

Genetic Analysis of Coho Salmon collected on Vashon Island in 2022

December 29, 2022

Garrett McKinney, WDFW Molecular Genetics Lab, Olympia, WA

Bianca Perla, Vashon Nature Center

Introduction

Chum salmon juveniles from Minter Creek Hatchery are regularly planted in Shingle Mill Creek on Vashon Island each May and up juvenile Coho salmon from Soos hatchery are regularly released into Judd and Shinglemill creeks (WDFW records). Vashon Nature Center salmonwatchers monitor creeks for spawning salmon each fall. Adult Chum and Coho salmon spawners were found in Shingle Mill Creek and Judd Creek on Vashon Island between 2019 and 2020. The Vashon Nature Center has been monitoring animals and plants on Vashon Island and was interested in the origins of these adult salmon. WDFW is developing a Chum salmon and Coho salmon SNP genetic baseline and can compare these unknown adult Chum and Coho salmon spawners to the baseline to estimate their origins. This study will build on an initial pilot study of Chum DNA samples from Shinglemill Creek in 2018.

Methods

Genomic DNA was extracted from unknown adult Coho salmon tissue samples using Machery-Nagel spin columns. Samples were genotyped at 348 Coho salmon SNP genotypes in the GTseq panel used for the Coho salmon SNP baseline (McKinney et al. 2022). 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 Coho 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, 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, six were identified as coho salmon and had sufficient genotype data to be assigned to the coho salmon genetic baseline (Table 1).

Samples were assigned to population of origin using the Coho salmon SNP baseline. Populations were removed from results if no samples had at least 1% assignment probability to that population. Two samples had high assignment probabilities to a single population (20QI0010 – Hoh River, 20QI0016 – Green River), while the remaining samples had approximately equal assignments to multiple populations ranging from South Puget Sound to the Strait of Juan de Fuca (Table 2). This does not

necessarily mean that these individuals have mixed ancestry. The Coho salmon baseline currently has limited power to distinguish among populations in Puget Sound and between Puget Sound and the Elwha River, and this assignment pattern may be signal of that limited resolving power.

These results are consistent with individuals straying from other populations or return of stocked Soos Creek (Green River stock) individuals; 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. Differentiation would also be prevented through continued stocking if transplanted individuals successfully returned and reproduced each year. 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.
- McKinney GM, Loudon A, Candy J, Spidle A, Nichols K, Smith C, O'Malley K, Litz M, Seamons T. 2022. Phase II of Coho Salmon GSI: SNP baseline development. Report to the Southern Fund Panel, PSC, 13 pp.

Table 1. Biological data and WDFW codes for Coho salmon samples analyzed in 2022. Only samples listed as Coho 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	Pcumings	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 2. Population assignments for samples identified as coho salmon. Assignment probabilities are color coded from white (0) to green (100).

Reporting Group	Population	Sample					
		20QI0010	20QI0013	20QI0014	20QI0016	20QI0019	20QJ0005
Stillaguamish/Snohomish	Skykomish_2017	0%	0%	4%	0%	0%	0%
Mid Puget Sound	Cedar_2019	0%	3%	23%	0%	0%	15%
Hood Canal	Duckabush_2018	0%	0%	1%	0%	0%	1%
Hood Canal	Dewatto_R	0%	28%	0%	0%	0%	0%
South Puget Sound	Green_2019	0%	0%	33%	77%	30%	8%
South Puget Sound	Nisqually_2019	0%	5%	0%	0%	0%	0%
South Puget Sound	Voights_H_2001	0%	0%	4%	0%	18%	0%
South Puget Sound	Green_2018	0%	0%	26%	0%	6%	36%
South Puget Sound	Nisqually_2018	0%	36%	7%	0%	1%	39%
US Strait of Juan de Fuca	Clallam_2001	8%	20%	0%	0%	20%	0%
US Strait of Juan de Fuca	Dungeness_2017	8%	3%	0%	19%	14%	0%
US Strait of Juan de Fuca	Elwha_2019	0%	0%	1%	0%	11%	0%
US Strait of Juan de Fuca	Elwha_2012	0%	0%	1%	3%	0%	0%
Hoh	Hoh_2006	83%	4%	0%	0%	0%	0%