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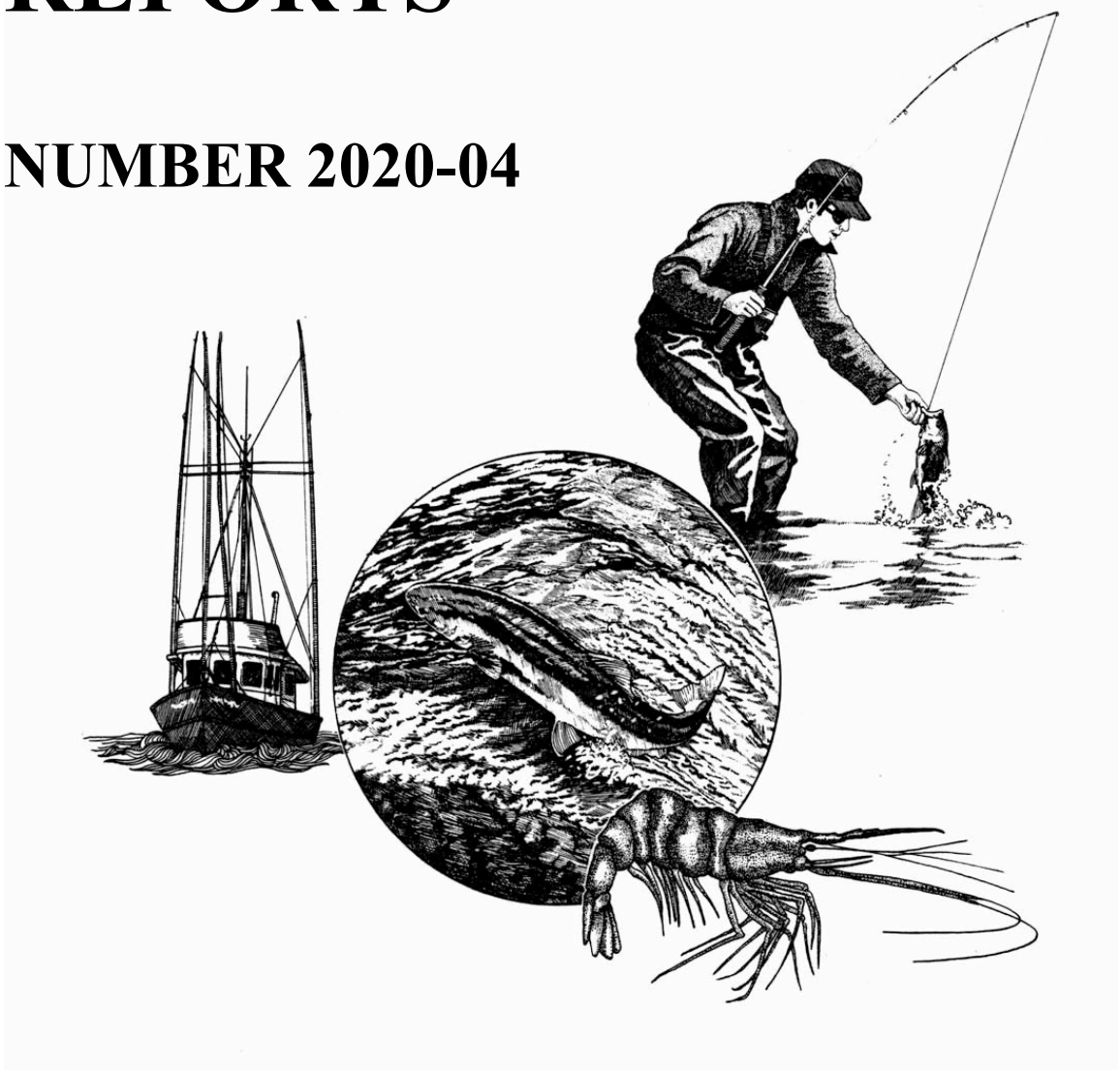

FISH DIVISION

Oregon Department of Fish and Wildlife

Genetic analysis of Chinook salmon (*Oncorhynchus tshawytscha*) in the Clackamas basin, 2015-2018

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CONTENTS

SUMMARY

We performed genetic analysis of Chinook salmon carcass samples collected from the Clackamas basin in 2015-2018. We found evidence for weak population structure based on neutral genetic markers which appears to be associated with collection date (early vs. late). We also found evidence for weak population structure among carcass samples based on collection location (upper vs. lower basin). Based on variation at the run timing marker, *Greb1L*, there was a mixture of spring, fall, and heterozygous genotypes within each year. Over 90% of the carcass samples assigned to the Upper Willamette River Chinook salmon evolutionarily significant unit (ESU), which includes naturally spawned spring-run Chinook salmon originating from the Clackamas River, the Willamette River and its tributaries above Willamette Falls, as well as spring-run Chinook salmon from six artificial propagation programs.

INTRODUCTION

The Clackamas River is a tributary of the Willamette River in northwestern Oregon. This basin supports Chinook salmon populations exhibiting two life history types. The spring-run Chinook salmon population is part of the Upper Willamette River Spring Chinook ESU, which is currently listed as threatened under the Endangered Species Act (ESA) (NMFS 2014). The Fall-run Chinook salmon population is part of the Lower Columbia River ESU, which is currently listed as threatened under the Endangered Species Act (ESA) (NMFS 2014). The terms spring run and fall run refer to the general migration timing of adult fish returning from the ocean to freshwater for spawning. Additional general differences between these two life history types include: spawning timing, fry emergence timing, freshwater life-histories, and juvenile ocean migration timing (NMFS 2013). Although there are substantial life-history differences between these two Chinook populations, there is still spatial and temporal overlap among spawners within the Clackamas River basin. When spawner abundance estimates rely on visual characteristics, this overlap creates difficulties in enumerating individual fish to spring-run or fall-run populations. Managers at the Oregon Department of Fish and Wildlife (ODFW) sought to determine if there are patterns in the spatial and temporal distributions of fall and spring run Chinook salmon in the Clackamas basin. If present, these patterns can be used to better delineate monitoring designs and provide better status assessments for managing these two listed Chinook populations.

Spring-run fish are counted as they pass the North Fork Clackamas Dam. Typical spawn timing is August-October (peak in September) ODFW (2011), and most of their spawning areas are above the dam

(Schroeder et al. 2007). These counts are done by Portland General Electric (PGE) staff and reported on their website. Based on life-history characteristics and historic timing, the PGE website characterizes typical North Fork Dam migration timing of spring Chinook as March through mid-October, and of fall Chinook as August through December. This relatively early timing for fall Chinook is likely the result of prior releases of an early spawning (Tule) stock of hatchery Chinook. In recent years, Clackamas spring-run Chinook spawning abundance has been in the thousands of fish. Fall-run Chinook historically spawned above and below PGE's River Mill-North Fork hydroelectric complex (ODFW 2010), but currently are limited to areas below this complex. In recent years Clackamas fall-run Chinook spawning abundance has been in the hundreds of fish. It was suspected that poor water quality in the lower Clackamas River contributed to a decline in the natural run of fall Chinook salmon (Taylor 1999). Tule fall Chinook salmon were released into the Clackamas basin in 1952, and a naturally sustaining population of fall Chinook salmon was reported in the Clackamas through 1991. Tule Chinook are a fall Chinook population in which adults return to freshwater relatively early (mid-August), in an advanced state of maturation, and typically spawn within a few weeks (ODFW 2010).

The primary goal of this research was to determine if there were two genetically distinct groups of Chinook salmon present on the Clackamas basin spawning grounds in 2015-2018. The secondary goal, predicated on the results from the first, was to determine the spatial and/or temporal distribution patterns of any genetically distinct groups that are relevant to management. We used neutral genetic markers as well as genetic markers associated with run timing (Thompson et al. 2019) to test for population structure among carcass samples within each of the four consecutive years. We also used the neutral genetic markers to assign individual carcass samples to previously established genetic reporting groups (Hess et al. 2015), which include Chinook salmon from the Upper Willamette River and Lower Columbia River ESUs.

METHODS

Sample collection

Caudal fin tissue was sampled from Chinook salmon carcasses collected during the 2015-2018 spawning ground surveys in the Clackamas basin and from live Chinook salmon trapped at the North Fork Dam Adult Sorting Facility in 2017 and 2018 (Table 1, Figure 1). These spawning surveys are conducted each year as part of ODFW's long-term monitoring of naturally spawning populations of Oregon salmonids. There are two main spawning survey efforts for Chinook in the Clackamas basin, one targeting spring-run

fish and one fall-run fish (Whitman et al. 2017 and ODFW 2019, respectively). The two programs use similar field methods. Stream reaches that are small enough to be walked safely are sampled by individual surveyors in an upstream direction. Larger stream reaches are sampled by two or more surveyors, from inflatable non-motorized boats, in a downstream direction. Surveyors enumerate redds and all live and dead adult salmonids observed. Surveyors record species, sex, length, and all fin clips and tags observed on all carcasses collected. Scales, otoliths and fin clip samples are collected, with the fin clips preserved in 95% ethanol. All surveys are conducted on a 7 to 10 day rotation through the spawning survey season. The repeat schedule is intended to increase the probability of adequately documenting peak redd counts. These repeat visits also provide carcass samples throughout the spawning season to avoid temporal biases and increase the number of carcasses sampled. Typically, spring Chinook spawning surveys are conducted from mid-July through mid-October and fall Chinook surveys September through mid-January. Spring Chinook spawning surveys are based on a census design, thus include annually sampling all known Spring Chinook spawning habitat in the Clackamas River basin. Fall Chinook spawning surveys are based on a random spatially-balanced sampling design (Stevens 2002) to annually select survey sites representing 30% of the Fall Chinook spawning habitat below the North Fork Clackamas Dam. This equates to an annual sampling goal of 11 sites (~1 mile in length) from the 36.2 miles of fall Chinook spawning habitat in this area. Further detail on the methods and design for these two spawner estimates are found in Schroder et al. (2013) and Jacobs et al. (2002). The design of these two efforts provides substantial spatial and temporal overlap in spawning surveys.

Tissue samples were collected from live Chinook by Portland General Electric staff at the North Fork Clackamas Dam trapping facilities. This sampling was conducted as an addition to normal operations at the facility. The 2017 samples from live Chinook were presumed fall Chinook salmon based on timing, collected in October. The 2018 live samples were part of a tagging study performed in June and July. Fin clips were preserved in 95% ethanol.

Table 1. Number of Chinook salmon collected from the Clackamas basin spawning grounds and North Fork Dam Adult Sorting Facility (16) in 2015-2018. Sampling dates, total number of samples collected, and number of samples successfully genotyped are listed for the 23 sampling locations for all three years. The appendix further reports sample sizes by year.

Location	Dates	Collected	Genotyped
1 Clackamas River 1	Sep 17 - Oct 12	26	17
2 Clackamas River 2	Aug 15 - Oct 15	283	159
3 Clackamas River 3	Sep 28 - Oct 12	65	33
4 Hot Springs Fork	Oct 5 - 6	3	0
5 Collawash River	Sep 24 - Oct 22	42	24
6 Clackamas River 4	Sep 20 - Oct 15	13	8
7 Oak Grove Fork 1	Sep 29	1	1
8 Oak Grove Fork 2	Sep 29 - Oct 15	7	6
9 Oak Grove Fork 3	Oct 1 - 15	5	2
10 Clackamas River 5	Sep 20 - Oct 15	9	7
11 Clackamas River 6	Sep 29 - Oct 28	14	8
12 Roaring River	Oct 5	3	2
13 Clackamas River 7	Jul 21 - Oct 28	5	1
14 South Fork Clackamas	Sep 29 - Oct 28	13	6
15 Clackamas River 8	Sep 29 - Oct 28	16	12
16 North Fork Dam	Jun 7 - Oct 27	96	91
17 Clackamas River 9	Oct 15	1	1
18 Clackamas River 10	Jul 15 - Nov 22	99	43
19 Clackamas River 11	Jul 25 - Nov 22	13	2
20 Clackamas River 12	Jul 15 - Oct 15	10	2
21 Clackamas River 13	Oct 8	1	1
22 Clackamas River 14	Jul 8 - Aug 29	10	6
23 Clackamas River 15	Jun 30 - Aug 30	13	7
Total		**748**	**439**

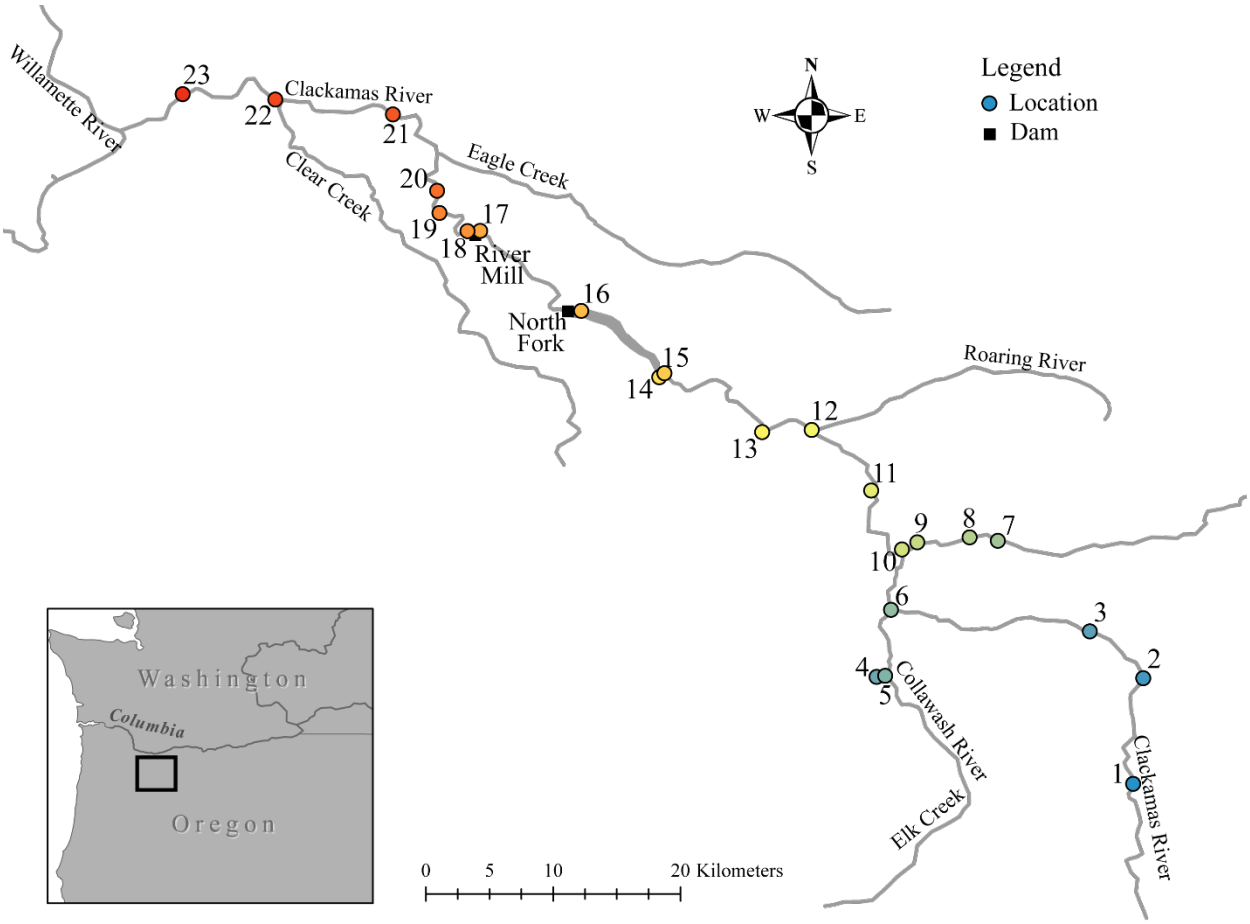


Figure 1. Map of Clackamas basin showing the Chinook salmon sampling locations. Locations are numbered from 1 (most upstream) to 23 (most downstream). Site names and sample sizes are listed in Table 1. Dams are indicated by black squares.

DNA extraction and sequencing

Genomic DNA was isolated following the protocol of Ivanova et al. (2006). Samples were genotyped at a panel of previously identified single nucleotide polymorphisms (SNPs) using the Genotyping-in-Thousands by sequencing (GT-seq) method of Campbell et al. (2015). The panel consisted of 299 SNPs including a sex marker (Ots_SEXY3-1) (Hess et al. 2015) and two SNPs in the *Greb1L* region (Thompson et al. 2019). The genotyping protocol followed Campbell et al. (2015), except the second polymerase chain reaction (PCR) used Ultra II Q5 master mix (New England Biolabs) to add i5 and i7 adapters. Amplicons were sequenced on an Illumina HiSeq 3000 at Oregon State University's Center for Genome Research and Biocomputing. Samples were sequenced on two lanes. The first three years were split evenly across lanes and 2018 samples were all sequenced on the second lane.

Genotyping

We used genotyping scripts previously developed by Campbell et al. (2015) which are available at https://github.com/GTseq/GTseq-Pipeline/. Reads were demultiplexed with GTseq_BarcodeSplit_MP.py. Genotypes were called with GTseq_Genotyper_v3.pl and compiled with GTseq_GenoCompile_v3.pl. The sex marker, Ots_SEXY3-1, was called using OtsSEX_test_v2. GTseq_Genotyper_v3.pl was used to calculate an individual fuzziness index (IFI), which estimates the amount of cross-contamination in a given sample. Only samples with an IFI less than 2.5 and at least 90% of SNPs genotyped were included in our analysis. Duplicate samples were identified in Coancestry (Wang 2011).

Twelve pairs of SNPs aligned within 10,000 base pairs of each other on the Chinook salmon genome (Genome accession number GCA_002872995). To account for potential linkage, we removed the member of each pair with the lower estimate of effective alleles calculated in GenAlEx (Peakall and Smouse 2012). We removed 12 SNPs from the dataset that had more than 20% missing data or failed to genotype in more than 10% of samples because alleles amplified unevenly, reducing the ability to call heterozygotes. After removing 23 monomorphic SNPs, the dataset consisted of 252 putatively neutral polymorphic SNPs. The two *Greb1L* SNPs, snp640165 and snp670329, which have previously been shown to be associated with run timing (Thompson et al. 2019), were analyzed separately. snp640165 has been found to be more informative when characterizing run timing in coastal Chinook salmon (Thompson Per. Comm.).

Analyses

Polymorphic SNPs were checked for deviations from Hardy-Weinberg proportions and linkage equilibrium in GENEPOP v. 4.2 (Raymond and Rousset 1995). Measures of genetic diversity were calculated in GENALEX v. 6.5 (Peakall and Smouse 2012).

The Bayesian clustering software STRUCTURE v. 2.3.4 (Pritchard et al. 2000, Falush et al. 2003) was used to assign individuals to genetic clusters that met expectations of Hardy-Weinberg and linkage equilibrium. The number of clusters, *K*, was allowed to vary from 1 to 5, with 10 runs for each *K*, using the admixture and correlated allele frequencies model. Burn-in and length of simulation were set at 50,000 iterations, each. We selected the K with the highest delta K (Evanno et al. 2005) in STRUCTURE HARVESTER (Earl and vonHoldt 2012).

Samples were also visualized using principal components analysis (PCA) in the R (R Core Team 2018) package adegenet v. 2.1.1 (Jombart 2008, Jombart and Ahmed 2011). Scatter plots were produced with R package ggplot2 v. 3.1.0 (Wickham 2016).

We used ONCOR (Kalinowski et al. 2007) to assign each sample to previously established genetic reporting groups (Hess et al. 2015). These groups, listed in Table 2, were identified by genotyping 7,084 Chinook salmon at 172 SNPs. Samples with assignment probabilities less than 0.95 were considered to be unassigned.

Table 2. Reporting groups and associated number of individuals (n) genotyped at 172 neutral SNPS to establish the GSI baseline (adapted from Hess et al. 2015).

Reporting group	**Description**	**n**
01_YOUNGS	Youngs Bay-Columbia Rogue stock	91
02_WCASSP	West Cascade spring-run	173
03_WCASFA	West Cascade fall-run	522
04_WILLAM	Willamette River spring-run	205
05_SPCRTU	Spring Creek tule fall-run	126
06_KLICKR	Klickitat River spring-run	84
07_DESCSP	Deschutes River spring-run	183
08_JOHNDR	John Day River spring-run	167
09_YAKIMA	Yakima River spring-run	164
10_UCOLSP	Upper Columbia River spring-run/Carson Hatchery spring-run	382
11_TUCANO	Tucannon River spring-run	81
12_HELLSC	Hells Canyon spring-run	1258
13_SFSALM	South Fork Salmon River spring/summer-run	528
14_CHMBLN	Chamberlain Creek spring/summer-run	219
15_MFSALM	Middle Fork Salmon River spring/summer-run	972
16_UPSALM	Upper Salmon River spring/summer-run	973
17_DESCFA	Deschutes River fall-run	252
18_UCOLSF	Upper Columbia River summer/fall-run	385
19_SRFALL	Snake River fall-run	318

RESULTS

Genetic Diversity

Two SNPs (*Ots_hnRNPL* and *Ots_U2305-63*) showed deviations from Hardy-Weinberg proportions, which may have been due to the presence of subpopulation structure (see below). The inclusion of these

SNPs did not change the results of the analyses. After removing closely mapped SNPs, no remaining SNPs showed evidence of linkage disequilibrium after correcting for multiple comparisons.
Levels of genetic diversity were similar across carcass sample collections by year (Table 3). The 2017 collection had slightly higher observed heterozygosity than expected heterozygosity, while the remaining years had slightly lower observed heterozygosity than expected heterozygosity.

Table 3. Genetic diversity of Clackamas basin Chinook salmon carcass samples at 252 putatively neutral SNPs. N = number of samples, N_A = average number of alleles per SNP, H_O = observed heterozygosity, H_E = expected heterozygosity, and F = fixation index.

Year	N	N_A	H_O	H_E	F
2015	85	1.958	0.297	0.298	0.006
2016	98	1.958	0.291	0.294	0.013
2017	79	1.947	0.290	0.287	-0.012
2018	86	1.966	0.286	0.291	0.017

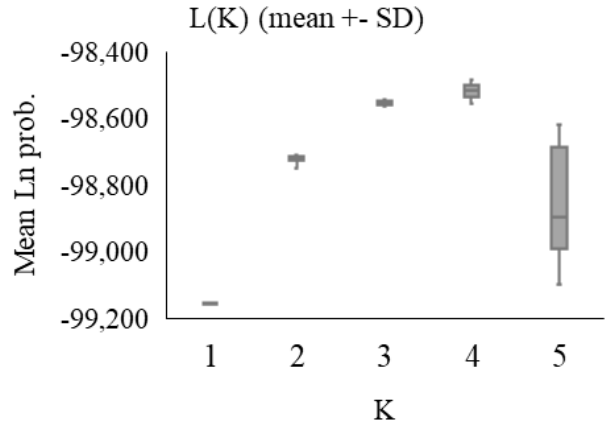
Population structure

Based on results from the software STRUCTURE, we found evidence for two genetic clusters, which roughly corresponded to early and late spawners (Figure 2). While STRUCTURE runs with K = 3 and K = 4 had higher mean log probability (Figure 2a), K = 2 had the highest delta K (Figure 2b) and runs with K > 2 evenly assigned all samples to every cluster, indicating that these results were not biologically meaningful.

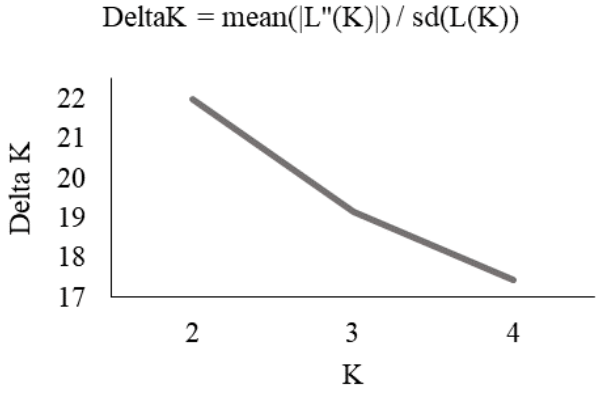
Carcass samples collected in late October and November of 2015, 2016, and 2018, also had strong assignment to the late-spawning group. This pattern was not found in the 2017 carcass samples, but no carcass samples were collected after October 12th of that year.

Figure 2. STRUCTURE results (a) Mean log probability for each K (b) Delta K from STRUCTURE HARVESTER and (c) Bar plot ($K = 2$) of Clackamas basin Chinook salmon based on 252 putatively neutral SNPs. Each row represents one individual, and the proportion of shading indicates assignment to each genetic cluster. Samples are listed in order by date of collection, with live samples collected from the North Fork Dam sorting facility listed before carcass samples collected during spawning ground surveys. Green represents the early spawning group and orange indicates the late spawning group. *Greb1L* genotypes at both SNPs are indicated to the right of the STRUCTURE plot. The first two blocks are snp640165 and the second two blocks are snp670329. Green indicates a spring allele, orange indicates a fall allele, and white indicates missing data. Sex of each individual is reported to the right of *Greb1L* genotype, with pink indicating females and blue indicating males.

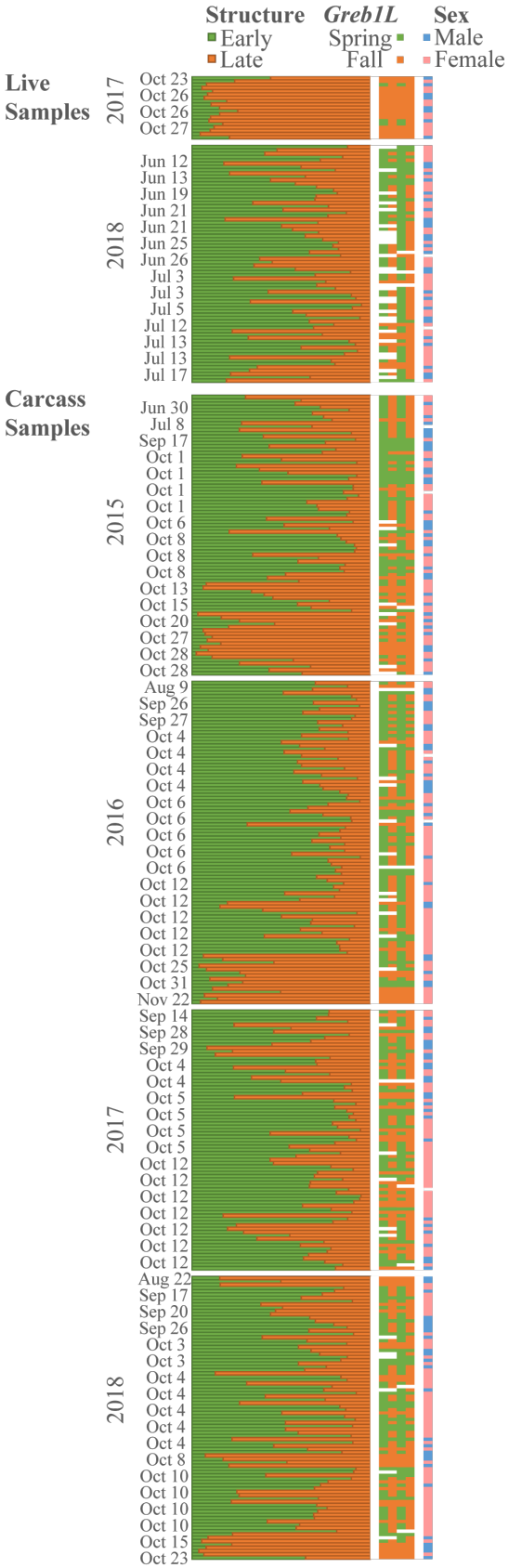
(a)



(b)



(c)



The live samples collected from the North Fork Dam in October, 2017, had the strongest assignment to the late spawning cluster (Figure 2c). This group of samples also had the highest frequency of fall *Greb1L* genotypes. Most samples (84.2%) were homozygous fall at both SNPs and the remaining samples were heterozygous at both SNPs.

Principal components analysis (PCA)

We did not find partitioning by date of carcass collection (Figure 3a-d). However, we did see evidence for partitioning by carcass location in 2015, 2016, and 2018. Samples collected in the upper basin were associated with the positive end of the first axis in 2015 (Figure 4a) and 2016 (Figure 4b) and with the negative end of the first axis in 2018 (Figure 4d). Samples collected in the lower basin were associated with the negative end of the first axis in 2015 and 2016 and with the positive end of the first axis in 2018. This pattern was absent in 2017 (Figure 4c), when few samples were collected from the lower basin.

There was a larger proportion of late spawners in the lower basin, but early and late spawners were found in both basins.

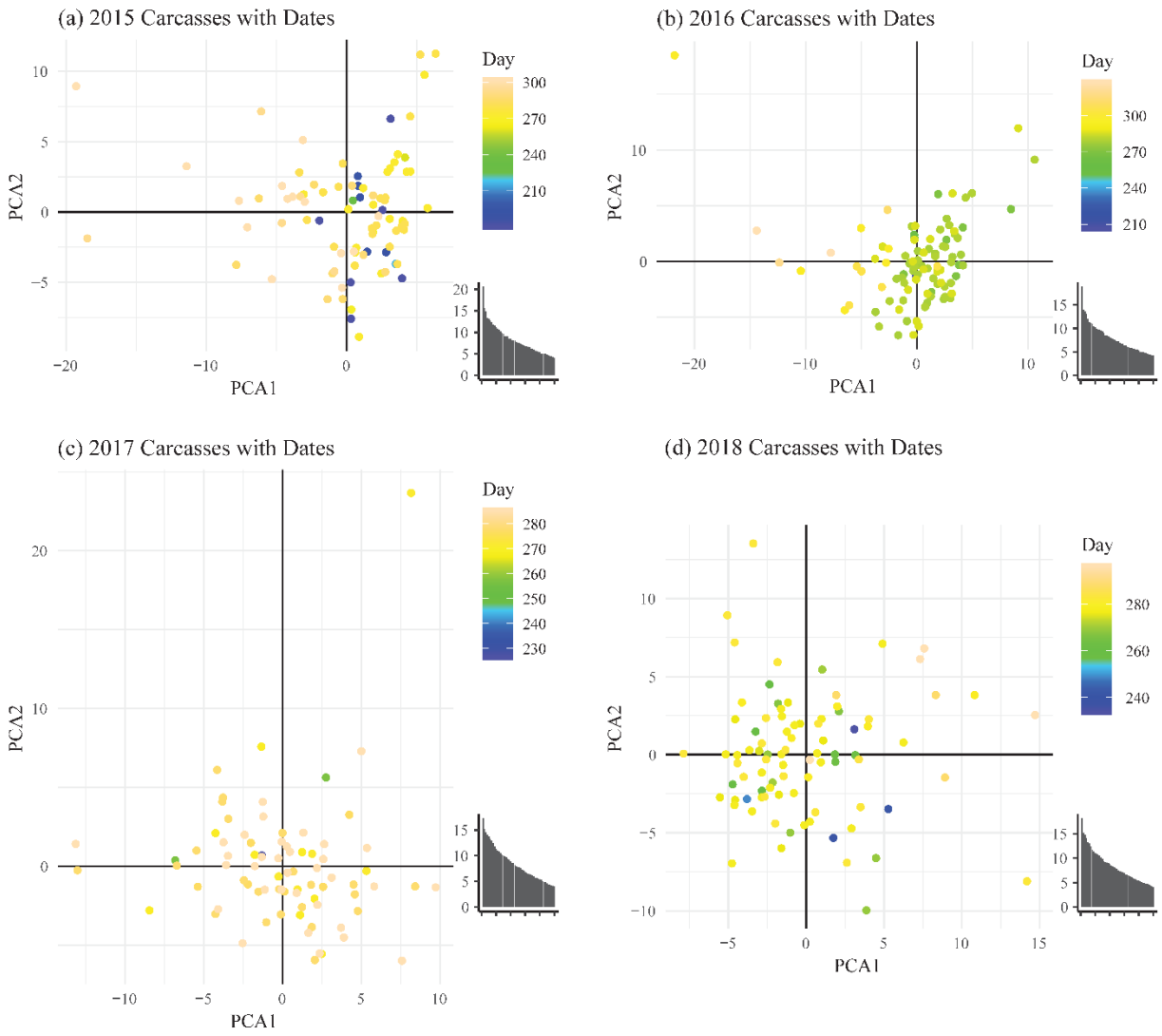


Figure 3. PCAs for each year of Clackamas basin carcass samples genotyped at 252 putatively neutral SNPs performed in adegenet. Eigenvalues for the first 50 axes are shown in the inset bar plots. Points are shaded to indicate the day of the year the carcass sample was collected from the spawning grounds, ranging from 181 (June 30th) to 327 (November 22nd). (a) 2015 samples. PCA axis 1 explained 4.2% of the variation and axis 2 explained 3.2% of the variation. (b) 2016 samples. PCA axis 1 explained 3.8% of the variation and axis 2 explained 2.9% of the variation. (c) 2017 samples. PCA axis 1 explained 3.5% of the variation and axis 2 explained 3.1% of the variation. (d) 2018 samples. PCA axis 1 explained 3.7% of the variation and axis 2 explained 3.1% of the variation.

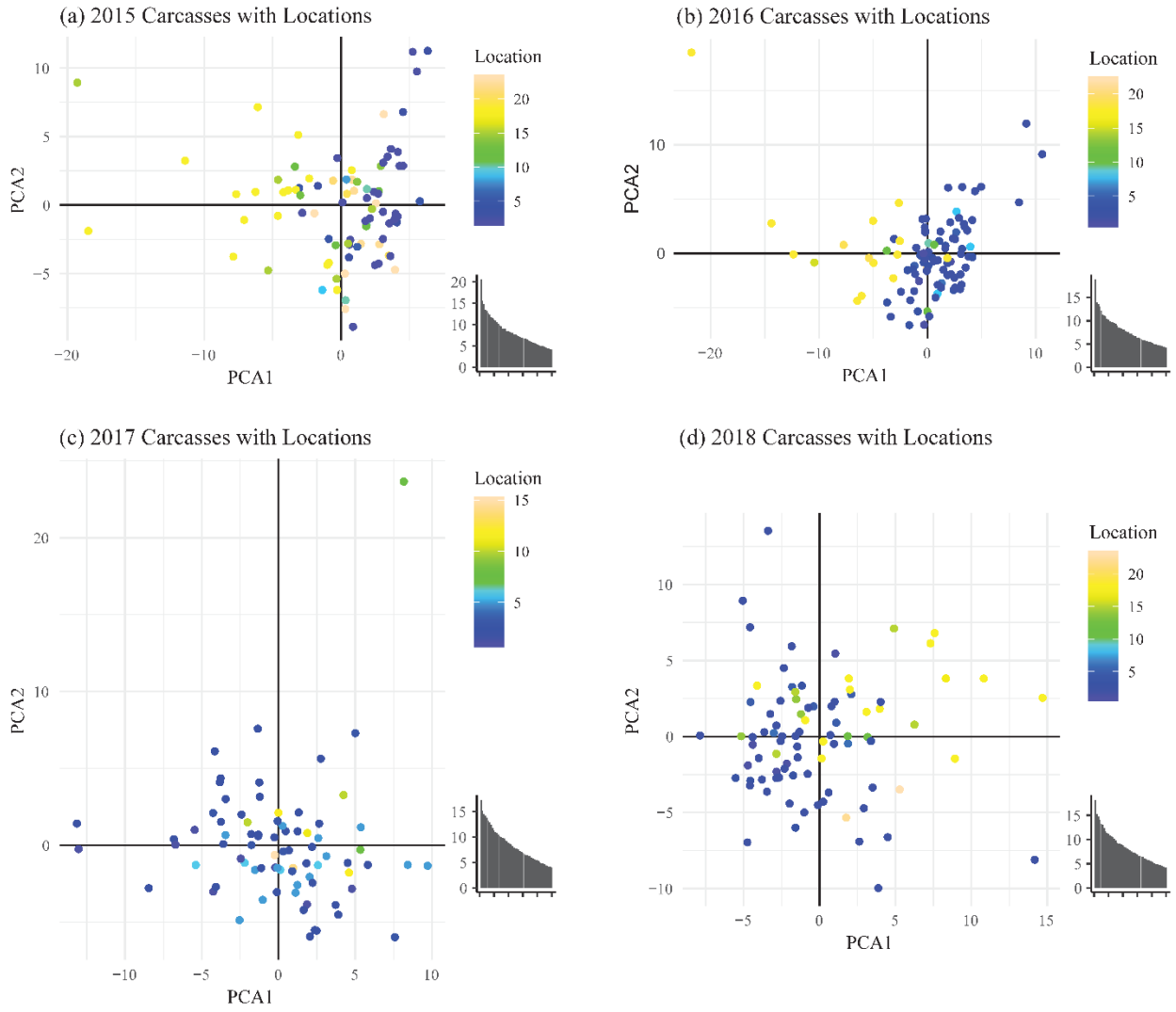
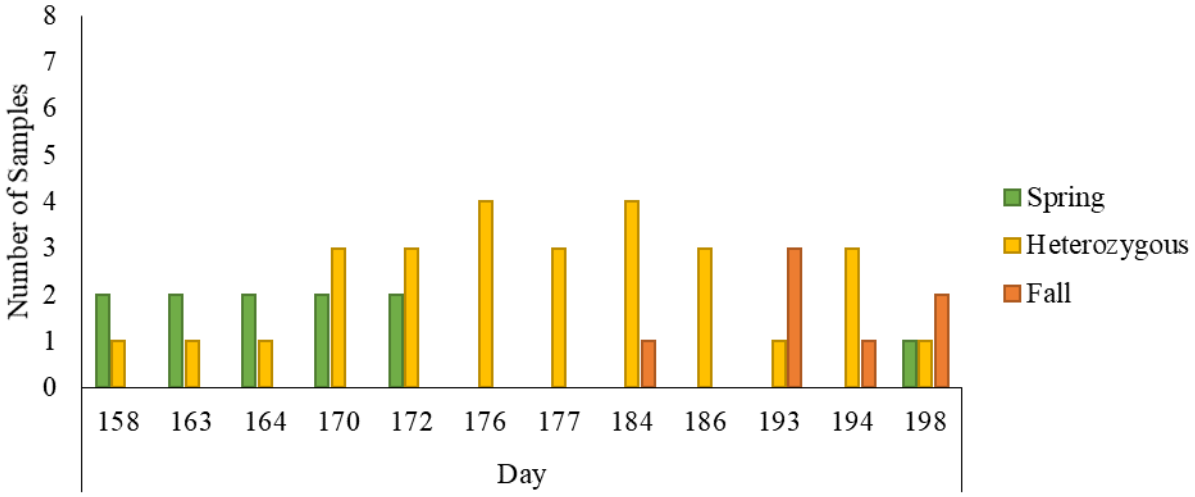


Figure 4. PCAs for each year of Clackamas basin carcass samples genotyped at 252 putatively neutral SNPs performed in adegenet. Eigenvalues for the first 50 axes are shown in the inset bar plots. Points are shaded to indicate the location where the carcass sample was collected, with locations numbered from 1 (most upstream) to 23 (most downstream) (Table 1, Figure 1). (a) 2015 samples. PCA axis 1 explained 4.2% of the variation and axis 2 explained 3.2% of the variation. (b) 2016 samples. PCA axis 1 explained 3.8% of the variation and axis 2 explained 2.9% of the variation. (c) 2017 samples. PCA axis 1 explained 3.5% of the variation and axis 2 explained 3.1% of the variation. (d) 2018 samples. PCA axis 1 explained 3.7% of the variation and axis 2 explained 3.1% of the variation.

Run timing markers

We saw a shift in *Greb1L* genotype frequencies at both SNPs during the one month sampling period at North Fork Dam in 2018 (Figure 5a-b). However, there was no clear relationship between the two *Greb1L* SNP genotype frequencies and carcass collection date (Figure 6). Further, *Greb1L* genotypes at either SNP did not correspond to the genetic clusters identified in STRUCTURE.

(a) snp640165



(b) snp670329

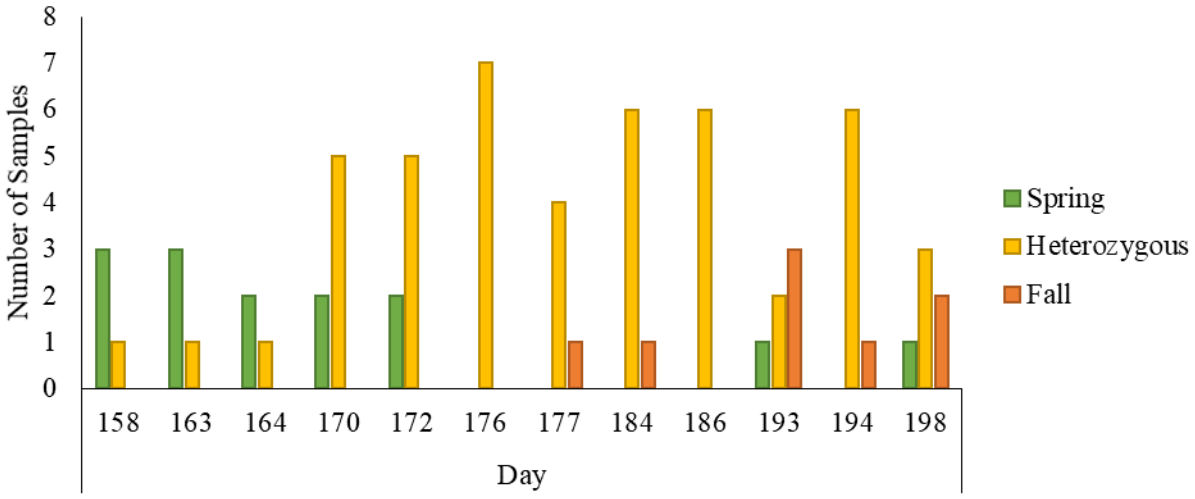
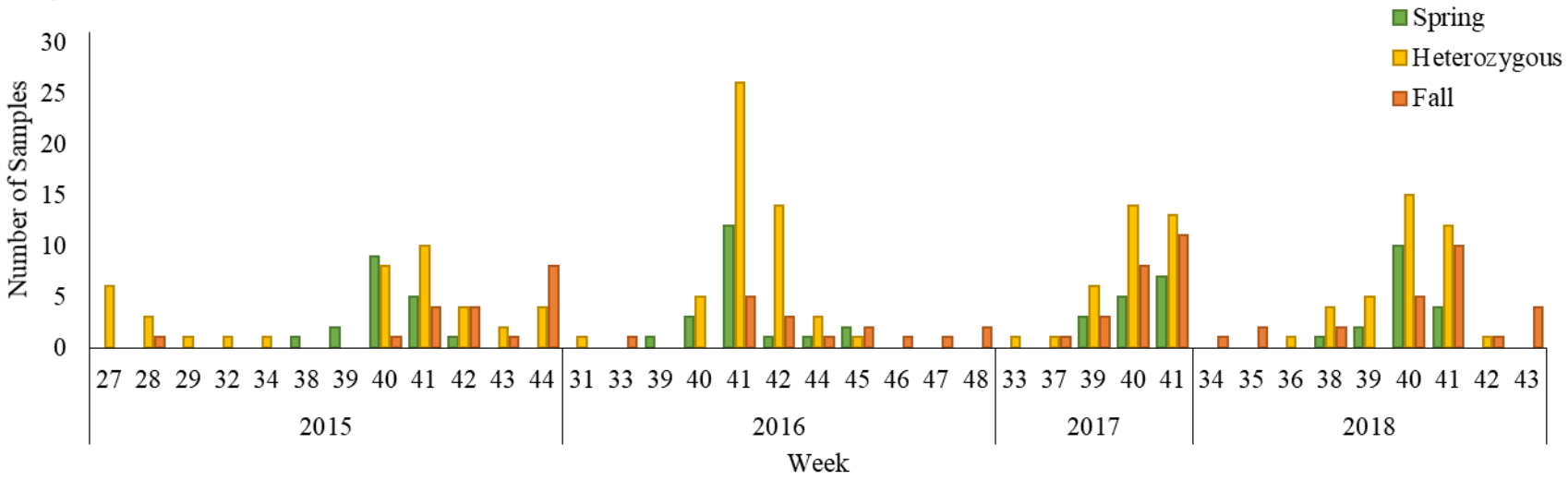


Figure 5. *Greb1L* (a) snp640165 and (b) snp670329 genotypes of adult Chinook salmon returning to the North Fork Dam from June 7 to July 17, 2018. snp640165 has been found to be more informative when characterizing run timing in coastal Chinook salmon (Thompson Per. Comm.).

(a) snp640165



(b) snp670329

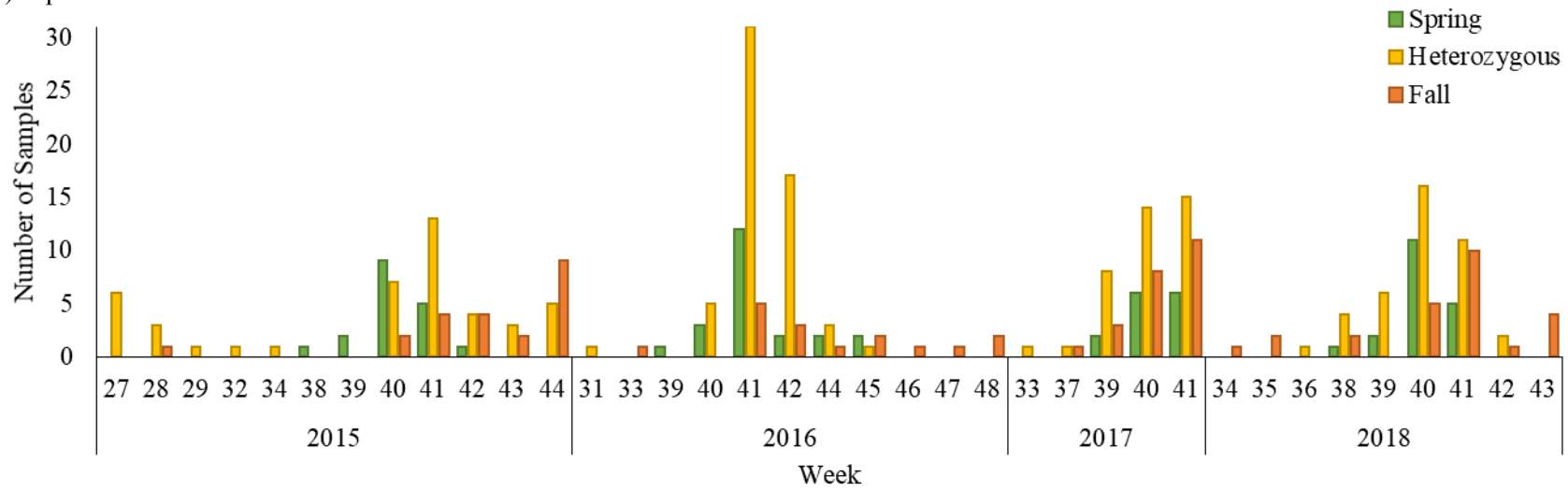


Figure 6. *Greb1L* (a) snp640165 and (b) snp670329 genotypes of Clackamas basin Chinook salmon carcasses sampled in 2015-2018. snp640165 has been found to be more informative when characterizing run timing in coastal Chinook salmon (Thompson Per. Comm.).

Genetic stock identification (GSI)

Most Clackamas basin Chinook salmon assigned to the Willamette genetic reporting group (91.8%), which corresponds to the Upper Willamette River ESU (Table 4). The remaining samples assigned to genetic groups within the Lower Columbia River ESU (1.4%), the Youngs Bay genetic reporting group (0.2%), or were unassigned (6.6%). Of the October 2017, North Fork Dam samples that appeared to have a fall run phenotype, 14 (73.7%) assigned to the Willamette genetic reporting group (Upper Willamette River ESU) and the remaining 5 samples were unassigned.

Table 4. Genetic stock identification of Clackamas basin Chinook salmon carcass samples to reporting group. Samples were classified as unassigned in ONCOR if their probability of assignment was less than 0.95.

Evolutionarily significant unit	**Reporting group**	**Live samples**		**Carcass samples**				
		2017	**2018**	**2015**	**2016**	**2017**	**2018**	**Total**
Upper Willamette River								
	04_WILLAM	14	69	73	92	78	77	**403**
Lower Columbia River								
	02_WCASSP						1	**1**
	03_WCASFA			4				**4**
	05_SPCRTU						1	**1**
Other								
	01_YOUNGS				1			**1**
	Unassigned	5	3	8	5	1	7	**29**
	Total	19	72	85	98	79	86	**439**

CONCLUSIONS

The primary goal of this research was to determine if there were two genetically distinct groups of Chinook salmon present on the Clackamas basin spawning grounds in 2015-2018. We found weak evidence for population structure among Chinook salmon sampled on the spawning grounds based on the program STRUCTURE. Carcass samples collected after October 12th in 2015, 2016, and 2018 had stronger assignment to a "late-spawning" group. In concordance, all live samples collected after October 22nd in 2017 had strong assignment to this "late-spawning" group. We found no evidence for population structure among carcass samples in 2017 when all samples were collected on or prior to October 12th. Our results correspond to findings for Chinook salmon in the nearby Sandy River where there was stronger evidence for population

structure and carcasses collected after October 15th comprised the "late-spawning" group (Whitman et al. in prep). We did not find similar evidence for population structure among Chinook salmon carcass samples based on collection date in the PCA. We found some evidence for separation between carcasses sampled in the upstream and downstream sites in 2015, 2016 and 2018 but not in 2017.

While there was a distinct shift in *Greb1L* snp640165 and snp670329 genotype frequencies for adult Chinook salmon returning to the North Fork Dam in 2017, individuals heterozygous at both SNPs were sampled throughout the entire time period. Further, there is no clear association between the *Greb1L* snp640165 or snp670329 genotypes and collection date and the *Greb1L* SNP genotypes do not corroborate results based on the neutral genetic markers. The secondary goal of this research was dependent upon distinct population differentiation in space and time. While there was some evidence of population structuring, it is unclear how to apply the ambiguous patterns of spatial and/or temporal distribution to managing the conservation of these ESA-listed populations. This result is substantially different than the companion analysis conducted with Chinook in the Sandy basin (Whitman et al. in prep.). The strong evidence of population structure for Chinook in the Sandy basin provide much clearer guidance on future monitoring design. Management and monitoring of the Clackamas Chinook population(s) could benefit from further genetic analysis to clarify these results.

Most carcass samples assigned to the Upper Willamette River ESU. Only four samples collected in 2015 assigned to the West Cascade Fall genetic reporting group, and these samples also had high assignment ($q >$ 0.89) to the "late-spawning" group.

Acknowledgments

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Appendix

Number of Chinook salmon samples collected from the Clackamas basin during the 2015-2018 spawning ground surveys and at the North Fork Dam Adult Sorting Facility (16). Collection dates are listed for each sampling location. N_C indicates the number of samples collected from each site. N_G indicates the number of samples that passed genotype quality filtering and were therefore included in the genetic analysis.

	2015			2016			2017			2018		
Location	**Dates**	**N_C**	**N_G**	**Dates**	**N_C**	**N_G**	**Dates**	**N_C**	**N_G**	**Dates**	**N_C**	**N_G**
1 Clackamas River 1				Oct 12	11	4	Oct 5	9	8	Sep 17 - Oct 10	6	5
2 Clackamas River 2	Sep 17 - Oct 15	65	28	Sep 19 - Oct 13	92	51	Aug 15 - Oct 12	61	37	Sep 6 - Oct 10	65	43
3 Clackamas River 3	Oct 6	9	5	Oct 4	23	15	Sep 28 - Oct 12	14	7	Oct 3 - 11	19	6
4 Hot Springs Fork				Oct 6	2		Oct 5	1				
5 Collawash River	Oct 1 - 22	10	3	Sep 26 - Oct 12	6	2	Sep 28 - Oct 12	20	14	Sep 24 - Oct 3	6	5
6 Clackamas River 4	Oct 15	3	1	Sep 27	2	1	Oct 4	6	4	Sep 20 - Oct 2	2	2
7 Oak Grove Fork 1							Sep 29	1	1			
8 Oak Grove Fork 2	Oct 15	1	1	Oct 4	5	4	Sep 29	1	1			
9 Oak Grove Fork 3	Oct 1 - 15	4	1	Oct 4	1	1						
10 Clackamas River 5	Sep 23 - Oct 15	5	3				Oct 4	2	2	Sep 20	2	2
11 Clackamas River 6	Oct 8 - 28	7	4	Oct 12	3	3	Sep 29	2	1	Oct 10	2	
12 Roaring River							Oct 5	3	2			
13 Clackamas River 7	Jul 21 - Oct 28	4	1				Sep 29	1				
14 South Fork Clackamas	Oct 1 - 28	7	2				Sep 29	1	1	Oct 4	5	3
15 Clackamas River 8	Oct 1 - 28	9	6	Oct 24	1	1	Sep 29	1	1	Oct 4	5	4
16 North Fork Dam							Oct 23 - Oct 27	21	19	Jun 7 - Jul 17	75	72
17 Clackamas River 9										Oct 15	1	1
18 Clackamas River 10	Jul 15 - Nov 3	45	17	Aug 9 - Nov 22	34	13				Aug 22 - Oct 23	20	13
19 Clackamas River 11	Aug 17 - Oct 20	3		Jul 25 - Nov 22	7	2	Aug 15 - Nov 1	3				
20 Clackamas River 12	Jul 15 - Oct 7	8	2	Aug 9	1					Oct 15	1	
21 Clackamas River 13	Oct 8	1	1									
22 Clackamas River 14	Jul 8	7	4	Jul 25	1	1	Aug 15	1		Aug 29	1	1
23 Clackamas River 15	Jun 30	10	6	Aug 22	2					Aug 30	1	1
Total		**198**	**85**		**191**	**98**		**148**	**98**		**211**	**158**

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