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EVALUATING SPRING CHINOOK SALMON REINTRODUCTIONS ABOVE DETROIT

DAM AND BELOW BIG CLIFF DAM, ON THE NORTH SANTIAM RIVER, USING GENETIC PARENTAGE ANALYSIS

Prepared for:

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# 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 (± 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 (± 1.0 SD; range = 0 - 5) and 0.058 (± 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 (± 0.53 SD; range = 0 – 3; based on age-3 and age-4 progeny only) and 0.035 (± 0.24 SD; range = 0 – 2; based on age-3 progeny only) offspring, respectively.

# 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. 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.

To evaluate the contribution of this reintroduction 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 ~5× (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 offspring 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, 358 adult progeny assigned to the 131 outplanted females in 2009. Of these progeny, 141 were females, resulting in a female CRR of 1.07 (141/131). In contrast, when considering all outplanted salmon, the CRR was only 0.54 (409/759). We will discuss whether we need to insert male CRR here and remove all CRR.

In a subsequent study, O’Malley *et al.* (2017) determined that 40% of the NOR sampled in the North Santiam in 2015 were progeny of previously sampled salmon. Among the 250 assigned progeny, 83% (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 ± 1.10 SD; range = 0 - 10 progeny). For the 2010 cohort, the female CRR was 0.19 and the male CCR was 0.27.

Outplanting programs on other rivers within the UWR basin currently release marked HOR fish, unmarked presumed NOR fish, or some combination of HOR and NOR spring Chinook salmon. 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 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 above dams), RPA 4.7 (increase the percent of outplanted adults that successfully spawn through development of new release locations), RPA 6.2.3 (continue adult Chinook outplanting, Willamette basin-wide), and RPA 9.3 (monitoring the effectiveness of fish passage facilities and strategies at Willamette Project dams).

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). However, 61 tissue samples failed to genotype. 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 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.

1. Estimate the effects of release date and release location on the total lifetime fitness of adult spring Chinook salmon outplanted 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.
2. Estimate Cohort Replacement Rate (CRR) for spring Chinook salmon outplanted above Detroit Dam in 2011, 2012, 2013, 2014 and 2015.
3. Estimate the effective number of breeders (Nb) for the adult salmon population outplanted above Detroit Dam in 2011, 2012, 2013, 2014 and 2015.
4. 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.
5. 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.
6. 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.
7. Estimate Cohort Replacement Rate (CRR) for spring Chinook salmon reintroduced below Big Cliff Dam in 2013, 2014 and 2015.
8. Estimate the effective number of breeders (Nb) for the adult salmon population salmon reintroduced below Big Cliff Dam in 2013, 2014 and 2015.
9. 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

Spring Chinook salmon migration is impeded by two large dams on the North Santiam River,

Big Cliff and Detroit, which are located at 44° 45′ 3.6″ N, 122° 16′ 59.16″ W and 44° 43′ 15.44″ N, 122° 14′ 59.27″ W, respectively (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). 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.

## Outplanting operations above Detroit Dam

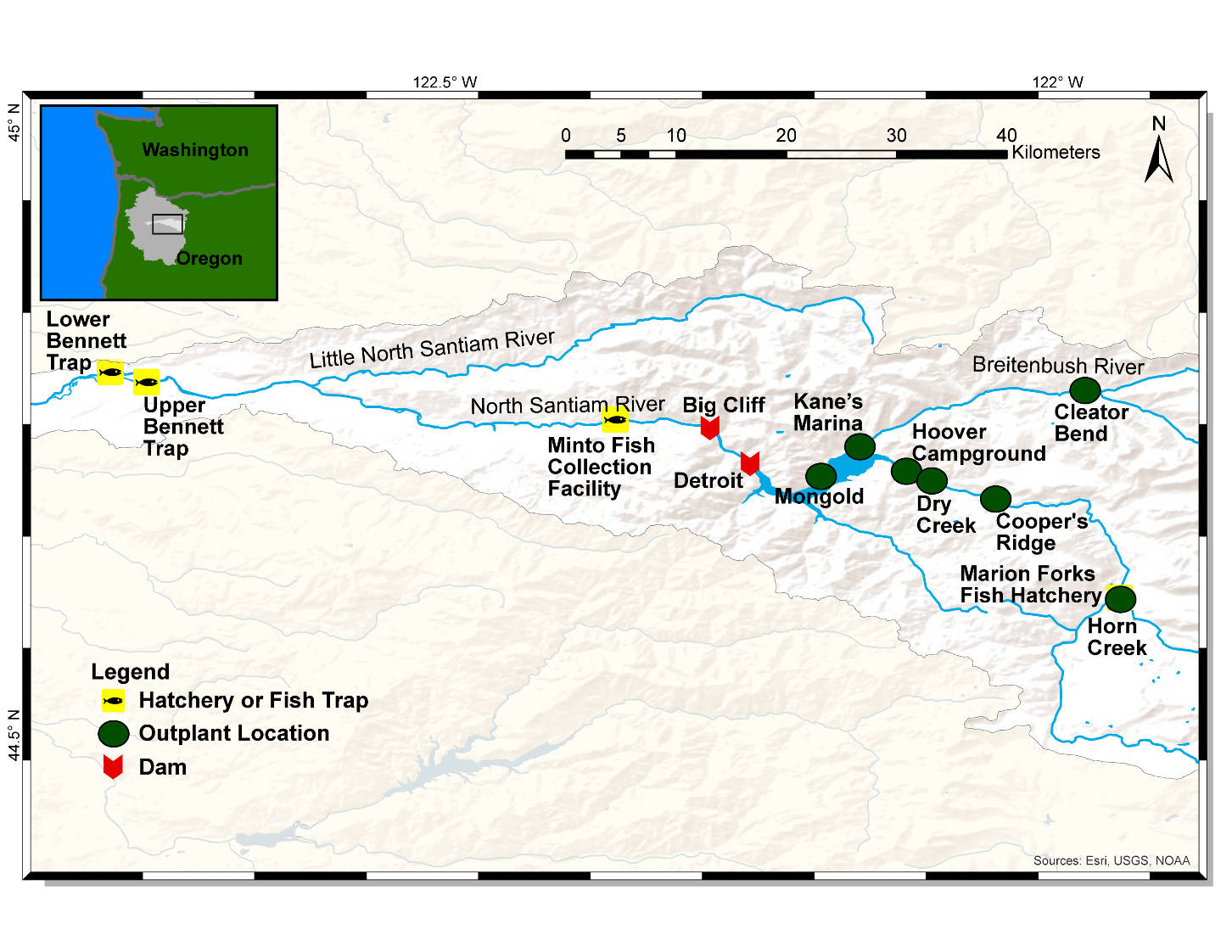
While outplanting of HOR salmon above Detroit Dam was initiated in the 1990s, tissue sampling of salmon did not begin until 2007 (O’Malley *et al.* 2015; Table 1). Multiple release locations have been used above Detroit Dam since outplanting operations began, but from 2011 - 2015, release locations included 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; Figure 1; Table 2).

## 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 collected from NOR salmon carcasses below Big Cliff Dam in 2014, 2015, 2016, 2017, 2018 and 2019 were included as potential progeny of previously outplanted salmon (see Figure 2 for assignment details). Note, 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 in 2011, 2012, 2013, 2014, and 2015 were included as potential parents of progeny sampled at the Minto Fish Collection Facility or during spawning ground surveys in 2014, 2015, 2016, 2017, 2018, and 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 seven release locations used in spring Chinook salmon outplanting operations and the Marion Forks Fish Hatchery.

## Genetic parentage analysis

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).

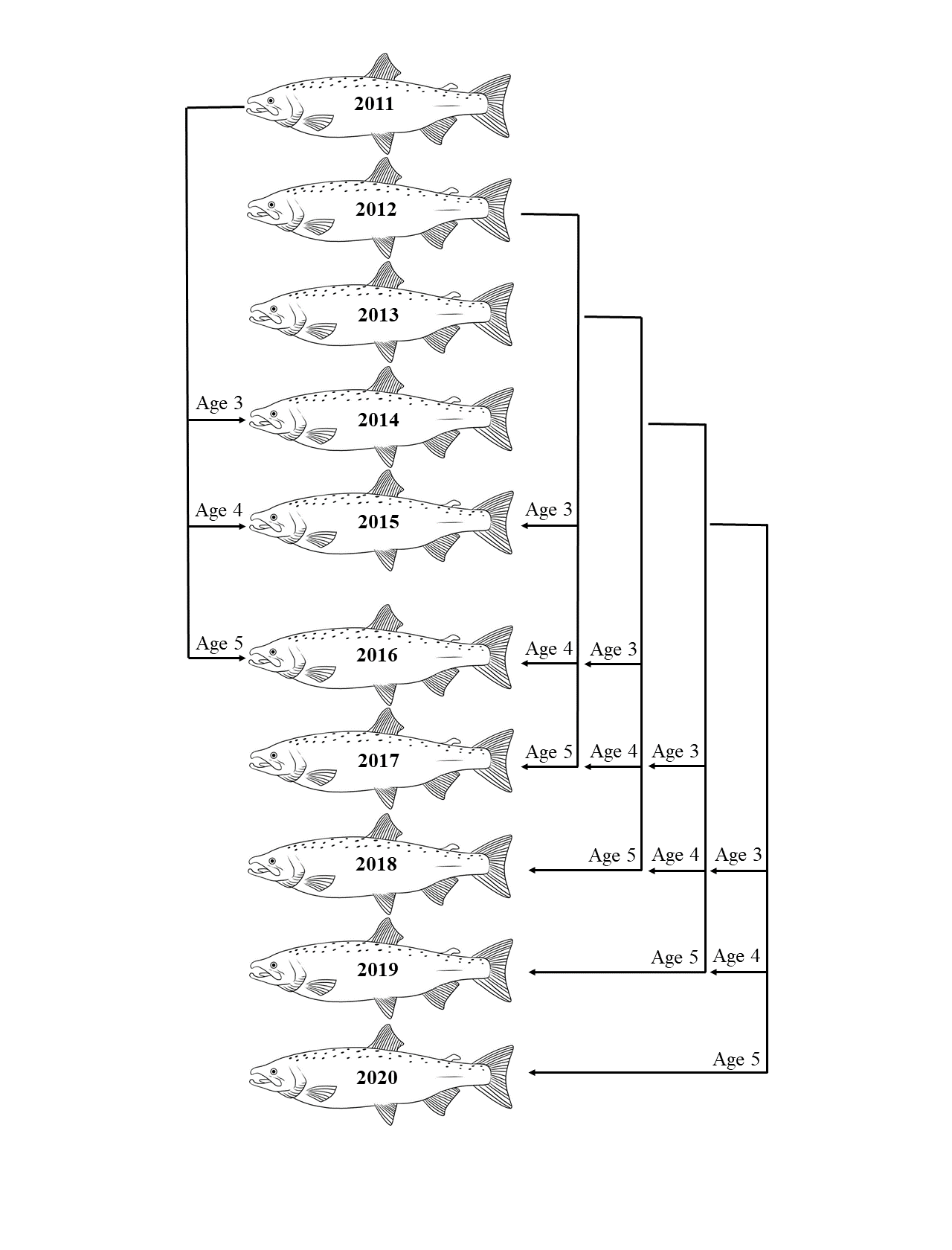
As 2015 represented the first large-scale reintroduction of NOR salmon above Detroit Dam, carcass samples were also examined from above dam habitat. These NOR carcass samples were included in the analysis for duplicate genotypes in the event that a reintroduced live fish was not sampled (i.e. field sampling error) or genotyped (i.e. poor DNA quality or genotyping rate). Genotypes that were identical at all loci were assumed to represent a single individual and duplicated genotypes were removed from subsequent analysis. As reported in O’Malley *et al.* (2017), 15 carcasses had unique genotypes.

We did integrate a few NOR’s in the N Santiam in 2018 and/or 2019.

**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. Individuals were removed from the analysis if they were genotyped at < 7 loci, there was no genotypic or phenotypic sex information, or represented a duplicate multi-locus genotype.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Year  *Tissue Source* | Tissue samples | # Genotyped < 7 markers | # Duplicates removed | Females | Males |
| 2011 |  |  |  |  |  |
| *Carcass* | 330 | 126 | 8 | 104 | 92 |
| 2012 |  |  |  |  |  |
| *Carcass* | 130 | 46 | 0 | 45 | 39 |
| 2013 |  |  |  |  |  |
| *Live* | 560 | 1 | 5 | 165 | 389 |
| *Carcass* | 58 | 4 | 15 | 20 | 19 |
| 2014 |  |  |  |  |  |
| *Live* | 770 | 1 | 15 | 294 | 460 |
| *Carcass* | 94 | 29 | 19 | 23 | 23 |
| 2015 |  |  |  |  |  |
| Above Detroit |  |  |  |  |  |
| *Live* | 498 | 62 | 5 | 144 | 287 |
| *Carcass* | 41 | 6 | 20 | 6 | 9 |
| Below Big Cliff |  |  |  |  |  |
| *Live* | 170 | 15 | 7 | 70 | 78 |
| *Carcass* | 47 | 18 | 10 | 7 | 12 |
| 2016 |  |  |  |  |  |
| *Live* | 531 | 1 | 10 | 220 | 300 |
| *Carcass* | 48 | 18 | 11 | 10 | 9 |
| 2017 |  |  |  |  |  |
| *Live* | 513 | 1 | 7 | 201 | 304 |
| *Carcass* | 31 | 7 | 10 | 8 | 6 |
| 2018 |  |  |  |  |  |
| *Live* | 257 | 0 | 9 | 82 | 166 |
| *Carcass* | 9 | 4 | 2 | 2 | 1 |
| 2019 |  |  |  |  |  |
| *Live* | 832 | 6 | 13 | 304 | 509 |
| *Carcass* | 73 | 30 | 37 | 5 | 1 |
| 2020 |  |  |  |  |  |
| *Live* | 1622 | 0 | 28 | 630 | 963 |

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 Figures 2 and 3. 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, using a minimum of seven loci and a maximum of one mismatch between parent - offspring pairs (maximum of two mismatches for trios). Parentage assignments from CERVUS were then verified using the combined PLS - FL algorithm implemented in COLONY (Version 2.061; 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). Unknown parental contributions to NOR salmon, i.e. from below dam spawners or strays from other systems, could therefore impact the assignment accuracy of CERVUS. 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.



**Figure 2.** Framework used to reconstruct parent(s) - offspring relationships for spring Chinook salmon sampled in the North Santiam River, Oregon from 2011-2020. Five cohorts (2011-2015) of primarily HOR salmon outplanted above Detroit Dam were identified through pedigree reconstruction. Note that in 2015, 498 NOR salmon were outplanted above Detroit Dam. These individuals are potential progeny of previously outplanted salmon in 2010-2012 and potential parents of adult recruits in 2017-2020.

## Diagram Description automatically generated

**Figure 3.** Framework used to reconstruct parent(s) - offspring relationships for NOR spring Chinook salmon sampled below Big Cliff Dam in the North Santiam River, Oregon from 2011-2020. Five cohorts (2011-2015) were identified through pedigree reconstruction. Note that in 2011 and 2012, only carcasses were sampled since the Minto Fish Collection Facility was not operational. From 2013-2019 samples were collected from both carcasses and live fish handled at the Minto Fish Collection Facility. In 2020, only samples from live fish sampled at the Minto Fish Collection Facility were included in the genetic pedigree analysis.

## Parentage assignments and inferred age at maturity

The assignment rate was calculated by 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 above Detroit Dam

Thetotal lifetime fitness (TLF) of 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).

## Predictors of total lifetime fitness

A generalized linear model (GLM; using a negative binomial distribution and log link function) was used to examine the influence of *sex*, *release date*, *release location*, and the interaction between *sex* ~ *release date*, on the TLF of salmon outplanted above Detroit Dam in 2011, 2012, 2013, 2014 and 2015. The interaction between *release date* ~ *release location* was not examined as only one location was typically used per date. The full model was fit in R by *lme4*. Significance was tested using a likelihood-ratio test against a null model that included only an intercept and the model was validated by (a) comparing the scaled residuals against rank transformed predicted values and (b) examining a QQ plot for goodness of fit (Kolmogorov–Smirnov test), overdispersion, and outliers. Model validation was conducted using the *DHARMa* package in R. Significance of individual predictors in the full model was evaluated with a Wald test. Estimates of the effects of predictors and their standard error are presented on the scale of the link function of the GLM (logarithm). Backtransformed estimates of the effects of the predictors are also presented in the text.

## 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, live NOR salmon reintroduced below Big Cliff Dam in 2013, 2014, and 2015, and live NOR salmon reintroduced above Detroit Dam in 2015. We report both a female-only CRR (CRRF) and a male-only CRR (CRRM). 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 (*Nb*) among outplanted salmon in 2011, 2012, 2013, 2014 and 2015, among salmon reintroduced below Big Cliff Dam in 2013, 2014, and 2015 and among salmon reintroduced above Detroit Dam in 2015 was estimated using the linkage disequilibrium (LD) method, as implemented in the program NEESTIMATOR (Version 2; 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. *Nb* was calculated using a minimum allele frequency cutoff of 0.02 and 95% confidence intervals were generated using a jackknife re-sampling method (Waples and Do 2008).

## Total lifetime fitness of salmon reintroduced below Big Cliff Dam or above Detroit Dam

Thetotal 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 3). TLF was similarly estimated for salmon reintroduced above Detroit Dam in 2015.

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

Thetotal 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 3). Note, TLF estimates of salmon in 2015 were based 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 2.** Summary of release dates, release locations and number of 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) and removing duplicates. Note, the number of candidate parents is always fewer than the number of fish outplanted.

| Year | Release date | Release location | Candidate Dams | Candidate Sires | 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 |
| 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 |
|  | 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 | Breitenbush (Undefined) | 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 |
|  |  | 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.

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

# RESULTS

## Genotyping

2016 - Of the 579 NOR tissue samples collected during 2016, one batch-collected sample failed to genotype and DNA was severely degraded for 18 carcass samples (due to decomposition); these samples were removed from the analysis. Comparing the multi-locus genotypes among all adult returns and carcass samples collected during 2016 revealed 21 duplicate genotypes, which were subsequently removed from the analysis (Table 1). The remaining 539 NOR samples were then used in parentage analysis as putative adult progeny.

2017 - Of the 544 NOR tissue samples collected during 2017, one batch-collected sample failed to genotype and DNA was severely degraded for seven carcass samples (due to decomposition); these samples were removed from the analysis. Comparing the multi-locus genotypes among all adult returns and carcass samples collected during 2017 revealed 17 duplicate genotypes, which were subsequently removed from the analysis (Table 1). The remaining 519 NOR samples were then used in parentage analysis as putative adult progeny.

Of the 1674 tissue samples collected from HOR salmon outplanted above Detroit Dam, one failed to genotype at greater than 7 microsatellite loci and one had neither genotypic nor phenotypic sex information and was excluded. Comparing the multi-locus genotypes among all outplants sampled during 2017 revealed 69 duplicate genotypes, which were subsequently removed from the analysis. The remaining 1604 outplants were then used in parentage analysis as candidate parents.

2018 - Of the 266 NOR tissue samples collected during 2018, DNA was severely degraded for four carcass samples (due to decomposition); these samples were removed from the analysis. Comparing the multi-locus genotypes among all adult returns and carcass samples collected during 2018 revealed 11 duplicate genotypes, which were subsequently removed from the analysis (Table 1). The remaining 251 NOR samples were then used in parentage analysis as putative adult progeny.

2019 - Of the 905 NOR tissue samples collected during 2019, six batch-collected samples failed to genotype and DNA was severely degraded for 30 carcass samples (due to decomposition); these samples were removed from the analysis. Comparing the multi-locus genotypes among all adult returns and carcass samples collected during 2019 revealed 50 duplicate genotypes, which were subsequently removed from the analysis (Table 1). The remaining 819 NOR samples were then used in parentage analysis as putative adult progeny.

2020 - Of the 1622 NOR tissue samples collected during 2020, all were successfully genotyped at greater than 7 microsatellite loci. One had neither genotypic nor phenotypic sex information and was excluded. Comparing the multi-locus genotypes among all adult returns and carcass samples collected during 2020 revealed 28 duplicate genotypes, which were subsequently removed from the analysis (Table 1). The remaining 1593 NOR samples were then used in parentage analysis as putative adult progeny.

## 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 3). 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 3).

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 3). 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 salmon reintroduced below Big Cliff dam and a carcass sample (Table 3).

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 3).

2018 - Results from genetic parentage analysis revealed that 71% (180 / 251) of the 2018 NOR adult offspring assigned to previously sampled salmon (Table 3). 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 outplanted (HOR)/reintroduced (NOR) salmon in 2015), with 6% (10 / 180) assigning solely to salmon reintroduced (NOR) above Detroit Dam in 2015, < 1% (1 / 180) assigning to salmon carcasses sampled below Big Cliff Dam, and 33% (59 / 180) assigning to NOR salmon reintroduced 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 3).

2019 - Results from genetic parentage analysis revealed that 81% (665 / 819) of the 2019 NOR adult offspring assigned to previously sampled salmon (Table 3). Among the 665 assigned progeny, 66% (436 / 665) assigned to salmon previously outplanted above Detroit Dam (including 119 that assigned to parent pairs of outplanted (HOR)/reintroduced (NOR) salmon in 2015 and 1 that assigned to parent pairs of outplanted salmon (HOR) and carcasses (NOR) recovered in 2015), with 22% (146 / 665) assigning solely to salmon reintroduced (NOR) above Detroit Dam in 2015, < 1% (4 / 665) assigning solely to salmon carcasses previously sampled below Big Cliff Dam, < 1% (1 / 665) assigning to a parent pair of salmon reintroduced (NOR) above Detroit Dam and a carcass recovered above Detroit Dam in 2015, < 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 12% (77 / 665) assigning to NOR salmon reintroduced below Big Cliff Dam (Table 3).

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 3).

2020 – Results from genetic parentage analysis revealed that 91% (1449 / 1593) of the 2020 NOR adult offspring assigned to previously sampled salmon (Table 3). Among the 1449 assigned progeny, 87% (1261 / 1449) assigned to salmon previously outplanted above Detroit Dam (including 56 that assigned to parent pairs of outplanted (HOR)/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 a parent pair of 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 3).

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 3).

## Total lifetime fitness of salmon outplanted 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 and thus still had the potential to spawn. Mean fitness of males was 0.87 ± 2.12 SD, whereas the mean fitness of females was 1.14 ± 2.11 SD (Table 4).

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 and thus still had the potential to spawn. Mean fitness of males was 1.31 ± 2.47 SD, whereas the mean fitness of females was 1.13 ± 2.05 SD (Table 4).

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 and thus still had the potential to spawn. Mean fitness of males was 0.34 ± 0.86 SD, whereas the mean fitness of females was 0.45 ± 0.95 SD (Table 4).

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 and thus still had the potential to spawn. Mean fitness of males was 0.14 ± 0.49 SD, whereas the mean fitness of females was 0.24 ± 0.76 SD (Table 4).

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 / 1125, 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 and thus still had the potential to spawn. Mean fitness of males was 0.56 ± 1.24 SD, whereas the mean fitness of females was 0.82 ± 1.55 SD (Table 4).

## Predictors of total lifetime fitness of salmon outplanted above Detroit Dam

2011 - *Release location* was not included in the model because all outplants were released at the same location, Reservoir (Mongold). The full model containing *sex* and *release date* was not significant (p = 0.78, likelihood-ratio test) and no significant effects were found. (Table 5).

2012 – The full model containing *sex,* *release date,* and *location* was not significant (p = 0.55, likelihood-ratio test) and no significant effects were found (Table 5).

2013 - The full model containing *sex* and *release date,* was not significant (p = 0.32, likelihood-ratio test) and no significant effects were found (Table 5).

2014 – The full model containing *sex,* *release date,* and *location* was not significant (p = 0.39, likelihood-ratio test). There was a significant effect of *sex* on fitness (Wald Test, p = 0.014). However, the model failed validation: the scale of the residuals depended on the predicted values and the model failed our test of goodness-of-fit (Kolmogorov Smirnov test, p = 0.02, outlier test, p = 0.03). Males are predicted to have 57% of the fitness of females in 2014.

2015 - The full model containing *sex,* *release date,* and *location* was not significant (p = 7.7 x 10-5, likelihood-ratio test). There was a significant effect of *sex* on fitness (Wald Test, p = 0.015). However, the model failed validation: the scale of the residuals depended on the predicted values. Males are predicted to have 72% of the fitness of females in 2015.

## Cohort replacement rates of salmon outplanted above Detroit Dam

2011 - During 2014 - 2016, 94 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 of the 149 genotyped salmon that were outplanted above Detroit in 2011. Both male and female replacement rates were less than 1, with a CRRM of 0.49 and a CRRF of 0.54.

2012 - During 2015 - 2017, 174 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 the 258 genotyped salmon that were outplanted above Detroit in 2012. Both male and female replacement rates were less than 1, with a CRRM of 0.77 and a CRRF of 0.43.

2013 - During 2016 - 2018, 242 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 the 1125 genotyped salmon that were outplanted above Detroit in 2013. Both male and female replacement rates were less than 1, with a CRRM of 0.20 and a CRRF of 0.18.

2014 - During 2017 - 2019, 87 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 the 861 genotyped salmon that were outplanted above Detroit in 2014. Both male and female replacement rates were less than 1, with a CRRM of 0.07 and a CRRF of 0.13.

2015 - During 2018 - 2020, 498 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 the 1042 genotyped salmon that were outplanted above Detroit in 2015. Both male and female replacement rates were less than 1, with a CRRM of 0.33 and a CRRF of 0.33.

## Effective number of breeders of salmon outplanted above Detroit Dam

2011 - The estimated number of breeders (*Nb)* for the 2011 outplant cohort was 49.1 (95% C.I. = 34.6 - 73.3). This estimated value is less than the number of outplants that produced one or more adult progeny (*N* = 50) in 2011. The ratio of *Nb* to the census size (*N*) of the outplanted cohort was 0.33 (49.1 / 149). *Nb*estimated among salmon for 2011 was a fraction of the estimates for 2009 (*Nb*= 130.7) and 2010 (*Nb*= 435.4); however, the *Nb / N*ratio estimated for 2011 is higher than those calculated for 2009 (*Nb / N* = 0.17) and 2010 (*Nb / N* = 0.20).

2012 - The estimated number of breeders (*Nb)* for the 2012 outplant cohort was 88.7 (95% C.I. = 70.2 - 114.8). This estimated value is less than the number of outplants that produced one or more adult progeny (*N* = 102) in 2012. The ratio of *Nb* to the census size (*N*) of the outplanted cohort was 0.34 (88.7 / 258). The *Nb / N*ratio estimated for 2012 is higher than those calculated for previous years, which ranged from 0.17 to 0.33.

2013 - The estimated number of breeders (*Nb)* for the 2013 outplant cohort was 224.0 (95% C.I. = 179.3 – 289.8). This estimated value is less than the number of outplants that produced one or more adult progeny (*N* = 242) in 2013. The ratio of *Nb* to the census size (*N*) of the outplanted cohort was 0.19 (224 / 1125). The *Nb / N*ratio estimated for 2013 is similar to those calculated for 2009 – 2010, which ranged from 0.17 to 0.19.

2014 - The estimated number of breeders (*Nb)* for the 2014 outplant cohort was 109.8 (95% C.I. = 63.1 – 270.3). This estimated value is higher than the number of outplants that produced one or more adult progeny (*N* = 104) in 2014, but some progeny were assigned as single parent assignments and *Nb* therefore represents more than 104 individuals. The ratio of *Nb* to the census size (*N*) of the outplanted cohort was 0.13 (109.8 / 861). The *Nb / N*ratio estimated for 2014 is lower than those calculated for 2009 – 2013, which ranged from 0.17 to 0.34.

2015 - The estimated number of breeders (*Nb)* for the 2015 outplant cohort was 291.5 (95% C.I. = 223.2 – 394.9). This estimated value is less than the number of outplants that produced one or more adult progeny (*N* = 308) in 2013. The ratio of *Nb* to the census size (*N*) of the outplanted cohort was 0.28 (291.5/ 1042). The *Nb / N*ratio estimated for 2014 is similar that calculated for 2012.

*Total lifetime fitness of NOR salmon reintroduced below Big Cliff Dam and above Detroit 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.

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. For reintroduced samples collected during 2015, male (mean **=** 1.12 ± 2.72 SD, *n =* 287) salmon showed lower fitness than female (mean = 1.39 ± 2.45 SD, *n =* 144), with 39% (167 / 431) of the salmon reintroduced above Detroit Dam producing one or more progeny.

*Cohort replacement rates of NOR salmon reintroduced below Big Cliff Dam and Above Detroit Dam*

2013 - During 2016 - 2018, 91 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 CRRM of 0.12 and a CRRF of 0.13, signifying that replacement was not met for 2013.

2014 - During 2017 - 2019, 50 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 CRRM of 0.05 and a CRRF of 0.04, signifying that replacement was not met for 2014.

2015 - During 2018 - 2020, 83 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 CRRM of 0.44 and a CRRF of 0.41, signifying that replacement was not met for 2015.

During 2018 - 2020, 396 salmon returning to the North Santiam River (all passed over Minto) were determined to be progeny of the 431 genotyped salmon that were reintroduced above Detroit Dam in 2015. Both male and female replacement rates were less than 1, with a CRRM of 0.66 and a CRRF of 0.55, signifying that replacement was not met for 2015.

## Effective number of breeders of NOR salmon reintroduced below Big Cliff Dam and above Detroit Dam

2013 - The estimated number of breeders (*Nb)* for the 2013 reintroduced cohort below Big Cliff was 155.3 (95% C.I. = 96.4 – 329.3). This estimated value is higher than the number of reintroduced salmon that produced one or more adult progeny (*N* = 97) in 2013, but some progeny were assigned as single parent assignments and *Nb* therefore represents more than 97 individuals. The ratio of *Nb* to the census size (*N*) of the reintroduced cohort was 0.28 (174.3 / 554).

2014 - The estimated number of breeders (*Nb)* 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 (*N* = 60) in 2014, but the confidence interval of the estimate was large. The ratio of *Nb* to the census size (*N*) of the reintroduced cohort was 0.31 (291.6 / 754).

2015 - The estimated number of breeders (*Nb)* for the 2015 reintroduced cohort below Big Cliff was 69.9 (95% C.I. = 51.1 – 101.3). This estimated value is higher than the number of reintroduced salmon that produced one or more adult progeny (*N* = 49) in 2015, but some progeny were assigned as single parent assignments and *Nb* therefore represents more than 49 individuals. The ratio of *Nb* to the census size (*N*) of the reintroduced cohort was 0.47 (69.9 / 148).

The estimated number of breeders (*Nb)* for the 2015 reintroduced cohort above Detroit Dam was 153.7 (95% C.I. = 118.0 – 204.8). This estimated value less than the number of reintroduced salmon above Detroit Dam that produced one or more adult progeny (*N* = 167) in 2015. The ratio of *Nb* to the census size (*N*) of the cohort was 0.36 (153.7 / 431).

## 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 3.** 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), or carcasses collected below Big Cliff Dam (Carcass), 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 (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).

1. 2016

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Offspring |  |  | Parents | | | | | | |  |
|  |  | 2011 | | 2012 | | 2013 | | | Assigned (%) |
|  |  | Outplant | Carcass | Outplant | Carcass | Outplant | Reintro. | Carcass |
| Sample type | *N* | (*N* = 149) | (*N* = 197) | (*N* = 258) | (*N* = 84) | (*N* = 1125) | (*N* = 554) | (*N* = 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%)** |

1. 2017

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Offspring |  |  | Parents | | | | | | | |  |
|  |  | 2012 | | 2013 | | | 2014 | | | Assigned (%) |
|  |  | Outplant | Carcass | Outplant | Reintro. | Carcass/ Reintro | Outplant | Reintro. | Carcass |
| Sample type | *N* | (*N* = 258) | (*N* = 84) | (N = 1125) | (*N* = 554) | (*N* = 39/554) | (N = 861) | (*N* = 754) | (*N* = 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%)*** |

1. 2018

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Offspring |  |  | Parents | | | | | | | | | | |  |
|  |  | 2013 | | | 2014 | | | 2015 | | | | | Assigned (%) |
|  |  | Outplant | Reintro. | Carcass | Outplant | Reintro. | Carcass | Outplant | Reintro. Above | Outplant/ Reintro. Above | Reintro. Below | Carcass |
| Sample type | *N* | (*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 | 14 3 5 | 0 0 0 | 178 (72%) |
| 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%)*** |

1. 2019

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Offspring |  |  |  | Parents | | | | | | | | | | | | |  |
|  |  | 2014 | | |  | 2015 | | | | | | | 2016 | | | Assigned (%) |
|  |  | Outplant | Reintro. | Carcass | Outplant | Reintro. Above | Outplant/ Reintro. Above | Outplant/ Carcass | Reintro. Above/ Carcass | Reintro. Below | Reintro Below / Carcass | Carcass | Outplant | Reintro. | Carcass |
| Sample type | *N* | (*N* =  861) | (*N* = 754) | (*N* =  46) | (*N* =  1042) | (*N* =  431) |  |  |  | (*N* = 148) |  | (*N* =  34) | (*N* = 1310) | (*N* = 520) | (*N* =  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 | 5 4 3 | 0 0 1 | 662 (81%) |
| 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%)*** |

1. 2020

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Offspring |  |  |  |  | | Parents | | | | | | | | | | | | | |
|  |  |  | | 2015 | | | | | | | | 2016 | | | 2017 | | |  |
|  |  | Outplant | | Reintro. Above | | Outplant/ Reintro. Above | Outplant/ Carcass | Reintro. Above/ Carcass | Reintro. Below | Reintro Below / Carcass | Carcass | Outplant | Reintro. | Carcass | Outplant | Reintro. | Carcass |  |
| Sample type | *N* | (*N* =  1042) | | (*N* =  431) | |  |  |  | (*N* = 148) |  | (*N* =  34) | (*N* = 1310) | (*N* = 520) | (*N* =  19) | (*N = 1604*) | (*N = 505*) | (*N = 14*) | Assigned (%) |
| 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 4.** Total lifetime fitness estimates for spring Chinook salmon outplanted above Detroit Dam (2011 - 2015), collected as carcasses below Big Cliff Dam (2011 - 2015), or 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 or Carcass), 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 | *N* | Mean | SD | Range |
| 2011 (age-3, age-4, age-5 progeny) |  |  |  |  |  |  |
|  | Outplant | M  F | 77  72 | 0.87  1.13 | 2.12  2.11 | 0 - 15  0 - 8 |
|  | Carcass | M  F | 93  104 | 0.25  0.27 | 0.58  0.58 | 0 - 3  0 - 3 |
| 2012 (age-3, age-4, age-5 progeny) |  |  |  |  |  |  |
|  | Outplant | M  F | 112  146 | 1.31  1.13 | 2.47  2.04 | 0-17  0-10 |
| Carcass | M  F | 39  45 | 0.31  0.29 | 0.57  0.63 | 0-2  0-2 |
| 2013 (age-3, age-4, age-5 progeny) |  |  |  |  |  |  |
|  | Reintro. | M  F | 165  389 | 0.19  0.39 | 0.57  0.76 | 0-5  0-5 |
|  | Outplant | M  F | 647  478 | 0.34  0.45 | 0.86  0.96 | 0-7  0-6 |
| Carcass | M  F | 19  20 | 0.05  0.10 | 0.23  0.31 | 0-1  0-1 |
| 2014 (age-3, age-4, age-5 progeny) |  |  |  |  |  |  |
|  | Reintro. | M  F | 460  294 | 0.08  0.12 | 0.33  0.37 | 0-2  0-2 |
|  | Outplant | M  F | 569  292 | 0.14  0.24 | 0.49  0.76 | 0-5  0-8 |
| Carcass | M  F | 23  23 | 0.04  0.04 | 0.21  0.21 | 0-1  0-1 |
| 2015 (age-3, age-4, age-5 progeny) |  |  |  |  |  |  |
|  | Reintro. Below | M  F | 78 70 | 0.76 0.93 | 1.66 1.70 | 0-10 0-10 |
|  | Reintro. Above | M  F | 287  144 | 1.12  1.39 | 2.72  2.45 | 0-26  0-19 |
| Outplant | M  F | 523  519 | 0.56  0.82 | 1.24  1.55 | 0-8  0-10 |
|  | Carcass Above | M  F | 9  6 | 0.56  0.17 | 1.13  0.41 | 0-1  0-1 |
|  | Carcass Below | M  F | 11  8 | 0.18  0.12 | 0.41  0.35 | 0-1  0-1 |

**Table 5.** Results of generalized linear models examining the influence of *release location,* *release date,* and *sex* on the fitness of outplanted spring Chinook salmon from the North Santiam River. Separate models were run for each outplant cohort (2011 - 2015) and results are summarized for each year. The factor *release location* was not included for the 2011 model (see methods section). Interaction terms were not significant and thus not included in any of the final models. The null hypothesis that each predictor did not significantly improve the model effect was tested with a likelihood-ratio test. P-values falling below the critical α (0.05) are shown in boldface. Estimates (β) and standard error (s.e.) of effects on log(fitness) are indicated where significant.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  | β | s.e. | P-value |
| 2011 (age-3, age-4, age-5 progeny) | Model |  |  | 0.776 |
|  | *sex* [Male] |  |  | 0.508 |
|  | *release date* |  |  | 0.951 |
| 2012 (age-3, age-4, age-5 progeny) | Model |  |  | 0.552 |
|  | *sex* [Male] |  |  | 0.460 |
|  | *release date* |  |  | 0.244 |
|  | *release location* |  |  | 0.873 |
| 2013 (age-3, age-4, age-5 progeny) | Model |  |  | 0.319 |
|  | *sex* [Male] |  |  | 0.093 |
|  | *release location* |  |  | 0.564 |
|  | *release date* |  |  | 0.928 |
| 2014 (age-3, age-4, age-5 progeny) | Model |  |  | 0.386 |
|  | *sex* [Male] | -0.550 | 0.223 | **0.014** |
|  | *release location* |  |  | 0.989 |
|  | *release date* |  |  | 0.901 |
| 2015 (age-3, age-4, age-5 progeny) | Model |  | - | 7.7 x 10-5 |
|  | *sex* [Male] | -0.329 | 0.135 | **0.016** |
|  | *release location* |  | - | 0.076 |
|  | *release date* |  | - | 0.860 |

# DISCUSSION

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.

1. The 2015 cohort exhibited an unexpectedly geriatric adult age structure, charcaterized 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.

1. 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.

1. The *Nb* of the 2010 outplant cohort was 435.4 (95% C.I. = 388.8 – 490.9), leading to an *Nb* / *N* ratio of 0.20.

1. 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).

1. 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.

1. 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.

# REFERENCES

Botsford, L. W., and J. G. Brittnacher. 1998. Viability of Sacramento River winter-run Chinook salmon. Conservation Biology 12:65-79.

Brunelli, J. P., K. J. Wertzler, K. Sundin, and G. H. Thorgaard. 2008. Y-specific sequences and polymorphisms in rainbow trout and Chinook salmon. Genome 51:739-48.

Cairney, M., J. Taggart, and B. Hoyheim. 2000. Characterization of microsatellite and minisatellite loci in Atlantic salmon and cross-species amplification in other salmonids. Molecular Ecology 9:2175-2178.

Do, C., R. S. Waples, D. Peel, G. M. Macbeth, B. J. Tillett, and J. R. Ovenden. 2014.

NeEstimator v2: re-implementation of software for the estimation of contemporary effective population size (Ne) from genetic data. Molecular Ecology Resources 14:209-14.

Greig, C., D. P. Jacobson, and M. a. Banks. 2003. New tetranucleotide microsatellites for finescale discrimination among endangered chinook salmon. Molecular Ecology Notes 3:376379.

Harrison, H. B., P. Saenz-Agudelo, S. Planes, G. P. Jones, and M. L. Berumen. 2013. Relative accuracy of three common methods of parentage analysis in natural populations. Molecular Ecology 22:1158-70.

Ivanova, N., J. R. Dewaard, and P. D. N. Hebert. 2006. An inexpensive, automation-friendly protocol for recovering high-quality DNA. Molecular Ecology Notes 6:998-1002.

Jones, O. R., and J. Wang. 2010. COLONY: a program for parentage and sibship inference from multilocus genotype data. Molecular Ecology Resources 10:551-555.

Kalinowski, S. T., M. L. Taper, and T. C. Marshall. 2007. Revising how the computer program CERVUS accommodates genotyping error increases success in paternity assignment. Molecular Ecology 16:1099-1106.

Naish, K. A., and L. K. Park. 2002. Linkage relationships for 35 new microsatellite loci in Chinook salmon. Animal Genetics 33:316-8.

NMFS. 2008. Endangered species act-section 7 consultation biological opinion and MagnusonStevens fishery conservation and management act consultation on the Willamette River basin flood control project. Portland, OR.

O’Malley, K. G., M. L. Evans, M. A. Johnson, D. P. Jacobson, and M. Hogansen. 2015. An evaluation of spring Chinook salmon reintroductions above Detroit Dam, North Santiam River, using genetic pedigree analysis. Pp. 25. Portland, OR.

O’Malley, K. G., A. N. Black, M. L. Evans, M. A. Johnson, and D. P. Jacobson. 2017. Evaluating Spring Chinook salmon reintroductions above Detroit Dam, on the North Santiam River, using genetic parentage analysis. Pp. 25. Portland, OR.

Olsen, J. B., P. Bentzen, and J. E. Seeb. 1998. Characterization of seven microsatellite loci derived from pink salmon. Molecular Ecology 7:1087-1089.

Peakall, R.O.D. and Smouse, P.E. 2006. GENALEX 6: genetic analysis in Excel. Population genetic software for teaching and research. Molecular ecology notes 6:288-295.

Raymond, M., and F. Rousset. 1995. GENEPOP (Version 1.2): Population genetics software for exact tests and ecumenicism. Journal of Heredity 86:248-249.

Waples, R. S., and C. Do. 2008. LDNE: a program for estimating effective population size from data on linkage disequilibrium. Molecular Ecology Resources 8:753-6.

Williamson, K. S., J. F. Cordes, and B. May. 2002. Characterization of microstellite loci in Chinook salmon (*Oncorhynchus tshawytscha*) and cross-species amplification in other salmonids. Molecular Ecology Notes 2:17-19.

# APPENDIX

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 … 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 ×10-15, as estimated by CERVUS. Results from GENEPOP analysis indicated that heterozygosity (patterns of genetic variation) deviated from Hardy-Weinberg proportions at … 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 (HO and HE, respectively) are indicated. Shown in bold are loci exhibiting significantly (P < 0.05 with FDR correction) lower HO than expected, according to Hardy-Weinberg exact tests conducted in GENEPOP (Version 4.51). Years 2011 and 2012 include marked outplants released above Detroit Dam and carcass samples. Years 2013, 2014, 2015, 2016, and 2017 include marked outplants released above Detroit Dam, unmarked salmon reintroduced below Big Cliff Dam, and carcass samples. Years 2018, 2019, and 2020 include unmarked salmon reintroduced below Big Cliff Dam and carcass samples.

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