Second generation fitness consequences of Pink Salmon hatchery-origin strays in Prince William Sound

Kyle R. Shedd[1], Erika M. King[1], Kristen M. Gruenthal[1], Milo D. Adkison[2], Lorna I. Wilson[3], Peter H. Westley[4], Samuel A. May[5], Peter S. Rand[6]

[1] Alaska Department of Fish & Game (ADF&G), Gene Conservation Laboratory; [2]ADF&G, Headquarters; [3]ADF&G, Aquaculture Section; [4]University of Alaska Fairbanks; [5]AquaTechCenter; [6]Prince William Sound Science Center

Do offspring of hatchery strays have lower fitness than offspring of natural-origin fish?

BACKGROUND

- As part of the Alaska Hatchery Research Program (AHRP), we investigated the effects of hatcheries on the fitness (productivity) of naturally spawning Pink Salmon in Prince William Sound (PWS)
- ~70% of the total return of Pink Salmon to PWS are hatchery-origin (Fig. 1)[1]
- ~97% hatchery-origin return is harvested in commercial fisheries or spawned as broodstock[1]
- Unharvested hatchery-origin Pink Salmon stray into streams and spawn alongside wild stocks[1,2]
- 5–15% of Pink Salmon spawners in PWS are hatchery-origin strays, with substantial variation among streams (0–92%)[1,2]
- First generation (F_0) hatchery strays produce **~50% fewer** returning adults[3]
- Multiple mechanisms likely reduce fitness – run timing, spawning location, etc.
- Unknown whether fitness reductions persist across generations

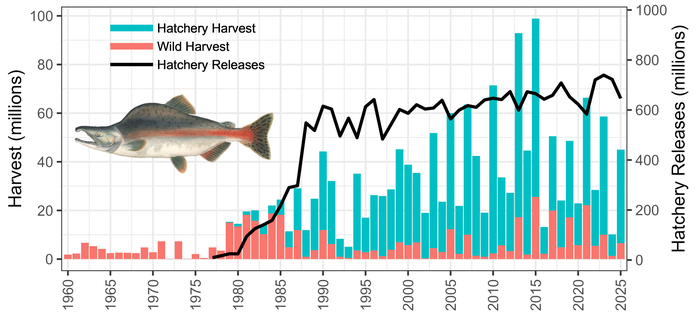


Figure 1. Prince William Sound Pink Salmon hatchery releases and commercial harvest in millions, 1960–2025

METHODS

Determine the relative fitness of offspring of hatchery strays vs. offspring of natural-origin Pink Salmon ($F_1 \rightarrow F_2$) with genetic pedigrees

Field Collections

- Five fitness streams sampled 2013–2020 (Fig. 2)
- Not all streams sampled in each year
- **Incomplete sampling of post-spawn adults**
- Higher sampling rate in even- than odd-lineage years
- Collected paired otoliths (origin) and genetic tissues (pedigree reconstruction; Fig. 3 & 4)
- Phenotypic data: body length, date, stream location[4]

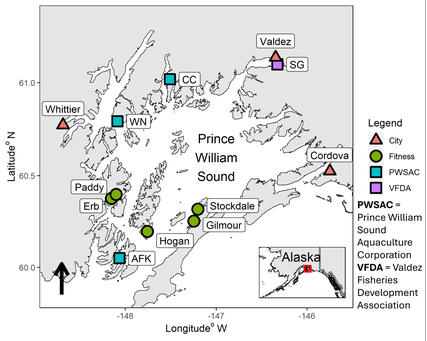


Figure 2. Map of five fitness streams (green circles) and hatcheries (blue and purple squares).

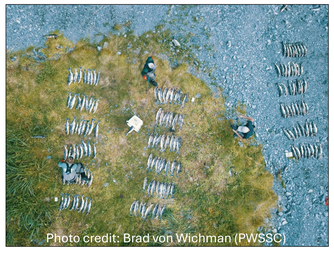


Figure 3. Post-spawn Pink Salmon organized for sampling paired otoliths and genetic tissue.

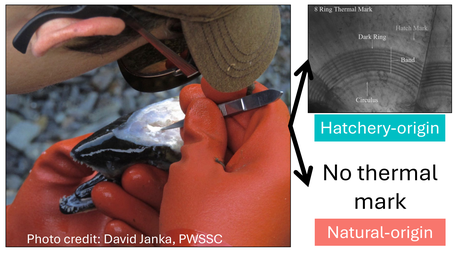
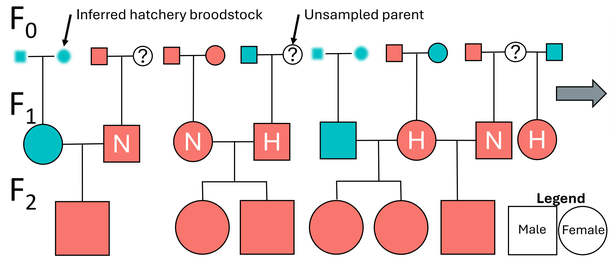


Figure 4. Otolith thermal marks determine hatchery- vs. natural-origin.

Pedigree Reconstruction

- Samples genotyped with 298 SNP GT-seq panel[3]
- *FRANz* pedigree reconstruction software[5] used to identify parent-offspring relationships
- All streams combined for pedigree reconstruction to account for natural straying among streams
- F_1: **hatchery-ancestry** if either F_0 parent was a hatchery stray (Fig. 5)
- F_1: **natural-ancestry** if either F_0 parent was natural-origin and neither was a hatchery stray



Reproductive Success Data

F_1 ancestry	F_1 sex	# F_2 offspring
Natural	Male	1
Natural	Female	2
Hatchery	Male	2
Hatchery	Female	3
Natural	Male	1
Hatchery	Female	0

RRS Analysis

	Male		Female	
F_1 ancestry	N	H	N	H
# F_1 parents	2	1	1	2
# F_2 offspring	2	2	2	3
RS	1.0	2.0	2.0	1.5
$RRS_{H/N}$	2.00		0.75	

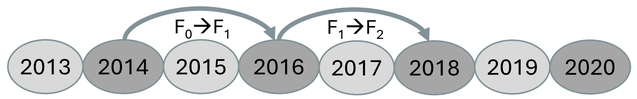
Figure 5. Multi-generational pedigree example. F_0 represents the first year of sampling. Colors depict fish origin as determined by otoliths. Unsampled parents are represented by "?". White letters show ancestry for F_1's as determined by F_0 origin in the pedigree (N = natural-ancestry and H = hatchery-ancestry). Note that F_1's without any assigned F_0 parents or any new hatchery strays are not included in the $F_1 \rightarrow F_2$ analysis. Tables show calculation of RRS from pedigree data.

Fitness Analysis

- **Reproductive Success (RS) = number of offspring** assigned per parent (fitness)
- Calculated average RS ($\overline{RS}$) for males and females for each stream/year/ancestry
- **Relative reproductive success (RRS)** = $\overline{RS}_{Hatchery} / \overline{RS}_{Natural}$ for each stream/year/sex with 95% CIs[6] (Fig. 5)
- Calculated geometric mean RRS weighted by parent sample size to compare across streams and years

F_0 Hatchery-origin: Returning adults reared in a hatchery that strayed into a stream to spawn. These fish mate in the wild with other hatchery strays and/or natural-origin fish.

F_0 Natural-origin: Entire lives spent in wild. These fish mate in the wild with hatchery strays and/or natural-origin fish on the spawning grounds.



F_1 Hatchery-ancestry: Entire lives spent in wild; at least one F_0 parent was a hatchery stray

F_1 Natural-ancestry: Entire lives spent in wild; at least one F_0 parent was a natural-origin fish, but no hatchery strays as parents.

RESULTS

Pedigree Reconstruction

- 235,542 samples collected
- Incomplete pedigrees due to unsampled offspring/parents/grandparents
  - Odd-lineage: average of 13% offspring assigned to parents (2.1–20.7%)
  - Even-lineage: average of 40% offspring assigned to parents (13.2–46.7%)
- Most potential parents assigned 0 offspring (93.6% odd, 80.3% even; Fig. 6)
- First generation: 113,259 total F_0 potential parents
  - 33,599 $F_0 \rightarrow F_1$ parent-offspring relationships
- Second generation: 15,213 total F_1 potential parents with known ancestry (Table 1)
  - 6,457 $F_1 \rightarrow F_2$ parent-offspring relationships

Table 1. Sample size of F_1 potential parents with known ancestry, successful F_1 parents (assigned at least 1 offspring), and number of F_2 offspring assigned. Dyads have only one known parent, triads have both parents.

		F_1 Parents		Successful F_1		F_2 Offspring Assigned			
Stream	Year	H	N	H	N	H	N	Dyad	Triad
Hogan	2015	6	114	0	8	0	11	11	0
	2016	2,456	418	213	40	792	146	810	64
	2017	84	408	5	28	11	76	71	8
Stockdale	2015	10	122	2	13	3	20	23	0
	2016	762	746	33	57	46	83	125	2
	2017	72	510	10	50	11	69	74	3
Gilmour	2016	638	401	76	63	168	145	257	28
	2017	27	176	2	15	2	21	17	3
Paddy	2016	370	245	119	95	301	277	466	56
	2018	189	1053	46	355	104	723	713	57
Erb	2016	430	2,270	127	804	297	2,093	1796	297
	2018	155	3,551	18	536	30	1,028	868	95

Fitness Analysis $F_0 \rightarrow F_1$

- First generation hatchery strays have lower fitness
  - Even-lineage mean RRS = **0.48**
  - Odd-lineage mean RRS = **0.28**
- First generation hatchery strays less likely to have any offspring assigned (Fig. 6), limiting sample size of F_1 parents with known ancestry
- Phenotypic differences (e.g., run timing) between F_0 hatchery strays and natural-origin fish[4] do not fully account for fitness reductions[3]

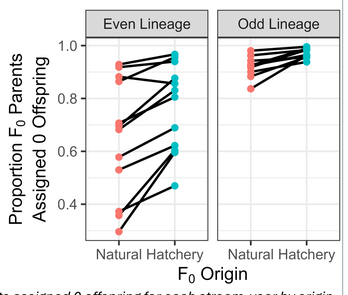


Figure 6. Difference in the proportion of F_0 parents assigned 0 offspring for each stream-year by origin

RESULTS (CONT.)

Fitness Analysis $F_1 \rightarrow F_2$

- Skewed distribution of RS ~ negative binomial (Fig. 7)
- Second generation offspring of hatchery strays have lower fitness relative to natural-origin fish (Fig. 8)
  - Even-lineage mean RRS = **0.73**
  - Odd-lineage mean RRS = **0.85**
- Second generation offspring of hatchery strays also less likely to have any offspring assigned
  - Even-lineage mean 82.5% (N) vs. 77.7% (H)
  - Odd-lineage mean 90.6% (N) vs. 91.4% (H)

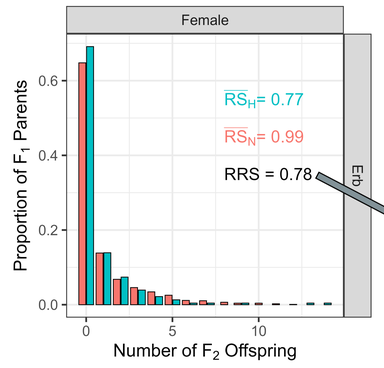


Figure 7. Example of negative binomial distribution of RS by F_1 ancestry for Erb Creek 2016 females.

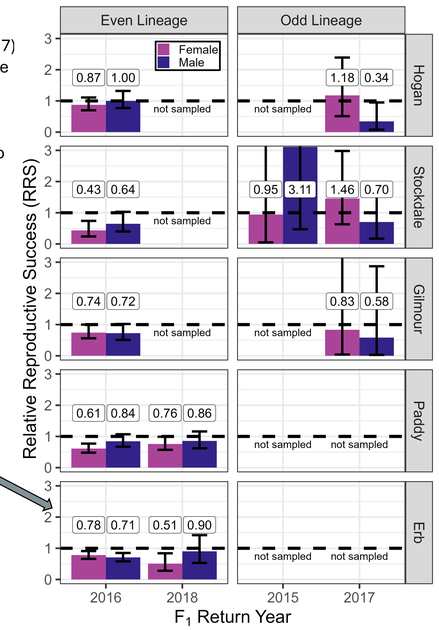


Figure 8. $F_1 \rightarrow F_2$ RRS estimates with 95% CIs by lineage, stream, year, and sex. RRS values less than 1 indicate that offspring of hatchery-origin strays were assigned fewer returning adult offspring than offspring of natural-origin pink salmon.

CONCLUSIONS

- **First generation hatchery strays have lower fitness than natural-origin Pink Salmon[3]**
- **Second generation offspring of hatchery strays have lower fitness (carry-over effect)**
- **Fitness reductions are less severe than in the first generation, especially odd-lineage**

FUTURE WORK

- Use generalized linear models to determine the relative importance of ancestry to other covariates (date, location, body length) in explaining variation in reproductive success
- Investigate phenotypic changes between hatchery strays and their offspring in response to stream-specific selection pressures (i.e., run timing due to stream temperature).

REFERENCES

1. Knudsen, E. E., Rand, P. R., Gorman, K. B., Bernard, D. R., & Templin, W. D. (2021). Hatchery-origin stray rates and total run characteristics for Pink Salmon and Chum Salmon returning to Prince William Sound, Alaska, in 2013–2015. Marine and Coastal Fisheries, 13(1), 41–68.
2. Brenner, R. E., Moffitt, S. D., & Grant, W. S. (2012). Straying of hatchery salmon in Prince William Sound, Alaska. Environmental Biology of Fishes, 94(1), 179–195.
3. Shedd, K. R., Lescak, E. A., Habicht C., Knudsen, E. E., Dann, T. H., Hoyt, H. A., Prince, D. J., & Templin, W. D. (2022). Reduced relative fitness in hatchery-origin Pink Salmon in two streams in Prince William Sound, Alaska. Evolutionary Applications, 15 (3), 429-446.
4. McMahon, J., May, S. A., Rand, P. S., Gorman, K. B., McPhee, M. V., & Westley, P. A. 2025. Phenotypic sorting of pink salmon hatchery strays may alleviate adverse impacts of reduced variation in fitness-associated traits. external link Ecology and Evolution 15(1):e70781.
5. Riester, M., Stadler, P. F., & Klemm, K. (2009). FRANz: Reconstruction of wild multi-generation pedigrees. Bioinformatics, 25(16), 2134–2139.
6. Kalinowski, S. T. & Taper, M. L. (2005). Likelihood-based confidence intervals of relative fitness for a common experimental design. Canadian Journal of Fisheries and Aquatic Sciences, 62(3), 693–699.

ACKNOWLEDGEMENTS & ADDITIONAL INFO

This study is part of the larger Alaska Hatchery Research Program (AHRP). The AHRP Science Panel developed research questions and experimental design. A complete roster of current and former Science Panel members can be found on the website. Funding for the AHRP has been provided by seven of Alaska's largest private nonprofit hatchery corporations (NSRAA, SSRAA, DIPAC, PWSAC, VFDA, KRAA, and CIAA), Seafood Processors Association, and the State of Alaska. Additional funding for genetic analyses came from the North Pacific Research Board (project number 1619) and the NOAA Saltonstall-Kennedy Grant Program (NA16NMF4270251). The statements, findings, conclusions, and recommendations are those of the author(s) and do not necessarily reflect the views of NOAA Fisheries. All field work was conducted by Prince William Sound Science Center. Electronic data collection software was designed by Rick Busch. Otoliths were read by the ADF&G Cordova Otolith Lab and Mark, Tag, and Age Lab. Genetic markers were developed by the Seeb Lab at the University of Washington. Genotyping was done at the ADF&G Gene Conservation Lab.