

August 2022 Report

EVALUATING SPRING CHINOOK SALMON RELEASES ABOVE DETROIT
DAM AND BELOW BIG CLIFF DAM, ON THE NORTH SANTIAM RIVER, USING
GENETIC PARENTAGE ANALYSIS

Prepared for:

U. S. ARMY CORPS OF ENGINEERS
PORTLAND DISTRICT - WILLAMETTE VALLEY
PROJECT
333 SW First Ave.
Portland, Oregon 97204

Prepared by:

Kathleen G. O'Malley, David I. Dayan, Sandra Bohn, Cristín K. Fitzpatrick, Greg A.
Grenbemer

Oregon State University
State Fisheries Genomics Lab,
Coastal Oregon Marine Experiment Station
Department of Fisheries, Wildlife and Conservation Sciences,
Hatfield Marine Science Center,
2030 SE Marine Science Drive
Newport, Oregon 97365

SUMMARY

For approximately two decades, hatchery-origin (HOR; adipose fin removed) spring Chinook salmon have been released (“outplanted”) above Detroit Dam on the North Santiam River. Previous research has used genetic parentage analysis to evaluate the population productivity of spring Chinook salmon (*Oncorhynchus tshawytscha*) outplanted above Detroit Dam. Here, we extended the genetic pedigree reported in O’Malley *et al.* (2015, 2017) by assigning the 2016 – 2020 adult returns to salmon previously outplanted above Detroit Dam (2011 – 2017). This updated pedigree was then used to estimate total lifetime fitness and a cohort replacement rate for salmon released above Detroit Dam in 2011 – 2015.

Of the 613 natural-origin (NOR) salmon successfully genotyped in 2015, 40% (250 / 613) were progeny of previously sampled salmon (2010 - 2012). Among the 250 assigned progeny, 83% (209 / 250) were identified as adult offspring of salmon previously outplanted above Detroit Dam (2010 - 2012), while the remaining 16% (41 / 250) assigned to salmon sampled as carcasses below Big Cliff Dam (2011 - 2012).

Replacement of salmon outplanted in 2010 was not met, as determined by a cohort replacement rate of 0.27 (males only) and 0.19 (females only). Overall, total lifetime fitness estimates for salmon outplanted above Detroit Dam in 2010 were low, averaging 0.47 (\pm 1.17 SD; range = 0 - 16) offspring. Preliminary fitness estimates for 2011 (based on age-3 and age-4 progeny only) and 2012 (based on age-3 progeny only) hatchery-origin (HOR) salmon outplants averaged 0.40 (\pm 1.0 SD; range = 0 - 5) and 0.058 (\pm 0.25 SD; range = 0 - 2) offspring, respectively. Preliminary fitness estimates for NOR carcasses sampled below Big Cliff Dam in 2011 and 2012 were slightly lower compared to HOR salmon outplants, averaging 0.21 (\pm 0.53 SD; range = 0 - 3; based on age-3 and age-4 progeny only) and 0.035 (\pm 0.24 SD; range = 0 - 2; based on age-3 progeny only) offspring, respectively.

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INTRODUCTION

Upper Willamette River (UWR) spring Chinook salmon (*Oncorhynchus tshawytscha*) are currently listed as threatened under the U.S. Endangered Species Act (NMFS 2008). To facilitate dispersal to historical habitats and increase the abundance and distribution of naturally produced fish, adult spring Chinook salmon are released above USACE dams throughout the UWR basin. The North Santiam River is a major tributary of the UWR and supports both hatchery-origin (HOR; adipose fin removed) and natural-origin (NOR; adipose fin intact) spring Chinook salmon.

Spring Chinook salmon migration is impeded by two large dams on the North Santiam River, Detroit and Big Cliff (Figure 1). Dam operations began in the early 1950s, as did operation of the original Minto Fish Collection Facility, which was used to collect broodstock for Marion Forks Fish Hatchery, located upstream of the dams (Figure 1). For almost two decades, primarily HOR spring Chinook salmon have been released above the Detroit-Big Cliff Dam complex on the North Santiam River with the goal of reestablishing natural spawning activity in historical habitats. Additionally, NOR spring Chinook salmon that enter the Minto Fish Collection Facility are released into the river below Big Cliff Dam, or, rarely, above Detroit Dam. Throughout this report, we distinguish releases of HOR individuals from releases of NOR individuals by referring to them as outplanted or reintroduced salmon, respectively.

To evaluate the contribution of the outplanting program to adult salmon recruitment in the North Santiam River, tissue samples for genetic parentage analysis have been collected from spring Chinook salmon prior to release above Detroit Dam since 2007, from NOR carcass samples below Big Cliff Dam since 2011, and from NOR salmon collected at the new Minto Fish Collection Facility since 2013. It is important to note that in some of the earlier years there was incomplete sampling of putative parents, which downwardly biased assignment rates of the progeny. Similarly, incomplete sampling of progeny downwardly biased fitness estimates for the putative parents. Except for a small number of unmarked NOR fish reintroduced above Detroit Dam in 2010 (N = 50), only HOR salmon were outplanted from 2007 – 2014.

Despite the sampling limitations, O'Malley *et al.* (2015) determined that most NOR salmon sampled in the North Santiam in 2013 (59%) and 2014 (66%) were progeny of salmon outplanted

above Detroit Dam. These are minimum estimates of outplant program contributions to NOR recruitment due to incomplete sampling of parents in 2008 – 2011. For the 2007 and 2008 cohorts outplanted above Detroit Dam, 15% of salmon outplants produced progeny that were detected using pedigree reconstruction. These are also minimum estimates due to limited sampling of NOR adult recruits (i.e. putative progeny) in 2011 – 2012 when the Minto Fish Collection Facility was not operational. By comparison, 29% (218/759) of salmon outplants in 2009 produced at least one adult offspring despite limited sampling of potential age-3 progeny in 2012. Among females, the limiting sex in 2009, 64% (84/131) produced progeny whereas only 21% (134/628) of males produced adult progeny. Female total lifetime fitness (based on age-3, age-4, and age-5 progeny) was on average $\sim 5\times$ (2.72:0.52 progeny) that of males and fitness was highly variable among individuals (range: 0-20 progeny). Cohort replacement rate (CRR), or “the number of future spawners produced by a spawner” (Botsford and Brittnacher 1998), was calculated for salmon outplanted above Detroit Dam in 2009. CRR, an index of the demographic viability, was based on age-4 and age-5 NOR returns to the new Minto Fish Collection Facility in 2013 and 2014, respectively. In addition, parentage assignments to 2012 carcass samples provided an estimate of age-3 progeny returns, although, a likely downwardly biased one. In total, 357 adult progeny assigned to the 131 outplanted females in 2009. Of these progeny, 140 were females, resulting in a female CRR of 1.07 (140/131). Three hundred twenty-eight adult progeny assigned to the 628 outplanted males in 2009. Of these, 194 were males, resulting in a male CRR of 0.31 (194/628).

In a subsequent study, O’Malley *et al.* (2017) determined that 40% of the NOR spring Chinook salmon sampled in the North Santiam in 2015 were progeny of previously sampled parents. Among the 250 assigned progeny, 84% (209/250) were identified as adult offspring of salmon previously outplanted above Detroit Dam in 2010 – 2012, while the remaining 16% (41/250) assigned to salmon sampled as carcasses below Big Cliff Dam in 2011 – 2012. For the 2010 cohort, 75% (1587/2109) of outplanted salmon produced no adult progeny that were detected in subsequent years. Total lifetime fitness (based on age-3, age-4, and age-5 progeny) for salmon outplanted above Detroit Dam averaged 0.47 offspring with no significant difference between males (mean fitness = 0.44 ± 1.22 SD; range = 0 – 16 progeny) and females (mean fitness = 0.50

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Commented [DD3R2]: There’s at least 4 separate problems here. First, there’s a simple typo on my part. 328, not 358 offspring assign to male parents.

Second, even if the value was 358 for both male and female, 141 and 194 would not need to add up to 358, because these values reflect the number of female offspring assigned to female parents, and male offspring assigned to male parents respectively. They don’t need to sum up to any shared value because they don’t include male offspring of female parents or female offspring of male parents.

Third, I think there’s an error in the original report. Previously, I only recalculated the male CRR and took the other values included in this draft at face value. Using Evan’s spreadsheets to check all the number this time, I think they included the header column when counting. All values are 1 more than in any version of Evans’ CRR spreadsheets. I revised 358 adult progeny assigned to females to 357, and “141 were females” to “140 were females”.

Finally, I found an additional spreadsheet in Evans’ files that caught an error. Some parents that were not outplanted above Detroit, but actually from Shelburn were included. What’s confusing here is that Evans clearly caught this mistake, but the Shelburn-corrected spreadsheet is not used to calculate the final values in the 2015 report. I used the uncorrected file, since that was the decision made in 2015, and I assume there was a rationale.

I’ve attached the spreadsheets if anyone would like to try to proof these values themselves. They are a good example of the reproducibility challenges associated with these projects. Note that in one spreadsheet, there are two columns of assigned offspring (I can’t figure out why). The second column (E) is the one to use (confirmed using raw colony and cervus outputs from 2015 report), and the first (A) should be ignored.

± 1.10 SD; range = 0 – 10 progeny). For the 2010 cohort, the female CRR was 0.19 and the male CCR was 0.27.

Programs on other rivers within the UWR basin currently release marked HOR spring Chinook salmon, unmarked presumed NOR spring Chinook salmon, or some combination of HOR and NOR above dams. As stated above, primarily HOR salmon were outplanted above Detroit Dam from 2007-2014. However, in 2015, a large number of NOR salmon were reintroduced above Detroit Dam (N = 498). It is important to note that these NOR adults were placed above Detroit Dam as a special measure to spread the risk of potentially high prespawn mortality that was expected to occur in that extremely low-water year. The adult offspring of these reintroduced NOR salmon returned in 2018, 2019, and 2020 and are evaluated in this current study. Since 2015, primarily HOR salmon were once again outplanted above Detroit Dam. Our study evaluates the productivity of all salmon released above Detroit Dam, within the context of current passage conditions, to inform management decisions regarding the future use of NOR spring Chinook salmon in outplanting operations.

This work will meet the specific information needs of Reasonable and Prudent Alternative (RPA) 9.5.1(4) of the Willamette Project Biological Opinion (NMFS 2008) in determining the reproductive success of hatchery fish in the wild. Results of the research will also address RPA 4.1 (restoration of productivity by outplanting Chinook salmon above dams), RPA 6.2.3 (continue adult Chinook salmon outplanting, Willamette basin-wide), and RPA 9.3 (monitoring the effectiveness of fish passage facilities and strategies at Willamette Project dams). This research did not address RPA 4.7 (increase the percent of outplanted adults that successfully spawn through development of new release locations) because the outplanting strategy did not permit evaluation of release location as a predictor of total lifetime fitness in outplanted or reintroduced salmon.

OBJECTIVES

1. Determine the number and proportion of unmarked, presumed NOR adult Chinook salmon sampled at the Minto Fish Collection Facility in 2016, 2017, 2018, 2019 and 2020 that assign as progeny of spring Chinook salmon outplanted above Detroit Dam in 2011,

2012, 2013, 2014, 2015, 2016 and 2017. Note, 2015 was the first year a large number of presumed NOR salmon were reintroduced above Detroit Dam ($N = 498$). The adult offspring of these reintroduced NOR salmon returned in 2018, 2019, and 2020.

2. Determine the number and proportion of unmarked, presumed NOR adult Chinook salmon sampled on the North Santiam River spawning grounds as carcasses in 2016, 2017, 2018, and 2019 that assign as progeny of spring Chinook salmon outplanted above Detroit Dam in 2011, 2012, 2013, 2014, 2015, and 2016.
3. Estimate the total lifetime fitness of spring Chinook salmon outplanted or reintroduced above Detroit Dam in 2011, 2012, 2013, 2014 and 2015. This estimate will be based on parentage analysis of unmarked adult spring Chinook salmon sampled at the Minto Fish Collection Facility in 2014, 2015, 2016, 2017, 2018, 2019, and 2020, as well as unmarked salmon encountered on the spawning grounds below Big Cliff Dam in 2014, 2015, 2016, 2017, 2018 and 2019.
4. Estimate the effects of sex, release date, release location, sex ratio and number of released individuals on the total lifetime fitness of adult spring Chinook salmon outplanted or reintroduced above Detroit Dam in 2011, 2012, 2013, 2014 and 2015. Note, there were three release dates and one release location in 2011, ten release dates and two release locations in 2012, 19 release dates and three release locations in 2013, and 16 release dates and one unknown and four known release locations in 2014 and 14 release dates and two release locations in 2015.
5. Estimate Cohort Replacement Rate (CRR) for spring Chinook salmon outplanted or reintroduced above Detroit Dam in 2011, 2012, 2013, 2014 and 2015.
6. Estimate the effective number of breeders (N_b) for the adult salmon population outplanted or reintroduced above Detroit Dam in 2011, 2012, 2013, 2014 and 2015.

7. Determine the number and proportion of unmarked, presumed NOR adult Chinook salmon sampled at the Minto Fish Collection Facility in 2016, 2017, 2018, 2019 and 2020 that assign as progeny of unmarked, presumed NOR adult Chinook salmon released into the North Santiam River below Big Cliff Dam in 2013, 2014, 2015, 2016 and 2017.
8. Determine the number and proportion of unmarked, presumed NOR adult Chinook salmon sampled as carcasses on the spawning grounds below Big Cliff Dam in 2016, 2017, 2018, and 2019 that assign as progeny of spring Chinook salmon reintroduced or sampled as carcasses below Big Cliff Dam in 2011, 2012, 2013, 2014, 2015, and 2016.
9. Estimate the total lifetime fitness of spring Chinook salmon reintroduced below Big Cliff Dam in 2013, 2014 and 2015 or sampled as carcasses below Big Cliff Dam in 2011, 2012, 2013, and 2014. This estimate will be based on parentage analysis of unmarked, presumed NOR adult spring Chinook salmon sampled at the Minto Fish Collection Facility in 2016, 2017, 2018, 2019, and 2020, as well as unmarked salmon encountered on the spawning grounds as carcasses below Big Cliff Dam in 2016, 2017, 2018 and 2019.
10. Estimate Cohort Replacement Rate (CRR) for spring Chinook salmon reintroduced below Big Cliff Dam in 2013, 2014 and 2015.
11. Estimate the effective number of breeders (N_b) for the adult salmon population salmon reintroduced below Big Cliff Dam in 2013, 2014 and 2015.
12. Estimate and report the annual abundance and age structure of adult Chinook salmon that returned to the North Santiam River in 2016, 2017, 2018, 2019 and 2020 that can be confidently assigned to parents through genetic parentage analysis.

METHODS

Outplanting operations above Detroit Dam

While outplanting of HOR salmon above Detroit Dam was initiated in the 1990s, tissue sampling of salmon did not begin until 2007 (O'Malley *et al.* 2015; Table 1). Multiple release locations have been used above Detroit Dam since outplanting operations began, but from 2011 - 2015, release locations included Detroit Reservoir (Mongold), Breitenbush River (Kane's Marina, Cleator Bend), and along the mainstem North Santiam River (Hoover Campground, Dry Creek, Coopers Ridge, Horn Creek, Log Deck; Figure 1; Table 3). During construction of the new Minto Fish Collection Facility in 2011 – 2012, adult salmon were collected in a temporary trap at Upper Bennett Dam and outplanted above Detroit Dam. These outplants were hauled a longer distance to release locations and thus were likely exposed to greater handling and transport stresses than those from the new Minto Fish Collection Facility which began operation in 2013.

NOR recruitment and carcass surveys for adult offspring and parents

Beginning in 2011, tissue samples were collected from NOR salmon carcasses during spawning ground surveys occurring below Big Cliff Dam (Figure 1). To examine the contribution of salmon outplanting operations to below dam recruitment and to increase the accuracy of total lifetime fitness estimates of salmon outplanted in 2011 – 2015, tissue samples were collected from NOR spring Chinook salmon sampled live at the Minto Fish Collection Facility prior to reintroduction below Big Cliff Dam in 2013 – 2020 or from NOR carcasses during spawning ground surveys below Big Cliff Dam in 2011 – 2019. Spawning ground surveys were conducted on the North Santiam River from below Big Cliff Dam (44.7513°, -122.2838°) to the confluence of the North and South Santiam rivers (44.6863°, 123.0066°). In 2015, NOR carcasses were also sampled during spawning ground surveys on the North Santiam River above Detroit Dam from Blowout Bridge (44.7080°, -122.1100°) to Parish Lake Road (44.5244°, -121.9968°) and at the Minto Creek weir (44.6116°, -121.9459°). Collectively, NOR spring Chinook salmon sampled live or as carcasses from 2014 – 2020 were included as potential progeny of previously outplanted or reintroduced salmon (see Figure 2 for assignment details). Note, any carcass samples collected in 2020 were not included in the genetic parentage analysis.

In addition, tissue samples collected from NOR salmon carcasses below Big Cliff Dam from 2011 – 2015 and above Detroit Dam in 2015 were included as potential parents of progeny

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The survey area described here covers >20 river miles and only sampled a single fish, which was caught in the first section. Was a SGS really completed for the entire river from the reservoir to well above the hatchery and only found a single fish? I don't have these intake forms.

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sampled at the Minto Fish Collection Facility in 2014 – 2020 or during spawning ground surveys in 2014 – 2019 (see Figure 2 for assignment details). As noted above, carcass samples collected in 2020 were not included in the genetic parentage analysis.

Lastly, tissue samples collected from NOR salmon at the Minto Fish Collection Facility in 2013, 2014 and 2015 were included as potential parents of progeny sampled at the Minto Fish Collection Facility or during spawning ground surveys in 2016, 2017, 2018, 2019 and 2020 (see Figure 2 for assignment details). As noted above, carcass samples collected in 2020 were not included in the genetic parentage analysis.

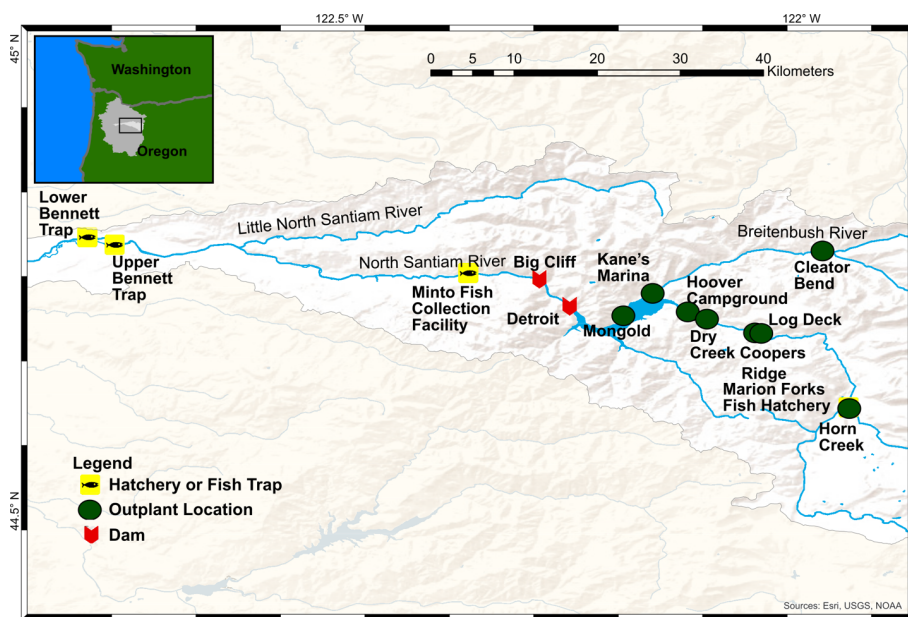


Figure 1. A map of the North Santiam River in Oregon. Shown are the locations of the Minto Fish Collection Facility, Big Cliff Dam, Detroit Dam, the eight release locations used in spring Chinook salmon outplanting operations and the Marion Forks Fish Hatchery.

Genotyping

In addition to genotype data used in previously published reports (O'Malley *et al.* 2015, O'Malley *et al.* 2017), NOR spring Chinook salmon sampled from 2016 – 2020 and HOR spring Chinook salmon sampled from 2013 – 2017 were genotyped at a panel of microsatellite loci. Whole genomic DNA was isolated from tissue samples using the protocol of Ivanova *et al.* (2006). Each DNA sample was then genotyped at 12 microsatellite loci: *Ots201*, *Ots211*, *Ots212*, *Ots215*, *OtsG249*, *OtsG311*, *OtsG409*, *OtsG474*, *Ots515*, *Ssa408*, *Ogo4*, and *Ogo2* (Olsen *et al.* 1998, Cairney *et al.* 2000, Naish and Park 2002, Williamson *et al.* 2002, Greig *et al.* 2003) and at the sex-linked marker, *Oty3*, to determine sex (Brunelli *et al.* 2008). Loci were amplified using polymerase chain reaction (PCR), PCR products were visualized on an ABI 3730xl DNA analyzer, and allele sizes scored using GENEMAPPER software (Version 5.0, Applied Biosystems, Inc., Foster City, CA).

Individuals with genotypes at < 7 loci were excluded, a threshold determined based on the sequential cumulative non-exclusion probabilities observed among loci (O'Malley *et al.* 2015). Multilocus genotypes were then compared among individuals to identify salmon that could have been sampled more than once (i.e. duplicate genotypes) using GENALEX (Version 6.5; Peakall and Smouse 2006). If individuals failed to genotype at the sex-linked marker *Oty3*, phenotypic information was used to infer sex. If no phenotypic sex information was available for individuals that failed to genotype at the sex-linked marker, the individual was excluded from the analysis.

Table 1. Summary of NOR spring Chinook salmon sampled live at the Minto Fish Collection Facility prior to reintroduction in 2013 – 2020 or as carcasses during spawning ground surveys below Big Cliff Dam in 2011 – 2019 or above Detroit Dam in 2015. Individuals were removed from the analysis if they were genotyped at < 7 loci or there was no sex information (missingness filtered), or if they represented a duplicate multi-locus genotype (duplicate filtered).

Year	Tissue samples	Missingness Filtered	Duplicate Filtered	Final Females	Final Males
<i>Tissue Source</i>					
2011					
<i>Carcass*</i>	330	126	8	104	92
2012					
<i>Carcass*</i>	130	46	0	45	39

2013					
<i>Live*</i>	560	1	5	165	389
<i>Carcass*</i>	58	4	15	20	19
2014					
<i>Live*</i>	770	1	15	294	460
<i>Carcass*</i>	94	29	19	23	23
2015					
Above Detroit					
<i>Live*</i>	498	62	5	144	287
<i>Carcass*</i>	41	6	20	6	9
Below Big Cliff					
<i>Live*</i>	170	15	7	70	78
<i>Carcass*</i>	47	18	10	7	12
2016					
<i>Live</i>	531	1	10	220	300
<i>Carcass</i>	48	18	11	10	9
2017					
<i>Live</i>	513	1	7	201	304
<i>Carcass</i>	31	7	10	8	6
2018					
<i>Live</i>	257	0	9	82	166
<i>Carcass</i>	9	4	2	2	1
2019					
<i>Live</i>	832	6	13	304	509
<i>Carcass</i>	73	30	37	5	1
2020**					
<i>Live</i>	1622	1	28	630	963

* Indicates groups previously genotyped in prior reports (O'Malley *et al.* 2015, O'Malley *et al.* 2017)

** In 2020, 46 additional NOR spring Chinook salmon including 23 females, 22 males and one jack, were collected at the Minto Fish Collection Facility and integrated into the spring Chinook broodstock. These 46 fish were not sampled for genetic analysis and were not included as potential offspring in the parentage analysis.

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Table 2. Summary of HOR spring Chinook salmon sampled prior to outplanting above Detroit Dam in 2011 – 2017. Individuals were removed from the analysis if they were genotyped at < 7 loci or there was no sex information (missingness filtered), or if they represented a duplicate multi-locus genotype (duplicate filtered).

Year	Tissue samples	Missingness Filtered	Duplicate Filtered	Final Females	Final Males
2011*	151	1	1	72	77
2012*	258	0	0	146	112
2013	1149	16	9	478	647
2014	869	7	24	292	569
2015	1062	11	9	519	523
2016	1378	2	66	858	452
2017	1674	1	69	913	691

* Indicates groups previously genotyped in prior reports (O'Malley *et al.* 2015, O'Malley *et al.* 2017)

Genetic parentage analysis

To estimate the number of NOR adult returns that were progeny of previously sampled salmon (live or carcass), the microsatellite genotypes of putative progeny were compared to the genotypes of adults, as indicated in Figure 2. The comparisons were first conducted within the maximum-likelihood framework of the parentage assignment program CERVUS (Version 3.07; Kalinowski *et al.* 2007). Parent(s) - offspring assignments were made using a strict 95% confidence criterion, a minimum of seven loci and a maximum of one mismatch between parent - offspring pairs (maximum of two mismatches for parent - offspring trios). Parentage assignments from CERVUS were then verified using the combined PLS - FL algorithm implemented in COLONY (Version 2.0.6.8; Jones and Wang 2010). The second analysis was conducted as CERVUS's likelihood-based parentage assignment method requires an accurate estimate of the number of parents contributing to a cohort (Harrison *et al.* 2013). Moreover, simulation studies have suggested that COLONY's assignment protocol is the most accurate of three alternate pedigree reconstruction methods (Harrison *et al.* 2013). COLONY was run using the following parameters: medium run length, polygamous male and female setting, allele dropout, and an error rate of 1% per locus.

Given the longitudinal nature of the genetic parentage analysis of North Santiam spring Chinook salmon, we developed an automated, reproducible procedure for choosing the best consensus parentage from the outputs of CERVUS and COLONY that does not allow for technician bias. Other changes from previously reported parentage analysis methods include application of an updated version of COLONY and an approach to avoid memory limitations in CERVUS. When the dataset was too large, we first removed candidate parents that had greater than one mismatch with all putative progeny in the dataset, then ran CERVUS on this filtered dataset. Note that HOR outplants sampled in 2011 and 2012 and evaluated as potential parents in prior reports were reanalyzed in this report using the updated procedure. A computational notebook provided as a supplement to this report ([assignment_notebook.html](#)) can be used to assign parentage from genotypic data collected in future years.

Parentage assignments and inferred age at maturity

The assignment rate was calculated using parentage analysis to determine the proportion of adult returns that were identified as progeny of previously sampled parents. For each assigned progeny, the return year (i.e. 2016) was subtracted by each parent(s) outplant year (e.g. 2013) to infer the age at maturity of progeny (e.g. age-3) and determine overall age structure among the adult returns in 2016, 2017, 2018, 2019 and 2020.

Total lifetime fitness of salmon outplanted or reintroduced above Detroit Dam

The total lifetime fitness (TLF) of HOR salmon outplanted above Detroit Dam in 2011, 2012, 2013, 2014 and 2015 was estimated from the number of NOR adult progeny (live or carcass) identified in subsequent return years. For instance, the TLF of salmon from the 2011 outplant cohort was estimated from the number of age-3, age-4, and age-5 progeny identified among NOR salmon sampled in 2014, 2015 and 2016 (Figure 2). TLF was similarly estimated for NOR salmon reintroduced above Detroit Dam in 2015.

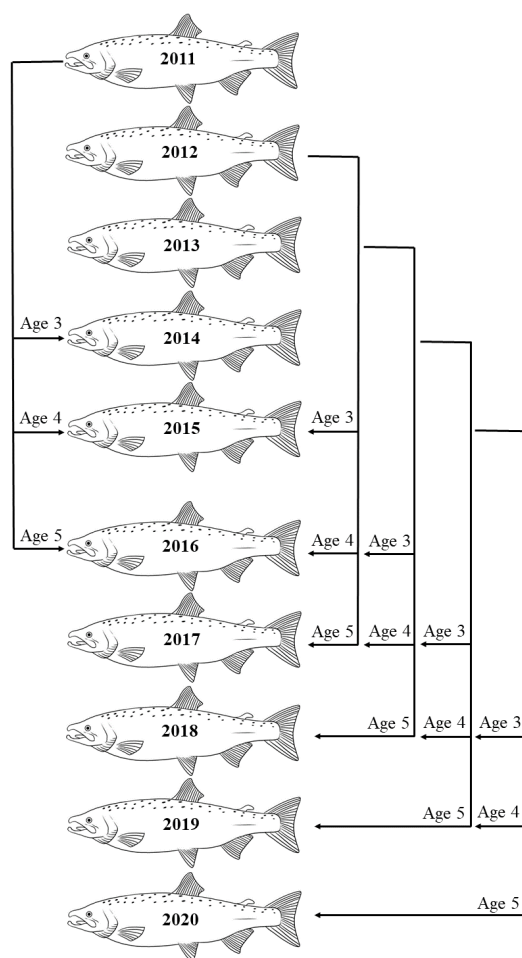


Figure 2. Framework used to reconstruct parent(s) - offspring relationships for spring Chinook salmon sampled in the North Santiam River, Oregon from 2011 – 2020. Throughout the report we present results focused on candidate parents sampled from 2011 – 2015. We also present results focused on potential NOR offspring sampled from 2016 – 2020. In both cases, results are based on assignments of potential age-3, age-4 and age 5 offspring to candidate parents.

Predictors of total lifetime fitness

We applied generalized linear models (GLMs) and generalized linear mixed models (GLMMs) to identify predictors of TLF of salmon outplanted or reintroduced above Detroit Dam from 2011 to 2015. We fit five individual GLMs to the data from each release year, and also fit a single GLMM using data across all release years. For the annual GLMs, we considered the influence of *sex*, *release day*, *release location*, *release group density*, *release group sex ratio*, and three interactions we believed may be biologically meaningful, *sex*release day*, *sex*release group density*, and *sex*release group sex ratio*. *Release day* is the Julian day that individuals were released and was modeled as a continuous fixed effect. A release group is defined as the individuals released at a single location during a single day. *Release group density* is the number of individuals in a release group. *Release group sex ratio* is the ratio of males to females in a release group. Sex ratios were log-transformed before inclusion as predictors in a model. For the GLMM across all years, we considered four additional predictors of TLF: *total number of fish released annually*, *annual sex ratio*, *year* (random effect), and *release group* (random effect).

Our modeling approach primarily followed the recommendations of Zuur *et al.* (2009) and Bolker (2015). For each year of the annual GLMs, we conducted an exploratory data analysis to identify the distribution and link function that provided the best fit to the data, calculated variance inflation factors of main effects to examine the data for multicollinearity and determined if non-linear effects of *release day* or *release group density* improved the fit to the data. After exploratory data analysis, we fit a full model using the negative binomial distribution and a log link function using the *glm.nb* function from the *MASS* package in *R*. We conducted model selection on the basis of both likelihood ratio tests for each predictor and backward stepwise selection using Wald tests for significant effects of each predictor. After a final model was selected, we conducted model validation using rootograms and QQ-plots of randomized quantile residuals from the *COUNTREG* package in *R*. We also examined models for goodness of fit, overdispersion and influence of outliers using residuals simulated by the *DHARMa* package in *R*. Effect plots of significant predictors retained in the final model were generated using the *effects* package in *R* and conditioned on the typical values of all other significant predictors in the final model.

For the GLMM using data across all years, we used a similar approach with the following changes to model fitting, selection and validation. All model fits were made using the *glmmTMB* function from the *glmmTMB* package in *R*. For model selection, we first identified the best random effects structure by fitting a fully saturated fixed effect model using restricted maximum likelihood and varying the random effects. Model selection of random effects was by AIC. After refitting the fully saturated fixed effects model with the final random effects structure using maximum likelihood, model selection of fixed effects was conducted using the same procedure as the annual GLMs. We validated the final model using only simulated residuals from the *DHARMA* package in *R*.

Cohort replacement rate

Cohort replacement rate (CRR), or “the number of future spawners produced by a spawner” (Botsford and Brittnacher 1998), was estimated for HOR salmon outplanted above Detroit Dam in 2011, 2012, 2013, 2014 and 2015, NOR salmon reintroduced above Detroit Dam in 2015, and NOR salmon reintroduced below Big Cliff Dam in 2013, 2014, and 2015. We report both a female-only CRR (CRR_F) and a male-only CRR (CRR_M). CRR metrics were calculated by totaling the number of assigned same-sex progeny and dividing it by the total number of outplanted females or males. For example, a female-only CRR = total number of age-3, age-4 and age-5 female progeny produced by outplanted females / the total number of outplanted females (see O’Malley *et al.* 2015; page 12).

Effective number of breeders

The effective number of breeders (N_b) among HOR salmon outplanted above Detroit Dam in 2011, 2012, 2013, 2014 and 2015, among NOR salmon released above Detroit Dam in 2015, and among NOR salmon reintroduced below Big Cliff Dam in 2013, 2014, and 2015 was estimated using the linkage disequilibrium (LD) method, as implemented in the program NEESTIMATOR (Version 2.1; Waples and Do 2008, Do *et al.* 2014). This method examines patterns of LD (nonrandom allelic associations, which are suggestive of common ancestry) among offspring of a cohort. N_b was calculated after filtering the input dataset to exclude singletons and 95% confidence intervals were generated using a jackknife re-sampling method (Waples and Do

Commented [OMKG8]: David is going to revise using S+ (no singletons).

Commented [DD9R8]: updated

2008). In each year, we compare the effective number of breeders (N_b) to the number of candidate parents (N_{cand}). N_{cand} is defined as the number of released salmon that are potential parents of NOR offspring and are present in our genetic dataset after filtering. N_{cand} potentially differs from the total number of salmon released due to incomplete sampling or incomplete genotyping. We also compare N_{cand} to the number of candidate parents with assigned progeny.

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Commented [DD11R10]: Revised

Total lifetime fitness of salmon reintroduced below Big Cliff Dam

The total lifetime fitness (TLF) of salmon reintroduced below Big Cliff Dam in 2013, 2014 and 2015 was estimated from the number of NOR adult progeny (live or carcass) identified in subsequent return years. For instance, the TLF of salmon from the 2013 reintroduced cohort was estimated from the number of age-3, age-4, and age-5 progeny identified among NOR salmon sampled in 2016, 2017 and 2018 (Figure 2).

Total lifetime fitness of NOR carcass samples collected below Big Cliff Dam

The total lifetime fitness of salmon sampled as carcasses below Big Cliff Dam in 2013, 2014 and 2015 was estimated from the NOR adult progeny (live or carcass) identified in subsequent return years (Figure 2). Note, TLF estimates of salmon in 2015 were based on samples collected from live fish and carcasses in all years except 2020 when only samples from live fish were included in the genetic parentage analysis.

Table 3. Summary of release dates, release locations and number of HOR female and male spring Chinook salmon outplanted above Detroit Dam on the North Santiam River in 2011 – 2017 and included as candidate parents in our parentage analysis after filtering for missingness (genotyped at < 7 microsatellite loci or no sex information) and removing duplicates. Note that the number of candidate parents is potentially fewer than the number of fish outplanted.

Year	Release date	Release location	Candidate Females	Candidate Males	Total Candidate Parents
2011	Jul. 21	Reservoir (Mongold)	7	16	23
	Jul. 28	Reservoir (Mongold)	46	43	89
	Aug. 10	Reservoir (Mongold)	19	17	36
	Unknown			1	1
Total			72	77	149

Year	Release date	Release location	Candidate Females	Candidate Males	Total Candidate Parents
2012	Jun. 1	Mainstem (Hoover)	16	9	25
	Jun. 14	Breitenbush (Undefined)	26	20	46
	Jul. 8	Mainstem (Hoover)	11	11	22
	Jul. 10	Mainstem (Hoover)	31	27	58
	Jul. 12	Mainstem (Hoover)	10	4	14
	Jul. 18	Mainstem (Hoover)	5	2	7
	Jul. 27	Mainstem (Hoover)	14	16	30
	Aug. 1	Mainstem (Hoover)	14	8	22
	Aug. 3	Mainstem (Hoover)	7	4	11
	Aug. 6	Mainstem (Hoover)	12	11	23
Total			146	112	258
2013	Jun. 10	Mainstem (Hoover)	23	25	48
	Jun. 13	Breitenbush (Kane's Marina)	15	22	37
	Jun. 20	Breitenbush (Kane's Marina)	11	8	19
	Jun. 28	Mainstem (Hoover)	27	33	60
	Jul. 1	Breitenbush (Kane's Marina)	24	28	52
	Jul. 3	Mainstem (Hoover)	28	32	60
	Jul. 8	Mainstem (Hoover)	8	24	32
	Jul. 12	Breitenbush (Kane's Marina)	20	14	34
	Jul. 18	Mainstem (Hoover)	24	35	59
	Jul. 22	Mainstem (Hoover)	32	40	72
	Jul. 25	Breitenbush (Kane's Marina)	22	54	76
	Jul. 29	Mainstem (Hoover)	31	33	64
	Aug. 5	Breitenbush (Kane's Marina)	30	65	95
	Aug. 7	Mainstem (Hoover)	19	33	52
	Aug. 20	Mainstem (Hoover)	24	48	72
	Aug. 29	Mainstem (Hoover)	11	27	38
	Sep. 18	Reservoir (Mongold)	25	33	58
	Sep. 24	Reservoir (Mongold)	68	38	106
	Sep. 26	Reservoir (Mongold)	35	46	81
	Unknown	Unknown	1	9	10
Total			478	647	1125
2014	Jun. 19	Mainstem (Coopers Ridge)	33	39	72
	Jun. 27	Mainstem (Hoover)	12	22	34
	Jul. 7	Breitenbush (Kane's Marina)	27	35	62
	Jul. 11	Mainstem (Hoover)	18	36	54
	Jul. 14	Breitenbush (Kane's Marina)	25	40	65
	Jul. 16	Breitenbush (Undefined)	5	8	13
	Jul. 21	Mainstem (Hoover)	23	50	73
	Jul. 28	Mainstem (Hoover)	19	43	62

Year	Release date	Release location	Candidate Females	Candidate Males	Total Candidate Parents
	Aug. 4	Breitenbush (Kane's Marina)	27	58	85
	Aug. 11	Mainstem (Horn Creek)	21	42	63
	Aug. 14	Mainstem (Horn Creek)	5	12	17
	Aug. 25	Breitenbush (Undefined)	11	29	40
	Sep. 4	Breitenbush (Undefined)	5	53	58
	Sep. 11	Breitenbush (Undefined)	26	56	82
	Sep. 19	Breitenbush (Undefined)	28	29	57
	Sep. 24	Breitenbush (Undefined)	7	17	24
		Total	292	569	861
2015*	Jun. 16	Breitenbush (Undefined)	70	66	136
	Jun. 24	Breitenbush (Undefined)	56	81	137
	Jul. 9	Breitenbush (Undefined)	63	106	169
	Jul. 22	Breitenbush (Undefined)	41	17	58
	Aug. 3	Breitenbush (Undefined)	48	45	93
	Aug. 17	Breitenbush (Undefined)	31	2	33
	Aug. 18	Mainstem (Dry Creek)	1	12	13
	Aug. 26	Mainstem (Dry Creek)	14	4	18
	Aug. 31	Mainstem (Dry Creek)	30	11	41
	Sep. 2	Mainstem (Dry Creek)	19	17	36
	Sep. 7	Mainstem (Dry Creek)	9	19	28
	Sep. 11	Mainstem (Dry Creek)	21	11	32
	Sep. 15	Mainstem (Dry Creek)	75	133	208
	Sep. 29	Mainstem (Dry Creek)	42	0	42
		Total	520	524	1044
2016	Unknown	Dry Creek or Breitenbush	830	423	1253
**	Unknown	Mainstem (Horn Creek)	28	29	57
		Total	858	452	1310
2017	Jun. 27	Log Deck	89	86	175
	Jul. 06	Breitenbush (Undefined)	59	108	167
	Jul. 10	Log Deck	66	89	155
	Jul. 13	Breitenbush (Undefined)	0	1	1
	Jul. 13	Mainstem (Horn Creek)	30	35	65
	Jul. 17	Log Deck	71	82	153
	Jul. 26	Log Deck	74	68	142
	Aug. 08	Breitenbush (Undefined)	26	50	76
	Aug. 14	Log Deck	25	32	57
	Aug. 22	Breitenbush (Undefined)	24	44	68
	Aug. 31	Log Deck	72	93	165
	Sep. 13	Log Deck	23	80	103
	Sep. 18	Breitenbush (Undefined)	132	145	277

Year	Release date	Release location	Candidate Females	Candidate Males	Total Candidate Parents
Total			691	913	1604

*498 natural-origin spring Chinook salmon were sampled and outplanted above Detroit Dam in 2015. This information is not included in the table. 431 individuals including 144 females and 237 males remained after genotype filtering for missingness and duplication. These individuals are candidate parents of the 2018, 2019, and 2020 adult returns.

**2016 release dates are unknown due to mislabeling of sample jars. There were 37 release dates across three locations: Mainstem (Dry Creek), Mainstem (Horn Creek), and Breitenbush.

RESULTS

Genotyping

After filtering for missing data and potential duplicates arising from multiple tissue samples drawn from the same individual, the complete genotypic dataset used for parentage analysis consisted of 12,357 individuals. Results of genotype filtering for NOR and HOR individuals is presented in tables 1 and 2 respectively.

Parentage assignments and inferred age at maturity

2016 - Results from genetic parentage analysis revealed that 35% (191 / 539) of the 2016 NOR adult offspring assigned to previously sampled salmon (Table 4). Among the 191 assigned progeny, 80% (153 / 191) assigned to salmon previously outplanted above Detroit Dam, with 11% (21 / 191) assigning to salmon sampled as carcasses below Big Cliff Dam and 9% (17 / 191) assigning to NOR salmon reintroduced below Big Cliff Dam in 2013, the first year the Minto Fish Collection Facility was operational (Table 4).

Out of the 191 assigned salmon, 48 were identified as age-5 (i.e. assigned to parents from 2011; 25%), 100 as age-4 (i.e. assigned to parents from 2012; 52%), and 43 as age-3 (i.e. assigned to parents from 2013; 23%; Table 3). The observed age structure is likely influenced by relatively few number of salmon outplanted above Detroit Dam in 2011 and 2012. We also note that samples from NOR salmon reintroduced below Big Cliff Dam were only available from 2013, which likely upwardly biased the proportion of progeny assigned as age-3.

2017 - Results from genetic parentage analysis revealed that 66% (343 / 519) of the 2017 NOR adult offspring assigned to previously sampled salmon (Table 4). Among the 343 assigned progeny, 75% (257 / 343) assigned to salmon previously outplanted above Detroit Dam, with 3% (9 / 343) assigning to salmon carcasses previously sampled below Big Cliff Dam, 22% (76 / 343) assigning to NOR salmon reintroduced below Big Cliff Dam in 2013 and 2014, and < 1% (1 / 343) assigning to a parent pair of a salmon reintroduced below Big Cliff dam and a carcass sample (Table 4).

Out of the 343 assigned salmon, 85 were identified as age-5 (i.e. assigned to parents from 2012; 25%), 234 as age-4 (i.e. assigned to parents from 2013; 68%), and 24 as age-3 (i.e. assigned to parents from 2014; 7%; Table 4).

2018 - Results from genetic parentage analysis revealed that 72% (180 / 251) of the 2018 NOR adult offspring assigned to previously sampled salmon (Table 4). Among the 180 assigned progeny, 61% (110 / 180) assigned to salmon previously outplanted above Detroit Dam (including 4 individuals that assigned to parent pairs of an outplanted (HOR) and a reintroduced (NOR) salmon in 2015), with 6% (10 / 180) assigning solely to salmon reintroduced (NOR) above Detroit Dam in 2015, 33% (59 / 180) assigning to NOR salmon reintroduced below Big Cliff Dam, and < 1% (1 / 180) assigning to salmon carcasses sampled below Big Cliff Dam (Table 3).

Out of the 251 assigned 2018 salmon, 58 were identified as age-5 (i.e. assigned to parents from 2013; 32%), 69 as age-4 (i.e. assigned to parents from 2014; 38%), and 53 as age-3 (i.e. assigned to parents from 2015; 29%; Table 4).

2019 - Results from genetic parentage analysis revealed that 81% (665 / 819) of the 2019 NOR adult offspring assigned to previously sampled salmon (Table 4). Among the 665 assigned progeny, 66% (436 / 665) assigned to salmon previously outplanted above Detroit Dam (including 119 that assigned to parent pairs of an outplanted (HOR) and a reintroduced (NOR) salmon in 2015, as well as one that assigned to a parent pair of an outplanted salmon (HOR) and

a carcass (NOR) recovered in 2015), with 22% (146 / 665) assigning solely to salmon reintroduced (NOR) above Detroit Dam in 2015, , < 1% (1 / 665) assigning to a parent pair of salmon reintroduced (NOR) above Detroit Dam and a carcass recovered above Detroit Dam in 2015, 12% (77 / 665) assigning to NOR salmon reintroduced below Big Cliff Dam, < 1% (1 / 665) assigning to a parent pair of salmon reintroduced (NOR) below Big Cliff Dam and a carcass recovered below Big Cliff Dam in 2015, and < 1% (4 / 665) assigning solely to salmon carcasses previously sampled below Big Cliff Dam (Table 4).

Out of the 665 assigned 2019 salmon, 46 were identified as age-5 (i.e. assigned to parents from 2014; 7%), 533 as age-4 (i.e. assigned to parents from 2015; 80%), and 86 as age-3 (i.e. assigned to parents from 2016; 13%; Table 4).

2020 – Results from genetic parentage analysis revealed that 91% (1449 / 1593) of the 2020 NOR adult offspring assigned to previously sampled salmon (Table 4). Among the 1449 assigned progeny, 87% (1261 / 1449) assigned to salmon previously outplanted above Detroit Dam (including 56 that assigned to parent pairs of an outplanted (HOR) and a reintroduced (NOR) salmon in 2015), with 4% (58 / 1449) assigning solely to salmon reintroduced (NOR) above Detroit Dam in 2015, < 1% (4 / 1449) assigning solely to salmon carcasses previously sampled below Big Cliff Dam, < 1% (2 / 1449) assigning to parent pairs of a salmon reintroduced (NOR) above Detroit Dam and a carcass recovered above Detroit Dam in 2015, and 9% (124 / 1449) assigning to NOR salmon reintroduced below Big Cliff Dam (Table 4).

Out of the 1449 assigned 2020 salmon, 216 were identified as age-5 (i.e. assigned to parents from 2015; 15%), 1211 as age-4 (i.e. assigned to parents from 2016; 84%), and 22 as age-3 (i.e. assigned to parents from 2017; 2%; Table 4).

Total lifetime fitness of salmon outplanted or reintroduced above Detroit Dam

2011 - As estimated from age-3, age-4, and age-5 progeny, the mean TLF for salmon outplanted above Detroit Dam during 2011 was 1.00 ± 2.11 SD offspring. Most salmon (99 / 149, or 66%) produced no adult offspring that were detected in subsequent years. It is possible the NOR adult

offspring were not sampled or strayed to another river. Mean fitness of males was 0.87 ± 2.12 SD, whereas the mean fitness of females was 1.14 ± 2.11 SD (Table 5).

2012 - As estimated from age-3, age-4, and age-5 progeny, the mean TLF for salmon outplanted above Detroit Dam during 2012 was 1.21 ± 2.24 SD offspring. Most salmon (156 / 258, or 60%) produced no adult offspring that were detected in subsequent years. It is possible the NOR adult offspring were not sampled or strayed to another river. Mean fitness of males was 1.31 ± 2.47 SD, whereas the mean fitness of females was 1.13 ± 2.05 SD (Table 5).

2013 - As estimated from age-3, age-4, and age-5 progeny, the mean TLF for salmon outplanted above Detroit Dam during 2013 was 0.39 ± 0.90 SD offspring. Most salmon (877 / 1125, or 78%) produced no adult offspring that were detected in subsequent years. It is possible the NOR adult offspring were not sampled or strayed to another river. Mean fitness of males was 0.34 ± 0.86 SD, whereas the mean fitness of females was 0.45 ± 0.95 SD (Table 5).

2014 - As estimated from age-3, age-4, and age-5 progeny, the mean TLF for salmon outplanted above Detroit Dam during 2014 was 0.17 ± 0.60 SD offspring. Most salmon (757 / 861, or 88%) produced no adult offspring that were detected in subsequent years. It is possible the NOR adult offspring were not sampled or strayed to another river. Mean fitness of males was 0.14 ± 0.49 SD, whereas the mean fitness of females was 0.24 ± 0.76 SD (Table 5).

2015 - As estimated from age-3, age-4, and age-5 progeny, the mean TLF for salmon outplanted above Detroit Dam during 2015 was 0.69 ± 1.41 SD offspring. Most salmon (734 / 1042, or 65%) produced no adult offspring that were detected in subsequent years. It is possible the NOR adult offspring were not sampled or strayed to another river. Mean fitness of males was 0.56 ± 1.24 SD, whereas the mean fitness of females was 0.82 ± 1.55 SD (Table 5).

As estimated from age-3, age-4, and age-5 progeny, the mean TLF for salmon reintroduced above Detroit Dam in 2015 was 1.21 ± 2.63 SD offspring. Most salmon (264 / 431, or 61%) produced no adult offspring that were detected in subsequent years. Mean fitness of males was

1.12 ± 2.72 SD, (*n* = 287), whereas the mean fitness of females was 1.39 ± 2.45 SD (*n* = 144) (Table 5).

The mean TLF of HOR salmon outplanted above Detroit Dam and NOR salmon reintroduced above Detroit Dam together in 2015 was 0.83 ± 1.87 SD offspring. Most salmon (998 / 1473, or 68%) produced no adult offspring that were detected in subsequent years. Mean fitness of males was 0.76 ± 1.92 SD, (*n* = 810), whereas the mean fitness of females was 0.95 ± 1.80 SD (*n* = 663) (Table 5).

Predictors of total lifetime fitness of salmon outplanted or reintroduced above Detroit Dam

2011 - *Release location* was not included in the model because all outplants were released at the same location, Reservoir (Mongold). There were only three release dates at this single location, and consequently only three unique values of *release group density* and *release group sex ratio* included in the model. We were unable to parse the potential effects of these three predictors due to multicollinearity when all were included in the model. Instead, we fit a simplified model with only *sex*, *release day*, *release group density* and the interaction *sex * release group density*. No predictors were retained after model selection by either likelihood ratio tests of individual predictors or backward selection using Wald tests (Table 6).

2012 - *Release location* was not included in the model because outplants were released at only two locations and of the two locations, one was utilized on only a single day, late in the season and at high density. Therefore, we are unable to parse the effect of *release location* from the effects of *release group density* or *release day*. After model selection, only a single predictor was included in the final model: *release group density* (Table 6). The effect of *release group density* was positive and is presented on the response scale (TLF) in supplemental figure 1a.

2013 - *Release location* was not included in the model because outplants were released at only three locations and there was strong collinearity between *release location* and *release day*. Salmon were released at one location only after releases at the other two locations were complete. Therefore, we are unable to parse the effect of *release location* from the effect of *release day*. After model selection, three predictors were included in the final model: *release*

Commented [OMKG12]: David will standardize the y-axis within years

Commented [DD13R12]: Done, but do we want to keep it this way? See comment in supplement.

group sex ratio, release group density and release day (Table 6). TLF decreased as sex ratio within release groups became more male-biased, but the range of sex ratios include more strongly male-biased than female biased ratios. There was a second order effect of the density of release groups with an optimal density around 50 individuals, and reduced TLF further from this optimal value. Finally, individuals released later in the season were estimated to have higher TLF. The effect of these predictors is presented on the response scale (TLF) in supplemental figures 1b, 1c and 1d, respectively.

2014 - Release location was not included in the model because of collinearity between release location and release day. Therefore, we are unable to parse the effect of release location from the effect of release day. After model selection, two predictors and their interaction were included in the final model: sex, release group density, and sex * release group density (Table 6). Males were estimated to have lower fitness overall and the overall effect of density was negative, but the difference in the effect of density between sexes was strong enough that females were estimated have higher TLF at the lower range of densities used in individual release groups (less than approximately 50 individuals), and males were predicted to have higher TLF at high densities (more than approximately 50 individuals). The effect of these predictors is presented on the response scale (TLF) in supplemental figures 1e.

2015 - Release location was not included in the model because of strongly unbalanced releases among the three locations used in 2015. Therefore, we did not evaluate the effect of release location. After model selection, four predictors and two interactions were included in the final model: release day, sex, release group density, release group sex ratio, sex * release group density and sex * release sex ratio (Table 6). Individuals released later in the season were estimated to have a higher TLF. Sex, release group density, and release group sex ratio did not have significant main effects but were included in the model because of significant interactions. Males were estimated to have an optimal TLF at a slightly male-biased sex ratio, while females were estimated to have a monotonically increasing TLF as sex ratios became more male-biased. Both males and females had increased TLF when released in smaller groups, but this effect was stronger in males than females. The effect of these predictors is presented on the response scale (TLF) in supplemental figures 1f, 1g and 1h.

Commented [OMKG14]: Is this phrase needed?

Commented [DD15R14]: I'm trying to emphasize that throughout the GLM and GLMM the problem appears to be strongly male-biased sex ratios (both annual and release group), but we rarely observe strongly female biased sex ratios, so we can't say much about them.

In other words, we should emphasize that the problem isn't male-biased sex ratios *per se*, but potentially unbalanced sex ratios generally. A precautionary response would be to try to balance sex ratios, but we don't know what the effect of female biased sex ratios might be.

Perhaps this gets relegated to the discussion.

Commented [OMKG16]: Positive?

Commented [DD17R16]: -0.018 on the log-link scale for the main effect of density. +0.036 for the interaction with sex [Male]. So density has a negative effect overall, but there is a sex specific effect of density such that it's effect is negative for females and positive for males (supplemental figure 1e makes this easier to understand)

Mixed Model (2011 – 2015) – *Release location* was not included in the model because of issues identified during exploratory data analysis within each year. We used a random effects structure that included random intercepts for both *year* and *release group*. After model selection of fixed effects, two predictors and their interaction were included in the final model: *sex*, *annual sex ratio*, and *sex*annual sex ratio* (Table 7). Males were estimated to have lower TLF than females and increasingly male-biased sex ratios reduced TLF in both sexes. Females were estimated to have higher fitness than males when the sex ratio was male biased, and males were estimated to have higher fitness than females when sex ratio was female biased. The effect of these predictors is presented on the response scale (TLF) in supplemental figure 2.

Cohort replacement rates of salmon outplanted or reintroduced above Detroit Dam

2011 - During 2014 - 2016, 94 **NOR** salmon returning to the North Santiam River (91 passed over Minto or released above Detroit, three sampled as a carcass below Big Cliff) were determined to be progeny some of the HOR salmon that were outplanted above Detroit in 2011 (N = 149). Both male and female replacement rates were less than 1, with a CRR_M of 0.49 and a CRR_F of 0.54.

Commented [OMKG18]: Could insert for all years below as a reminder?

2012 - During 2015 - 2017, 174 NOR salmon returning to the North Santiam River (172 passed over Minto or released above Detroit, two sampled as a carcass below Big Cliff) were determined to be progeny of some of the HOR salmon that were outplanted above Detroit in 2012 (N = 258). Both male and female replacement rates were less than 1, with a CRR_M of 0.77 and a CRR_F of 0.43.

2013 - During 2016 - 2018, 242 NOR salmon returning to the North Santiam River (239 passed over Minto, three sampled as a carcass below Big Cliff) were determined to be progeny of some of the HOR salmon that were outplanted above Detroit in 2013 (N = 1125). Both male and female replacement rates were less than 1, with a CRR_M of 0.20 and a CRR_F of 0.18.

2014 - During 2017 - 2019, 87 NOR salmon returning to the North Santiam River (86 passed over Minto, one sampled as a carcass below Big Cliff) were determined to be progeny of some of

the HOR salmon that were outplanted above Detroit in 2014 ($N = 861$). Both male and female replacement rates were less than 1, with a CRR_M of 0.07 and a CRR_F of 0.13.

2015 - During 2018 - 2020, 498 NOR salmon returning to the North Santiam River (496 passed over Minto, two sampled as a carcass below Big Cliff) were determined to be progeny of some of the HOR salmon that were outplanted above Detroit in 2015 ($N = 1042$). Both male and female replacement rates were less than 1, with a CRR_M of 0.33 and a CRR_F of 0.33.

During 2018 - 2020, 396 NOR salmon returning to the North Santiam River (all passed over Minto) were determined to be progeny of some of the NOR salmon that were reintroduced above Detroit Dam in 2015 ($N = 431$). Both male and female replacement rates were less than 1, with a CRR_M of 0.66 and a CRR_F of 0.55, signifying that replacement was not met for 2015.

During 2018 - 2020, 715 **NOR** salmon returning to the North Santiam River (all passed over Minto) were determined to be progeny of either the 431 genotyped NOR salmon that were reintroduced or the 1042 genotyped HOR salmon that were outplanted above Detroit Dam in 2015. Considering these two groups together, both male and female replacement rates were less than 1, with a CRR_M of 0.44 and a CRR_F of 0.38, signifying that replacement was not met for 2015.

Effective number of breeders of salmon outplanted or reintroduced above Detroit Dam

2011 - The effective number of breeders (N_b) for the 2011 outplant cohort was 57.1 (95% C.I. = 42.4 – 80.6). This estimated value is nearly the same as the number of outplants that produced one or more adult progeny (i.e. successful parents) in 2011 (50) based on the genetic parentage analysis. The ratio of N_b to the number of candidate parents (N_{cand}) was 0.38 (57.1/149).

2012 - The effective number of breeders (N_b) for the 2012 outplant cohort was 113.0 (95% C.I. = 91.1 – 143.5). This estimated value is similar to the number of outplants that produced one or more adult progeny (i.e. successful parents) in 2012 (102) based on the genetic parentage analysis. The ratio of N_b to N_{cand} was 0.44 (113.0/258).

Commented [DD19]: Previously this cutoff was seemingly arbitrary and around 10%. Changed to only highlight differences if N_b confidence interval did not include the number of parents that produced one or more offspring.

e.g. if 100 parents produced offspring in the pedigree, and the N_b estimate was 130 (95% CI: 80 – 140), then I wouldn't highlight the difference and refer to the values as similar.

2013 - The effective number of breeders (N_b) for the 2013 outplant cohort was 317.5 (95% C.I. = 251.7 – 418.7). This estimated value is higher than the number of outplants that produced one or more adult progeny in 2013 (248) based on the genetic parentage analysis. An N_b estimate greater than the number of successful parents in the pedigree may be due to disassortative mating, or due to unsampled parents or underassignment of offspring to parents (e.g. offspring assigns only to a single parent because the second parent was not sampled or incorrectly rejected as a parent during assignment). The ratio of N_b to N_{cand} was 0.28 (317.5/1125).

2014 - The effective number of breeders (N_b) for the 2014 outplant cohort was 145.4 (95% C.I. = 89.7 – 312.1). This estimated value is similar to the number of outplants that produced one or more adult progeny (i.e. successful parents) in 2014 (104) based on the genetic parentage analysis. The ratio of N_b to N_{cand} was 0.17 (109.8/861).

2015 - We estimated the effective number of breeders (N_b) for the combined cohort of outplanted HOR and reintroduced NOR spring Chinook salmon released above Detroit Dam, because the parentage analysis revealed that NOR and HOR individuals frequently spawned together. The effective number of breeders (N_b) for the total cohort above Detroit Dam in 2015 was 370.4 (95% C.I. = 321.6 – 430.2). This estimated value is less than the number of salmon above Detroit Dam that produced one or more adult progeny in 2015 (475) based on the genetic parentage analysis. An N_b estimate less than the number of successful parents in the estimated pedigree may be due to unbalanced sex ratios, fluctuations in N_b over time, assortative mating, or spurious assignments of offspring to parents. The ratio of N_b to N_{cand} was 0.25 (370.4/1473).

Total lifetime fitness of NOR salmon reintroduced below Big Cliff Dam

2013 - As estimated from age-3, age-4, and age-5 progeny, the mean TLF for reintroduced salmon sampled below Big Cliff Dam in 2013 was 0.25 ± 0.64 SD offspring. For reintroduced samples collected during 2013, male (mean = 0.19 ± 0.57 SD, $n = 389$) salmon showed lower fitness than female (mean = 0.39 ± 0.76 SD, $n = 165$) salmon, with 18% (97 / 554) of the reintroduced salmon sampled below Big Cliff producing one or more progeny.

2014 - As estimated from age-3, age-4, and age-5 progeny, the mean TLF for reintroduced salmon sampled below Big Cliff Dam in 2014 was 0.10 ± 0.34 SD offspring. For reintroduced samples collected during 2014, both male (mean = 0.08 ± 0.33 SD, $n = 460$) and female (mean = 0.12 ± 0.37 SD, $n = 294$) salmon showed similar fitness profiles, with 8% (60 / 754) of the reintroduced salmon sampled below Big Cliff producing one or more progeny.

2015 - As estimated from age-3, age-4, and age-5 progeny, the mean TLF for reintroduced salmon sampled below Big Cliff Dam in 2014 was 0.10 ± 0.34 SD offspring. For reintroduced samples collected during 2014, both male (mean = 0.76 ± 1.66 SD, $n = 78$) and female (mean = 0.93 ± 1.70 SD, $n = 70$) salmon showed similar fitness profiles, with 8% (49 / 148) of the reintroduced salmon sampled below Big Cliff producing one or more progeny.

Cohort replacement rates of NOR salmon reintroduced below Big Cliff

2013 - During 2016 - 2018, 91 NOR salmon returning to the North Santiam River (89 passed over Minto, two sampled as a carcass below Big Cliff) were determined to be progeny of the 554 genotyped salmon that were reintroduced below Big Cliff in 2013. Both male and female replacement rates were less than 1, with a CRR_M of 0.12 and a CRR_F of 0.13.

2014 - During 2017 - 2019, 50 NOR salmon returning to the North Santiam River (49 passed over Minto, one sampled as a carcass below Big Cliff) were determined to be progeny of the 754 genotyped salmon that were reintroduced below Big Cliff in 2014. Both male and female replacement rates were less than 1, with a CRR_M of 0.05 and a CRR_F of 0.04, signifying that replacement was not met for 2014.

2015 - During 2018 - 2020, 83 NOR salmon returning to the North Santiam River (82 passed over Minto, one sampled as a carcass below Big Cliff) were determined to be progeny of the 1042 genotyped salmon that were reintroduced below Big Cliff in 2015. Both male and female replacement rates were less than 1, with a CRR_M of 0.44 and a CRR_F of 0.41, signifying that replacement was not met for 2015.

Effective number of breeders of NOR salmon reintroduced below Big Cliff

2013 - The effective number of breeders (N_b) for the 2013 reintroduced cohort below Big Cliff was 162.0 (95% C.I. = 103.2 – 323.8). This estimated value is similar to the number of reintroduced salmon that produced one or more adult progeny (i.e. successful parents) in 2013 (97) based on the genetic parentage analysis. The ratio of N_b to the number of candidate parents in the reintroduced cohort (N_{cand}) was 0.29 (162/554).

Commented [DD20]: See note in N_b section above. Changed to “similar to” for any N_b estimate confidence interval that includes the number of parents that produced offspring in the pedigree.

2014 - The effective number of breeders (N_b) for the 2014 reintroduced cohort below Big Cliff was 230.6 (95% C.I. = 111.9 – 4527.3). This estimated value is higher than the number of reintroduced salmon that produced one or more adult progeny in 2014 (60). An N_b estimate greater than the number of successful parents in the pedigree may be due to disassortative mating, or due to unsampled parents or underassignment of offspring to parents (e.g. offspring assigns only to a single parent because the second parent was not sampled or incorrectly rejected as a parent during assignment). The ratio of N_b to N_{cand} was 0.31 (230.6/754).

2015 - The effective number of breeders (N_b) for the 2015 reintroduced cohort below Big Cliff was 80.1 (95% C.I. = 56.8 – 123.5). This estimated value is higher than the number of reintroduced salmon that produced one or more adult progeny in 2015 (49) based on the genetic parentage analysis. An N_b estimate greater than the number of successful parents in the pedigree may be due to disassortative mating, or due to unsampled parents or underassignment of offspring to parents (e.g. offspring assigns only to a single parent because the second parent was not sampled or incorrectly rejected as a parent during assignment). The ratio of N_b to N_{cand} was 0.54 (80.1/148).

Total lifetime fitness of NOR carcass samples

2011 - As estimated from age-3, age-4, and age-5 progeny, the mean TLF for carcasses sampled below Big Cliff Dam in 2011 was 0.26 ± 0.58 SD offspring. For carcass samples collected during 2011, both male (mean = 0.25 ± 0.58 SD) and female (mean = 0.27 ± 0.58 SD) salmon showed

similar fitness profiles, with 20% (40/196) of the salmon sampled below Big Cliff producing one or more progeny.

2012 - As estimated from age-3, age-4, and age-5 progeny, the mean TLF for carcasses sampled below Big Cliff Dam in 2012 was 0.30 ± 0.60 SD offspring. For carcass samples collected during 2012, both male (mean = 0.31 ± 0.57 SD) and female (mean = 0.29 ± 0.63 SD) salmon showed similar fitness profiles, with 23% (19/84) of the salmon sampled below Big Cliff producing one or more progeny.

2013 - As estimated from age-3, age-4, and age-5 progeny, the mean TLF for carcasses sampled below Big Cliff Dam in 2013 was 0.08 ± 0.27 SD offspring. For carcass samples collected during 2013, both male (mean = 0.05 ± 0.23 SD) and female (mean = 0.10 ± 0.31 SD) salmon showed similar fitness profiles, with 8% (3/39) of the carcasses sampled below Big Cliff producing one or more progeny.

2014 - As estimated from age-3, age-4, and age-5 progeny, the mean TLF for carcasses sampled below Big Cliff Dam in 2014 was 0.04 ± 0.21 SD offspring. For carcass samples collected during 2014, both male (mean = 0.04 ± 0.21 SD) and female (mean = 0.04 ± 0.21 SD) salmon showed similar fitness profiles, with 4% (2/46) of the carcasses sampled below Big Cliff producing one or more progeny.

2015 - As estimated from age-3, age-4, and age-5 progeny, the mean TLF for carcasses sampled below Big Cliff Dam in 2015 was 0.16 ± 0.37 SD offspring. For carcass samples collected during 2014, both male (mean = 0.18 ± 0.41 SD) and female (mean = 0.13 ± 0.35 SD) salmon showed similar fitness profiles, with 16% (3/19) of the carcasses sampled below Big Cliff producing one or more progeny.

Table 4. Summary of adult offspring assigned to Chinook salmon outplanted above Detroit Dam (Outplant), salmon reintroduced below Big Cliff Dam (Reintro.), salmon reintroduced above Detroit Dam (Reintro. Above), carcasses collected below Big Cliff Dam (Carcass), or carcasses collected above Detroit Dam (Carcass Above) on the North Santiam River in (a) 2016, (b) 2017, (c) 2018, (d) 2019 and (e) 2020. Indicated are the total number of putative offspring and parents considered in the pedigree analysis (*N*), summarized by sample type (Outplant Reintro. or Carcass), and the number assigned to a parental pair (P), or to a Female (F) or Male (M) parent only. Offspring assigned to parent pairs that included parents from different sample types (Outplant/Reintro., Outplant/Carcass, Reintro./Carcass) are indicated by M/F (male parent from first sample type and female parent from second sample type) or F/M (female parent from first sample type and male parent from second sample type).

(a) 2016

Offspring	Parents													Assigned (%)									
	Sample type <i>N</i>	2011			2012			2013															
		Outplant (<i>N</i> = 149)			Carcass (<i>N</i> = 197)			Outplant (<i>N</i> = 258)			Carcass (<i>N</i> = 84)				Outplant (<i>N</i> = 1125)			Reintro. (<i>N</i> = 554)			Carcass (<i>N</i> = 39)		
		P	F	M	P	F	M	P	F	M	P	F	M		P	F	M	P	F	M	P	F	M
Reintro.	520	32	7	4	1	3	0	69	14	3	0	6	6	5	7	11	3	8	5	0	0	1	185 (36%)
Carcass	19	0	0	0	0	1	0	0	0	0	0	1	1	0	0	1	0	0	1	0	1	0	6 (31%)
Total	539	32	7	4	1	4	0	69	14	3	0	7	7	5	7	12	3	8	6	0	1	1	191 (35%)

(b) 2017

Offspring	Parents																	Assigned (%)								
	Sample type <i>N</i>	2012						2013						2014												
		Outplant (<i>N</i> = 258)			Carcass (<i>N</i> = 84)			Outplant (<i>N</i> = 1125)			Reintro. (<i>N</i> = 554)			Carcass/ Reintro (<i>N</i> = 39/554)			Outplant (<i>N</i> = 861)			Reintro. (<i>N</i> = 754)			Carcass (<i>N</i> = 46)			
		P	F	M	P	F	M	P	F	M	P	F	M	M/F	F/M	P	F		M	P	F	M	P	F	M	
Reintro.	505	66	10	1	1	2	4	147	11	12	37	7	16	0	0	2	3	2	8	3	3	0	1	1	337 (67%)	
Carcass	14	0	0	1	0	0	0	1	0	1	0	0	1	0	1	0	0	0	0	0	1	0	0	0	6 (42%)	
Total	519	66	10	2	1	2	4	148	11	13	37	7	17	0	1	2	3	2	8	3	4	0	1	1	343 (66%)	

(c) 2018

Offspring	Parents													Assigned (%)
	Sample type	N	2013			2014			2015					
			Outplant	Reintro.	Carcass	Outplant	Reintro.	Carcass	Outplant	Reintro. Above	Outplant/ Reintro. Above	Reintro. Below	Carcass	
			(N = 1125)	(N = 554)	(N = 39)	(N = 861)	(N = 754)	(N = 46)	(N = 1042)	(N = 431)		(N = 148)	(N = 34)	
			P F M	P F M	P F M	P F M	P F M	P F M	P F M	P F M	M/F F/M	P F M	P F M	
			Reintro.	248	42 2 2	8 2 2	0 0 0	38 2 3	11 8 6	0 0 0	9 3 4	2 6 2	1 3	
Carcass	3	0 0 0	0 0 0	0 0 0	0 0 1	0 0 0	0 0 0	0 0 0	0 0 0	0 0	0 0 0	0 0 1	1 (33%)	
Total	251	42 2 2	8 2 2	0 0 0	38 2 4	11 8 6	0 0 0	9 3 4	2 6 2	1 3	14 3 5	0 0 0	179 (71%)	

(d) 2019

Offspring	Parents															Assigned (%)
	Sample type <i>N</i>	2014			2015								2016			
		Outplant	Reintro.	Carcass	Outplant	Reintro. Above	Outplant / Reintro. Above	Outplant/ Carcass Above	Reintro. Above / Carcass Above	Reintro. Below	Reintro Below / Carcass	Carcass	Outplant	Reintro.	Carcass	
		(<i>N</i> = 861)	(<i>N</i> = 754)	(<i>N</i> = 46)	(<i>N</i> = 1042)	(<i>N</i> = 431)				(<i>N</i> = 148)		(<i>N</i> = 34)	(<i>N</i> = 1310)	(<i>N</i> = 520)	(<i>N</i> = 19)	
		P F M	P F M	P F M	P F M	P F M	M/F F/M	M/F F/M	M/F F/M	P F M	M/F F/M	P F M	P F M	P F M	P F M	
		Reintro.	813	24 2 10	3 3 4	0 0 0	157 28 20	90 26 30	17 102	1 0	0 1	26 18 10	0 1	0 1 2	56 7 10	
Carcass	6	0 0 0	0 0 0	0 0 0	0 1 1	0 0 0	0 0	0 0	0 0	0 1 0	0 0	0 0 0	0 0 0	0 0 0	0 0 0	3 (50%)
Total	819	24 2 10	3 3 4	0 0 0	157 29 21	90 26 30	17 102	1 0	0 1	26 19 10	0 1	0 1 2	56 7 10	5 4 3	0 0 1	665 (81%)

(e) 2020

Offspring	Parents																
	Sample type	N	2015							2016			2017			Assigned (%)	
			Outplant	Reintro. Above	Outplant/ Reintro. Above	Outplant/ Carcass Above	Reintro. Above/ Carcass Above	Reintro. Below	Reintro Below / Carcass	Carcass	Outplant	Reintro.	Carcass	Outplant	Reintro.		Carcass
			(N = 1042)	(N = 431)				(N = 148)		(N = 34)	(N = 1310)	(N = 520)	(N = 19)	(N = 1604)	(N = 505)		(N = 14)
			P F M	P F M	M/F F/M	M/F F/M	M/F F/M	P F M	M/F F/M	P F M	P F M	P F M	P F M	P F M	P F M		P F M
Reintro.	1593	55 21 19	34 13 11	8 48	0 0	0 2	1 1 3	0 0	0 0 0	981 76 44	67 22 17	0 3 1	7 1 1	7 3 3	0 0 0	1449 (91%)	

Table 5. Total lifetime fitness estimates for spring Chinook salmon outplanted above Detroit Dam (2011 – 2015), collected as carcasses below Big Cliff Dam (2011 – 2015), or sampled live at the Minto Fish Collection Facility and reintroduced below Big Cliff Dam (2013 – 2015) on the North Santiam River. See Figure 2 for an overview of assignment approach. Indicated are the cohort year (and the age classes considered), sample type (Outplant, Carcass, or Reintro), Sex (M = Male; F = Female), number of outplanted, carcass samples or reintroduced salmon evaluated (*N*), and the mean, standard deviation (SD), and range (min - max) of fitness values observed for each year.

Cohort year	Sample type	Sex	<i>N</i>	Mean	SD	Range
2011 (age-3, age-4, age-5 progeny)						
	Outplant	M	77	0.87	2.12	0 - 15
		F	72	1.13	2.11	0 - 8
	Carcass	M	93	0.25	0.58	0 - 3
		F	104	0.27	0.58	0 - 3
2012 (age-3, age-4, age-5 progeny)						
	Outplant	M	112	1.31	2.47	0-17
		F	146	1.13	2.04	0-10
	Carcass	M	39	0.31	0.57	0-2
		F	45	0.29	0.63	0-2
2013 (age-3, age-4, age-5 progeny)						
	Reintro.	M	389	0.19	0.57	0-5
		F	165	0.39	0.76	0-5
	Outplant	M	647	0.34	0.86	0-7
		F	478	0.45	0.96	0-6
	Carcass	M	19	0.05	0.23	0-1
		F	20	0.10	0.31	0-1
2014 (age-3, age-4, age-5 progeny)						
	Reintro.	M	460	0.08	0.33	0-2
		F	294	0.12	0.37	0-2
	Outplant	M	569	0.14	0.49	0-5
		F	292	0.24	0.76	0-8
	Carcass	M	23	0.04	0.21	0-1
		F	23	0.04	0.21	0-1
2015 (age-3, age-4, age-5 progeny)						
	Reintro.	M	78	0.76	1.66	0-10
	Below	F	70	0.93	1.70	0-10

Reintro.	M	287	1.12	2.72	0-26
Above	F	144	1.39	2.45	0-19
Outplant	M	523	0.56	1.24	0-8
	F	519	0.82	1.55	0-10
Carcass	M	9	0.56	1.13	0-1
Above	F	6	0.17	0.41	0-1
Reintro.	M	810	0.76	1.92	0-26
Above and	F	663	0.95	1.80	0-19
Outplant					
Carcass	M	11	0.18	0.41	0-1
Below	F	8	0.12	0.35	0-1

Table 6. Results of generalized linear models examining the influence of *sex*, *release day*, *release location*, *release group density*, *release group sex ratio*, *sex*release day*, *sex*release group density*, and *sex*release group sex ratio* on the fitness of spring Chinook salmon from the North Santiam River reintroduced above Detroit Dam in each year from 2011 to 2015. Estimated effect (β) and standard error (s.e.) of each predictor on the link (log) scale for predictors that were retained in the final model are presented below. The null hypothesis that each predictor did not significantly improve the model fit was tested with a likelihood ratio test (LRT p-value). The null hypothesis that each predictor had an effect significantly different than zero was tested with the Wald test (Wald p-value). Estimated effects on the response scale (TLF) are presented in supplemental figure 1. Predictors indicated with [†] demonstrated collinearity with *release location*

Year	Predictor	β	s.e.	LRT p-value	Wald p-value
2011					
	(Intercept)	0.006	0.180		
2012					
	(Intercept)	-0.694	0.287		
	[†] <i>release group density</i>	0.024	0.007	0.002	0.001
2013					
	(Intercept)	-2.306	0.674		
	[†] <i>release day</i>	0.007	0.003	0.026	0.028
	<i>release group density</i>	-7.575	3.723		0.042
	(<i>release group density</i>) ²	-9.763	3.781	0.027	0.010

<i>Release group sex ratio</i>	-0.637	0.239	0.008	0.008
2014				
(Intercept)	-0.797	0.350		
<i>sex</i> [Male]	-1.842	0.484		<0.001
<i>release group density</i>	-0.018	0.009		0.043
<i>sex</i> [Male] * <i>release group density</i>	0.036	0.011	0.002	0.003
2015				
(Intercept)	-1.544	0.422		
<i>sex</i> [Male]	-0.008	0.235		0.973
<i>release day</i>	0.008	0.002	<0.001	<0.001
<i>release group density</i>	-0.002	0.002		0.310
<i>release group sex ratio</i>	5.276	3.086		0.087
<i>(release group sex ratio)²</i>	-0.678	3.234		0.834
<i>sex</i> [Male] * <i>release group density</i>	-0.004	0.002	0.045	0.047
<i>sex</i> [Male] * <i>release group sex ratio</i>	19.603	9.035		0.030
<i>sex</i> [Male] * <i>(release group sex ratio)²</i>	-21.362	7.273	0.009	0.003

Table 7: Results of generalized linear mixed model examining the influence of *sex*, *release day*, *release location*, *release group density*, *release group sex ratio*, *total number of fish released annually*, *annual sex ratio*, *sex*release group density*, *sex*release group sex ratio* and *sex*annual sex ratio* on the fitness of spring Chinook salmon from the North Santiam River reintroduced above Detroit Dam in each year from 2011 to 2015. *Year* and *release group* are included as random effects. Estimated effect (β) and standard error (s.e.) of each fixed predictor on the link (log) scale for predictors that were retained in the final model are presented below. The null hypothesis that each predictor did not significantly improve the model effect was tested with a likelihood ratio test (LRT p-value). The null hypothesis that each predictor has an effect significantly different than zero was evaluated with the Wald test (Wald p-value). Estimated variance (σ^2) and standard deviation (s.d.) are presented for random effects. Estimated effects on the response scale (TLF) are presented in supplemental figure 2.

Fixed Effects	β	s.e	LRT p-value	Wald p-value
(Intercept)	-0.1161	0.1781		
<i>Sex</i> [Male]	-0.0881	0.1141		0.440
<i>annual sex ratio</i>	-1.7541	0.4890		<0.001
<i>sex</i> [Male] * <i>annual sex ratio</i>	-0.6951	0.3490	0.040	0.046

Random Effects	σ^2	s.d.
<i>Year</i>	0.0734	0.2710
<i>Release Group</i>	0.0944	0.3074

DISCUSSION

Predictors of fitness **discussion** points

- Location
 - Identifying the effect of release location on fitness is a primary objective, but the release strategy employed by USACE precludes us from drawing any conclusions about release location, and to a lesser extent, release day, because releases locations are not spread across time. Our analyses can tolerate some heterogeneity in predictors or moderate collinearity among predictors, but the case with location is too extreme.
 - Collinearity between variables within years in the mixed model will still produce problems, even if the apparent collinearity disappears when data are pooled across years. However, none of the variables that are collinear with location are included in the final mixed model, so there is little reason to believe experimental design issues related to location produce type I error or unstable parameter estimates for the significant predictors retained in the final mixed model.
- Annual GLMs
 - Statistical power to detect significant relationships between predictors and TLF is limited in the GLMs, there are multiple predictors in each year, and we conduct many independent model selection / hypothesis testing procedures when we separate the data out into separate years. As a consequence, our results are subject to a multiple comparisons problem that we are not able to fully address and spurious associations between predictors and TLF are possible (a lot of effects are only marginally significant). Therefore the significance of predictors within each year should be approached with caution. Instead we should attempt to identify consistent patterns across years or rely on the mixed modeling results.

Some patterns within the annual GLMs are described below.

- Density: Release group density has a significant effect (Wald test $p < 0.05$) and/or improves the fit the data (LRT $p < 0.05$) in 4 of the 5 annual GLMs. While it can be challenging to detect because different release years employ different ranges of release group densities and the estimated effect over the within year levels of density varies across years, there is possibly some consensus in the effect of release group density on TLF. When averaged across both males and females, density appears to improve TLF up to an optimum value somewhere above 75, then it declines. However, females and males demonstrate different fitness

Commented [OMKG21]: I will circle back to this after we complete the methods and results.

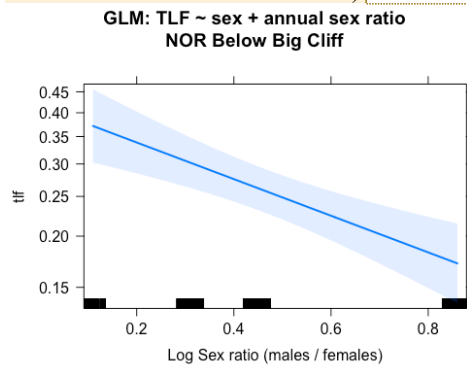
Commented [DD22R21]: Okay. Values in the highlighted section are not updated with the revised assignments and results.

Commented [DD23]: I summarized the most salient results from the modeling results here. I also have a more detailed, informal discussion of the results I can share if you'd like more context for these conclusions. We can also discuss the results.

Commented [DD24]: Kathleen, I included these for us to consider together, but my inclination given the audience/nature of the report is to rely on the mixed modeling results and not get into the weeds here, because of the issues I outlined above.

- relationships with density. The effect is not significant when data are combined across years in the mixed model.
- Release day: A later release day is associated with increased TLF in 3 of the 5 annual GLMs. However the consistent confounding of release day and location precludes us from drawing any strong conclusions here. Release day does not appear to have a consistent effect in the mixed model that combines data across all years
 - Release group sex ratio: Sex ratio at the level of release group is a significant predictor in 2 of 5 years. Similar to our findings on the effect of release group density, inconsistency among the parameter estimates in the different years may be driven by the different ranges of release group sex ratios employed from year to year. Taken together, the two years with significant predicted effects of release group density comport with biological expectations: extreme sex ratios of individual release groups ($> \sim 2$ / $< \sim 0.5$) are associated with reduced TLF. Release group sex ratio does not have a significant effect in the mixed model when data is combined across all years.
- GLMM (probably prioritize these results over annual GLMs)
 - Sex * Annual Sex Ratio Interaction
 - Many results point to an effect of sex ratios on TLF among salmon outplanted or reintroduced above Detroit Dam from 2011 to 2015. Overall cohort replacement rates are often well below the sex specific CRRs, and this is strongest in years where the sex ratio is particularly skewed. Mean TLF is also strongly correlated with the strength of the departure from a balanced sex ratio and sex specific differences in mean TLF between sexes are consistent with the direction of the sex bias. We subjected this relationship to hypothesis testing in the GLMM.
 - The GLMM estimates that the effect of annual sex ratio is strong and significant. The strongest bias in sex ratio among salmon outplanted or reintroduced above the dam was in 2014. There were 1.95 fold more males than females in this year. This level of male bias in sex ratio is estimated by the GLMM to reduce TLF to 31% and 19% of the TLF at a perfectly balanced sex ratio for females and males, respectively. This modeling result suggests that fitness could be substantially improved if efforts are made to balance sex ratios.
 - Our results are only useful over the range of predictors used to train the model. Therefore, while it is tempting to suggest that female biased sex ratios will increase fitness when looking at the model fit, I think it is best to provide a more conservative suggestion: strongly biased sex ratios, like the one used in 2014, should be avoided.
 - Interestingly, while the GLMM was fit using data from only salmon outplanted or reintroduced above Detroit Dam, we can evaluate the accuracy of our predictions using (somewhat) independent data: the fitness of NOR salmon reintroduced below Big Cliff Dam. A similar

effect of annual sex ratio can also be observed among salmon reintroduced below the dam. As sex ratio become more male biased, fitness is reduced. When evaluated with a simple GLM, this relationship appears to be significant (see effect plot of GLM for TLF of salmon below Big Cliff below, likelihood ratio test for annual sex ratio p-value = $1.7e-5$), although it is smaller (beta = -1.03 ± 0.24 (s.e.) below Big Cliff vs. beta = -1.75 ± 0.49 above Detroit).



- A second source of independent data against which to corroborate the effect of annual sex ratio are the 2016 outplants. These were excluded from the GLMM because we do not have the year 5 (2021) returns to include as potential offspring and there is no release date information for 2016 outplants. 2016 is the only year with a strong female bias (about 2x fold more females than males). From the model, we can predict 2016 outplants should have the highest overall fitness of any year, and that males should have much higher fitness than females. Indeed, 2016 has the highest CRR and fitness of any year, despite only including year 3 and 4 offspring. The interaction between sex ratio and sex is also corroborated by these new data. These fitness measurements are not in table 5 or the text, but I included a plot of mean empirical “TLF” for each sex over the range of annual sex ratios below (2016 is the new set of points on the left) to help make this point here.

Commented [DD25]: If we want to make this assertion we should probably include this GLM in the report. Instead of a full model selection and a lot of work, we could just fit the simple model, validate it, and report the parameter estimates and p-values like this.

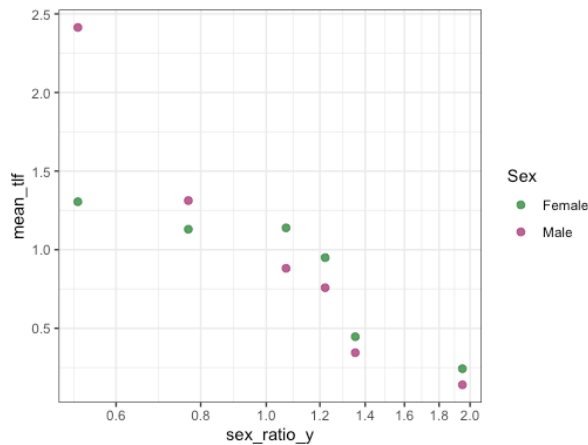
Commented [DD26R25]: Added a second appendix of post-hoc analyses

Commented [DD27]: I only thought to check this today and was very pleased to corroborate the modeling results.

Commented [DD28]: Discussed below in a comment below as well. We don't currently include these results in the main text, so if we want to use this piece of corroborating information then the fitness and/or partial CRR for 2016 outplants needs to be included in the discussion or added to the results.

Commented [DD29R28]: Added these as a second appendix

Commented [OMKG30R28]: Reference appendix?

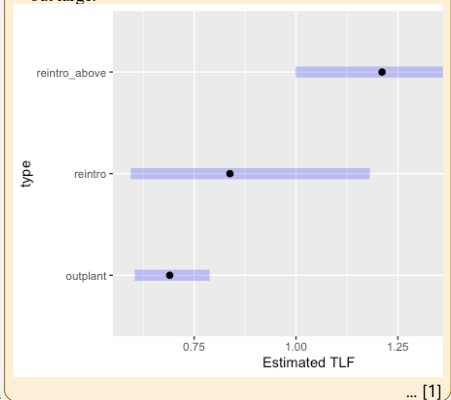


In addition to the main findings of our study, we highlight several salient results:

- **Comparisons within 2015:** TLF for NOR salmon reintroduced above Detroit Dam (1.21 ± 2.63) is substantially greater than TLF of NOR salmon reintroduced below Big Cliff (0.84 ± 1.67) and HOR salmon outplanted above Detroit Dam (0.69 ± 1.41) in 2015.
- **2016 outplants:** Although we did not sample 5 year old offspring of parent outplanted in 2016, and therefore do not include the full age structure of potential offspring of 2016 parents (and also do not report 2016 parent-level results in the report), the number and proportion of returning offspring that assigned to 2016 parents was exceptionally high. During 2019 and 2020, 1174 salmon returning to the North Santiam River (1174 passed over Minto) were determined to be progeny of the 1310 genotyped salmon that were outplanted above Detroit in 2016. The CRR_m (including only age 3 and 4 offspring) was 1.60, the CRR_f (including only age 3 and 4 offspring) was 0.45. Even excluding contributions to total lifetime fitness from age 5 offspring, the mean fitness of male 2016 outplants was 2.41 (the highest of any group analyzed) and the fitness of females was 1.3.

Commented [OMKG31]: Again, I think it makes most sense to compare location first – above Detroit NOR vs HOR then NOR above and NOR below.

Commented [DD32]: I didn't take the time to do a full exploration of this, but I fit a simple negative binomial glm on TLF with "type" (reintro above, reintro below, outplant above) as a fixed factor with no other effects. Type was very significant (delta AIC = 19, likelihood ratio test p-value = $1e-5$). Estimated effects of the GLM suggest that reintros above have significantly greater fitness than outplants above, but not reintros below. This seems like important information to highlight if the report is seeking to inform the decision to place NOR fish above the dam. It also suggests that we can't be sure the management decision to move NOR salmon above the dam in 2015 due to poor conditions was justified or not, TLF was higher but not significantly so. Effect plot below. Because we are dealing with count data that has a lot of dispersion and/or zero-inflation, the strength of the differences between these groups is not apparent when just looking at the means and standard deviation of empirical TLF as presented in table 4. We really need the GLM to highlight that effect size is not only significant, but large.



Commented [DD33R32]: Added this as a second appendix (post-hoc analyses)

Commented [DD34]: We can either add the text above to the appropriate section of the report with the caveat that it only includes age 3 and 4 offspring, or we can just highlight this result in the discussion. If we want to highlight that 2016 outplants corroborate the GLMM results, this needs to be included.

Commented [OMKG35R34]: I think this would fit best in the Discussion and Future Research sections. The information could be included in a supplemental file

Commented [DD36R34]: Added this as a second appendix (post-hoc analyses)

The main findings of our study are:

1. Of the NOR salmon reintroduced or sampled as carcasses in 2015, 40% (250 / 613) were progeny of spring Chinook salmon previously sampled in 2010 - 2012. This is a minimum estimate of outplant program contribution to subsequent NOR recruitment, because sampling of outplants (potential parents) was incomplete in 2010.
2. The 2015 cohort exhibited an unexpectedly geriatric adult age structure, characterized by the following composition: 66% age-5, 27% age-4, and 6% age-3 progeny. This age structure was likely influenced by the relatively few number of salmon outplanted above Detroit Dam in 2011 and 2012. The Minto Fish Collection Facility was under construction in 2011 and 2012, and alternative methods were used collect and transport adult salmon during these years.
3. Cohort replacement rate, an index of the demographic viability of the outplant program, was 0.27 (males only) and 0.19 (females only) for the 2010 cohort, signifying that replacement was not met. For the 2009 cohort, cohort replacement rate was 1.07 as estimated from female replacement whereas male CRR was only 0.29.
4. The N_b of the 2010 outplant cohort was 435.4 (95% C.I. = 388.8 – 490.9), leading to an N_b / N ratio of 0.20.
5. Total lifetime fitness for salmon outplanted during 2010 averaged 0.47 offspring with no significant difference between males (mean fitness = 0.44 ± 1.22 SD; range = 0 - 16 progeny) and females (mean fitness = 0.50 ± 1.10 SD; range = 0 - 10 progeny).
6. There was a significant relationship between fitness and *release location* for 2010, with high mean TLF at Coopers Ridge. No relationship was observed between *sex* or *release date* and preliminary fitness estimates for salmon outplanted above Detroit Dam during 2011 or 2012.
7. Overall, preliminary fitness estimates for carcasses sampled and successfully genotyped below Big Cliff Dam in 2011 ($N = 202$) and 2012 ($N = 84$) averaged 0.21 (± 0.53 SD, range = 0 - 3) and 0.035 (± 0.24 SD, range = 0 - 2) offspring, respectively. To provide full cohort data for the 2011 and 2012 carcass samples, the 2016 and 2017 NOR adult returns would also need to be genotyped. Given that the Minto Fish Collection Facility resumed operation in 2013, full cohort data for all NOR salmon released into the river below Big Cliff Dam this year could be achieved by genotyping the 2016, 2017, and 2018 adult returns.

This data will also be used by colleagues at the University of Idaho to further evaluate the effectiveness of this reintroduction program through modeling efforts.

Outplant program contributions to NOR salmon recruitment to the North Santiam River

Of the 613 NOR salmon successfully genotyped in 2015, only 40% were identified as progeny of previously sampled salmon. The observed assignment rate for 2015 is markedly lower than the rates reported in 2014 (66%) and 2013 (59%) (O'Malley et al. 2015). However, incomplete tissue sampling of putative parents in 2010 affected our ability to assign putative adult progeny sampled in 2015. As a result, our assignment rates are downwardly biased. Moreover, there were few salmon outplanted above Detroit Dam in 2011 ($N = 149$) and 2012 ($N = 258$), which could have resulted in reduced reproductive opportunity and low recruitment. Largely due to these limitations, results indicate that relatively few NOR spring Chinook salmon sampled in 2015 were progeny of outplanted salmon or individuals sampled as carcasses.

Replacement for the 2010 cohort was less than one for both males and females, indicating that adult offspring recruitment did not meet population replacement. The pre-spawn mortality rate for female salmon released above Detroit Dam in 2010 was 0.04. Under equal sex ratios, we observed similar total lifetime fitness (TLF) estimates for males and females; the mean TLF of male outplants was similar to that of females as was the range (males: 0 - 16 vs. females: 0 - 10 progeny). While preliminary, estimates of fitness for the 2011 and 2012 cohorts show low fitness means, variances, and ranges. However, it remains to be seen how population productivity measures after evaluating the full cohort for 2011 (inclusion of age-5 progeny returning in 2016) and 2012 (inclusion of age-4, age-5 progeny returning in 2016 and 2017, respectively).

Outplant program and spring Chinook salmon fitness

In addition to quantifying outplant contributions to subsequent NOR salmon recruitment to the North Santiam River, an objective of the study was to investigate how different outplanting protocols, including differences in *release date* and *release location*, might influence fitness. Analysis of the 2010 cohort revealed a positive relationship between *release location* and TLF, indicating that fitness was higher at Coopers Ridge for 2010. However, despite a significant effect of *release date* previously reported in O'Malley et al. (2015), no significant effect of *release date* and fitness was found here. Yet, given a predominance of zero and low fitness estimate, we may have had insufficient power to detect a positive effect of *release date* on fitness.

In conclusion, this study provides updated measures on the viability of salmon released above the Detroit-Big Cliff Dam complex on the North Santiam River. Results indicate low replacement rates and fitness for the 2010 cohort, despite the large-scale release of HOR fish ($N = 2\,735$). The results also reveal low fitness estimates for salmon outplanted above Detroit Dam or sampled as carcasses below Big Cliff Dam during 2011 and 2012. The observed annual variability in population productivity metrics underscores the need to continue genetic evaluation of this population to help provide an accurate representation of the efficacy of evolving outplanting operations occurring on the North Santiam River. Additionally,

continuation of the North Santiam genetic pedigree would provide the first fitness estimates of salmon handled at the new Minto Fish Collection Facility and help determine the productivity of NOR salmon reintroduced above Detroit Dam in 2015.

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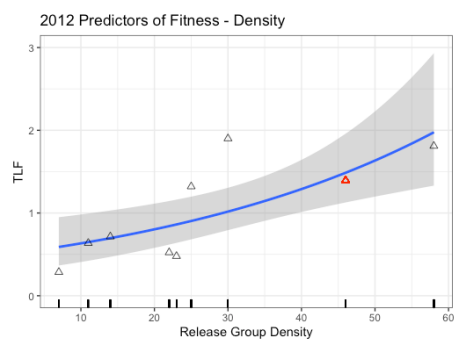
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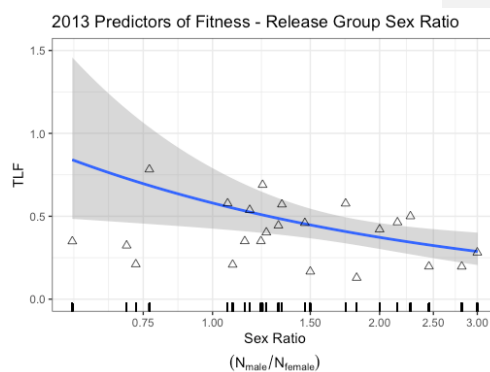
Supplemental Figures

Commented [DD37]: Embedded as pixel-based images to facilitate revision, will need to re-export these as vector-based later.

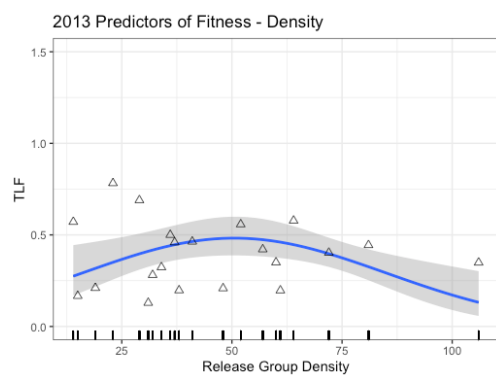
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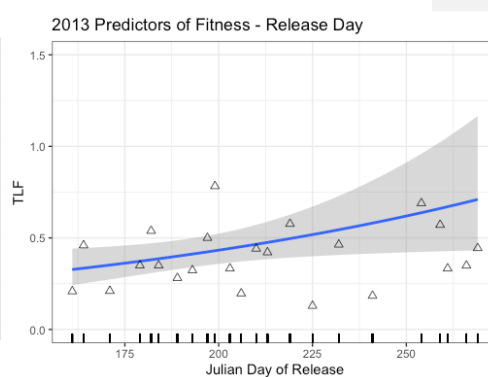
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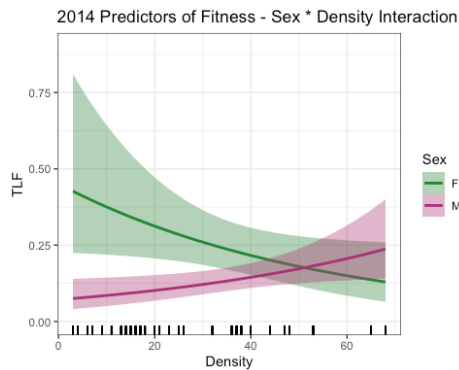
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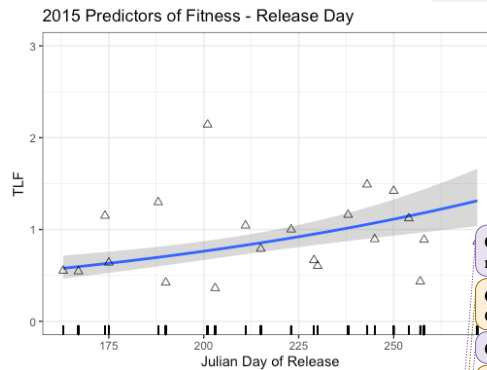
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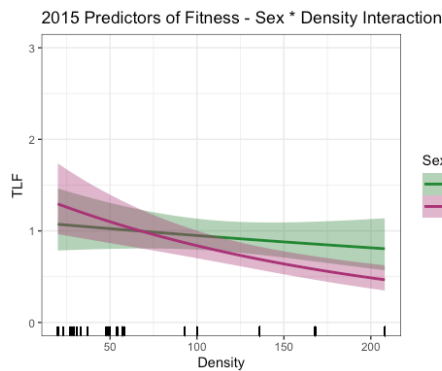
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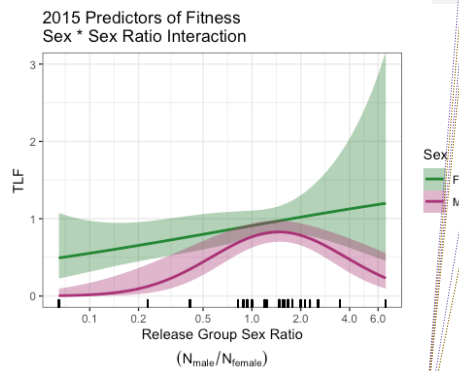
(f)



(g)



(h)



Supplemental Figure 1: Effect plots of significant predictors of TLF from the annual GLMs. Estimated effects of significant predictors are presented as lines with 95% confidence intervals. Estimated effects of predictors from final models with more than one predictor are conditioned on the mean value of other numeric predictors, or the weighted average of the within-level fitted values for categorical predictors. Empirical TLF averaged over each level of the predictor are presented as triangles for main effects. The rug plot at the bottom of each figure displays the levels of the predictors used to fit the model.

(a) Estimated effect of *release group density* on TLF in 2012. Red triangle highlights the observations from the single release of salmon at the Breitenbush River. No other predictors were retained in the final model. Location was not evaluated as a potential predictor of TLF in 2012 during model selection and validation due to multicollinearity.

Commented [OMKG38]: I'm surprised the max TLF never exceeded 3? In 2009, it was 20 for males

Commented [DD39R38]: This is estimated TLF + 95% CIs. The line should approximate the estimated mean TLF.

Commented [OMKG40]: Can we standardize the y axis?

Commented [DD41R40]: Yes we can
This would better convey magnitude of the effect size of a predictor vs others, or across years, but come at the cost that individual effects might be hard to interpret. Plots b, c, e, f and g would look like flat lines, because the effects in plots a, d and h are so much larger (or their CIs are larger) than others.
As a compromise, we could also standardize the y-axis within a year.

Commented [OMKG42R40]: Yes, standardize within year

Commented [DD43R40]: Realizing now that KGO did not have confidence intervals, so the Y-axes on these figures must have been very strange. Was this the motivation to standardize y axis?

Do we still want to standardize y-axis within year (as revised here), or go back to more typical data visualization with axis limits scaled to the data presented in each figure?

Commented [OMKG44]: I only see one triangle

Commented [DD45R44]: These are embedded as pdfs to preserve resolution, which has presented some problems when passing drafts back and forth before. I've attached a pdf of this draft of the report.

Commented [OMKG46R44]: Hmm, not sure I saw a PDF. I'll go back and check my emails.

Commented [DD47]: These can be removed if they are a little confusing/misleading. The data is fit on TLF at the level of the individual parent, not averaged over predictors. Putting them both on the same plot might confuse some readers. I originally included them to highlight how collinearity between location and density in 2011 may drive the parameter estimate for the effect density.

Commented [DD48R47]: Highlighting that it would still be good to get others' input here. Are the triangles misleading? They are not the data that the lines (predictions) are fit on, but instead, a summary.

(b) Estimated effect of *release group sex ratio* on TLF in 2013. *Release group density* and *release day* were also included in the final model. Location was not evaluated as a potential predictor of TLF in 2013 during model selection and validation due to multicollinearity.

(c) Estimated effect of *release group density* on TLF in 2013. *Release group sex ratio* and *release day* were also included in the final model. Location was not evaluated as a potential predictor of TLF in 2013 during model selection and validation due to multicollinearity.

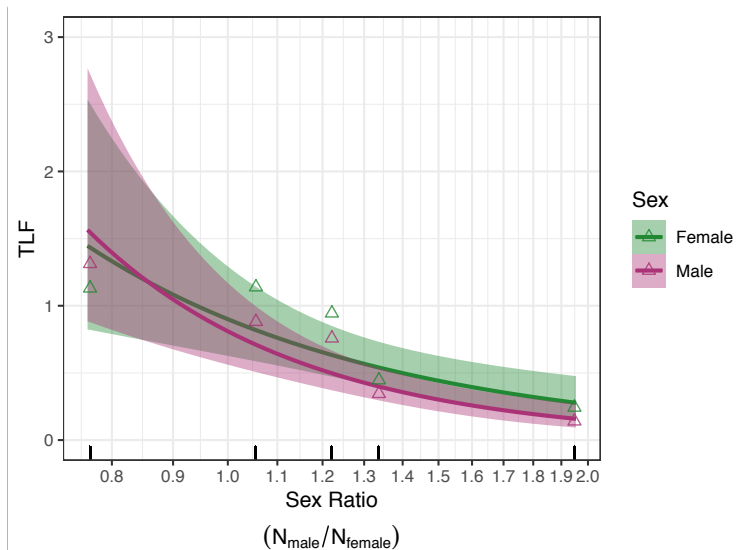
(d) Estimated effect of *release day* on TLF in 2013. *Release group density* and *release day* were also included in the final model. Location was not evaluated as a potential predictor of TLF in 2013 during model selection and validation due to multicollinearity.

(e) Estimated effect of *release density*, *sex* and their interaction on TLF in 2014. No other predictors were included in the final model. Location was not evaluated as a potential predictor of TLF in 2014 during model selection and validation due to multicollinearity.

(f) Estimated effect of *release day* on TLF in 2015. *Sex*, *release group density*, *release group sex ratio*, and two interactions, *sex * release group density* and *sex * release group sex ratio*, were also included in the final model. Location was not evaluated as a potential predictor of TLF in 2015 during model selection and validation due to strongly unbalanced design.

(g) Estimated effect of *release group density*, *sex* and their interaction on TLF in 2015. *Release day*, *release group sex ratio*, and the interaction *sex * release group sex ratio* were also included in the final model. Location was not evaluated as a potential predictor of TLF in 2015 during model selection and validation due to strongly unbalanced design.

(h) Estimated effect of *release group sex ratio*, *sex* and their interaction on TLF in 2015. *Release day*, *release group sex density*, and the interaction *sex * release group density* were also included in the final model. Location was not evaluated as a potential predictor of TLF in 2015 during model selection and validation due to strongly unbalanced design.



Supplemental Figure 2: Estimated effect of *sex*, *annual sex ratio*, and their interaction TLF of salmon outplanted or reintroduced above Detroit Dam from 2011 to 2015 (lines with 95% confidence intervals). Empirical TLF averaged over each level of the predictor are presented as triangles. The rug plot at the bottom of the figure displays the levels of the predictors used to fit the model.

Commented [DD49]: Is this figure broken for others? It should have two lines (different colors), two confidence intervals and 10 triangles.

I'll render the whole report as a pdf to show what it should look like.

APPENDIX A: ALLELE FREQUENCIES

As reported in O'Malley *et al.* (2015), the 12 microsatellite loci were highly polymorphic (Table A1). Allele frequencies among 2011, 2012, and 2013 salmon outplants and carcass samples and 2013 unmarked reintroduced salmon, putative parents of 2016 NOR salmon returns, provided a non-exclusion probability for a candidate parental pair of 1.47×10^{-15} , as estimated by CERVUS. Results from GENEPOP analysis (Version 4.51; Raymond and Rousset 1995) indicated that heterozygosity (patterns of genetic variation) deviated from Hardy-Weinberg proportions at all but three loci (*Ots515*, *Ogo2*, and *Ogo4*) for the 2016 adult returns (Table A1).

Allele frequencies among 2012, 2013, and 2014 salmon outplants and carcass samples and 2013 and 2014 unmarked reintroduced salmon, putative parents of 2017 NOR salmon returns, provided a non-exclusion probability for a candidate parental pair of 1.54×10^{-15} , as estimated by CERVUS. Results from GENEPOP analysis indicated that heterozygosity (patterns of genetic variation) deviated from Hardy-Weinberg proportions at two loci (*Ots215* and *OtsG311*) for the 2017 adult returns (Table A1).

Allele frequencies among 2013, 2014, and 2015 salmon outplants, unmarked reintroduced salmon, and carcass samples, putative parents of 2018 NOR salmon returns, provided a non-exclusion probability for a candidate parental pair of 1.61×10^{-15} , as estimated by CERVUS. Results from GENEPOP analysis indicated that heterozygosity (patterns of genetic variation) conformed to Hardy-Weinberg proportions at all loci for the 2018 adult returns (Table A1).

Allele frequencies among 2014, 2015, and 2016 salmon outplants, unmarked reintroduced salmon, and carcass samples, putative parents of 2019 NOR salmon returns, provided a non-exclusion probability for a candidate parental pair of 1.55×10^{-15} , as estimated by CERVUS. Results from GENEPOP analysis indicated that heterozygosity (patterns of genetic variation) conformed to Hardy-Weinberg proportions at all but one locus (*OtsG311*) for the 2019 adult returns (Table A1).

Allele frequencies among 2015, 2016, and 2017 salmon outplants, unmarked reintroduced salmon, and carcass samples, putative parents of 2020 NOR salmon returns, provided a non-exclusion probability for a candidate parental pair of 1.55×10^{-15} , as estimated by CERVUS. Results from GENEPOP analysis indicated that heterozygosity (patterns of genetic variation) deviated from Hardy-Weinberg proportions at all but four loci (*Ots211*, *Ots515*, *Ogo2*, and *Ots212*) for the 2020 adult returns (Table A1).

Table A1. Heterozygosity (genetic variation) at 12 microsatellite loci used in genetic parentage analysis of spring Chinook salmon from the North Santiam River, Oregon. For each locus and year, the observed and expected proportion of heterozygotes (H_O and H_E , respectively) are indicated. Shown in bold are loci exhibiting significantly ($P < 0.05$ with FDR correction) lower H_O than expected, according to Hardy-Weinberg exact tests conducted in GENEPOP (Version 4.51). Years 2011 and 2012 include HOR salmon outplanted above Detroit Dam and carcass samples. Years 2013, 2014, 2015, 2016, and 2017 include HOR and NOR salmon released above Detroit Dam, NOR salmon reintroduced below Big Cliff Dam, and carcass samples. Years 2018, 2019, and 2020 include NOR salmon reintroduced below Big Cliff Dam and carcass samples.

	2011 <i>N</i> = 345		2012 <i>N</i> = 342		2013 <i>N</i> = 1713		2014 <i>N</i> = 1653		2015 <i>N</i> = 1647		2016 <i>N</i> = 1845		2017 <i>N</i> = 2123		2018 <i>N</i> = 251		2019 <i>N</i> = 819		2020 <i>N</i> = 1593	
Locus	H_O	H_E	H_O	H_E	H_O	H_E	H_O	H_E	H_O	H_E	H_O	H_E	H_O	H_E	H_O	H_E	H_O	H_E	H_O	H_E
<i>Ots211</i>	0.918	0.917	0.917	0.909	0.920	0.916	0.910	0.915	0.907	0.913	0.913	0.910	0.918	0.916	0.899	0.915	0.919	0.912	0.919	0.914
<i>OtsG409</i>	0.971	0.952	0.944	0.949	0.943	0.944	0.951	0.949	0.946	0.949	0.951	0.948	0.947	0.948	0.947	0.949	0.953	0.950	0.950	0.949
<i>Ots215</i>	0.890	0.940	0.935	0.941	0.930	0.936	0.936	0.933	0.946	0.937	0.945	0.942	0.933	0.938	0.936	0.935	0.946	0.936	0.933	0.939
<i>Ots515</i>	0.862	0.858	0.853	0.858	0.871	0.863	0.870	0.868	0.872	0.867	0.862	0.865	0.87	0.865	0.820	0.865	0.867	0.872	0.857	0.864
<i>Ots201</i>	0.930	0.916	0.918	0.908	0.928	0.911	0.921	0.911	0.920	0.916	0.914	0.911	0.92	0.912	0.873	0.907	0.913	0.910	0.917	0.915
<i>Ogo2</i>	0.798	0.809	0.806	0.793	0.798	0.805	0.838	0.814	0.825	0.805	0.815	0.809	0.815	0.807	0.813	0.803	0.819	0.813	0.813	0.812
<i>Ssa408</i>	0.861	0.907	0.906	0.913	0.911	0.910	0.918	0.910	0.904	0.909	0.909	0.904	0.913	0.912	0.892	0.906	0.926	0.915	0.908	0.909
<i>OtsG249</i>	0.951	0.941	0.935	0.941	0.931	0.943	0.945	0.948	0.935	0.942	0.938	0.941	0.936	0.946	0.928	0.947	0.944	0.944	0.935	0.943
<i>Ots212</i>	0.888	0.892	0.860	0.882	0.900	0.882	0.878	0.883	0.888	0.893	0.910	0.896	0.884	0.885	0.928	0.890	0.878	0.896	0.894	0.893
<i>OtsG474</i>	0.744	0.765	0.772	0.763	0.785	0.768	0.785	0.762	0.738	0.744	0.741	0.748	0.787	0.768	0.753	0.747	0.736	0.743	0.758	0.759
<i>Ogo4</i>	0.761	0.738	0.751	0.735	0.733	0.715	0.729	0.714	0.728	0.730	0.737	0.730	0.728	0.718	0.689	0.709	0.714	0.723	0.730	0.730
<i>OtsG311</i>	0.943	0.957	0.953	0.959	0.952	0.961	0.953	0.959	0.950	0.958	0.951	0.959	0.952	0.96	0.948	0.953	0.958	0.956	0.952	0.959

Commented [SB50]: I did a two-tail comparison and then noticed this says “lower”. Some of these are higher.

Commented [DD51R50]: I kept consistent with what was done (two-tailed). So the caption should be changed. Left comment in case we only want to present one tailed test, but if not this should be changed to “different”

Commented [DD52R50]: Proof again

APPENDIX B: POST-HOC ANALYSES

Comparisons within 2015

We noted that the mean TLF of NOR salmon reintroduced above Detroit dam was greater than both TLF of HOR salmon outplanted above Detroit Dam and NOR salmon reintroduced below Big Cliff. To evaluate if these differences were significant, we fit a generalized linear model with a log-link function and negative binomial distribution that modeled TLF as a function of *type* and *sex*. *Type* was a factor with three levels: reintroduced NOR salmon above Detroit Dam, outplanted HOR salmon above Detroit Dam, and reintroduced NOR salmon below Big Cliff Dam. We validated the model using randomized and simulated residuals as in the GLM of predictors of fitness in the main text. We evaluated the significance of the effect of *type* on TLF using a likelihood ratio test and a Wald Test. We plotted the estimated marginal means and s.e. of the effect of *type* using the *emmeans* package in R.

Including *type* significantly improved the fit to the data over a simple model that included only an effect of *sex* and an intercept (likelihood ratio test p-value: 8.7×10^{-7}). NOR salmon released above Detroit Dam had significantly greater fitness than both HOR salmon outplanted into the same habitat above Detroit Dam (Wald test p-value: 2.0×10^{-7}) and NOR salmon reintroduced into the Wild Fish Sanctuary below Big Cliff Dam (Wald test p-value: 0.039).

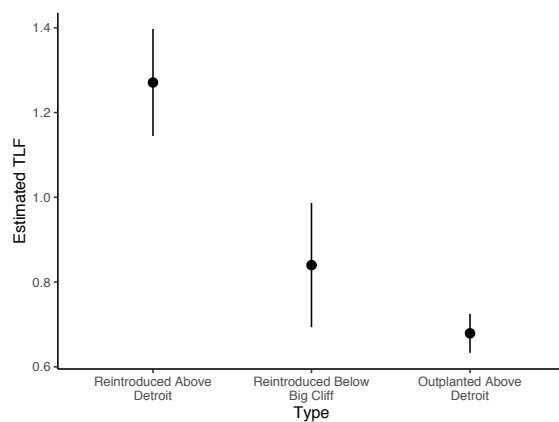


Figure A1: Estimated marginal means and standard errors of the effect of *type* on TLF of spring Chinook salmon releases in 2015.

Commented [DD53]: A note that I was wrong when we last met. When we decided to include this as a data supplement, I more carefully reviewed the results and realized I read them incorrectly. I was comparing outplants to reintros above and reintros below, when I said only the comparison against reintros above was significant.

I've corrected this now. Reintros above have greater fitness than outplants AND reintros below

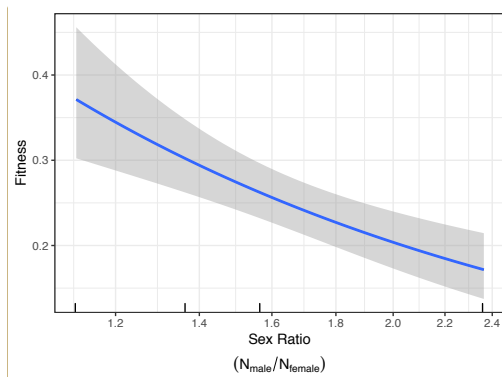
Corroborating Estimated Effect of Annual Sex Ratio

We hypothesized that if annual sex ratio was predictive of fitness among spring Chinook salmon released above Detroit Dam from 2011-2015, then it should also be predictive of fitness among 2016 HOR outplants above Detroit Dam and NOR salmon reintroduced below Big Cliff Dam from 2013-2016.

NOR Salmon Reintroduced Below Big Cliff

To evaluate if annual sex ratio was predictive of fitness among NOR spring Chinook salmon reintroduced below Big Cliff Dam, we fit a generalized linear model with a log-link function and negative binomial distribution that modeled fitness of NOR spring Chinook salmon reintroduced below Big Cliff Dam in 2013-2016 as a function of *sex*, *annual sex ratio* and their interaction. The range of sex ratios observed each year below Big Cliff Dam was comparable to the range above Detroit dam: 1.1 - 2.4 (males to females) and 0.8 – 2.0, respectively. We validated the model using randomized and simulated residuals as described in the methods concerning GLM of predictors of fitness in the main text. We evaluated the significance of the effects of *sex*, *annual sex ratio* and their interaction on fitness using a likelihood ratio test and a Wald Test. We prepared an effect plot in the same fashion as the models in main text.

The interaction term was not significant, so we refit the main effects without the interaction. Inclusion of both *sex* and *annual sex ratio* significantly improved model fit (likelihood ratio test p-values: 2.1×10^{-4} and 1.7×10^{-5} , respectively), and both estimated effects were significantly different than zero (Wald Test, 2.1×10^{-4} and 1.7×10^{-5} , respectively). The effect of *annual sex ratio* was negative over the range that occurred from 2013-2016 ($\beta = -1.03 \pm 0.24$). This estimated effect of annual sex ratio is presented on the response scale in figure A2.



Commented [DD54]: Again, this should show up with a confidence interval. If not, see the PDF.

Figure A2: Estimated effect of Annual Sex Ratio on Fitness of NOR spring Chinook salmon reintroduced below Big Cliff Dam from 2013-2016.

The finding that strongly male-biased sex ratios is estimated to impact fitness in a similar direction and magnitude among NOR salmon reintroduced below Big Cliff as all salmon released above Detroit Dam provides corroborating evidence of an effect of annual sex ratio on fitness. Sex ratios were not correlated between the Below Big Cliff and Above Detroit cohorts in the three years that overlapped between these analyses.

2016 Outplants Above Detroit Dam

The sex ratio for salmon outplanted above Detroit Dam in 2016 was female biased with approximately 2 fold more females than males (452 males, 858 females). Using the effects of sex, sex ratio and their interaction estimated in the final GLMM, we predicted 2016 outplants should have the highest overall fitness of any year, and that males should have much higher fitness than females. Although we did not sample 5 year old offspring of HOR parents outplanted above Detroit Dam in 2016, and therefore do not include the full age structure of potential offspring of 2016 parents, the number and proportion of returning offspring that assigned to 2016 was the highest of any year. In addition to the main effects, the interaction between sex ratio and sex is also corroborated by these new data with males demonstrating much higher fitness and CRR than females.

During 2019 and 2020, 1174 salmon returning to the North Santiam River (1174 passed over Minto) were determined to be progeny of the 1310 genotyped salmon that were outplanted above Detroit in 2016. The CRR_m (including only age 3 and 4 offspring) was 1.60, the CRR_f (including only age 3 and 4 offspring) was 0.45. Excluding contributions to total lifetime fitness from age 5 offspring, the mean fitness of male 2016 outplants was 2.41 and the fitness of females was 1.3.

We also attempted to use the average age at maturity estimated from offspring in years 2016-2020 to adjust the empirical mean TLF for 2016 HOR salmon outplanted above Detroit Dam and compare this value to quantitative model predictions. Year 5 offspring represent an average of 20.8% of TLF for 2011 – 2015 parents. The actual mean fitness for 2016 HOR salmon outplanted above Detroit Dam 1.3 and 2.41 for females and males respectively. After adjusting the values to account for the unsampled year 5 returns, the predicted mean TLFs are 1.64 and 3.04 for females and males respectively. These TLFs are within the 95% confidence intervals for predicted TLF from the GLMM at the sex ratio observed in 2016 of 2.74 ± 1.2 for females and 3.9 ± 1.8 for females.

The capacity of the mixed model to predict TLF in years that were not used to train the model provides some corroborating evidence that sex ratios influence TLF of spring Chinook salmon released above Detroit Dam, but some caution is warranted because we are predicting TLF from an annual sex ratio that is not observed in the data used to fit the model. For example, an extremely female biased sex ratio would assuredly have a negative effect on TLF, but our model would not predict this effect, because it is not trained on data from a year with such a sex ratio.

Commented [DD55]: If adjusting the 2016 TLF for the missing year 5 returns is too hand-wavey for this report, we can delete it. It seemed appropriate given the post-hoc nature of this test, but I understand that maybe it should go.

Commented [DD56]: This is something that might belong in the discussion. Our model is parameterized over mostly male-biased sex ratios and predicts that strongly male-biased sex ratios used in 2013 and 2014 reduce fitness relative to the more balanced sex ratios used in 2011, 2012 and 2015.

Therefore, I think **the prudent management take-away here is that strongly biased sex ratios should be avoided if possible**, but there is a possibility for the GLMM results to be over-interpreted and predict that a female biased sex ratio will increase TLF. We don't have sufficient data to support the latter claim.

I didn't take the time to do a full exploration of this, but I fit a simple negative binomial glm on TLF with "type" (reintro above, reintro below, outplant above) as a fixed factor with no other effects. Type was very significant (delta AIC = 19, likelihood ratio test p-value = $1e-5$). Estimated effects of the GLM suggest that reintros above have significantly greater fitness than outplants above, **but not reintros below**. This seems like important information to highlight if the report is seeking to inform the decision to place NOR fish above the dam. It also suggests that we can't be sure the management decision to move NOR salmon above the dam in 2015 due to poor conditions was justified or not, TLF was higher but not significantly so. Effect plot below.

Because we are dealing with count data that has a lot of dispersion and/or zero-inflation, the strength of the differences between these groups is not apparent when just looking at the means and standard deviation of empirical TLF as presented in table 4. We really need the GLM to highlight that effect size is not only significant, but large.

