

REPORT TO SOUTHERN BOUNDARY RESTORATION AND ENHANCEMENT FUND: PUGET SOUND CHUM SALMON GSI

Marisa Litz¹, Maureen Small¹, Kwasi Addae¹, Bill Patton², Adrian Spidle²

¹Washington Department of Fish and Wildlife, 1111 Washington St. SE., Olympia, WA 98501

²Northwest Indian Fisheries Commission, 6730 Martin Way E, Olympia WA 98516

Contract dates: July 1, 2019 – June 30, 2020

July 2020, corrected Aug. 11, 2020

Project funded by the Pacific Salmon Commission's Southern Boundary Restoration and Enhancement Program: File SF-2019-13

ACKNOWLEDGEMENTS

This project was funded by the Southern Boundary Restoration and Enhancement Fund, Washington State General Funds. Archived samples added to the Chum salmon baseline were collected by tribal and state personnel. The fishery samples were collected from the WA Area 10 and 11 commercial Chum salmon fisheries by WDFW personnel. We thank Todd Kassler (WDFW) for administering the contract. We thank Dale Gombert (WDFW) for the map. We thank the Southern Boundary Restoration and Enhancement Fund for supporting the project.

TABLE OF CONTENTS

Report to Southern Boundary Restoration and Enhancement Fund: Puget Sound Chum salmon GSI	1
Acknowledgements	1
List of Figures.....	3
List of Tables.....	3
Executive Summary.....	4
Introduction.....	4
Objectives.....	4
Methods.....	5
Baseline Improvement	5
Genotyping	5
Mixed Fishery Sampling.....	5
Mixed Fishery Analysis.....	6
Results.....	6
Baseline Enhancement	6
Mixed Fishery Analysis.....	6
Discussion and Conclusions	7
References	8

LIST OF FIGURES

Figure 1. Map of Puget Sound and marine areas 10 and 11	9
Figure 2. Map of the Chum salmon Evolutionary Significant Units (ESUs).....	9
Figure 3. Map showing distribution of Chum salmon populations.....	10
Figure 4. Plot of the ONCOR assignment in 100% simulation.	11

LIST OF TABLES

Table 1. List of Chum salmon samples added to the Chum SNP baseline in 2019.	12
Table 2. List of US and CAN Chum salmon samples in the Chum SNP baseline.....	13
Table 3. Self-assignment results from ONCOR 100% simulation for Chum SNP baseline.....	14
Table 4. Mixed stock fishery analysis for the 2018 Area 10 and 11	15
Table 5. Mixed stock fishery analysis for the 2017 Area 10 and 11	17

EXECUTIVE SUMMARY

This project addressed two Southern Panel priorities: genetic stock identification (GSI) sampling of Chum salmon and developing the Chum salmon Single Nucleotide Polymorphism (SNP) genetic baseline. The project identified fall-, winter-, and summer-run Chum salmon population contributions to mixed fisheries in the commercial Chum salmon fishery in US Marine Areas 10 and 11. The project added six key Chum salmon populations to the SNP baseline and augmented four other key Chum salmon populations in the baseline (Table 1) to improve baseline representation of Puget Sound Chum salmon populations. We applied the baseline to the Area 10/11 fishery in 2018 and re-analyzed the fishery from 2017 with the improved baseline. In the 2018 fishery the baseline identified roughly one Canadian-origin fish per collection week and no Hood Canal summer-run Chum salmon. The South Puget Sound and the Hood Canal falls were the largest and second largest components, respectively, and the South Puget Sound winters were a distant third component at less than 2% of the fishery, mostly from Diru Hatchery. The baseline identified contributions from hatchery and wild-origin Chum salmon throughout South Puget Sound and Hood Canal. In the 2017 fishery, similar to the original analysis, the improved baseline identified the Canadian Chum salmon and Hood Canal Summer Chum salmon. In contrast to the original 2017 fishery analysis, the improved baseline showed the relative contributions of hatchery and wild-origin Chum salmon and showed that the majority of the contributions of winter-run Chum salmon were from Diru Hatchery and relatively few were from Nisqually River.

INTRODUCTION

OBJECTIVES

1. Improve representation of Puget Sound Chum salmon in the bilateral Chum SNP baseline by adding up to 10 populations to the baseline - completed
2. Sample mixed fisheries in the southern region of the Puget Sound/Strait of Georgia ESU over time and space in four consecutive years – year 1 completed.
3. Genotype Chum salmon sampled from the mixed fishery at the Chum-GTseq350 SNP loci – year 1 completed.
4. Assign Chum salmon from the mixed fishery to expanded Chum SNP genetic baseline to identify home population and region – year 1 completed.

The outcome of this project will be more thorough representation of Puget Sound fall-, winter-, and summer-run Chum salmon from the Southern Boundary Region in the Chum salmon SNP baseline and better understanding of the distribution and abundance of CAN and US fish caught in the Areas 10 and 11 fishery (Figure 1). The higher-resolution baseline will be tested with mixed fishery samples collected in 2017 (Small et al. 2018a) and 2018 to identify improvements and to identify populations that may need better representation. The goal is to monitor and assess the abundance of Canadian Chum salmon, as well as winter- and summer-run Chum salmon caught in a mixed-fishery directed on US fall-run Chum salmon.

Abundance of some Chum salmon populations in the Southern Boundary has trended downward in the past 20 years. Preliminary GSI analysis of the fall Chum salmon fishery in Areas 10 and 11 showed that stocks of concern were harvested, including summer-run Chum salmon from Hood Canal and winter-run Chum salmon from the Nisqually River. Hood Canal summer-run Chum salmon are of high conservation concern and low fishery relevance, and winter-run Chum salmon

are of medium conservation concern and medium fishery relevance. Because CAN is currently moving their Chum salmon baseline to SNPs (Candy and Small 2018), improving Puget Sound Chum salmon population representation in the baseline will improve both CAN and US ability to manage low abundance populations caught in the Southern Boundary Region and improve survival rate estimates in cohort reconstruction.

The Chum salmon fishery in Areas 10 and 11 is managed to minimize impacts on ESA-listed Hood Canal Summer-run Chum salmon and other stocks of conservation concern, including Canadian, North Puget Sound fall-run and South Puget Sound winter-run Chum salmon. Better understanding of the abundance of these stocks in the fishery will support management actions to modify fisheries to avoid taking these fish. Conducting GSI of mixed fisheries in Areas 10 and 11 will provide better adjustment to capture allocations the following year in fulfillment of Treaty agreements. Another potential benefit is the ability to manage fisheries at the individual stock level in Puget Sound. This study would support domestic fishery goals to prevent over-harvest of stocks of conservation concern, and guide fishery timing to prevent unnecessary restrictions on fisheries.

METHODS

BASELINE IMPROVEMENT

The first major element of the proposed study was to increase population representation of Puget Sound Chum salmon in the Chum SNP baseline (Table 1, Table 2 and Figure 3) to improve accuracy and precision in Chum salmon mixed-fishery estimates. Part of this goal is to standardize collection representation to 95 fish per population in the baseline (Table 2) to equalize sample sizes and to improve power to assign fish back to their population of origin. For the collection effort, WDFW biological technicians sampled fin tissue during regular spawning surveys in terminal area streams or from hatcheries identified in Table 1. The population samples were genotyped with the ChumGTseq_350 panel following Small et al. (2018b).

GENOTYPING

Genomic DNA was extracted from tissue samples using Clone-tech® extraction kits, following manufacturer's instructions. SNP genotypes were generated with a GT-seq protocol (Campbell et al. 2015): briefly, samples are subjected to an initial tailed, multiplex PCR reaction that adds sequencing primer sites to target DNA, in a second PCR reaction unique barcode DNA sequences are added to the target DNA (amplicon), barcoded amplicons are pooled and sequenced on a next-generation sequencer. Using the barcodes, perl scripts split pooled sample sequences into individual files and assembles the SNP genotypes for each individual. The final genotypes consisted of 350 loci in the ChumGTseq_350 panel, the standard Chum SNP locus panel for the bilateral Chum SNP baseline (Small et al. 2018b).

MIXED FISHERY SAMPLING

Mixed-stock purse seine fisheries of the non-treaty commercial fleet were sampled in the southern region of the Puget Sound/Strait of Georgia ESU identified by the US Biological Review Team (Figure 2). Sampling was conducted in four successive years over a four-week period, from management week 42 through week 45, in US Areas 10 and 11 (Figure 1). Year 1 (2018) is complete and described in this report. We include a description of the 2017 mixed stock fishery which was our pilot program (Small et al. 2018a) and was re-analyzed for this report with the enhanced baseline. Puget Sound Commercial Salmon Monitoring Biologists recorded the GIS coordinates for each purse seine set where samples were collected. The sampling objective was to

collect spatially and temporally stratified random samples representing the stocks harvested in the fishery throughout the geographic area over the specified harvest time directed at US fall Chum salmon. The sample size was derived from a power analysis and verified with the pilot study in 2017 (Small et al. 2018a). The power analysis suggested that a minimum of 10 fish per observed purse seine set was sufficient to characterize the fishery.

Observers collected fin tissue samples onto Whatman blotter paper supplied by the WDFW Molecular Genetics Laboratory (MGL). Sampling occurred on commercial purse seine vessels at the completion of each set.

MIXED FISHERY ANALYSIS

Fishery tissue samples were genotyped with 350 SNP loci in the ChumGTseq_350 panel, using the GTseq protocol. The genotypes of the fish were compared to the Chum salmon baseline (Small et al. 2018b) to estimate their population of origin and to identify components of the mixed fishery using the program ONCOR (Kalinowski et al. 2007). The program uses the conditional maximum likelihood method of Anderson et al. (2007) and genotype probabilities calculated with the Rannala and Mountain method (1997), to estimate the proportions of fish from different populations that likely contributed to the mixed stock fishery. The analysis proceeds iteratively: it conditions the estimated mixture proportion based on the perceived mixture and recalculates the mixture proportions until there is no change. The analysis estimates the portions of the mixture from each population in the baseline and summarizes the portions of the mixed fishery to reporting groups. The reporting groups are groups of populations in the same management area that are more closely related to each other than to populations in other management areas (see “region” in Tables 1 and 2). With the exception of the summer- and fall-run from Sherwood Creek that are closely related, the reporting groups are assembled with populations from the same run group in the same general geographic area (Sherwood summers are part of the South Puget Sound fall-run group). The Chum SNP baseline was tested for assignment power (Small et al. 2018b) and accurately assigned components of the mixed fishery in the pilot project (Small et al. 2018a).

RESULTS

BASELINE ENHANCEMENT

Most samples genotyped well, with the exception of the Green River Hatchery samples; only half (N = 47) of the Green River Hatchery samples had sufficient data to include them in the baseline. Fifteen of the Sherwood Creek summer-run samples also failed, but the remaining samples (N = 76) may characterize the population adequately. We plan to collect additional samples for both populations. In addition to the collections added to the baseline through this project, we added collections from other projects, such as the Chum SNP baseline development with DFO (Candy and Small 2018) and used this enhanced baseline for the mixed fishery analysis described below. We will continue to improve collection sizes and improve population representation in the baseline.

MIXED FISHERY ANALYSIS

We tested the baseline for the power to identify fish back to their home population in a 100% simulation test in ONCOR (Table3, Figure 4). This test is a best-case scenario in which ONCOR simulated a collection of 200 fish from each population in turn and assigned the 200 fish to collections in the baseline and to regional groups identified in the baseline. All collections assigned well to their region (average 97% correct) and some assigned well back to their home population

(range 5%-99%, average 58%). The smallest collections had lowest self-assignments, e.g. North Fork Skokomish (N = 30), which likely insufficiently captured the genetic variation in the population to distinguish it from other Hood Canal fall populations.

We conducted mixed fishery analyses on the Areas 10 and 11 2018 fishery (Table 4). We also re-analyzed the 2017 fishery pilot project data with the updated baseline (Table 5). As the baseline improves, we will reanalyze these mixed fisheries to document any changes. In the 2018 fishery, the South Puget Sound Chum salmon stocks comprised the largest portion overall (79%) and each week (Table 4). Among the South Puget Sound Chum salmon stocks, Minter Creek Hatchery and Kennedy Creek were the largest components. The distribution of the fishery components changed over time, with Minter Creek contributing 3% in week 42 and increasing to 31% in week 45. The Hood Canal fall Chum salmon stocks were the next largest component (18%), mainly composed of fish from Hoodspout Hatchery and Dewatto Creek. A few South Puget Sound winter-run Chum salmon were caught in weeks 43, 44 and 45. Most of these arose from Diru Hatchery and two fish assigned to Nisqually River in week 44. A few fish from Strait of Juan de Fuca were caught in weeks 42 and 44, and one Canadian-origin fish from the Strait of Georgia was caught each week.

The 2017 fishery differed from the 2018 fishery in that the overall collection size was larger (N = 1447). Similar to the 2018 fishery, the South Puget Sound and Hood Canal falls were the largest and second largest components, respectively, and the South Puget Sound winters were a distant third component (6% overall). With the enhanced baseline, we were able to identify that 75% of the winter-run Chum salmon estimated in the fishery were from Diru Hatchery and that the Nisqually winters were mostly caught in week 45.

DISCUSSION AND CONCLUSIONS

This project added six key Chum salmon populations from South Puget Sound to the baseline and increased the collection sizes for another four key populations. These additions improved our ability to identify components of the mixed stock fishery in Areas 10 and 11 in South Puget Sound. We found that some Canadian-origin Chum salmon were captured in the fishery, which is important to know for international treaty obligations, as well as a Hood Canal summer-run Chum salmon, which is a stock listed in the US under the Endangered Species Act. The most important finding for US domestic fishery management was the winter-run Chum salmon in the fall-run directed fishery. The winter-run Chum salmon from Nisqually River are a unique stock in South Puget Sound and the fishery is timed to avoid them. With the improvements to the Chum SNP baseline, specifically increasing the representation of Nisqually River Chum salmon and Diru Creek Hatchery Chum salmon, we found that the majority of the winter-run component were Diru Hatchery-origin Chum salmon, rather than Nisqually River Chum salmon. The increased collection sizes better characterized the winter-run populations so that they were genetically distinguishable. The Diru Creek broodstock originated from the Nisqually River winter-run, but over time had been selected for earlier return timing and the hatchery gene pool had drifted from its source populations. Thus, their genetic origin as winter-run Chum salmon was still detectable, but they were being caught throughout the fishery directed at fall-run Chum salmon because of their run timing shift. Analyzing the components of the 2019 fishery will add to our understanding of how well the fishery timing captures intended fall-run stocks and avoids stocks of concern.

REFERENCES

- Anderson EC, RS Waples, and ST Kalinowski. 2007. An improved method for estimating the accuracy of genetic stock identification. *Canadian Journal of Fisheries and Aquatic Sciences* 44:866-881.
- Campbell NR, Harmon SA, Narum SR. 2015. Genotyping-in-Thousands by sequencing (GT-seq): A cost effective SNP genotyping method based on custom amplicon sequencing. *Mol Ecol Resour* 15: 855-867.
- Candy, J and M. Small. 2018. Expanded Bilateral Chum Salmon SNP Genetic Baseline for Genetic Stock Identification. Grant SF-2018-SP-22.
- Rannala, B., and Mountain, J.L. 1997. Detecting immigration by using multilocus genotypes. *Proc. Natl. Acad. Sci. USA* 94:9197-9201
- Small, MP, K Addae, M Litz, and M Kissler. 2018a. Genetic analysis of Chum Salmon from commercial non-treaty fleet in Marine Areas 10 and 11 in 2017. WDFW draft report, 8pp.
- Small MP, Warheit K, Pascal C, Seeb L, Ruff C, Zischke J, Winans G, Seeb J. 2018b. Chum Salmon Southern Area Genetic Baseline Enhancement Part 1 and Part 2: Amplicon Development, Expanded Baseline Collections, and Genotyping. Report to the Southern Fund Panel, Pacific Salmon Commission, 45 pp.

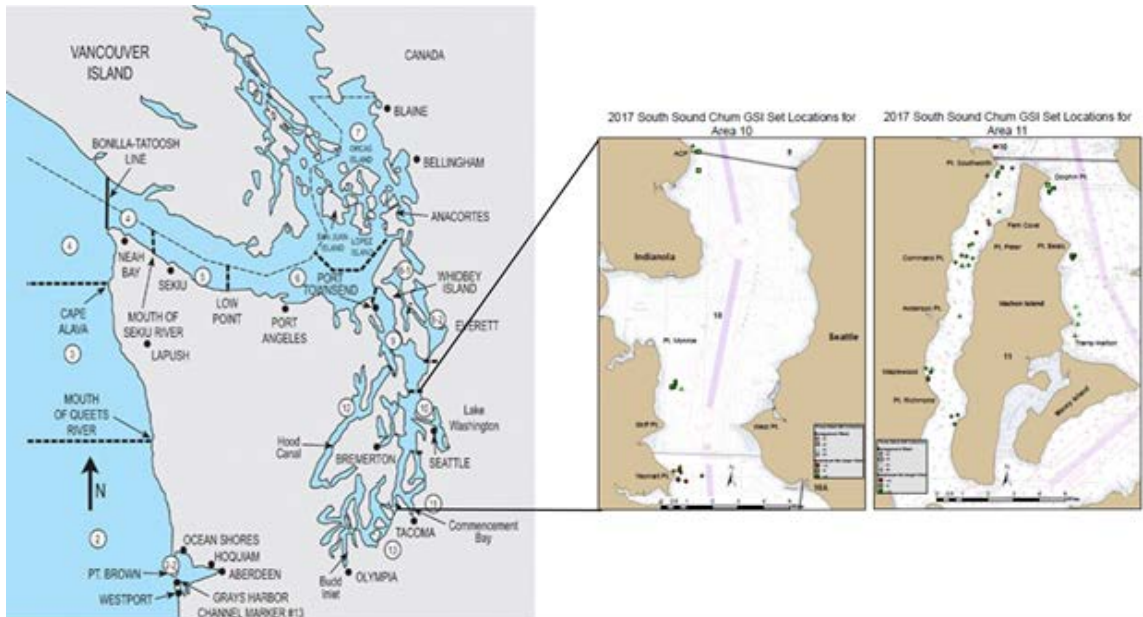


Figure 1. Map of Puget Sound and nearby regions showing the location of marine areas 10 and 11 within Puget Sound (areas expanded to right) and the locations of the purse seine fisheries.

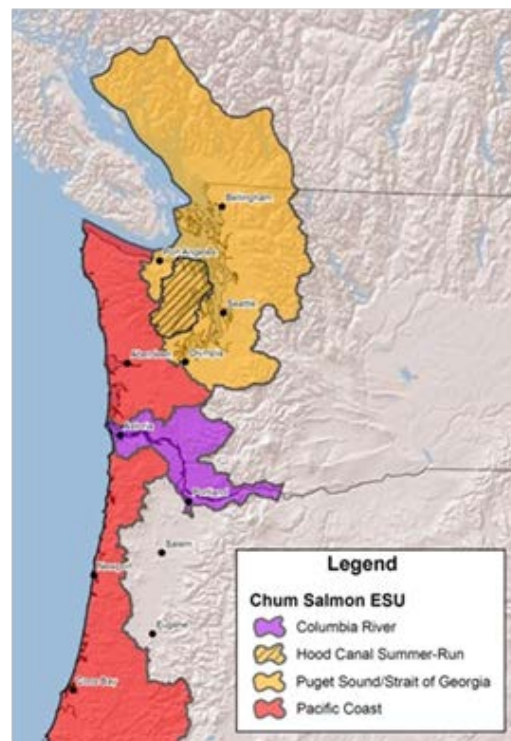


Figure 2. Map created by S. Stone (NOAA) of the Chum salmon Evolutionary Significant Units (ESUs) in the Pacific Northwest from NOAA_NMFS_NWFSC TM-32: Status Review of Chum salmon.

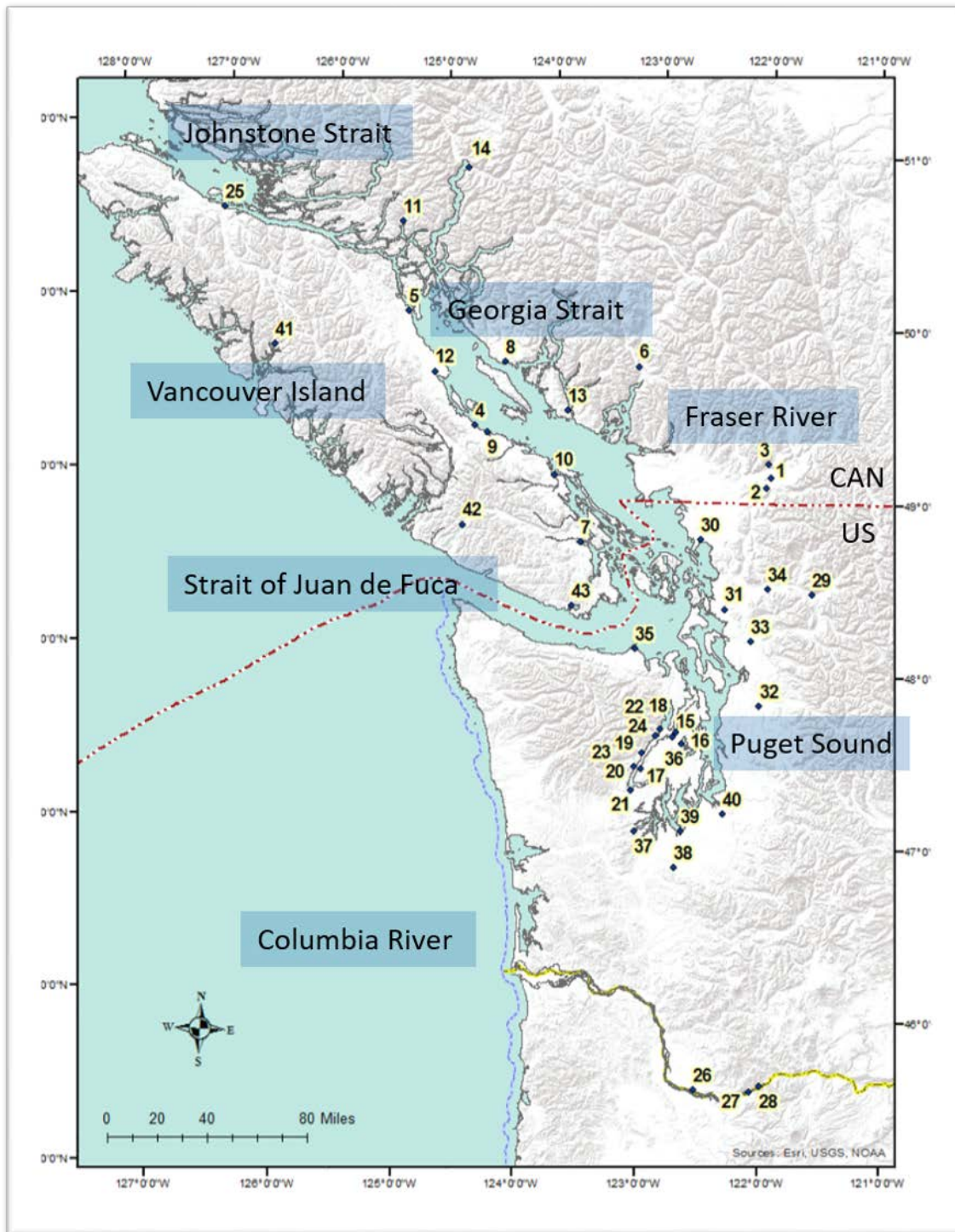


Figure 3. Map showing distribution of Chum salmon populations in the Chum SNP baseline. Numbers correspond to some locations for Chum salmon populations described in this report, but new locations were sampled since map was constructed and the map is included to show the regions represented in the Chum SNP baseline.

SPS Chum baseline and GSI report to SBRF, WDFW Molecular Genetics Lab, 2020

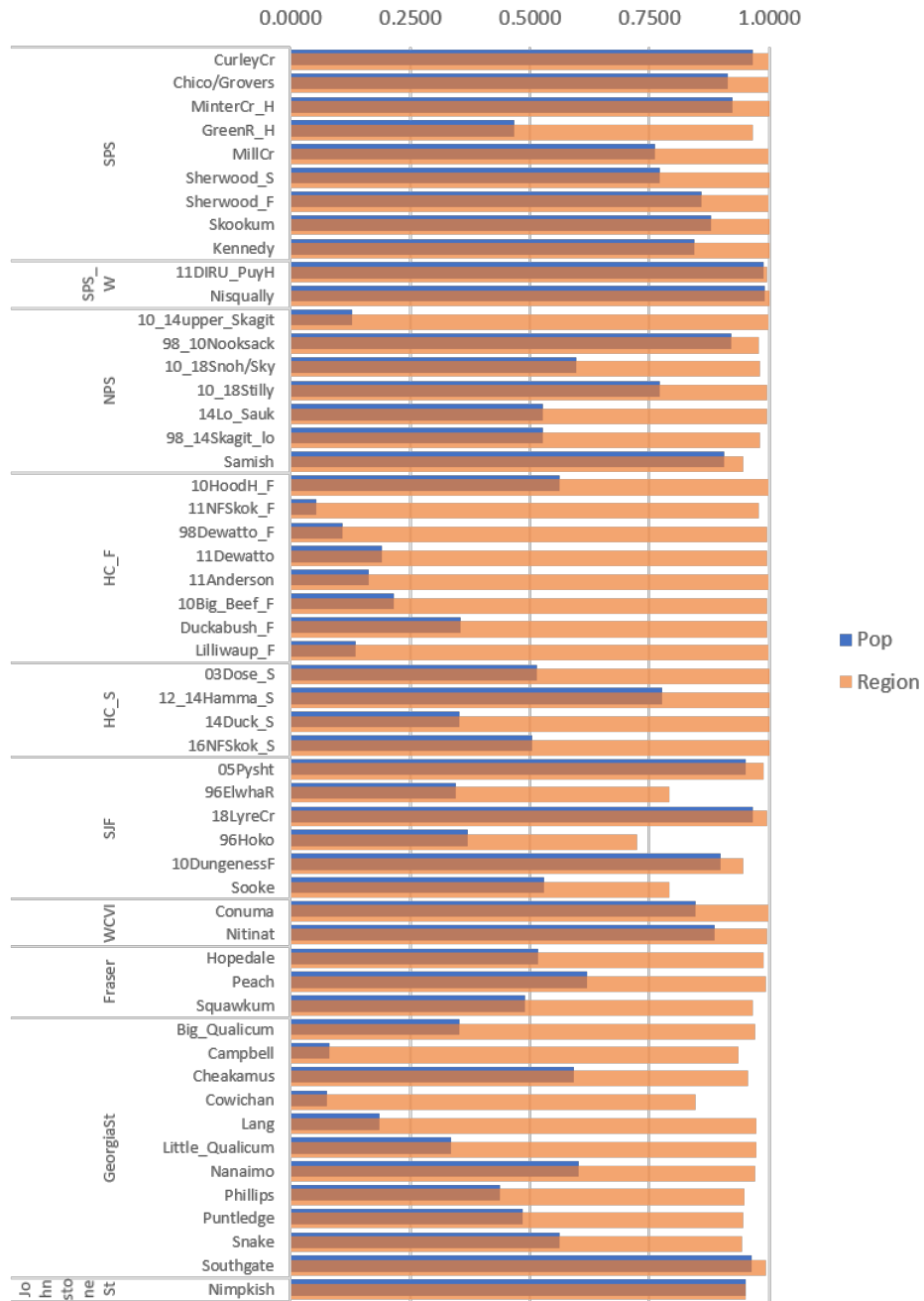


Figure 4. Plot of the average assignment back to home population (Pop) and to regional group (Region) in ONCOR 100% simulation. The averages and their standard deviations are in Table 3.

Table 1. List of Chum salmon samples added to the Chum SNP baseline in 2019 under this proposal.

Add or supplement	region	Collection	Add for 95	WDFW Code
add	Central_PS	Curley Cr	95	02KS
add	South_PS	MinterCr_H	95	03JO
add	South_PS	MillCr (by Shelton)	67	11KW
add	South_PS	Sherwood (F)	95	94GS
add	South_PS	Sherwood (S)	91	94GR
add	Central_PS	GreenR Hatchery	95	07LB
supplement	SouthPS_W	Nisqually	21	10ME
supplement	SouthPS_F	Chico/Grovers	40	11ML
supplement	SouthPS_F	Kennedy	44	10MG
supplement	SouthPS_F	Skookum	58	11KU

SPS Chum baseline and GSI report to SBRF, WDFW Molecular Genetics Lab, 2020

Table 2. List of US and CAN Chum salmon samples in the Chum SNP baseline and the collections underway to standardize collection sizes to 95 and improve population distribution. An existing grant will be used to genotype several collections that were not covered by the grant in this report (Small et al. 2019). The CAN baseline samples in this table were genotyped during the SNP panel development and additional collections will be genotyped by the DFO lab.

Region_US	Pop	N		Region_CAN	Pop	N
S_PugetSound	CurleyCr	95		St_JuandeFuca	Sooke	32
S_PugetSound	Chico/Grovers	93		WCVI	Conuma	44
S_PugetSound	MinterCr_H	91		WCVI	Nitinat	48
S_PugetSound	GreenR_H	47	collecting	Fraser	Hopedale	39
S_PugetSound	MillCr	66	collecting	Fraser	Peach	43
S_PugetSound	Sherwood_S	76	collecting	Fraser	Squawkum	32
S_PugetSound	Sherwood_F	94		GeorgiaSt	Big_Qualicum	48
S_PugetSound	Skookum	94		GeorgiaSt	Campbell	32
S_PugetSound	Kennedy	91		GeorgiaSt	Cheakamus	42
S_PugetSound_W	11DIRU_PuyH	94		GeorgiaSt	Cowichan	25
S_PugetSound_W	Nisqually	95		GeorgiaSt	Lang	33
N_PugetSound	10_14up_Skagit	21	collecting	GeorgiaSt	Little_Qualicum	46
N_PugetSound	98_10Nooksack	92		GeorgiaSt	Nanaimo	50
N_PugetSound	10_18Snoh/Sky	87	collecting	GeorgiaSt	Phillips	44
N_PugetSound	10_18Stilly	91		GeorgiaSt	Puntledge	48
N_PugetSound	14Lo_Sauk	67	collecting	GeorgiaSt	Snake	44
N_PugetSound	98_14Skagit_lo	77	collecting	GeorgiaSt	Southgate	32
N_PugetSound	Samish	73	updating	JohnstoneSt	Nimpkish	41
HoodCanal_F	10Hoodsporth_H	88				
HoodCanal_F	11NFSkok_F	30	collecting			
HoodCanal_F	98_11Dewatto_F	94				
HoodCanal_F	11Anderson	48	collecting			
HoodCanal_F	10Big_Beef_F	47	collecting			
HoodCanal_F	Duckabush_F	46	collecting			
HoodCanal_F	Lilliwaup_F	47				
HoodCanal_S	03_14Dose_S	84				
HoodCanal_S	12_14Hamma_S	58	collecting			
HoodCanal_S	14Duck_S	47	collecting			
HoodCanal_S	16NFSkok_S	41	collecting			
St_JuandeFuca	05Pysht	93				
St_JuandeFuca	96ElwhaR	45				
St_JuandeFuca	18LyreCr	94				
St_JuandeFuca	96Hoko	43	collecting			
St_JuandeFuca	10DungenessF	77				

SPS Chum baseline and GSI report to SBRF, WDFW Molecular Genetics Lab, 2020

Table 3. Self-assignment results from ONCOR 100% simulation for Chum SNP baseline – assigned back to baseline collection and assignments summarized per regional reporting group.

Region	Pop (US)	POPULATION		REPORTING GROUP		Region	Pop (CAN)	POPULATION		REPORTING GROUP	
		AVG	ST DEV	AVG	ST DEV			AVG	ST DEV	AVG	ST DEV
SPS	CurleyCr	0.9665	0.0182	0.9987	0.0026	SJF	Sooke	0.5298	0.0451	0.7903	0.0392
SPS	Chico/Grovers	0.9127	0.0243	0.9992	0.0018	WCVI	Conuma	0.8455	0.0313	0.9969	0.0044
SPS	MinterCr_H	0.9226	0.0269	0.9995	0.0016	WCVI	Nitinat	0.8859	0.0281	0.9954	0.0045
SPS	GreenR_H	0.4687	0.0395	0.9659	0.0164	Fraser	Hopedale	0.5178	0.0446	0.9889	0.0078
SPS	MillCr	0.7617	0.0363	0.9992	0.0020	Fraser	Peach	0.6196	0.0386	0.9937	0.0064
SPS	Sherwood_S	0.7702	0.0402	0.9997	0.0011	Fraser	Squawkum	0.4888	0.0410	0.9663	0.0159
SPS	Sherwood_F	0.8578	0.0345	0.9987	0.0026	GeorgiaSt	Big_Qualicum	0.3531	0.0498	0.9698	0.0147
SPS	Skookum	0.8785	0.0331	0.9996	0.0013	GeorgiaSt	Campbell	0.0805	0.0271	0.9365	0.0248
SPS	Kennedy	0.8431	0.0368	0.9998	0.0008	GeorgiaSt	Cheakamus	0.5919	0.0487	0.9556	0.0171
SPS_W	11DIRU_PuyH	0.9875	0.0108	0.9968	0.0040	GeorgiaSt	Cowichan	0.0771	0.0245	0.8471	0.0374
SPS_W	Nisqually	0.9906	0.0085	0.9996	0.0013	GeorgiaSt	Lang	0.1868	0.0366	0.9721	0.0154
NPS	10_14upper_Skagit	0.1287	0.0308	0.9971	0.0042	GeorgiaSt	Little_Qualicum	0.3360	0.0433	0.9730	0.0132
NPS	98_10Nooksack	0.9213	0.0258	0.9789	0.0133	GeorgiaSt	Nanaimo	0.6016	0.0436	0.9710	0.0161
NPS	10_18Snoh/Sky	0.5982	0.0450	0.9803	0.0116	GeorgiaSt	Phillips	0.4377	0.0411	0.9475	0.0220
NPS	10_18Stilly	0.7720	0.0415	0.9961	0.0044	GeorgiaSt	Puntledge	0.4850	0.0446	0.9455	0.0223
NPS	14Lo_Sauk	0.5270	0.0482	0.9964	0.0038	GeorgiaSt	Snake	0.5630	0.0431	0.9428	0.0216
NPS	98_14Skagit_lo	0.5277	0.0528	0.9814	0.0116	GeorgiaSt	Southgate	0.9638	0.0151	0.9927	0.0058
NPS	Samish	0.9058	0.0280	0.9453	0.0239	JohnstoneSt	Nimpkish	0.9510	0.0170	0.9510	0.0170
HC_F	10HoodH_F	0.5632	0.0558	0.9969	0.0040						
HC_F	11NFSkok_F	0.0536	0.0238	0.9779	0.0132						
HC_F	98Dewatto_F	0.1091	0.0343	0.9965	0.0042						
HC_F	11Dewatto	0.1919	0.0417	0.9944	0.0061						
HC_F	11Anderson	0.1637	0.0322	0.9983	0.0027						
HC_F	10Big_Beef_F	0.2158	0.0407	0.9960	0.0044						
HC_F	Duckabush_F	0.3564	0.0467	0.9962	0.0038						
HC_F	Lilliwaup_F	0.1365	0.0373	0.9987	0.0025						
HC_S	03_14Dose_S	0.5150	0.0484	1.0000	0.0004						
HC_S	12_14Hamma_S	0.7773	0.0368	1.0000	NaN						
HC_S	14Duck_S	0.3519	0.0427	1.0000	0.0000						
HC_S	16NFSkok_S	0.5052	0.0444	1.0000	0.0000						
SJF	05Pysht	0.9519	0.0188	0.9890	0.0074						
SJF	96ElwhaR	0.3466	0.0480	0.7916	0.0398						
SJF	18LyreCr	0.9664	0.0194	0.9947	0.0047						
SJF	96Hoko	0.3714	0.0507	0.7237	0.0407						
SJF	10DungenessF	0.8982	0.0285	0.9470	0.0211						

SPS Chum baseline and GSI report to SBRF, WDFW Molecular Genetics Lab, 2020

Table 4. Mixed stock fishery analysis for the 2018 Area 10 and 11 Chum salmon fishery in South Puget Sound. Upper table has the fishery proportions summed up per reporting group (number in first column identifies the reporting group for each population listed in the lower part of the table) and lower table has the fishery proportions assigned per individual population in the baseline. The first data column to the left has the fishery proportion estimate summed over all weeks. The data columns to the right have the fishery proportion estimates per week. The numbers following "NMixture" in the first row are the number of fish analyzed in the fishery per time strata. The second row identifies the fishing gear.

	NMixture 730		NMixture 212		NMixture 77		NMixture 201		NMixture 240	
	Purse seine and gill net		Purse seine and gill net		Gill net only		Purse seine and gill net		Purse seine and gill net	
	ALL WEEKS		week 42		week 43		week 44		week 45	
	REPORTING GROUP EST		REPORTING GROUP EST		REPORTING GROUP EST		REPORTING GROUP EST		REPORTING GROUP EST	
1	SPugetSound	0.7942	SPugetSound	0.7273	SPugetSound	0.7283	SPugetSound	0.8442	SPugetSound	0.8446
2	SPugetSound_W	0.0158	SPugetSound_W	0	SPugetSound_W	0.0132	SPugetSound_W	0.0203	SPugetSound_W	0.0259
3	NPugetSound	0.0037	NPugetSound	0	NPugetSound	0.0129	NPugetSound	0	NPugetSound	0.0043
4	HoodCanal_F	0.1775	HoodCanal_F	0.2638	HoodCanal_F	0.2326	HoodCanal_F	0.1202	HoodCanal_F	0.1211
5	HoodCanal_S	0	HoodCanal_S	0	HoodCanal_S	0	HoodCanal_S	0	HoodCanal_S	0
6	St_JuandeFuca	0.0048	St_JuandeFuca	0.0047	St_JuandeFuca	0	St_JuandeFuca	0.0104	St_JuandeFuca	0
7	WCVI	0	WCVI	0	WCVI	0	WCVI	0	WCVI	0
8	Fraser	0	Fraser	0	Fraser	0	Fraser	0	Fraser	0
9	GeorgiaSt	0.0041	GeorgiaSt	0.0041	GeorgiaSt	0.0130	GeorgiaSt	0.0050	GeorgiaSt	0.0041
10	JohnstoneSt	0	JohnstoneSt	0	JohnstoneSt	0	JohnstoneSt	0	JohnstoneSt	0
	ALL WEEKS		week 42		week 43		week 44		week 45	
	POPULATION EST		POPULATION EST		POPULATION EST		POPULATION EST		POPULATION EST	
1	CurleyCr	0.0374	CurleyCr	0.0548	CurleyCr	0.0343	CurleyCr	0.0282	CurleyCr	0.0294
1	Chico/Grovers	0.1127	Chico/Grovers	0.1364	Chico/Grovers	0.1411	Chico/Grovers	0.1137	Chico/Grovers	0.0820
1	MinterCr_H	0.1640	MinterCr_H	0.0241	MinterCr_H	0.1269	MinterCr_H	0.1716	MinterCr_H	0.3093
1	GreenR_H	0.0715	GreenR_H	0.0438	GreenR_H	0.0617	GreenR_H	0.1187	GreenR_H	0.0673
1	MillCr	0.0844	MillCr	0.0790	MillCr	0.1663	MillCr	0.0846	MillCr	0.0676
1	Sherwood_S	0.0129	Sherwood_S	0.0346	Sherwood_S	0.0045	Sherwood_S	0	Sherwood_S	0.0075
1	Sherwood_F	0.0374	Sherwood_F	0.0689	Sherwood_F	0.0359	Sherwood_F	0.0226	Sherwood_F	0.0211
1	Skookum	0.0823	Skookum	0.0946	Skookum	0.0427	Skookum	0.0729	Skookum	0.0875
1	Kennedy	0.1917	Kennedy	0.1912	Kennedy	0.1149	Kennedy	0.2320	Kennedy	0.1729
2	11DIRU_PuyH	0.0131	11DIRU_PuyH	0	11DIRU_PuyH	0.0132	11DIRU_PuyH	0.0071	11DIRU_PuyH	0.0259
2	Nisqually	0.0026	Nisqually	0	Nisqually	0	Nisqually	0.0132	Nisqually	0
3	10_14up_Skagit	0.0019	10_14up_Skagit	0	10_14up_Skagit	0	10_14up_Skagit	0	10_14up_Skagit	0.0043
3	98_10Nooksack	0	98_10Nooksack	0	98_10Nooksack	0	98_10Nooksack	0	98_10Nooksack	0
3	10_18Snoh/Sky	0	10_18Snoh/Sky	0	10_18Snoh/Sky	0	10_18Snoh/Sky	0	10_18Snoh/Sky	0
3	10_18Stilly	0	10_18Stilly	0	10_18Stilly	0.0129	10_18Stilly	0	10_18Stilly	0
3	14Lo_Sauk	0	14Lo_Sauk	0	14Lo_Sauk	0	14Lo_Sauk	0	14Lo_Sauk	0

SPS Chum baseline and GSI report to SBRF, WDFW Molecular Genetics Lab, 2020

	ALL WEEKS		week 42		week 43		week 44		week 45	
3	98_14Skagit_lo	0.0018	98_14Skagit_lo	0	98_14Skagit_lo	0	98_14Skagit_lo	0	98_14Skagit_lo	0
3	Samish	0	Samish	0	Samish	0	Samish	0	Samish	0
4	10HoodH_F	0.0793	10HoodH_F	0.1417	10HoodH_F	0.0794	10HoodH_F	0.0587	10HoodH_F	0.0379
4	11NFSkok_F	0.0060	11NFSkok_F	0.0074	11NFSkok_F	0	11NFSkok_F	0.0031	11NFSkok_F	0.0059
4	98_11Dewatto_F	0.0549	98_11Dewatto_F	0.0644	98_11Dewatto_F	0.1096	98_11Dewatto_F	0.0322	98_11Dewatto_F	0.0499
4	11Anderson	0.0085	11Anderson	0.0099	11Anderson	0	11Anderson	0	11Anderson	0.0155
4	10Big_Beef_F	0.0149	10Big_Beef_F	0.0187	10Big_Beef_F	0.0157	10Big_Beef_F	0.0260	10Big_Beef_F	0
4	Duckabush_F	0.0074	Duckabush_F	0.0082	Duckabush_F	0.0280	Duckabush_F	0	Duckabush_F	0.0039
4	Lilliwaup_F	0.0066	Lilliwaup_F	0.0134	Lilliwaup_F	0	Lilliwaup_F	0.0001	Lilliwaup_F	0.0080
5	03_14Dose_S	0	03_14Dose_S	0	03_14Dose_S	0	03_14Dose_S	0	03_14Dose_S	0
5	12_14Hamma_S	0	12_14Hamma_S	0	12_14Hamma_S	0	12_14Hamma_S	0	12_14Hamma_S	0
5	14Duck_S	0	14Duck_S	0	14Duck_S	0	14Duck_S	0	14Duck_S	0
5	16NFSkok_S	0	16NFSkok_S	0	16NFSkok_S	0	16NFSkok_S	0	16NFSkok_S	0
6	05Pysht	0.0013	05Pysht	0	05Pysht	0	05Pysht	0.0046	05Pysht	0
6	96ElwhaR	0.0021	96ElwhaR	0	96ElwhaR	0	96ElwhaR	0	96ElwhaR	0
6	18LyreCr	0	18LyreCr	0	18LyreCr	0	18LyreCr	0	18LyreCr	0
6	96Hoko	0.0013	96Hoko	0.0047	96Hoko	0	96Hoko	0.0006	96Hoko	0
6	10DungenessF	0	10DungenessF	0	10DungenessF	0	10DungenessF	0.0052	10DungenessF	0
6	Sooke	0	Sooke	0	Sooke	0	Sooke	0	Sooke	0
7	Conuma	0	Conuma	0	Conuma	0	Conuma	0	Conuma	0
7	Nitinat	0	Nitinat	0	Nitinat	0	Nitinat	0	Nitinat	0
8	Hopedale	0	Hopedale	0	Hopedale	0	Hopedale	0	Hopedale	0
8	Peach	0	Peach	0	Peach	0	Peach	0	Peach	0
8	Squawkum	0	Squawkum	0	Squawkum	0	Squawkum	0	Squawkum	0
9	Big_Qual	0	Big_Qual	0	Big_Qual	0	Big_Qual	0	Big_Qual	0
9	Campbell	0	Campbell	0	Campbell	0	Campbell	0	Campbell	0
9	Cheakamus	0.0013	Cheakamus	0	Cheakamus	0	Cheakamus	0	Cheakamus	0.0041
9	Cowichan	0	Cowichan	0	Cowichan	0	Cowichan	0	Cowichan	0
9	Lang	0.0014	Lang	0	Lang	0	Lang	0.0050	Lang	0
9	Little_Qual	0	Little_Qual	0	Little_Qual	0	Little_Qual	0	Little_Qual	0
9	Nanaimo	0	Nanaimo	0	Nanaimo	0	Nanaimo	0	Nanaimo	0
9	Phillips	0.0014	Phillips	0	Phillips	0.0130	Phillips	0	Phillips	0
9	Puntledge	0	Puntledge	0.0041	Puntledge	0	Puntledge	0	Puntledge	0
9	Snake	0	Snake	0	Snake	0	Snake	0	Snake	0
9	Southgate	0	Southgate	0	Southgate	0	Southgate	0	Southgate	0
10	Nimpkish	0	Nimpkish	0	Nimpkish	0	Nimpkish	0	Nimpkish	0

SPS Chum baseline and GSI report to SBRF, WDFW Molecular Genetics Lab, 2020

Table 5. Mixed stock fishery analysis for the 2017 Area 10 and 11 Chum salmon fishery in South Puget Sound. Upper table has the fishery proportions summed up per reporting group (number in first column identifies the reporting group for each population listed in the lower part of the table) and lower table has the fishery proportions assigned per individual population in the baseline. The first data column to the left has the fishery proportion estimate summed over all weeks. The columns to the right have the fishery proportion estimates per week. The numbers following "NMixture" in the first row are the number of fish analyzed in the fishery per time strata. The second row identifies the fishing gear.

NMixture 1447 purse seine and gill net All_weeks	NMixture 765 GillNet_only All_weeks	NMixture 682 Purse Seine_only All_weeks	NMixture 217 purse seine and gill net Week 42	NMixture 395 purse seine and gill net Week 43	NMixture 326 purse seine and gill net Week 44	NMixture 509 purse seine and gill net Week 45
REPORTING GROUP EST	REPORTING GROUP EST	REPORTING GROUP EST	REPORTING GROUP EST	REPORTING GROUP EST	REPORTING GROUP EST	REPORTING GROUP EST
1 SPugetSound 0.6881	SPugetSound 0.5760	SPugetSound 0.8131	SPugetSound 0.7142	SPugetSound 0.7201	SPugetSound 0.5800	SPugetSound 0.7254
2 SPugetSound_W 0.0579	SPugetSound_W 0.0491	SPugetSound_W 0.0682	SPugetSound_W 0	SPugetSound_W 0.0190	SPugetSound_W 0.0504	SPugetSound_W 0.1154
3 NPugetSound 0.0112	NPugetSound 0.0174	NPugetSound 0.0040	NPugetSound 0	NPugetSound 0.0050	NPugetSound 0.0327	NPugetSound 0.0024
4 HoodCanal_F 0.2368	HoodCanal_F 0.3512	HoodCanal_F 0.1080	HoodCanal_F 0.2720	HoodCanal_F 0.2509	HoodCanal_F 0.3308	HoodCanal_F 0.1496
5 HoodCanal_S 0.0007	HoodCanal_S 0	HoodCanal_S 0.0015	HoodCanal_S 0.0046	HoodCanal_S 0	HoodCanal_S 0	HoodCanal_S 0
6 St_JuandeFuca 0.0016	St_JuandeFuca 0.0014	St_JuandeFuca 0.0023	St_JuandeFuca 0	St_JuandeFuca 0.0026	St_JuandeFuca 0	St_JuandeFuca 0.0041
7 WCVI 0	WCVI 0	WCVI 0	WCVI 0	WCVI 0	WCVI 0	WCVI 0
8 Fraser 0.0021	Fraser 0.0040	Fraser 0	Fraser 0.0046	Fraser 0.0024	Fraser 0.0031	Fraser 0
9 GeorgiaSt 0.0017	GeorgiaSt 0.0009	GeorgiaSt 0.0029	GeorgiaSt 0.0046	GeorgiaSt 0	GeorgiaSt 0.0031	GeorgiaSt 0.0031
10 JohnstoneSt 0	JohnstoneSt 0	JohnstoneSt 0	JohnstoneSt 0	JohnstoneSt 0	JohnstoneSt 0	JohnstoneSt 0
POPULATION EST	POPULATION EST	POPULATION EST	POPULATION EST	POPULATION EST	POPULATION EST	POPULATION EST
1 CurleyCr 0.0338	CurleyCr 0.0338	CurleyCr 0.0345	CurleyCr 0.0749	CurleyCr 0.0265	CurleyCr 0.0234	CurleyCr 0.0316
1 Chico/Grovers 0.1125	Chico/Grovers 0.1335	Chico/Grovers 0.0913	Chico/Grovers 0.2002	Chico/Grovers 0.1291	Chico/Grovers 0.0814	Chico/Grovers 0.0815
1 MinterCr_H 0.1863	MinterCr_H 0.1117	MinterCr_H 0.2703	MinterCr_H 0.0179	MinterCr_H 0.1585	MinterCr_H 0.1427	MinterCr_H 0.3104
1 GreenR_H 0.0408	GreenR_H 0.0523	GreenR_H 0.0290	GreenR_H 0.0632	GreenR_H 0.0323	GreenR_H 0.0181	GreenR_H 0.0542
1 MillCr 0.0650	MillCr 0.0390	MillCr 0.0946	MillCr 0.0603	MillCr 0.0895	MillCr 0.0767	MillCr 0.0414
1 Sherwood_S 0.0120	Sherwood_S 0.0087	Sherwood_S 0.0149	Sherwood_S 0.0034	Sherwood_S 0.0157	Sherwood_S 0.0060	Sherwood_S 0.0140
1 Sherwood_F 0.0305	Sherwood_F 0.0185	Sherwood_F 0.0431	Sherwood_F 0.0420	Sherwood_F 0.0444	Sherwood_F 0.0472	Sherwood_F 0.0095
1 Skookum 0.0740	Skookum 0.0543	Skookum 0.0936	Skookum 0.1052	Skookum 0.0752	Skookum 0.0686	Skookum 0.0605
1 Kennedy 0.1333	Kennedy 0.1243	Kennedy 0.1418	Kennedy 0.1471	Kennedy 0.1487	Kennedy 0.1158	Kennedy 0.1224
2 11DIRU_PuyH 0.0436	11DIRU_PuyH 0.0359	11DIRU_PuyH 0.0529	11DIRU_PuyH 0	11DIRU_PuyH 0.0122	11DIRU_PuyH 0.0412	11DIRU_PuyH 0.0842
2 Nisqually 0.0143	Nisqually 0.0132	Nisqually 0.0154	Nisqually 0	Nisqually 0.0069	Nisqually 0.0091	Nisqually 0.0312
3 10_14up_Skagit 0.0007	10_14up_Skagit 0.0014	10_14up_Skagit 0	10_14up_Skagit 0	10_14up_Skagit 0	10_14up_Skagit 0	10_14up_Skagit 0.0021
3 98_10Nooksack 0.0006	98_10Nooksack 0.0012	98_10Nooksack 0	98_10Nooksack 0	98_10Nooksack 0	98_10Nooksack 0.0018	98_10Nooksack 0
3 10_18Snoh/Sky 0.0053	10_18Snoh/Sky 0.0065	10_18Snoh/Sky 0.0018	10_18Snoh/Sky 0	10_18Snoh/Sky 0	10_18Snoh/Sky 0.0164	10_18Snoh/Sky 0.0003
3 10_18Stilly 0	10_18Stilly 0	10_18Stilly 0	10_18Stilly 0	10_18Stilly 0	10_18Stilly 0	10_18Stilly 0
3 14Lo_Sauk 0	14Lo_Sauk 0.0010	14Lo_Sauk 0	14Lo_Sauk 0	14Lo_Sauk 0.0025	14Lo_Sauk 0	14Lo_Sauk 0

SPS Chum baseline and GSI report to SBRF, WDFW Molecular Genetics Lab, 2020

POPULATION EST	POPULATION EST	POPULATION EST	POPULATION EST	POPULATION EST	POPULATION EST	POPULATION EST	POPULATION EST	POPULATION EST	POPULATION EST	POPULATION EST	POPULATION EST		
3 Samish	0.00350	Samish	0.0073	Samish	0	Samish	0	Samish	0	Samish	0.0145	Samish	0
4 10HoodH_F	0.07140	10HoodH_F	0.1038	10HoodH_F	0.0376	10HoodH_F	0.0798	10HoodH_F	0.09100	10HoodH_F	0.0786	10HoodH_F	0.0482
4 11NFSkok_F	0.00590	11NFSkok_F	0.0094	11NFSkok_F	0.0012	11NFSkok_F	0.0118	11NFSkok_F	0	11NFSkok_F	0.0052	11NFSkok_F	0.0107
4 98_11Dewatto_F	0.11860	98_11Dewatto_F	0.1709	98_11Dewatto_F	0.0602	98_11Dewatto_F	0.1173	98_11Dewatto_F	0.1421	98_11Dewatto_F	0.1743	98_11Dewatto_F	0.0706
4 11Anderson	0.01460	11Anderson	0.0260	11Anderson	0.0012	11Anderson	0.0295	11Anderson	0.0114	11Anderson	0.0218	11Anderson	0
4 10Big_Beef_F	0.00700	10Big_Beef_F	0.0111	10Big_Beef_F	0.0018	10Big_Beef_F	0.0174	10Big_Beef_F	0.0029	10Big_Beef_F	0.0143	10Big_Beef_F	0
4 Duckabush_F	0.01280	Duckabush_F	0.0184	Duckabush_F	0.0061	Duckabush_F	0	Duckabush_F	0.0022	Duckabush_F	0.0237	Duckabush_F	0.0177
4 Lilliwaup_F	0.00640	Lilliwaup_F	0.0116	Lilliwaup_F	0	Lilliwaup_F	0.0162	Lilliwaup_F	0.0013	Lilliwaup_F	0.0129	Lilliwaup_F	0.0023
5 03_14Dose_S	0	03_14Dose_S	0	03_14Dose_S	0	03_14Dose_S	0	03_14Dose_S	0	03_14Dose_S	0	03_14Dose_S	0
5 12_14Hamma_S	0.0007	12_14Hamma_S	0	12_14Hamma_S	0.0015	12_14Hamma_S	0.0046	12_14Hamma_S	0	12_14Hamma_S	0	12_14Hamma_S	0
5 14Duck_S	0	14Duck_S	0	14Duck_S	0	14Duck_S	0	14Duck_S	0	14Duck_S	0	14Duck_S	0
5 16NFSkok_S	0	16NFSkok_S	0	16NFSkok_S	0	16NFSkok_S	0	16NFSkok_S	0	16NFSkok_S	0	16NFSkok_S	0
6 05Pysht	0	05Pysht	0	05Pysht	0	05Pysht	0	05Pysht	0	05Pysht	0	05Pysht	0.0041
6 96ElwhaR	0.0009	96ElwhaR	0.0014	96ElwhaR	0	96ElwhaR	0	96ElwhaR	0.0026	96ElwhaR	0	96ElwhaR	0
6 18LyreCr	0	18LyreCr	0	18LyreCr	0	18LyreCr	0	18LyreCr	0	18LyreCr	0	18LyreCr	0
6 96Hoko	0	96Hoko	0	96Hoko	0	96Hoko	0	96Hoko	0	96Hoko	0	96Hoko	0
6 10DungenessF	0.0007	10DungenessF	0	10DungenessF	0.0023	10DungenessF	0	10DungenessF	0	10DungenessF	0	10DungenessF	0
6 Sooke	0	Sooke	0	Sooke	0	Sooke	0	Sooke	0	Sooke	0	Sooke	0
7 Conuma	0	Conuma	0	Conuma	0	Conuma	0	Conuma	0	Conuma	0	Conuma	0
7 Nitinat	0	Nitinat	0	Nitinat	0	Nitinat	0	Nitinat	0	Nitinat	0	Nitinat	0
8 Hopedale	0.0007	Hopedale	0.0015	Hopedale	0	Hopedale	0	Hopedale	0.0024	Hopedale	0	Hopedale	0
8 Peach	0	Peach	0	Peach	0	Peach	0.0046	Peach	0	Peach	0	Peach	0
8 Squawkum	0.0013	Squawkum	0.0026	Squawkum	0	Squawkum	0	Squawkum	0	Squawkum	0.0031	Squawkum	0
9 Big_Qual	0	Big_Qual	0	Big_Qual	0	Big_Qual	0	Big_Qual	0	Big_Qual	0	Big_Qual	0
9 Campbell	0.0006	Campbell	0	Campbell	0.0015	Campbell	0	Campbell	0	Campbell	0.0031	Campbell	0
9 Cheakamus	0	Cheakamus	0	Cheakamus	0	Cheakamus	0	Cheakamus	0	Cheakamus	0	Cheakamus	0
9 Cowichan	0	Cowichan	0	Cowichan	0	Cowichan	0	Cowichan	0	Cowichan	0	Cowichan	0
9 Lang	0.0006	Lang	0	Lang	0.0014	Lang	0.0046	Lang	0	Lang	0	Lang	0
9 Little_Qual	0	Little_Qual	0	Little_Qual	0	Little_Qual	0	Little_Qual	0	Little_Qual	0	Little_Qual	0
9 Nanaimo	0.0004	Nanaimo	0.0009	Nanaimo	0	Nanaimo	0	Nanaimo	0	Nanaimo	0	Nanaimo	0.0031
9 Phillips	0	Phillips	0	Phillips	0	Phillips	0	Phillips	0	Phillips	0	Phillips	0
9 Puntledge	0	Puntledge	0	Puntledge	0	Puntledge	0	Puntledge	0	Puntledge	0	Puntledge	0
9 Snake	0	Snake	0	Snake	0	Snake	0	Snake	0	Snake	0	Snake	0
9 Southgate	0	Southgate	0	Southgate	0	Southgate	0	Southgate	0	Southgate	0	Southgate	0
10 Nimpkish	0	Nimpkish	0	Nimpkish	0	Nimpkish	0	Nimpkish	0	Nimpkish	0	Nimpkish	0