Joint US and CA Mixed-stock Chum Fisheries Sampling Design and Analysis 2018

Report to Southern Endowment Fund: Project 57536

Andres Araujo, John Candy, Pieter Van Will,

Department of Fisheries and Oceans 3190 Hammond Bay Road Nanaimo, B. C. V9T 6N7

and

Bill Patton

Northwest Indian Fisheries Commission 6730 Martin Way E. Olympia, WA 98516 Phone: (360) 528-4383

Contact: Phone: 250-756-3367 Fax: 250-756-7053

Email: andres.araujo @dfo-mpo.gc.ca

Abstract

We conducted Genetic Stock Identification (GSI) of 2932 Chum salmon migrating to natal streams through Johnstone Strait (Statistical Areas 12 and 13), along the central Strait of Georgia (Statistical Area 17) and the San Juan Islands (Statistical Areas 7 and 7A) for 2018 using analyses of microsatellite variation. A total of 2058 Chum salmon were analyzed for Canadian fisheries (Areas 12, 13, and 17) and 874 Chum salmon for U.S. fisheries (Area 7-7A).

The analysis of chum salmon sampled in the commercial and test fisheries in Johnstone Strait (JS) were mainly from Canadian populations (85.8% to 99.4%) comprised largely of sites in that local area, the Fraser River, and Strait of Georgia (east and west sides). The central Strait of Georgia (SoG) was composed of largely Canadian contributions (92.4% to 97.7%), mainly from sites in the easter and western portions of SoG and Johnstone Strait. The analysis of Chum salmon caught in U.S. commercial fisheries in the San Juan Islands (Area 7 and 7A) were mostly of Canadian origin stocks: 93.5% to 99.2%. U.S. contribution reached 6.5% in late October.

The failure rate was very high for Areas 7 and 7A, where 51.9% of the samples failed due to DNA degradation and contamination issues. In Canadian samples the failure rate was low at 0.097%. A total of 0.41% of the samples were excluded from the analysis because the number of loci amplified was below threshold (<9 from 14 loci), lower than the previous year (3.04%).

Acknowledgments

Financial support for the project was provided by the Southern Enhancement Fund, with support from the Department of Fisheries and Oceans, Washington Department of Fish and Wildlife, Northwest Indian Fisheries Commission.

TABLE OF CONTENTS

ABSTRACT	I
ACKNOWLEDGMENTS	Ш
INTRODUCTION	5
MATERIALS AND METHODS	7
RESULTS AND DISCUSSION	11
LITERATURE CITED	13
Table 1. Sample size of tissue collections for DNA analysis for Chum salmon directed fisheries in 2018. Samples anal are the number that was effectively analyzed by the GSI program. Samples excluded are those that were included in analyses but did not provide sufficient information for genetic stock identification. Samples that failed are those that not amplify due to poor quality and therefore did not make it to the analyses.	the
Table 2. Baseline of 130 sample sites/populations by regional genetic groups used to estimate stock composition of Cl salmon from southern British Columbia and Washington State in 2018 fisheries.	hum 10
Table 3. Estimated percentage stock composition of Chum salmon caught in Area 12 and 13 Test and Commercial Fisheries in 2018. Stock compositions were estimated using 14 microsatellite loci and the baseline outlined in Table 2 Number of fish excluded because of their inability to provide sufficient information for genetic stock identification in parentheses. Samples that failed due to lack of amplification are not included in these analyses (see Table 1 for more details). Standard error of the estimated stock composition is in parentheses.	
Table 4. Estimated percentage stock composition of Chum salmon caught in the Strait of Georgia (Areas 17) Fall Chr Fisheries in 2018. Stock compositions were estimated using 14 microsatellite loci and the baseline outlined in Table 2 Number of fish excluded because of their inability to provide sufficient information for genetic stock identification in parentheses. Samples that failed due to lack of amplification are not included in these analyses (see Table 1 for more details). Standard error of the estimated stock composition is in parentheses.	2.
Table 5. Estimated percentage stock composition of Chum salmon caught in Area 7 and 7A in 2018. Stock composition were estimated using 14 microsatellite loci and the baseline outlined in Table 1. Number of fish excluded because of inability to provide sufficient information for genetic stock identification in parentheses. Samples that failed due to la amplification are not included in these analyses (see Table 1 for more details). Standard error of the estimated stock composition is in parentheses.	their
FIGURES	20
Figure 1. Map of Statistical Areas outlining Chum salmon fishing locations in southern British Columbia 2013-2018	20
Figure 2. Map of Statistical Areas outlining Chum salmon fishing locations in Puget Sound 2013-2018.	21

Introduction

In order to facilitate management responses to Southern Chum stock strength, in accordance with Annex IV, Chapter 6 of the Pacific Salmon Treaty (The Treaty) it is necessary to provide the catch composition in fisheries targeting southern origin Chum salmon (*Oncorhynchus keta*). This information supports the treaty requirement Section 3 to account for US chum stocks in Canadian fisheries and to account for Canadian chum stocks in US fisheries. This is the third year of an additional four year project to sample and provide Genetic Stock Identification (GSI) on key chum mixed stock fisheries within Canada and the US. This work is replicating previous annual sample collections to obtain uniform and sufficient coverage to meet Treaty requirements.

The main fisheries targeted were Johnstone Strait purse seine commercial and test fisheries (Area 12 and Area 13 - Figure 1), Strait of Georgia gill net (Area 17), as well as the US commercial purse seine and gill net fisheries occurring in the areas described as San Juan Islands/Point Roberts (SJI/PR) Fishery Management Areas 7 and 7A (Figure 2).

Both Canadian and US Chum salmon populations were grouped into genetically distinguishable groups and must be evaluated for concordance with existing Canadian Conservation Units and Evolutionary Significant Units for conservation management purposes. Besides immediate Treaty obligations, the GSI work is part of the information required for accurate post-season run reconstructions which are essential in evaluating whether domestic management actions were consistent with meeting overall objectives of the Treaty. Run reconstructions are also important in monitoring the productivity of stocks and assessing the adequacy of current escapement targets and both pre-season forecasting and in-season run assessment techniques. Without this knowledge, managing to achieve Treaty obligations would be difficult and severely limits the assessment of factors influencing stock productivity, which appear to have fluctuated widely in recent years.

Stock specific data collected in these mixed stock areas will provide the information, deemed necessary by the PSC Joint Chum Technical Committee (Chum TC) and the PSC Southern Panel, to develop management options addressing conservation of stocks of concern while focusing fisheries on stocks of significant abundance. It will also provide a bilaterally agreed method to determine the catch composition on all mixed stock Chum fisheries in Johnstone Strait, US areas 7 and 7A and other border fisheries in accordance with Annex IV, Chapter 6 of the Treaty.

Materials and Methods

Collection of DNA Samples and Laboratory Analysis

Caudal punches were taken from sampled fish by sticking tissue on Whatman paper to air dry and DNA was extracted as described by Withler et al. (2000) or placed in vials with non-denatured ethanol preservative. The samples were collected from 2932 adult Chum salmon in 2018 captured in test and commercial fisheries from British Columbia Statistical Areas 12, 13, and 17 between September 12 and October 22. There were 874 Chum salmon captured for genetic analysis in commercial fisheries from Washington State Statistical Areas 7 and 7A between October 13 and October 21, 2018. Unfortunately 51.9% of these samples from 7 and 7A failed to amplify due to DNA degradation and contamination issues. Tissue samples or purified DNA from these collections are available to be analyzed by U.S. labs at their request.

In Canadian waters, fisheries were sampled across a broad range of dates and areas. Fall Chum directed fisheries were sampled in Johnstone Strait (Area 12 and 13), and Strait of Georgia terminal Chum fisheries (Area 17). Commercial and Test fisheries were sampled in Johnstone Strait. The Fall Chum test fishery occurred from September 12 to October 22. There were one commercial purse seine opening in Johnstone Strait that took place on October 15, simultaneously in Areas 12 and 13. Commercial Vessels were sampled as they were encountered at the offload locations and 25-30 fish were randomly sampled per vessel. The catch was sampled between Areas 12 and 13 proportionate to the catch in those areas during the fishery. A Fall Chum gill net fishery was sampled in the Strait of Georgia (SOG) Area 17 (Oct 28 to 29). Table 1 summarizes all sample collections by fishery in Canadian waters.

In U.S. waters the chum directed fishery was sampled weekly in Washington Catch

Management Areas 7 & 7A (San Juan Islands and Point Roberts). The goal of the test fishery in

Area 7 was to collect 200 samples per survey. The dates ranged from October 13 to October 21. In 7A fisheries began on October 13 and ended in October 14. Table 1 summarizes sample collections from Areas 7 & 7A.

We employed chum salmon genomic DNA surveys of variation at the following 14 microsatellite loci: *Ots3* (Withler et al. 1999), *Oke3* (Buchholz et al. 2001), *Oki2* (Smith et al. 1998), *Oki100* (Beacham et al. 2008b), Ots103 (Nelson and Beacham 1999), *Omm1070* (Rexroad et al. 2001), *Omy 1011* (Spies et al. 2005), *One101*, *One102*, *One104*, *One111*, and *One114* (Olsen et al. 2000), *Ssa419* (Cairney et al. 2000), and *OtsG68* (Williamson et al. 2002). Microsatellites were size fractionated in an Applied Biosystems (ABI) 3730 capillary DNA sequencer, and genotypes were scored by GeneMapper software 3.0 (Applied Biosystems, Foster City, CA) using an internal lane sizing standard.

In general, polymerase chain (PCR) reactions were conducted in 10 µl volumes consisting of 0.06 units of Taq polymerase, 1µl of 30ng DNA, 1.5-2.5mM MgCl₂, 1mM 10x buffer, 0.8mM dNTP's, 0.006-0.065µM of labeled forward primer (depending on the locus), 0.4µM unlabeled forward primer, 0.4µM unlabeled reverse primer, and deionized H₂O. PCR was completed on an MJResearch™ DNA Engine™ PCT-200 or a DNA Engine Tetrad™ PCT-225. The amplification profile involved one cycle of 2 min @ 92°C, 30 cycles of 15 sec @ 92°C, 15 sec @ 52-60°C (depending on the locus) and 30 sec @ 72°C, and a final extension for 10 min @ 72°C. Specific PCR conditions for a particular locus could vary from this general outline. Further information on laboratory equipment and techniques is available at the Molecular Genetics Laboratory website at http://www.pac.dfo-mpo.gc.ca/science/facilities-installations/pbs-sbp/mgl-lgm.

Baseline Populations

The baseline survey consisted of microsatellite analysis of chum salmon from 130 locations within Canada and the southern US (Table 2). Thirteen regional groupings of populations were identified based on genetic stock structure and the ability to accurately estimate known mixtures on of these groupings (DFO unpublished data). All annual baseline samples available for a specific sample location were combined to estimate population allele frequencies, as was recommended by Waples (1990).

Estimation of Stock Composition

Analysis of fishery samples was conducted with a Bayesian procedure (BAYES) as outlined by Pella and Masuda (2001). Each locus was assumed to be in Hardy-Weinberg equilibrium, and expected genotypic frequencies were determined from the observed allele frequencies and used as model inputs. For BAYES, the initial FORTRAN-based computer program as outlined by Pella and Masuda (2001) required large amounts of computer analytical time when applied to stock identification problems with a baseline as comprehensive as employed in the current study. Given this limitation, a new version of the program was developed by our laboratory as a C-based program which is available from the Molecular Genetics Laboratory website (Neaves et al. 2005). In the analysis, ten 20,000-iteration Monte Carlo Markov chains of estimated stock compositions were produced, with initial starting values for each chain set at 0.90 for a particular population which was different for each chain. Estimated stock compositions were estimated when all Monte Carlo Markov chains had converged producing a Gelman-Rubin coefficient < 1.2 (Pella and Masuda 2001). The last 1,000 iterations from each of the 10 chains were combined, and for each fish the probability of originating from each population in the baseline was determined. These individual probabilities were summed over all fish in the sample, and divided by the number of fish sampled to provide the point estimate of stock composition. Standard deviations of estimated stock compositions

were also determined from the last 1,000 iterations from each of the 10 Monte Carlo Markov chains incorporated in the analysis.

Results and Discussion

The southern British Columbia/Washington Chum salmon baseline consisting of fourteen microsatellite markers, a subset of the Pacific Rim baseline for Chum salmon ranging from Japan, across the North Pacific (including the Yukon River) to the southern range limit of Chum salmon in the Columbia River (Beacham et al. 2008; Beacham et al. 2008b) was used to determine the compositions of the fishery samples taken in 2018 (Table 2).

Samples collected in the summer and fall from the Canadian Area 12 test fishery consisted of Canadian origin fish (99.4% to 93.5%; Table 3) predominantly from the river systems in the area; as the weeks progressed catches switched from Johnstone Strait to the Strait of Georgia (east and west sides) and the Fraser River. Commercial samples from Areas 12 and 13 (weeks 43 and 44) were predominantly from the SoG east and west sides and the Fraser River. Fall samples from Johnstone Strait tended to see a buildup of Fraser stocks until week 39 then a steady decline through the end of October samples. Stocks from SoG West increased in composition through the fall reaching their peaking in week 41 while SoG east remained steady through the season until their decline in October. The Fall SoG terminal chum fishery catches (Table 4) were dominated by East Vancouver Island stocks (49.4% to 58.5%) and overall by Canadian stocks (92.4% to 97.7%).

Samples collected from commercial fisheries in U.S. Area 7 also were both Canadian and U.S. origin stocks with a larger contribution of the Fraser River and SoG West, overall by Canadian origin stocks: 93.5% to 94.5%. For Area 7A the same trend remained with a large proportion of Fraser River 78.8%; 99.2% were Canadian stocks.

Sample failure due to tissue quality (e.g. degradation, contamination) will result in absent or poor DNA amplification. Overall the failure to amplify rate was very high for Areas 7 and 7A where 51.9% of the samples failed. For Canadian samples the failure rate was low at 0.097%. A

total of 0.41% of the samples were excluded from the analysis because the number of loci amplified was below threshold (<9 from 14 loci), lower than the previous year (3.04%). The Fishery with larger number of failed samples was the Area7A gillnet— with 97%. The Fishery with more samples excluded from the analyses was the Area 12 TF Double Bay (Seine) with 1.4% of the samples failed to provide sufficient information for genetic stock identification. However no samples failed in this fishery.

Literature Cited

Banks, M. A., Blouin, M. S., Baldwin, B. A., Rashbrook, V. K., Fitzgerald, H. A., Blankenship, S. M and Hedgecock, D. 1999. Isolation and inheritance of novel microsatellites in chinook salmon (Oncorhynchus tshawytscha). J. Hered. 90: 281-288.

Beacham, T. D., S. Urawa, K. D. Le, and M. Wetklo 2008. Population structure and stock identification of chum salmon from Japan determined with microsatellite DNA variation.

Fisheries Science 74: 983-994.

Buchholz W.G, S. J. Miller, and W. J. Spearman . 2001. Isolation and characterization of chum salmon microsatellite loci and use across species. Animal Genetics 32: 160-167.

Cairney, M., Taggart, J. B., and Hoyheim, B. 2000. Characterization of microsatellite and minisatellite loci in Atlantic salmon (Salmo salar L.) and cross-species amplification in other salmonids. Mol. Ecol. 9: 2175-2178.

Neaves, P. I., C. G. Wallace, J. R. Candy, and T. D. Beacham. 2005. CBayes: Computer program for mixed stock analysis of allelic data. Version v4.02. Free program distributed by the authors over the internet from http://www.pac.dfo-mpo.gc.ca/sci/mgl/Cbayes_e.htm

Nelson, R. J., and T. D. Beacham. 1999. Isolation and cross species amplification of microsatellite loci useful for study of Pacific salmon. Animal Genetics. 30: 228-229.

Olsen, J. B., S. L. Wilson, E. J. Kretschmer, K. C. Jones, and J. E. Seeb. 2000. Characterization of 14 tetranucleotide microsatellite loci derived from sockeye salmon. Molecular Ecology 9: 2185-2187.

Pella, J. and Masuda, M. 2001. Bayesian methods for analysis of stock mixtures from genetic characters. Fish. Bull. 99: 151-167.

Rexroad, C. E., Coleman, R. L, Martin, A. M., Hershberger, W. K., and Killefer, J. 2001.

Thirty-five polymorphic microsatellite markers for rainbow trout (Oncorhynchus mykiss). Animal Genetics 32: 283-319

Small, M. P., T. D. Beacham, R. E. Withler, and R. J. Nelson. 1998. Discriminating coho salmon (Oncorhynchus kisutch) populations within the Fraser River, British Columbia using microsatellite DNA markers. Molecular Ecology 7: 141-155.

Smith, C. T., Koop, B. F., and Nelson, R. J. 1998. Isolation and characterization of Coho salmon (Oncorhynchus kisutch) microsatellites and their use in other salmonids. Mol. Ecol. 7: 1613-1621.

Spies, I. B., D. J. Brasier, P. T. L. O'Reilly, T. R. Seamons, and P. Bentzen. 2005.

Development and characterization of novel tetra-, tri-, and dinucleotide microsatellite markers in rainbow trout (Oncorhynchus mykiss). Molecular Ecology Notes 5: 278-281.

Williamson, K. S., J. F. Cordes, and B. May. 2002. Characterization of microsatellite loci in Chinook salmon (Oncorhynchus tshawytscha) and cross-species amplification in other salmonids. Molecular Ecology Notes 2: 17-19.

Withler, R. E, Le, K. D., Nelson, R. J., Miller, K. M., and Beacham, T. D. 2000. Intact genetic structure and high levels of genetic diversity in bottlenecked sockeye salmon,

Oncorhynchus nerka, populations of the Fraser River, British Columbia, Canada. Can. J. Fish.

Aquat. Sci. 57: 1985-1998.

Tables

Table 1. Sample size of tissue collections for DNA analysis for Chum salmon directed fisheries in 2018. Samples analyzed are the number that was effectively analyzed by the GSI program. Samples excluded are those that were included in the analyses but did not provide sufficient information for genetic stock identification. Samples that failed are those that did not amplify due to poor quality and therefore did not make it to the analyses.

Canadian Waters										
Region	Fishery	Gear	Dates		Analysed	Excluded	Failed	Total		
	Area 12 JST (Area B) Commercial	Seine	15-Oct	15-0 ct	250	0	0	250		
Johnston Strait	Area 12 TF Blinkhorn	Seine	24-S ep	30-S ep	579	2	0	581		
	Area 12 TF Double Bay	Seine	23-S ep	22-0 ct	483	7	0	490		
	Area 12 TF	Seine	12-S ep	20-S ep	373	0	1	374		
	Area 13 JST (Area B) Commercial	Seine	15-Oct	15-0 ct	249	1	0	250		
Central Strait of Georgia	Area 17 (Area E) Commercial	Gillnet	28-Oct	29-0 ct	112	0	1	113		
				Subtotal:	2046	10	2	2058		

U.S. Waters										
Region	Fishery	Gear	Dates		Analysed	Excluded	Failed	Total		
	Area 7	Gillnet	13-Oct	19-0ct	28	0	0	28		
Area 7 - U.S.	Area 7	Gillnet/Seine	20-0 ct	21-Oct	168	1	0	169		
	Area 7	Seine	13-Oct	16-0ct	95	0	222	317		
Area 7A - U.S.	Area 7A	Gillnet	13-Oct	14-0ct	7	0	232	239		
Alea /A - 0.5.	Area 7A	Seine	13-Oct	14-0ct	120	1	0	121		
				Subtotal:	418	2	454	874		

Total Samples Run	Analysed	Excluded	Failed	Total
	2464	12	456	2932

Table 2. Baseline of 130 sample sites/populations by regional genetic groups used to estimate stock composition of Chum salmon from southern British Columbia and Washington State in 2018 fisheries.

Region	Populations
Johnstone Strait	Heydon Cr, Klinaklini R, Ahta R, Viner Sound,
	Waump Cr, Nimpkish R, Kakweiken R, Glendale Cr, Ahnuhati
	Cr, Mackenzie Sound, Phillips R, Viner/Scott Cove
Strait of Georgia East	Tzoonie Cr, Cheakamus R, Sliammon R, Mamquam R, Wortley
	Cr, Squamish R, Indian R, Theodosia R, Southgate R, Algard
	Cr, Orford R, Shovelnose R, Mashiter Cr, Stawamus R,
	Homathko R, Kwalate Cr, Lang Cr, Deserted Cr, Myrtle Cr,
	Snake Cr, Anderson Cr
Strait of Georgia West	Goldstream R, Cowichan R, Nanaimo R, Chemainus R,
Strait of Georgia West	
	Puntledge R, Qualicum R, Little Qualicum R, Campbell R, Cold
West Osset Value and Island	Cr, Englishman R
West Coast Vancouver Island	Smith Cr, Kirby Cr, Demaniel R, Nitinat R, Hathaway Cr,
	Petattum Cr, Goodspeed, R, Cayeghle Cr, Colonial R, Sugsaw,
	Cr, Nahmint R, Hoiss Cr, Black Cr, Parks R, Tsowwin_R, Kaouk
	R, Sucwoa R, Canton R, Little Toquart R, Tranquil Cr, Salmon
	Cr, Bedwell R, Warner Bay, Burman Cr, Sooke R
Fraser River	Silverdale Cr, Squawkum Cr, Wahleach Cr, Chilliwack R,
	Chehalis R, Stave R, Alouette R, Vedder R, Harrison R, Inch Cr,
	Lower Lillooet R, Norrish-Worth Cr, North Alouette R, Widgeon
	Slough, Kawkawa Cr, Blaney Cr, Chilqua Cr, Serpentine R,
	Kanaka Cr, Worth Cr, Hopedale Cr, Hicks Cr, Harrison Lake,
	Peach Cr, Sweltzer Cr, Nathan Cr, McIntyre Cr, Street Cr,
	Railroad, Cr, Silverhope Cr
North Puget Sound	Skagit R, County Line Cr, Grant Cr, Siberia Cr, Skykomish R,
0	Snohomish R, Stilllaguamish R, Sauk R
South Puget Sound	Kennedy Cr, Minter Cr, Nisqually R, Mill Cr, Skookum Cr,
	Puyallup R, South Prairie Cr
Juan de Fuca/	Salmon R, Big Quilcene R
Hood Canal Summer	
Coastal Washington	Ellsworth Cr, Bitter Cr, Quinault R, Satsop R
Nooksack	Nooksack R
Tulalip	Tulalip R
Central Puget Sound	Green R, Grovers Cr
Juan de Fuca/	Elwha R, Hoodsport, Spencer Cr, Big Mission Cr, Dewatto R,
Hood Canal Fall	Hamma Hamma R, Big Beef Cr

Table 3. Estimated percentage stock composition of Chum salmon caught in Area 12 and 13 Test and Commercial Fisheries in 2018. Stock compositions were estimated using 14 microsatellite loci and the baseline outlined in Table 2. Number of fish excluded because of their inability to provide sufficient information for genetic stock identification in parentheses. Samples that failed due to lack of amplification are not included in these analyses (see Table 1 for more details). Standard error of the estimated stock composition is in parentheses.

Year	201	8	201	8	201	8	201	8	201	8	201	8	2018	2018		
Julian date	255-2	258	260-2	166	267-2	273	274-2	277	281-2	281-284 290-294		288		295-30	00	
Gear	seir	ne	sein	е	seir	ne	sein	ie	sein	ie	seir	ie	seine_c	omm	seine	
Stat Area	Area 12	2_T F	Area12	_T F	Area12	2_T F	Area12	_T F	Area12	_T F	Area12	_T F	Area12_13	Comm	Area12_13	C omm
Fishery Type	Weel	k37	Week	38	Weel	k 39	Week	(40	Week	41	Week	42	Week	42	Week	43
Dates	S ep12-9	Sep15	Sep17-S	ep23	Sep24-9	Sep30	Oct01-0	Oct04	Oct08-0	Oct11	Oct17-0	Ct21	Oct1	5	O ct22-0	ct27
sample Size	192(0)	231(0)	188(0)	145(1)	192(0)	258(8)	499(1	L)	229(0)
Region	E s tima t S	5 D	E s tima t e S	D	E s tima te S	D	E s tima t∈ S	D	E s tima t S	D	E s tima t S	D	Estimate S	D	Estimate SI)
Johnstone Strait	17.1	(4.2)	2.6	(3.5)	0.5	(1.9)	3.8	(5.3)	2.4	(3.6)	4.3	(3.7)	7.0	(3.7)	4.3	(1.8)
Strait of Georgia East (F)	11.9	(5.1)	9.9	(4.3)	19.5	(7.5)	12.9	(7.4)	15.7	(6.9)	16.5	(5.0)	11.7	(4.2)	27.8	(5.7)
Strait of Georgia West (F)	8.1	(5.5)	17.8	(5.1)	21.0	(7.2)	30.1	(7.6)	52.3	(7.5)	43.4	(5.5)	41.8	(4.6)	28.9	(6.1)
Fraser River (F)	57.1	(4.9)	67.1	(4.4)	57.5	(5.1)	47.0	(5.8)	27.5	(4.5)	27.0	(4.3)	36.7	(3.1)	23.8	(4.1)
West Coast Vancouver I(F)	1.6	(1.7)	2.0	(1.6)	0.4	(1.0)	5.6	(2.9)	0.6	(1.2)	2.3	(1.5)	0.3	(0.7)	1.0	(1.4)
North Puget Sound (F)	4.2	(2.8)	0.4	(0.9)	0.1	(0.5)	0.2	(0.9)	0.2	(8.0)	5.4	(3.8)	0.5	(1.1)	11.0	(3.7)
Central Puget Central (F)	0.0	(0.1)	0.0	(0.1)	0.4	(0.6)	0.0	(0.2)	0.0	(0.1)	0.0	(0.1)	0.0	(0.1)	0.0	(0.1)
South Puget Sound (F-W)	0.0	(0.2)	0.0	(0.2)	0.1	(0.5)	0.1	(0.5)	0.1	(0.4)	0.0	(0.2)	0.0	(0.2)	0.1	(0.5)
Hood Canal (S)	0.0	(0.1)	0.0	(0.1)	0.0	(0.1)	0.0	(0.1)	0.0	(0.1)	0.0	(0.1)	0.0	(0.0)	0.0	(0.1)
Hood Canal (F)	0.1	(0.4)	0.1	(0.5)	0.3	(0.8)	0.2	(0.7)	1.1	(1.5)	1.1	(1.4)	2.0	(1.2)	2.9	(1.4)
Juan de Fuca (F)	0.0	(0.1)	0.0	(0.1)	0.0	(0.1)	0.1	(0.6)	0.0	(0.2)	0.0	(0.1)	0.0	(0.0)	0.0	(0.3)
Coastal Washington (F)	0.0	(0.1)	0.0	(0.1)	0.0	(0.2)	0.1	(0.4)	0.1	(0.3)	0.0	(0.1)	0.0	(0.1)	0.0	(0.1)
Country																
Canada	95.7	(2.9)	99.4	(1.1)	99.0	(1.2)	99.3	(1.4)	98.5	(1.8)	93.5	(3.8)	97.5	(1.6)	85.8	(3.9)
US	4.3	(2.9)	0.6	(1.1)	1.0	(1.2)	0.7	(1.4)	1.5	(1.8)	6.5	(3.9)	2.5	(1.6)	14.2	(3.9)

Table 4. Estimated percentage stock composition of Chum salmon caught in the Strait of Georgia (Areas 17) Fall Chum Fisheries in 2018. Stock compositions were estimated using 14 microsatellite loci and the baseline outlined in Table 2. Number of fish excluded because of their inability to provide sufficient information for genetic stock identification in parentheses. Samples that failed due to lack of amplification are not included in these analyses (see Table 1 for more details). Standard error of the estimated stock composition is in parentheses.

Year	201	8	2018			
Julian date	301	1	302			
Gear	gil	I	gill			
Stat Area	A17_E_	Comm	A17_E_C omm			
Fishery Type	Weel	k43	Wee	k44		
Dates	Oct	28	Oct	29		
sample Size	87(0	0)	25(0)		
Region	E s tima te	S D	E s tima te	S D		
Johnstone Strait	19.0	(8.4)	0.1	(1.5)		
Strait of Georgia East (F)	19.3	(10.6)	38.9	(13.7)		
Strait of Georgia West (F)	58.5	(13.6)	49.4	(15.2)		
Fraser River (F)	0.6	(1.7)	3.6	(5.7)		
West Coast Vancouver I(F)	0.2	(0.9)	0.4	(2.4)		
North Puget Sound (F)	0.7	(1.8)	0.4	(2.3)		
Central Puget Central (F)	0.1	(0.5)	0.1	(1.0)		
South Puget Sound (F-W)	1.5	(2.4)	1.3	(3.3)		
Hood Canal (S)	0.0	(0.2)	0.0	(0.5)		
Hood Canal (F)	0.0	(0.4)	5.7	(8.2)		
Juan de Fuca (F)	0.0	(0.1)	0.0	(0.7)		
Coastal Washington (F)	0.0	(0.2)	0.0	(0.8)		
Country						
Canada	97.7	(2.9)	92.4	(8.9)		
US	2.3	(2.9)	7.6	(8.9)		

Table 5. Estimated percentage stock composition of Chum salmon caught in Area 7 and 7A in 2018. Stock compositions were estimated using 14 microsatellite loci and the baseline outlined in Table 1. Number of fish excluded because of their inability to provide sufficient information for genetic stock identification in parentheses. Samples that failed due to lack of amplification are not included in these analyses (see Table 1 for more details). Standard error of the estimated stock composition is in parentheses.

					· · · · · · · · · · · · · · · · · · ·		
Year	2018	3	201	8	2018		
Julian date	286		286-2	287	289-294		
Gear	G N-P	S	G N-I	PS	GN-GN_PS-PS		
Stat Area	Area	7	Area	7A	Are	a7	
Fishery Type	Week	41	Weel	<41	Wee	k42	
Dates	Oct1	.3	Oct13-0	Oct14	Oct16-	Oct21	
sample Size	52(0)	127(1)	239	(1)	
Region	E s tima te	S D	E s tima te	S D	Estimate	S D	
Johnstone Strait	0.1	(1.0)	1.5	(2.1)	0.2	(0.7)	
Strait of Georgia East (F)	7.6	(7.9)	8.8	(4.3)	11.3	(5.1)	
Strait of Georgia West (F)	22.7	(9.4)	9.3	(5.0)	22.6	(5.8)	
Fraser River (F)	63.5	(8.8)	78.8	(5.3)	58.8	(4.7)	
West Coast Vancouver I(F)	0.6	(1.9)	0.8	(1.3)	0.7	(1.1)	
North Puget Sound (F)	0.5	(1.9)	0.5	(1.4)	5.4	(2.5)	
Central Puget Central (F)	4.8	(3.6)	0.2	(0.6)	0.6	(1.0)	
South Puget Sound (F-W)	0.1	(0.7)	0.1	(0.5)	0.1	(0.5)	
Hood Canal (S)	0.0	(0.3)	0.0	(0.1)	0.0	(0.1)	
Hood Canal (F)	0.0	(0.6)	0.0	(0.2)	0.2	(0.5)	
Juan de Fuca (F)	0.0	(0.1)	0.0	(0.1)	0.0	(0.1)	
Coastal Washington (F)	0.0 (0.4)		0.0 (0.2)		2) 0.2		
Country							
Canada	94.5	(4.1)	99.2	(1.6)	93.5	(2.7)	
US	5.5	(4.1)	0.8	(1.6)	6.5	(2.7)	

Figures

Figure 1. Map of Statistical Areas outlining Chum salmon fishing locations in southern British Columbia 2013-2018

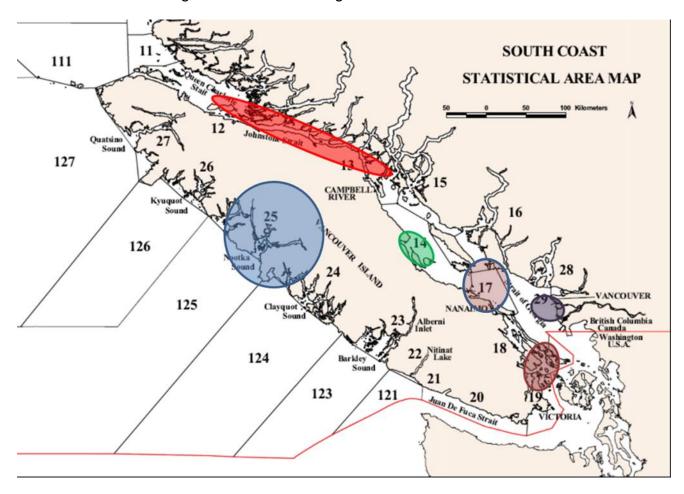


Figure 2. Map of Statistical Areas outlining Chum salmon fishing locations in Puget Sound 2013-2018.

