Genetic Analysis of Chum Salmon collected on Vashon Island in 2022

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Introduction

Up to 250 Chum salmon juveniles from Minter Creek Hatchery were planted in Shingle Mill Creek on Vashon Island each May beginning in 2012. In fall 2018, adult Chum salmon spawners were found in Shingle Mill Creek and Judd Creek on Vashon Island. The Vashon Nature Center has been monitoring animals and plants on Vashon Island and was interested in the origins of these adult Chum salmon. WDFW is developing a Chum salmon SNP genetic baseline and compared these unknown adult Chum salmon spawners to the baseline to estimate their origins.

Methods

Genomic DNA was extracted from unknown adult Chum salmon tissue samples using Machery-Nagel spin columns. Samples were genotyped at 350 Chum salmon SNP genotypes in the Oke_GTseq350 panel used for the Chum salmon SNP baseline (Small et al. 2018). 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.

Samples were assigned to the Chum salmon SNP baseline as unknown fish using the program Rubias (Moran and Anderson, 2019). The program calculates the likelihood of each unknown fish arising from each of the baseline collections (Table 2), based on the genotype of the fish and the allele frequencies of each baseline collection. The baseline population with the highest likelihood of assignment is hypothesized as the population of origin of the unknown fish.

Results

A Total of 27 samples were genotyped for the both the chum SNP panel and the coho SNP panel. Samples were genotyped with both panels due to uncertainty of species ID for about a third of the samples. Of the 27 samples, 14 were identified as chum salmon and had sufficient genotype data to be assigned to the chum salmon genetic baseline (Table 2).

Samples were assigned to population of origin using the Chum salmon SNP baseline. Populations were removed from results if no samples had at least 1% assignment probability to that population. Curly Creek, Chico/Grovers, and Minter Creek Hatchery each had samples assigned with high probability (Table 3). Keta Creek Hatchery had low assignment probabilities for all samples but passed the threshold of 1% for reporting. Eight of the samples had greater then 90% assignment to a population, five samples had greater than 70% assignment to a population, and one sample had approximately equal assignment to three populations.

These results are consistent with individuals straying from other populations; however, we cannot rule out the possibility of a self-sustaining population on Vashon Island. If a self-sustaining population arose from transplants to Vashon, individuals in this population would be genetically indistinguishable from the source population until enough generations had passed to accumulate genetic differences. In the short time since transplantation (2012-2018) we would not expect differentiation to arise. Discerning whether individuals returning to spawn are offspring of past natural spawners rather than hatchery strays would require different analyses such as genetic parentage assignment or examining fish for hatchery markings. Both of these methods have requirements which may limit their application. Parentage analysis requires sampling of putative parents each year which can be prohibitive if the number of spawners is large or if fish spawn in inaccessible areas. Hatcheries may not mark fish consistently, or even at all, so the ability to detect hatchery marks is dependent on the practices of the potential source hatcheries.

References:

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 Resources 15: 855-867.

Moran BM, Anderson EC. 2019. Bayesian inference from the conditional genetic stock identification model. CJFAS 76:4 551-560.

Small, MP, Warheit K, Pascal C, Seeb L, Ruff C, Zischke J, Winans G, Seeb J. 2018. 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, PSC, 45 pp.

Table 1. List of individual Chum salmon collections in the SNP genetic baseline and their reporting groups (geographic and run timing group).

Pop	Region	Pop	Region
CurleyCr	SPS	10DungenessF	SJF
MinterCr_H	SPS	10_14upper_Skagit	NPS
GreenR_H	SPS	98_10Nooksack	NPS
MillCr	SPS	10_18Snoh/Sky	NPS
Sherwood_S	SPS	10_18Stilly	NPS
Sherwood_F	SPS	14Lo_Sauk	NPS
Chico/Grovers	SPS	98_14Skagit_lo	NPS
Skookum	SPS	Samish	NPS
Kennedy	SPS	Sooke	WCVI
10HoodH_F	HC_F	Conuma	WCVI
11NFSkok_F	HC_F	Nitinat	WCVI
98_11Dewatto_F	HC_F	Hopedale	Fraser
11Anderson	HC_F	Peach	Fraser
10Big_Beef_F	HC_F	Squawkum	Fraser
Duckabush_F	HC_F	Big_Qualicum	GeorgiaSt
Lilliwaup_F	HC_F	Campbell	GeorgiaSt
11DIRU_PuyH	SPS_W	Cheakamus	GeorgiaSt
Nisqually	SPS_W	Cowichan	GeorgiaSt
03Dose_S	HC_S	Lang	GeorgiaSt
12_14Dose_S	HC_S	Little_Qualicum	GeorgiaSt
12_14Hamma_S	HC_S	Nanaimo	GeorgiaSt
14Duck_S	HC_S	Phillips	GeorgiaSt
16NFSkok_S	HC_S	Puntledge	GeorgiaSt
05Pysht	SJF	Snake	GeorgiaSt
18LyreCr	SJF	Southgate	GeorgiaSt
96Hoko	SJF	Nimpkish	JohnstoneSt

Table 2. Biological data and WDFW codes for Chum salmon samples analyzed in 2022. Only samples listed as Chum in genetic species were analyzed for population assignment. Samples listed as No Data for genetic species had insufficient genotypes for species assignment.

UNID	WDFW code	Genetic Species	Phenotypic Species	Sample date	Sampler	Creek	Notes
Vash1	19RD0001	Chum	chum	11/12/2019	Kkeenan	Shinglemill	predation, male, prespawn, 28"
Vash2	19RD0002	No Data	chum	11/15/2019	Bperla	Shinglemill	adipose, Male, 27", pre-spawn, reach 1
Vash3	19RD0003	Chum	chum	11/23/2019	KKeenan	KVI marsh	29", male, pre-spawn
Vash4	19RD0004	Chum	chum	12/13/2019	Bperla	Judd	26", not full carcass, reach 1
Vash5	20QJ0005	Coho	chum	11/11/2020	BPerla	Shinglemill	partial body
Vash6	20QJ0006	Chum	chum	11/15/2020	Kkeenan	Shinglemill	spawned, adipose, 24" female
Vash7	20QJ0007	Chum	chum	11/8/2020	KKeenan	Shinglemill	pre-spawn, 22", male, adipose, reach 1
Vash8	20QJ0008	No Data	chum	11/15/2020	Kkeenan	Shinglemill	pre-spawn, 30", adipose, male
Vash9	20QJ0009	No Data	chum	11/15/2020	Kkeenan	Shinglemill	spawned, adipose, 26", female, reach 2
Vash10	20QI0010	Coho	unknown	12/3/2020	Kkeenan	Shinglemill	partial body, reach 1
Vash11	20QJ0011	Chum	unknown	11/11/2020	Kkeenan	Shinglemill	spawned, 24", adipose, reach 1
Vash12	20QI0012	No Data	coho	12/3/2020	Kkeenan	Shinglemill	partial body, reach 3
Vash13	20QI0013	Coho	coho	12/3/2020	Kkeenan	Shinglemill	head only, reach 3
Vash14	20QI0014	Coho	coho	12/3/2020	Kkeenan	Shinglemill	20", female, spawned, adipose, reach 2
Vash15	20QI0015	No Data	coho	12/3/2020	Kkeenan	Shinglemill	adipose, predation, 26", reach 3
Vash16	20QI0016	Coho	coho	10/31/2020	Kkeenan	Shinglemill	21", female, pre-spawn, adipose, reach 2
Vash17	20QI0017	Pos. trout per Bianca	unknown	11/20/2020	Kkeenan	Shinglemill	reach 1, 47.485423, -122.487730 acc. 21 feet
Vash18	20QJ0018	Chum	unknown	12/12/2020	Pcummings	Judd	likely chum, partial body
Vash19	20QI0019	Coho	coho	10/16/2020	Lthorpe	Judd	reach 1
Vash20	21QX0020	Chum	unknown	10/22/2021	Gkuhns	Shinglemill	female, predation, eggs and head
Vash21	21QY0021	Chum	chum	10/22/2021	Kkeenan	Shinglemill	female, adipose, pre-spawn, 27"
Vash22	21QY0022	Chum	chum	10/22/2021	Kkeenan	Shinglemill	female, predation, prespawn, 27" adipose unknown
Vash23	21QX0023	Pos. trout per Bianca	coho	11/8/2021	Kkeenan	Shinglemill	16" long, predation, reach 4, 47.473791, -122.481374 acc. 79 ft.
Vash24	21QY0024	Chum	chum	11/22/2021	P Cummings	Judd	adipose, predation, male?
Vash25	21QY0025	Chum	chum	11/22/2021	P Cummings	Judd	female?, adipose
Vash26	21QY0026	Chum	chum	11/18/2021	P Cummings	Judd	24-30", adipose present
Vash27	21QY0027	Chum	chum	11/19/2021	P Cummings	Judd	20-24", adipose present

Table 3. Population assignments for samples identified as chum salmon. Assignment probabilities are color coded from white (0) to green (100).

WDFW ID	20KetaCrHat	02CurleyCr	10_15Chico/ Grovers	03MinterCr_H
19RD0001	0%	97%	2%	0%
19RD0003	4%	2%	71%	22%
19RD0004	0%	1%	18%	81%
20QJ0006	1%	18%	3%	76%
20QJ0007	0%	92%	7%	1%
20QJ0011	4%	1%	88%	6%
20QJ0018	0%	0%	0%	100%
21QX0020	0%	32%	40%	28%
21QY0021	0%	99%	1%	0%
21QY0022	2%	2%	96%	0%
21QY0024	0%	0%	0%	100%
21QY0025	0%	4%	0%	96%
21QY0026	1%	2%	97%	1%
21QY0027	1%	0%	11%	88%