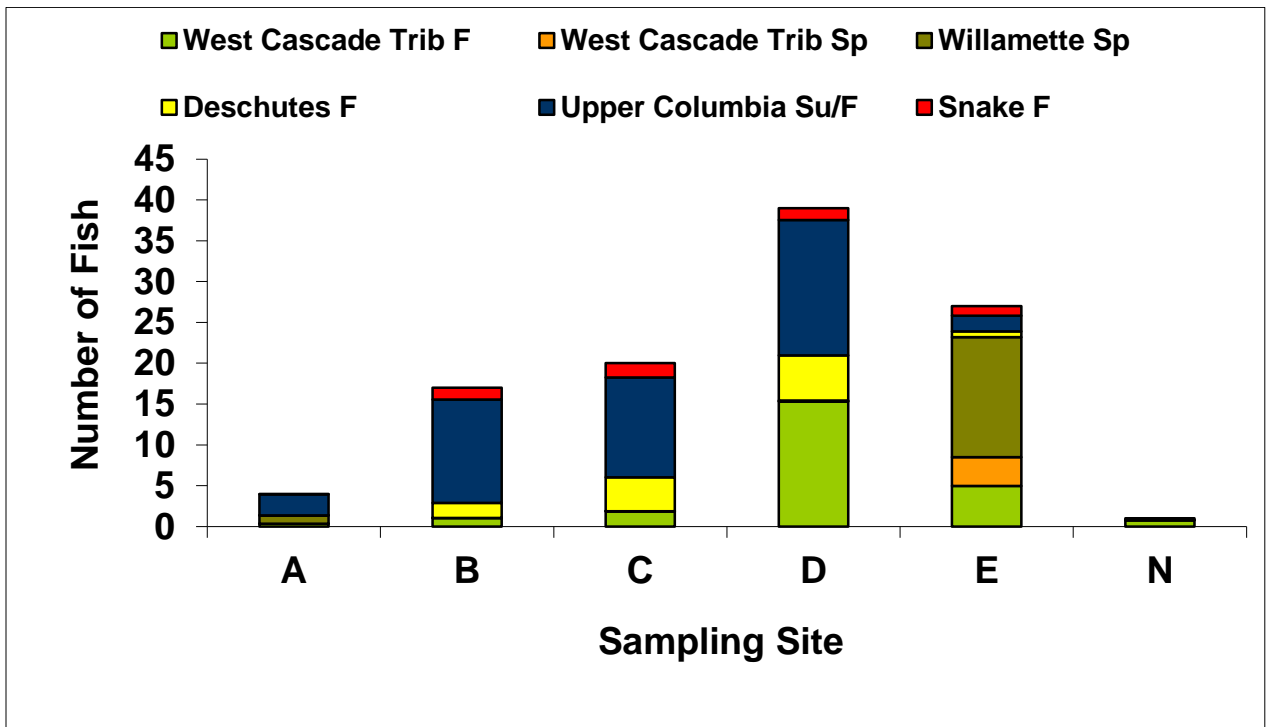


Figure 2. Sums of fractional genetic assignments of individual Chinook salmon by sampling site. Fractions for the Spring Creek Group Tule Falls, Mid and Upper Columbia Springs, and Snake Springs totaled to 0.25 and are not shown. F=fall run, Su=summer run, Sp=spring run.

Discussion

Our genetic analysis indicated that diverse stocks of Chinook salmon occupy habitats within the study area (Table 1). Genetic stock groups from both below (West Cascade Tributaries and Willamette River) and above (Deschutes River, Upper Columbia River, and Snake River) Bonneville Dam were estimated to contribute to the samples. In addition, we found that both fall and spring Chinook salmon were sampled. Estimates of Willamette River fish in our samples are surprising because the Willamette River enters the Columbia River below our study area. These results indicate that fish may have migrated upstream to our sites. An alternative explanation is that the fish that we allocated to the Willamette stock were Sandy River spring Chinook salmon. Willamette hatchery stocks has been outplanted extensively in the Sandy River and previous genetic studies have shown that Sandy River spring Chinook are genetically intermediate between the Willamette and Lower Columbia spring run groups (Myers et al. 2006). Additional analysis that includes Sandy River spring run data in the genetic baseline may help with the interpretation of these results.

We summed individual fish assignment probabilities by date to search for temporal patterns in Chinook salmon habitat use (Fig. 2). Sampling in early June produced our largest catches of juvenile Chinook salmon, and also the largest estimated catches of all of the interior Columbia Basin stock groups. In contrast, estimates for spring Chinook salmon from the Willamette River and West Cascade Tributaries were greatest in our late December sampling, which showed the greatest diversity of groups.

Our analysis of first-year samples indicates that genetic data can provide useful information on Chinook salmon use of the study sites. The microsatellite DNA baseline we used for the genetic analysis includes representative populations from all of the major Columbia River Basin stock groups (Waples et al. 2004). It is expected that the multi-agency standardized database supporting the baseline (Seeb et al. 2007) will continue to include more populations providing improved identification for some stock groups.

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