

Supporting Information

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SI Materials and Methods

Sample Collection and Genotyping. Samples were collected from the Hood River in Oregon, where winter-run steelhead are listed as threatened under the Endangered Species Act (1). Genetic samples for steelhead used in this study were collected from run-years 1992–2007, which corresponds to fish born in brood-years 1989 through 2005. Winter-run steelhead begin returning to their natal rivers in early December, the year of which designates the run-year, and do not spawn until spring of the next year. Thus, a steelhead that spawns in May of 2000 will belong to run-year 1999 (even if it returned in March of 2000), and its offspring will belong to brood-year 2000. Because of the accelerated growth rate in hatcheries (i.e., decreased time to smoltification), most hatchery-born steelhead (71%) return to spawn at 2.5 y of age, whereas most wild-born steelhead (64%) return at 3.5 y (Fig. 1). Adult fish returning in a single run-year come from multiple brood-years. Summer-run fish breed in different forks of the river and are genetically distinct (2).

Steelhead returning to spawning grounds in the Hood River were passed over the Powerdale Dam, which was a complete barrier to migrating fish. Every fish passed over the dam was individually handled, and samples of scales and fin tissue were collected for aging and genetic analysis by staff of the Oregon Department of Fish and Wildlife. Also recorded were the length, weight, sex, and run-timing of every fish. Steelhead were easily categorized as hatchery or wild origin because all hatchery fish had their adipose fin clipped before being released as juveniles. All wild fish and an approximately equal number of hatchery fish were passed over the dam each year. All broodstock were collected at the dam, and the winter-run hatchery fish were created using either two wild fish or one wild fish and a first-generation hatchery fish (i.e., F1 fish) as broodstock (3). The majority of broodstock fish (81%) were of wild ancestry, with the remainder being first-generation hatchery fish. Most broodstock fish were spawned with two (or occasionally more) partners, which created returning hatchery fish that were both full- and half-sibs. Fish used as hatchery broodstock were collected randomly from throughout the entire run period and were unlikely to be related. As confirmation, we calculated that 66% of broodstock pairs shared an allele at two or fewer loci and 88% of broodstock pairs shared an allele at three or fewer loci. We have tissue samples from all broodstock and comprehensive records on broodstock pairings in the hatchery.

The winter-run steelhead samples averaged 847 fish per run-year for a total of 12,700 samples. All samples were genotyped at eight highly polymorphic microsatellite loci (Omy 1001, Omy 1011, Omy 1191, Omy77, One108, One2, Ssa407, and Str2), which average 36 alleles per locus. Details about the genetic markers, laboratory methods, and genotyping can be found elsewhere (2–4). Extensive details on this study system, management practices, steelhead life history, and reproductive success can also be found elsewhere (2, 4–6). It is important to note that survivorship in this hatchery (measured from egg to smolt release) was an average of 65% across 6 y (6), such that we do not know whether selection was occurring in the hatchery, after release, or both.

F1 Return Times. Not all F1 hatchery fish were passed above the dam. All wild fish and an approximately equal number of hatchery

fish were passed over the dam each year, and the hatchery fish were passed over in a way to mimic the run-time distribution of the wild fish. Therefore, the only mechanism for a bias that we can imagine would be if hatchery fish from the best-performing families were not all passed over the dam because they showed up at the tails of the wild run-time distribution. Although such a relationship would be counterintuitive, we nonetheless examined whether F1 hatchery siblings had similar return dates. If F1 fish with many siblings had all been passed over the dam at the peak run-time, it is possible that F1 fish arriving at the tails of the run may have had siblings that were not passed over the dam. To investigate this possibility, we isolated all siblings for each of the 8 examined run-years and calculated their intraclass correlation coefficient (ICC) for return time using the “psy” library in R (7). For all run-years, the ICC was positive but very low, suggesting that there was only a very weak association between siblings for the date that they were passed over the dam (Table S4). We also looked for a relationship between F1 family size and their mean deviation from the median run date. If larger families were passed over the dam more frequently toward the median run date, smaller families may have been biased by virtue of their run date. However, we did not find evidence of a negative relationship in any run-years after a Bonferroni correction (and only slight evidence in 1 of 8 y, 1996, without a Bonferroni correction) (Fig. S3). Furthermore, there was no relationship between F1 reproductive success and the date the fish were passed over the dam. These results all suggest that the practice of passing a subset of hatchery fish over the dam had little bearing on our results. This practice was not a concern for estimating the reproductive success of F1 fish that were passed over the dam because all wild F2 fish were sampled (and subsequently passed above the dam).

Parentage of Broodstock. One striking pattern is that the tradeoff between success of wild broodstock and the subsequent success of their F1 offspring appears to increase sharply after the first 2 y (i.e., the tradeoff is stronger in F1 run-years 1998–2002 than it is in run-years 1996–1997; Fig. 2). One possibility is that the “wild” broodstock in later years had hatchery ancestry and that these fish would subsequently have higher fitness than broodstock without hatchery ancestry. To address this hypothesis, we performed parentage analyses on all broodstock that produced offspring that returned in run-years 1998–2002. We searched for broodstock parents among both wild and hatchery fish, and we searched among putative parents plus or minus 1 brood-year to account for any incorrect scale aging. For all relevant broodstock, we identified only 28 hatchery parents, which amounted to only 6% of the broodstock fish having hatchery parents. Furthermore, the broodstock fish with identified hatchery parents did not, on average, have high reproductive success (i.e., they were not to the far right of the x axis in Fig. 2). Thus, the greater tradeoff in later years is not attributable to some broodstock fish having a greater proportion of hatchery genes. One possible explanation is that the selection pressures, such as the crowding of fish (Table S3), may have gotten worse through time. Ocean conditions may have also played a role, as is suggested by the 1996 and 1997 run-years possessing the lowest maximum number of offspring per broodstock.

1. Good TP, Waples RS, Adams P, eds. (2005) *Updated status of federally listed ESUs of West Coast salmon and steelhead*. US Department of Commerce NOAA Tech. Memo.

NMFS-NWFSC-66, 598 p. Available at <http://www.nwr.noaa.gov/Publications/Biological-Status-Reviews/Salmon.cfm>. Accessed November 28, 2011.

Table S2. P values for the slope from a GLM and a sample-variance G-test for alternative approaches to analyzing the data

		1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	All years
Eight loci	Slope	—	—	0.902	0.106	0.007	0.002	<0.001	<0.001	<0.001	<0.001	<0.001
	G-test	—	—	0.138	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	0.015	<0.001
Broodstock pair	Slope	—	—	0.092	0.040	0.002	0.002	0.002	<0.001	<0.001	0.001	<0.001
	G-test	—	—	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	0.049	<0.001
Age 3 fish	Slope	—	—	0.252	0.202	0.078	0.008	<0.001	0.060	<0.001	<0.001	<0.001
	G-test	—	—	0.049	<0.001	0.627	0.138	<0.001	0.001	0.016	0.005	<0.001
F1 brood-year	Slope	0.813	0.077	0.347	0.006	<0.001	0.008	<0.001	<0.001	—	—	<0.001
	G-test	0.958	0.107	<0.001	<0.001	<0.001	0.002	<0.001	0.005	—	—	<0.001

“Eight loci” refers to analyses using only broodstock and F1 parentage assignments that matched at all eight loci. “Broodstock pair” refers to analyses in which the broodstock reproductive success was not measured for each individual fish but, rather, for each mated pair of fish. “Age 3 fish” refers to analyses in which fish in an F1 run-year came from only the most common brood-year. “F1 brood-year” refers to analyses in which F1 fish were grouped by their brood-year as opposed to run-year. “All years” refers to analyses performed with data points from all analyzed years (e.g., 1995–2002). Statistical methods used in this table are described in the *Materials and Methods* of the main text.

Table S3. Year and number of winter-run hatchery steelhead smolts released (N_{released}) into the Hood River

Year	N_{released}	Size, fish/lb	Return year
1992	4,600	4.6	1995
1993	38,034	5.8	1996
1994	42,860	5.0 (4.5–5.8)	1997
1995	50,896	5.4 (5.1–5.9)	1998
1996	59,837	5.4 (5.0–5.8)	1999
1997	59,837	7.1 (5.6–8.3)	2000
1998	62,136	6.4 (5.2–9.0)	2001
1999	46,598	6.0 (5.6–9.2)	2002
2000	61,335	7.6 (7.3–10.3)	2003

Also reported is the size of the fish released recorded as fish per pound (fish/lb). When multiple release locations were used, we report the mean fish size (weighted by the number of individuals released at each site), along with the range of mean fish sizes released across locations. Larger fish would allow for fewer fish per pound; thus, some of the largest fish produced were released in 1992. The return year in which the majority of these fish would return to their spawning grounds is also reported. The first year of the winter-run hatchery supplementation program was 1992, which corresponds to the year in which the fewest and largest smolts were released. The majority of fish released in 1992 returned in 1995 (Fig. 1). From Kostow et al. (1).

1. Kostow K, Olsen E, Jennings M, Newton J (2000) *Hood River Steelhead Hatchery Programs: (Goals Risk/Benefit Analysis and Assessment of Alternative Operational Protocols)*, Portland, OR.

Table S4. Intraclass correlation for run-timing of F1 families by run-year

F1 run-year	Intraclass correlation
1995	0.0043
1996	0.0454
1997	0.0576
1998	0.0279
1999	0.1033
2000	0.0534
2001	0.0377
2002	0.0608

These low but positive values suggest that there is a very weak association between siblings and their return date.

Table S5. Multiple linear regression for a suite of explanatory variables as predictors for broodstock reproductive success

Run-year	Sex	Output	Length	Weight	Date	SW age	Age	Temp	Eggs
1992	Male	Slope	-0.024	NA	0.041	0.541	-0.047	0.032	NA
		P value	0.739	NA	0.054	0.222	0.935	0.091	NA
	Female	Slope	-0.003	NA	0.015	-0.322	-0.562	-0.024	NA
		P value	0.944	NA	0.370	0.820	0.838	0.582	NA
1993	Male	Slope	-1.432	3.023	-0.074	-18.477	-0.049	0.084	NA
		P value	0.024	0.214	0.531	0.055	0.654	0.724	NA
	Female	Slope	-0.052	0.003	0.000	0.147	0.000	0.001	NA
		P value	0.392	0.984	0.986	0.694	0.633	0.954	NA
1994	Male	Slope	-0.077	0.249	0.020	0.372	0.269	-0.004	NA
		P value	0.093	0.270	0.251	0.301	0.583	0.905	NA
	Female	Slope	0.030	0.373	-0.002	-0.061	0.000	-0.042	NA
		P value	0.811	0.671	0.925	0.860	0.449	0.426	NA
1995	Male	Slope	-0.464	2.084	-0.131	-0.993	-0.002	-0.171	NA
		P value	0.368	0.542	0.110	0.789	0.653	0.104	NA
	Female	Slope	-0.427	4.950	-0.100	3.433	0.000	-0.172	NA
		P value	0.403	0.178	0.128	0.057	0.977	0.200	NA
1996	Male	Slope	-0.029	1.784	-0.013	2.373	-0.002	0.101	NA
		P value	0.863	0.347	0.892	0.391	0.703	0.550	NA
	Female	Slope	-0.121	0.801	-0.014	0.085	0.104	0.011	NA
		P value	0.438	0.380	0.261	0.819	0.767	0.695	NA
1997	Male	Slope	0.067	-0.542	0.009	0.097	0.000	0.006	NA
		P value	0.455	0.365	0.255	0.683	0.514	0.664	NA
	Female	Slope	2.272	-18.790	0.137	2.150	0.002	-0.038	NA
		P value	0.280	0.185	0.445	0.696	0.699	0.902	NA
1998	Male	Slope	0.139	-0.743	-0.015	-0.353	0.001	-0.016	NA
		P value	0.089	0.252	0.308	0.256	0.301	0.301	NA
	Female	Slope	1.902	-8.220	-0.219	-7.125	0.006	-0.257	NA
		P value	0.110	0.382	0.302	0.122	0.525	0.253	NA
1999	Male	Slope	-0.040	0.055	0.011	-0.128	0.000	0.020	0.003
		P value	0.858	0.972	0.445	0.890	0.717	0.263	0.449
	Female	Slope	0.130	-0.727	0.021	0.074	0.000	0.008	-0.001
		P value	0.457	0.453	0.245	0.869	0.828	0.715	0.786
2000	Male	Slope	0.163	-1.228	-0.005	0.205	0.001	0.008	-0.002
		P value	0.198	0.112	0.687	0.601	0.851	0.761	0.417
	Female	Slope	1.294	-8.111	-0.088	-0.118	0.021	0.024	-0.001
		P value	0.503	0.486	0.665	0.985	0.108	0.953	0.538
2001	Male	Slope	0.483	-3.011	0.064	-0.976	-0.316	0.017	-0.003
		P value	0.181	0.206	0.406	0.587	0.883	0.834	0.625
	Female	Slope	-0.303	1.598	0.016	0.218	0.023	0.022	0.000
		P value	0.129	0.231	0.471	0.602	0.972	0.440	0.724
2002	Male	Slope	-0.010	-0.122	-0.019	-0.136	-0.044	0.000	0.000
		P value	0.818	0.654	0.013	0.702	0.923	0.208	0.586
	Female	Slope	-0.081	0.521	0.010	0.442	-0.228	0.000	0.000
		P value	0.254	0.275	0.231	0.205	0.563	0.240	0.633

Explanatory variables for the broodstock parents included the total length (cm), weight (g), arrival date at the dam, salt water (SW) age, and age as determined by scale aging. Variables in the hatchery included the length of time eggs were chilled (Temp), and the number of eggs that successfully hatched. Data on egg counts were only available for run-years 1999–2002. The slope of the regression line and associated *P* value are presented. NA, data not available.