

## Isotopes and genes reveal freshwater origins of Chinook salmon *Oncorhynchus tshawytscha* aggregations in California's coastal ocean

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Table S1. Description of the 13 microsatellite loci and primer sequences used in genotyping Chinook salmon adults.

Locus	Reference	Primer Sequences <sup>1</sup>	Total number of alleles	Observed size range
<i>Ots201b</i>	Greig et al. 2003	F-CAG GGC GTG ACA ATT ATG C R-GTT TGG ACA TCT GTG CGT TGC*	26	139-275
<i>Ots208b</i>	Greig et al. 2003	F-GGA TGA ACT GCA GCT TGT TAT R-GTT TGG CAA TCA CAT ACT TCA ACT TCC*	34	152-316
<i>Ots211</i>	Greig et al. 2003	F-TAG GTT ACT GCT TCC GTC AAT G R-GTT TGA GAG GTG GTA GGA TTT GCA G*	21	205-285
<i>Ots212</i>	Greig et al. 2003	F-TCT TTC CCT GTT CTC GCT TC R-GTT TCC GAT GAA GAG CAG AAG AGA C*	17	134-222
<i>Ots213</i>	Greig et al. 2003	F-CCC TAC TCA TGT CTC TAT TTG GTG R-GTT TAG CCA AGG CAT TTC TAA GTG AC*	30	204-336
<i>OtsG474</i>	Williamson et al. 2002	F-TTA GCT TTG GAC ATT TTA TCA CAC R-GTT TCC AGA GCA GGG ACC AGA AC*	14	154-210
<i>Ots9</i>	Banks et al. 1999	F-ATC AGG GAA AGC TTT GGA GA R-GTT TCC CTC TGT TCA CAG CTA GCA*	3	106-110
<i>Ots3M</i>	Greig and Banks 1999	F-TGT CAC TCA CAC TCT TTC AGG AG* R-GTT TGA GAG TGC TGT CCA AAG GTG A*	9	138-158
<i>Omm1080</i>	Rexroad et al. 2001	F-GAG ACT GAC ACG GGT ATT GA R-GTT TGT TAT GTT GTC ATG CCT AGG*	34	174-342
<i>Ogo2</i>	Olsen et al. 1998	F-ACA TCG CAC ACC ATA AGC AT R-GTT TGT TTC GAC TGT TTC CTC TGT GTT GAG*	12	217-257
<i>Ogo4</i>	Olsen et al. 1998	F-GTC GTC ACT GGC ATC AGC TA R-GTT TGA GTG GAG ATG CAG CCA AAG*	8	134-168
<i>Oki100</i>	Seeb et al. 2007 <sup>2</sup>	F-CCA GCA CTC TCA CTA TTT R-GTT TCC AGA GTA GTC ATC TCT G*	25	188-312
<i>Ssa408</i>	Cairney et al. 2000	F-AAT GGA TTA CGG GTA CGT TAG ACA R-GTT TCT CTT GTG CAG GTT CTT CAT CTG T*	16	183-251

<sup>1</sup>An asterisk identifies the forward (F) or reverse (R) primer as modified for use as in Seeb et al. (2007). <sup>2</sup> Originally, Department of Fisheries and Oceans Canada, Personal Communication, Kristi Miller.

Table S2. Natal origin inferred by otolith  $^{87}\text{Sr}/^{86}\text{Sr}$  analysis of fish assigned to CV fall-run genetic reporting group and ocean region of collection.

Fish ID	Region	Aggregation <sup>1</sup>	$^{87}\text{Sr}/^{86}\text{Sr} \pm 2$ standard error	Hatchery/Natural Assignment <sup>2</sup>	Natal Origin Assignment <sup>3</sup>
RJ20165	Bodega Bay	BB1	0.705390 ± 0.000030	H	CNH
RJ20166	Bodega Bay	BB1	0.706158 ± 0.000057	H	CNH
RJ20167	Bolinas Bay	BB1	0.705923 ± 0.000078	H	CNH
RJ20168	Bodega Bay	BB1	0.707831 ± 0.000060	H	MOH
RJ20169	Bodega Bay	BB1	0.704912 ± 0.000065	H	CNH
RJ20172	Bodega Bay	BB1	0.707668 ± 0.000100	.	MOH
RJ20174	Bodega Bay	BB1	0.707425 ± 0.000053	H	MOH
RJ20212	Bodega Bay	BB2	0.705185 ± 0.000034	H	CNH
RJ20214	Bodega Bay	BB2	0.705690 ± 0.000056	H	CNH
RJ20216	Bodega Bay	BB2	0.705196 ± 0.000037	H	CNH
RJ20217	Bodega Bay	BB2	0.705196 ± 0.000054	H	CNH
RJ20219	Bodega Bay	BB2	0.704399 ± 0.000045	N	MIL
RJ20220	Bodega Bay	BB2	0.707561 ± 0.000033	H	MOH
JH20050	Bodega Bay	BB3	0.708740 ± 0.000046	H	MEH
JH20051	Bodega Bay	BB3	0.707294 ± 0.000040	H	MOH
JH20052	Bodega Bay	BB3	0.706433 ± 0.000056	.	STA
JH20053	Bodega Bay	BB3	0.707370 ± 0.000039	.	TUO
JH20054	Bodega Bay	BB3	0.706183 ± 0.000048	H	CNH
JH20055	Bodega Bay	BB3	0.705124 ± 0.000040	H	CNH
JH20056	Bodega Bay	BB3	0.706454 ± 0.000061	H	FRH
RJ20380	Bolinas Bay	BO1	0.709671 ± 0.000039	H	NIH
RJ20384	Bolinas Bay	BO1	0.703906 ± 0.000032	H	CNH
RJ20389	Bolinas Bay	BO1	0.706659 ± 0.000034	H	FRH
RJ20395	Bolinas Bay	BO1	0.709550 ± 0.000052	H	NIH
RJ20397	Bolinas Bay	BO2	0.705431 ± 0.000062	H	CNH
RJ20399	Bolinas Bay	BO2	0.709579 ± 0.000043	N	AME
RJ20400	Bolinas Bay	BO2	0.708943 ± 0.000027	H	MEH
RJ20401	Bolinas Bay	BO2	0.705201 ± 0.000042	H	CNH
RJ20403	Bolinas Bay	BO2	0.707352 ± 0.000027	H	MOH
RJ20405	Bolinas Bay	BO2	0.707439 ± 0.000066	.	TUO
RJ20406	Bolinas Bay	BO2	0.709623 ± 0.000048	H	NIH
RJ20407	Bolinas Bay	BO2	0.705384 ± 0.000044	H	CNH
RJ20409	Bolinas Bay	BO2	0.706289 ± 0.000077	H	FRH
RJ20410	Bolinas Bay	BO2	0.705834 ± 0.000053	H	CNH
RJ20276	Bolinas Bay	BO3	0.710208 ± 0.000044	H	NIH
RJ20277	Bolinas Bay	BO3	0.709648 ± 0.000063	.	NIH
RJ20278	Bolinas Bay	BO3	0.708761 ± 0.000046	H	MEH
RJ20279	Bolinas Bay	BO3	0.705231 ± 0.000038	.	CNH
RJ20280	Bolinas Bay	BO3	0.709295 ± 0.000051	H	NIH
RJ20282	Bolinas Bay	BO3	0.705823 ± 0.000031	H	CNH
RJ20283	Bolinas Bay	BO3	0.708858 ± 0.000082	N	MER
RJ20284	Bolinas Bay	BO3	0.707712 ± 0.000031	N	TUO
MK20018	Monterey Bay	MO1	0.706264 ± 0.000043	H	FRH
MK20023	Monterey Bay	MO1	0.708126 ± 0.000040	H	MEH

Fish ID	Region	Aggregation <sup>1</sup>	<sup>87</sup> Sr/ <sup>86</sup> Sr ± 2 standard error	Hatchery/Natural Assignment <sup>2</sup>	Natal Origin Assignment <sup>3</sup>
MK20025	Monterey Bay	MO1	0.707683 ± 0.000054	N	TUO
MK20029	Monterey Bay	MO1	0.709632 ± 0.000041	H	NIH
MK20030	Monterey Bay	MO1	0.709791 ± 0.000036	H	NIH
MK20031	Monterey Bay	MO1	0.705081 ± 0.000052	H	CNH
MK20035	Monterey Bay	MO1	0.704881 ± 0.000068	H	CNH
MK20036	Monterey Bay	MO1	0.705668 ± 0.000071	H	CNH
MK20037	Monterey Bay	MO1	0.706148 ± 0.000032	H	CNH
RJ20006	Monterey Bay	MO2	0.707313 ± 0.000038	.	TUO
RJ20007	Monterey Bay	MO2	0.709613 ± 0.000043	.	NIH
RJ20010	Monterey Bay	MO2	0.709548 ± 0.000040	N	AME
RJ20011	Monterey Bay	MO2	0.705979 ± 0.000058	H	CNH
RJ20012	Monterey Bay	MO2	0.707803 ± 0.000038	H	MOH
RJ20013	Monterey Bay	MO2	0.707245 ± 0.000026	H	FRH
RJ20015	Monterey Bay	MO2	0.706107 ± 0.000044	H	CNH
RJ20016	Monterey Bay	MO2	0.705117 ± 0.000049	H	CNH
RJ20017	Monterey Bay	MO2	0.706362 ± 0.000077	N	STA
RJ20018	Monterey Bay	MO2	0.705602 ± 0.000057	.	CNH

<sup>1</sup>Aggregation codes referenced in Table 2, <sup>2</sup>otolith microstructure assignment (Barnett-Johnson et al. 2007), <sup>3</sup>Otolith microstructure and <sup>87</sup>Sr/<sup>86</sup>Sr data used in a 'separate' discriminant function model unless otolith microstructure was unreadable (.) then 'full' model using only <sup>87</sup>Sr/<sup>86</sup>Sr was applied (Barnett-Johnson et al. 2008).

Table S3. Genetic assignment and  $^{87}\text{Sr}/^{86}\text{Sr}$  ratios for non-CV fall-run Chinook salmon in the ocean. Individuals highlighted in grey were caught in the same aggregation and had intact otoliths for additional  $^{87}\text{Sr}/^{86}\text{Sr}$  profile analysis to assess similarity in freshwater rearing.

Fish ID	Genetic Assignment	Loci (N) <sup>1</sup>	Post. Prob. <sup>2</sup>	Region	Aggregation <sup>3</sup>	$^{87}\text{Sr}/^{86}\text{Sr} \pm 2$ standard error	
MK20019	CV winter-run	11	100	Monterey Bay	MO1	0.704876	± 0.000050
MK20021	CV winter-run	10	100	Monterey Bay	MO1	0.704948	± 0.000049
MK20024	CV winter-run	11	100	Monterey Bay	MO1	0.704944	± 0.000045
MK20026	CV winter-run	8	100	Monterey Bay	MO1	0.704975	± 0.000072
MK20027	CV winter-run	6	100	Monterey Bay	MO1	0.704972	± 0.000044
MK20028	CV winter-run	10	100	Monterey Bay	MO1	0.705044	± 0.000039
MK20032	CV winter-run	12	100	Monterey Bay	MO1	0.705075	± 0.000036
MK20033	CV winter-run	13	100	Monterey Bay	MO1	0.705130	± 0.000058
MK20034	CV winter-run	11	100	Monterey Bay	MO1	0.704809	± 0.000040
RJ20377	Klamath	13	100	Bolinas Bay	BO1	0.706799	± 0.000041
RJ20378	Klamath	11	63	Bolinas Bay	BO1	0.704834	± 0.000047
RJ20379	Klamath	12	89	Bolinas Bay	BO1	0.704124	± 0.000065
RJ20381	Klamath	12	100	Bolinas Bay	BO1	0.705116	± 0.000062
RJ20387	Klamath	8	100	Bolinas Bay	BO1	0.706925	± 0.000051
RJ20396	Klamath	10	100	Bolinas Bay	BO1	0.706354	± 0.000060
RJ20173	OR-CA Coast	12	100	Bodega Bay	BB1	0.705888	± 0.000051
RJ20382	OR-CA Coast	9	90	Bolinas Bay	BO1	0.705870	± 0.000059
RJ20383	OR-CA Coast	12	100	Bolinas Bay	BO1	0.703742	± 0.000051
RJ20388	OR-CA Coast	8	100	Bolinas Bay	BO1	0.707316	± 0.000056
RJ20390	OR-CA Coast	13	100	Bolinas Bay	BO1	0.706177	± 0.000086
RJ20391	OR-CA Coast	13	97	Bolinas Bay	BO1	0.704220	± 0.000039
RJ20392	OR-CA Coast	11	100	Bolinas Bay	BO1	0.704167	± 0.000025
RJ20393	OR-CA Coast	13	100	Bolinas Bay	BO1	0.704393	± 0.000069
RJ20411	OR-CA Coast	7	100	Bolinas Bay	BO2	0.707647	± 0.000082
RJ20178	Puget Sound	9	66	Bodega Bay	BB1	0.707381	± 0.000030
RJ20218	Deschutes	11	93	Bodega Bay	BB2	0.709688	± 0.000040
RJ20394	BC Coast	11	60	Bolinas Bay	BO1	0.703881	± 0.000042

<sup>1</sup>Number of loci genotyped successfully. <sup>2</sup>Posterior probability (%) for genetic assignment, <sup>3</sup>Codes referenced in Table 2

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