December 2022 Report

EVALUATING SPRING CHINOOK SALMON RELEASES ABOVE COUGAR DAM, ON THE SOUTH FORK MCKENZIE RIVER, USING GENETIC PARENTAGE ANALYSIS

Prepared for:

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**Glossary**

* Assignment – Offspring are *assigned to* parents.
* Candidate Parent – Individual released above Cougar Dam included in our parentage analysis as a potential parent (i.e in the filtered dataset)
* Cohort – Set of individuals that could potentially spawn together. Not set of offspring descended from a set of parents that spawned together.
* CRR (Cohort Replacement Rate) – Number of offspring produced a cohort of parents, divided by the number of parents in the cohort.
* Fitness – Number of offspring produced by an individual that return as an adult
* Hatchery Outplant – HOR salmon initially collected at a hatchery and outplanted above Cougar Dam. NOT HOR salmon collected at Cougar Trap and released above Cougar Dam.
* HOR (hatchery origin) –
* LSDR (late season downstream release) - Double floy tag and release salmon at Forest Glen (in mainstem, below confluence with South Fork) after September 1st. Only release above Cougar Dam if collected a second time at trap.
* *Nb* (Effective Number of Breeders) -
* NOR (natural origin) –
* Offspring Year – Calendar year an individual returns the South Fork McKenzie River to spawn
* Origin –
* Outplant – release HOR individual into inaccessible habitat (use as verb, not noun)
* Parent Year – Calendar year an individual returns the South Fork McKenzie River to spawn
* Potential Offspring – Any NOR individual sampled in the South Fork McKenzie that remains in the dataset after genotype quality filtering
* Progeny – sometimes used in place of offspring in NSNT report, avoid
* Recycle – double floy tag and all release salmon at Forest Glen (in mainstem, below confluence with South Fork). Only release above Cougar Dam if collected a second time at trap.
* Reintroduce – release NOR individual into inaccessible habitat (use as verb, not noun)
* Release – trap and haul salmon from below the dam to above the dam (use as verb, not noun)
* Source – Where was a fish initially encountered for this study? This can be one of hatchery outplant (initially encountered at a hatchery), at the Cougar Trap, as a carcass sample or as a precocial male above the dam. Note th
* TLF (Total Lifetime Fitness) –
* Marked/Unmarked – avoid in favor of HOR/NOR

**Summary**

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**Objectives**

1. Determine the number and proportion of unmarked adult Chinook salmon sampled at various locations in the South Fork McKenzie River (e.g. Cougar Trap and spawning grounds below Cougar dam) in 2016 - 2020 that can be assigned as progeny of Chinook salmon previously released above Cougar Dam, South Fork McKenzie River in 2011 - 2017.
2. Estimate and report the annual abundance and age structure of adult Chinook salmon that return to the South Fork McKenzie River that can be confidently assigned to parents through genetic pedigree in 2016-2020.
3. Estimate the TLF for Chinook salmon reintroduced above Cougar Dam in 2011-2015. These estimates include unmarked adult offspring sampled at Cougar Dam, as well as unmarked spawners encountered on spawning grounds below the dam in 2014 - 2019.
4. Estimate cohort replacement rate (CRR), or “the number of future spawners produced by a spawner” for spring Chinook salmon released above Cougar Dam in 2011 - 2015.
5. Estimate the effective number of breeders (Nb) for the adult salmon population reintroduced above Cougar Dam in 2011-2015.
6. Estimate the effects of release date and release site on the total lifetime fitness of adult spring Chinook salmon released above Cougar Dam in 2011 - 2015.
7. Evaluate fitness differences between HOR and NOR Chinook salmon released above Cougar Dam in 2011-2015 through assignment of adult offspring returns in 2014-2020.

**Introduction**

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**Methods**

Study System and Sample Collection

Adult hatchery origin (HOR) Chinook salmon from the McKenzie River Hatchery and, infrequently, the Leaburg Hatchery have been reintroduced above Cougar Dam annually since 1996. The construction of a trap and transport facility near the base of Cougar Dam, hereafter referred to as the Cougar Trap, was completed in July 2010 (Fig. 1). Since that time, this facility has collected sexually mature, natural origin (NOR) Chinook salmon for reintroduction above Cougar Dam, while the population has continued to be supplemented with HOR salmon from both the Cougar Trap and from the McKenzie and Leaburg hatcheries. Since its construction, the Cougar trap has been operational throughout the spawning migration each year, with the exception of 19 July–6 August 2011, due to repairs. At both the hatchery and the trap, adults were collected using small fish ladders that end in holding tanks. Adults are placed in fish transportation trucks, driven above the dam and released into the river at one of six sites to spawn. To date, there is no assisted downstream passage for juveniles produced above the dam. Instead, juvenile fish can exit the reservoir volitionally, either by passage through hydroelectric turbines or over a steep, 73 m ‘regulating outlet’ spillway (Duncan, 2011).

Diagram

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**Figure. 1:** Map of the study system.

Beginning in 2013, all NOR Chinook salmon collected at Cougar Trap after September 1st were double floy-tagged and released into the mainstem, beneath the confluence with the South Fork. After September 1st, only floy-tagged NOR Chinook salmon were released above the dam. We refer to this program as late-season downstream release (LSDR). The function of the LSDR program was to limit transportation above the dam of NOR Chinook salmon that were not produced in the above Dam habitat. LSDR was implemented in 2013 and 2014. Beginning in 2015, all NOR Chinook salmon collected at Cougar Trap, regardless of date, were double floy-tagged and released into the mainstem, beneath the confluence with the South Fork. Only floy-tagged NOR salmon collected at Cougar Trap were released above the dam. We refer to this program as recycling. The recycling program has been implemented each year since 2015.

Tissue samples for genetic analysis were collected from nearly all NOR Chinook salmon that entered the Cougar trap and nearly all Chinook salmon released above the dam, regardless of origin. Tissue samples were also collected from NOR Chinook salmon carcasses identified during spawning ground surveys (SGSs) on the South Fork McKenzie River from 2011 - 2019, including SGSs above the dam and SGS between the confluence with the mainstem and the dam. Additionally, tissue samples were collected from precocial male Chinook salmon identified on the spawning grounds during 2014.

Genotyping

Consistent with previously published reports (add Banks and Sard cites), all NOR Chinook salmon sampled from 2016 – 2020, and all sampled Chinook salmon released above Cougar Dam from 2014 - 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 reformat cite). Each DNA sample was then genotyped at 11 microsatellite loci: *Ots201*, *Ots208b, Ots209*, *Ots211*, *Ots212*, *Ots215*, *OtsG249*, *Ots253b, OtsG311*, *OtsG409*, *Ots515* (Olsen *et al.* 1998, Cairney *et al.* 2000, Naish and Park 2002, Williamson *et al.* 2002, Greig *et al.* 2003 reformat and confirm cites) 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 (Appendix A). Multilocus genotypes were then compared among individuals to identify salmon that could have been sampled more than once. For example, NOR Chinook salmon sampled at Cougar Trap that were later sampled as carcasses. We describe individuals first encountered at Cougar Trap and later sampled as carcasses during SGSs as Cougar Trap individuals. If individuals failed to genotype at the sex-linked marker *Oty3*, phenotypic information was used to infer sex.

Genetic Parentage Analysis

The primary objective of this report is to evaluate spring Chinook salmon releases above Cougar Dam, on the South Fork Mckenzie River. Therefore, when inferring pedigrees we define *potential offspring* as NOR Chinook salmon sampled anywhere on the South Fork McKenzie River and *candidate parents* as any Chinook salmon, regardless of origin, released or sampled on the South Fork McKenzie River above Cougar Dam (Fig. 2). Potential offspring that do not assign to at least a single candidate parent are assumed to be NOR immigrants descended from parents that spawned below the dam or in the mainstem.

Previous reports and manuscripts evaluating the reintroduction of Chinook salmon above Cougar Dam on the South Fork McKenzie river have considered offspring from 2010 – 2015 and candidate parents from 2007 – 2012 (cites). Most Chinook salmon on the South Fork McKenzie River express an age at maturity of 3 - 6 years (cite). Therefore, previous reports have assigned potential offspring to all candidate parents salmon 2007 – 2009. Results based on the pedigree of salmon released above Cougar Dam in 2010 were also provided along with the caveat that age 6 offspring were not yet evaluated.

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**Fig. 2:** Illustration of how groups of individuals are organized into sets of potential offspring and candidate parents for parentage analysis. Here potential offspring that returned to the South Fork McKenzie in 2014 are assigned to candidate parents in 2008 – 2011. Source refers to where an individual was initially encountered: during a spawning ground survey on the South Fork McKenzie River (SGS), at the Cougar Trap (Cougar Trap) or at either the McKenzie or Leaburg Hatchery (Hatchery Outplant). Note that while all individuals initially encountered during SGS are NOR, and all individuals initially encountered at a Hatchery are HOR, individuals initially encountered at Cougar Trap are both NOR and HOR. Final disposition refers to whether a group was eventually released above the dam and is considered a candidate parent.

\* Note that 5 NOR SGS individuals and 12 precocial males from above the dam are also included as both candidate parents and potential offspring and are not depicted in the figure.

Continuing this work, we assigned potential offspring sampled on the South Fork McKenzie from 2016 to 2020 to candidate parents from 2010 to 2017. Combined with the pedigrees inferred in previous reports (cites), these new results allow us to identify all offspring of salmon released above Cougar Dam from 2007 - 2014, most offspring of salmon released above Cougar Dam in 2015 and some offspring of salmon released above the dam from 2016 – 2017 (Fig. 3).

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**Fig. 3:** Illustration of how results from genetic parentage analysis (Fig. 2) are combined to make demographic inferences about parental cohorts. Here we demonstrate how inferences about the 2013 parental cohort are drawn. Assignments between 2013 candidate parents (purple dashed rectangle) and their offspring in 2014 – 2017 (red rectangle) are depicted as black arrows. Labels are as in figure 2 except the values inside circles.

We inferred pedigrees by comparing microsatellite genotypes of potential offspring in each year to the genotypes of all candidate parents 3, 4, 5 and 6 years prior, as indicated in Fig. 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, an assumed parent sampling rate of 95%, and a maximum of one mismatch between parent - offspring pairs (maximum of two mismatches for parent - offspring trios). We also estimated non-exclusion probabilities and expected number of false parent-offspring pairs. 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, weak sibship prior of 1, allele dropout and miscalled allele rate prior of 2% per locus, and an assumed 95% rate of sampled parents.

Given the longitudinal nature of the genetic parentage analysis of South Fork 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. To evaluate how these changes to software versions and parentage assignment may impact results we reassigned all potential offspring from 2010 – 2020 to candidate parents from 2007 – 2017 and compared results between pedigrees inferred in previous reports and new pedigrees.

Assignments

We summarized the number and proportion of unmarked adult Chinook salmon sampled at either the Cougar Trap or spawning grounds below Cougar dam in 2016 - 2020 that can be assigned as progeny of Chinook salmon previously released above Cougar Dam, South Fork McKenzie River in 2011 - 2017.

To evaluate the efficacy of the LSDR / recycling program, we also determined the number of NOR immigrants collected at Cougar Trap each day. To better understand the relationship between time and the probability that an individual collected at Cougar Trap was not produced above the dam, we fit a binomial generalized linear model (GLM) using sex, Julian day, and their interaction across all years in our combined pedigree where we confidently evaluate all possible parentages (offspring years 2013 – 2020). Effects of Julian day, sex and their interaction were evaluated using likelihood ratio tests and Wald Tests.

Demography

*Age at Maturity*

For each assigned progeny, we subtracted the return year (e.g., 2016) by each parent(s) release year (e.g., 2013) to infer the age at maturity of progeny (e.g., age-3) and determined overall age structure among the adult returns from 2010 - 2020. Note that, because our candidate parents include salmon released above the dam from 2007 onwards, we were able to identify age 3, 4, 5, and 6 offspring in return years 2013 – 2020. For example, we cannot identify age 5 salmon returning in 2010, because we did not examine candidate parents from 2005.

*Total Lifetime Fitness*

TLF definition paragraph

*Cohort Replacement Rate*

CRR definition paragraph

*Effective Number of Breeders*

Nb methods paragraph. Include possible explanations for difference between number of successful parents and Nb here so it doesn’t need to be repeated in the results

Predictors of Fitness

GLMM Modeling methods.

**Results**

Sampling and Genotyping

After genotype quality filtering to remove individuals with fewer than 7 scored genotypes and to remove duplicate samples, there were 9,839 individuals genotyped at an average of 10.86 microsatellite loci (Table 1). There were 6,700 salmon initially collected at McKenzie or Leaburg Hatcheries and transported above Cougar Dam (hatchery outplants), 2,930 NOR and HOR salmon initially encountered at Cougar Trap and released above the dam, into the mainstem or immediately below the tailrace of the dam, 12 precocial males sampled on spawning grounds above the Dam, 192 carcasses sampled during SGSs below the dam and 5 carcasses sampled during SGSs above the dam (Table 2).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Year** | **Tissue Samples** | **Missingness Filtered** | **Duplicate Filtered** | **Nfinal** |
| 2007\* | 746 | 1 | 1 | 72 |
| 2008\* | 873 | 0 | 0 | 146 |
| 2009\* | 1386 | 16 | 9 | 478 |
| 2010\* | 748 | 7 | 24 | 292 |
| 2011\* | 791 | 11 | 9 | 519 |
| 2012\* | 962 | 2 | 66 | 858 |
| 2013\* | 695 | 1 | 69 | 913 |
| 2014\* | 744 | 1 | 1 | 72 |
| 2015\* | 917 | 0 | 0 | 146 |
| 2016 | 891 | 16 | 9 | 478 |
| 2017 | 718 | 7 | 24 | 292 |
| 2018 | 156 | 11 | 9 | 519 |
| 2019 | 193 | 2 | 66 | 858 |
| 2020 | 168 | 1 | 69 | 888 |

**Table 1.** Summary of genotype quality filtering. Individuals were removed from the analysis if they were genotyped at < 7 loci (missingness filtered), or if they represented a duplicate multi-locus genotype (duplicate filtered).

\* Indicates individuals from this year genotyped in prior reports (cites)

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Year** | **Hatchery Outplant** | **Cougar Trap** | | | **Precocial Male** | **SGS** | |
|  |  | HOR | NOR | Unknown |  | Below | Above |
| 2007 | 745 |  |  |  |  |  |  |
| 2008 | 873 |  |  |  |  |  |  |
| 2009 | 1383 |  |  |  |  |  |  |
| 2010 | 496 | 30 | 221 |  |  |  |  |
| 2011 | 340 | 29 | 356 |  |  | 45 |  |
| 2012 | 430 | 17 | 500 |  |  | 10 |  |
| 2013 | 440 | 22 | 223 |  |  | 5 |  |
| 2014 | 486 | 21 | 191 | 1 | 12 | 14 | 1 |
| 2015 | 600 | 19 | 241 |  |  | 24 |  |
| 2016 | 459 | 74 | 295 | 4 |  | 31 | 4 |
| 2017 | 448 | 6 | 239 | 1 |  | 13 |  |
| 2018 |  |  | 120 |  |  | 35 |  |
| 2019 |  |  | 158 |  |  | 15 |  |
| 2020 |  |  | 162 |  |  |  |  |

**Table 2:** Sample sizes after genotype quality filtering of salmon initially encountered at McKenzie or Leaburg Hatcheries (Hatchery Outplant), at Cougar Trap, during spawning ground surveys (SGS) above or below Cougar Dam, or as precocial males observed on the spawning grounds above Cougar Dam. Note that all Hatchery Outplants are HOR, Cougar Trap salmon include both NOR and HOR, and all precocial males and SGS salmon are NOR.

Parentage Assignment

We attempted to assign 2,915 potential offspring to 8,985 candidate parents (Tables 3 and 4, respectively). Of these 2,915 offspring, xxx assigned to yyy parents for an overall assignment rate of xxx (Table 4). Assignment rates per year varied substantially with just 6% of offspring in 2010 assigned to at least one candidate parent, and 94% of offspring in 2020 assigned to at least one candidate parent (Table 5). For the six offspring years when pedigrees were inferred in this report and in previous reports the average absolute difference in assignment rate for non-carcass samples was 0.7% (Table 5), indicating that changes to software versions, genotype quality filtering and assignment procedures had only a limited impact on the final pedigree.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Overall** | | |  | **Cougar Trap** | | | | | |
| **Year** | ***npotential offspring*** | ***nassigned*** | **% Assigned** |  | | ***npotential offspring*** | | ***nassigned*** | **% Assigned** | **Previous % Assigned** |
| 2010\* | 221 | 14 | 6% |  | | 221 | 14 | | 6% | 6% |
| 2011\* | 401 | 140 | 35% |  | | 356 | 138 | | 39% | 38% |
| 2012\* | 510 | 328 | 64% |  | | 500 | 326 | | 65% | 64% |
| 2013 | 228 | 153 | 67% |  | | 223 | 153 | | 69% | 67% |
| 2014 | 218 | 118 | 54% |  | | 191 | 117 | | 61% | 62% |
| 2015 | 265 | 179 | 68% |  | | 241 | 176 | | 73% | 72% |
| 2016 | 330 | 228 | 69% |  | | 295 | 212 | | 72% |  |
| 2017 | 252 | 173 | 69% |  | | 239 | 169 | | 71% |  |
| 2018 | 155 | 100 | 65% |  | | 120 | 92 | | 77% |  |
| 2019 | 173 | 84 | 49% |  | | 158 | 80 | | 51% |  |
| 2020 | 162 | 152 | 94% |  | | 162 | 152 | | 94% |  |

**Table 3:** Number of NOR Chinook salmon sampled in the South Fork McKenzie River and retained after genotype quality filtering (*npotential offspring*) in each year and the number (*nassigne****d***) and percent (% Assigned) assigned to candidate parents. Results for the full set of potential offspring (Overall) and potential offspring initially sampled at Cougar Trap (Cougar Trap) are presented separately. The previously reported assignment rate (Previous % Assigned) (for Cougar Trap only) is also presented.

\* Note that in 2010 – 2012, not all potential parents are included as candidate parents in the genetic parentage analysis.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Year** | **Hatchery Outplant** | **Cougar Trap** | | | **Precocial Male** | | **SGS** |
|  |  | HOR | NOR | Unknown | |  |  |
| 2007 | 745 |  |  |  | |  |  |
| 2008 | 873 |  |  |  | |  |  |
| 2009 | 1383 |  |  |  | |  |  |
| 2010 | 496 | 30 | 221 |  | |  |  |
| 2011 | 340 | 29 | 356 |  | |  |  |
| 2012 | 430 | 17 | 500 |  | |  |  |
| 2013 | 440 | 15 | 172 |  | |  |  |
| 2014 | 486 | 20 | 132 | 1 | | 12 | 1 |
| 2015 | 600 | 19 | 135 |  | |  |  |
| 2016 | 459 | 70 | 171 | 1 | |  | 4 |
| 2017 | 448 | 5 | 151 | 1 | |  |  |
| 2018 |  |  | 68 |  | |  |  |
| 2019 |  |  | 65 |  | |  |  |
| 2020 |  |  | 89 |  | |  |  |

**Table 4:** Number of individuals released or encountered above Cougar dam retained in the final filtered dataset. These values correspond to candidate parents used in genetic parentage analysis. All hatchery outplants are HOR, all precocial males and SGS individuals are NOR.

Considering only years where all potential parents were include in the genetic parentage analysis as candidate parents (2013 - 2020), the average proportion of individuals assigned to at least one parent above Cougar Dam was 71%. Assuming individuals that do not assign to at least one parent above the dam were not produced above the dam, this suggests 29% of NOR salmon collected at Cougar dam are immigrants. We found that the probability that an individual collected at Cougar Trap was produced above the dam decreased throughout the season, and that this effect was stronger for males than females (Table 5, Fig. 4).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Effect** | **β** | **s.e** | **LRT**  **p-value** | **Wald**  **p-value** |
| (Intercept) | 3.983 | 0.588 |  |  |
| *Julian Day* | -0.013 | 0.003 |  | **9.12 x 10-7** |
| *Sex[male]* | -1.203 | 0.778 |  | 0.122 |
| *sex* [male] \* *Julian Day* | -0.007 | 0.003 | **0.046** | **0.046** |

**Table 5:** Results of generalized linear mixed model examining the influence of *sex, Julian Day,* and their interaction on whether or not a NOR salmon sampled at Cougar Trap was assigned to at least one parent from above the dam. Estimated effect (β) and standard error (s.e.) of each fixed predictor on the link (logit) scale for predictors that were retained in the final model are presented. 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).

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**Figure 4:** Estimated effect of sex, Julian Day and their interaction on the probability that a NOR salmon collected at Cougar Trap is assigned to at least 1 parent above the dam (1 – predicted probability of NOR immigrant). Vertical dashed red line is Julian Day 245, which corresponds to either September 1st or October 31st, depending on the year.

Other assignment results text.

Demography

*Age at Maturity*

The average age at maturity for NOR Chinook salmon that we were able to successfully assign to a parent was 4.4 years. Most salmon were ages 4 or 5 (54.6% and 42.0%, respectively), with few returning at age 3 or 6 1.6% and 1.8%, respectively. This pattern was consistent across all offspring years where we are able to identify all of age 3, 4, 5, and 6 salmon (2013 – 2020). However, there was substantial variation in the proportion of age 4 and age 5 returns from year to year (figure 5).

Chart

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**Figure 5:** Inferred age at maturity for NOR salmon sampled in South Fork McKenzie River from 2010 – 2020.

\* Potential parents prior to 2007 are not included as candidate parents in the genetic parentage analysis. Therefore offspring in years 2010, 2011, and 2012 cannot be identified across the full range of potential ages.

*Total Lifetime Fitness*

TLF Results paragraphs

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Year** | **N** | **TLF** | **SD** | **Range** |
| 2007 | 745 | 0.79 | 1.53 | 0 - 17 |
| 2008 | 873 | 0.53 | 1.2 | 0 - 12 |
| 2009 | 1383 | 0.14 | 0.44 | 0 - 4 |
| 2010 | 747 | 0.22 | 0.63 | 0 - 6 |
| 2011 | 725 | 0.64 | 1.42 | 0 - 9 |
| 2012 | 947 | 0.31 | 0.68 | 0 - 5 |
| 2013 | 627 | 0.4 | 0.92 | 0 - 8 |
| 2014 | 652 | 0.19 | 0.55 | 0 - 4 |
| 2015\* | 754 | 0.17 | 0.48 | 0 - 6 |
| 2016\*\* | 705 | 0.36 | 0.8 | 0 - 8 |
| 2017\*\* | 605 | 0 | 0 | 0 - 0 |

**Table 6:** Average TLF and standard deviation per parent year.

\* Note that 2015 estimates do not include potential year 6 offspring. However we expect these offspring to contribute very little to TLF (< 2%)

\*\* Note that 2016 and 2017 offspring do not include potential year 5 and 6 offspring, and potential year 4 5 and 6 offspring, which are expected to substantially contribute to TLF for these parents years

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Year** | **Source\*\*\*** | **N** | **TLF** | **SD** | **Range** |
| 2007 | Hatchery Outplant | 745 | 0.79 | 1.53 | 0 - 17 |
| 2008 | Hatchery Outplant | 873 | 0.53 | 1.2 | 0 - 12 |
| 2009 | Hatchery Outplant | 1383 | 0.14 | 0.44 | 0 - 4 |
| 2010 | Cougar Trap | 251 | 0.26 | 0.65 | 0 - 4 |
| 2010 | Hatchery Outplant | 496 | 0.19 | 0.63 | 0 - 6 |
| 2011 | Cougar Trap | 385 | 0.74 | 1.54 | 0 - 9 |
| 2011 | Hatchery Outplant | 340 | 0.54 | 1.26 | 0 - 9 |
| 2012 | Cougar Trap | 517 | 0.38 | 0.77 | 0 - 5 |
| 2012 | Hatchery Outplant | 430 | 0.22 | 0.53 | 0 - 3 |
| 2013 | Cougar Trap | 187 | 0.75 | 1.3 | 0 - 8 |
| 2013 | Hatchery Outplant | 440 | 0.26 | 0.65 | 0 - 5 |
| 2014 | Cougar Trap | 153 | 0.27 | 0.74 | 0 - 4 |
| 2014 | Hatchery Outplant | 486 | 0.17 | 0.48 | 0 - 3 |
| 2015\* | Cougar Trap | 154 | 0.29 | 0.69 | 0 - 6 |
| 2015\* | Hatchery Outplant | 600 | 0.14 | 0.41 | 0 - 4 |
| 2016\*\* | Cougar Trap | 242 | 0.38 | 0.88 | 0 - 8 |
| 2016\*\* | Hatchery Outplant | 459 | 0.34 | 0.75 | 0 - 6 |
| 2017\*\* | Cougar Trap | 157 | 0 | 0 | 0 - 0 |
| 2017\*\* | Hatchery Outplant | 448 | 0 | 0 | 0 - 0 |

**Table 6b:** Average TLF and standard deviation per parent year and source.

\* Note that 2015 estimates do not include potential year 6 offspring. However we expect these offspring to contribute very little to TLF (< 2%)

\*\* Note that 2016 and 2017 offspring do not include potential year 5 and 6 offspring, and potential year 4 5 and 6 offspring, which are expected to substantially contribute to TLF for these parents years

*\*\*\** Note that there are 5 individuals sampled during spawning ground surveys above the dam and 12 precocial males sampled above the dam that were included as candidate parents. None had an offspring assigned to them and they are not presented in this table

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Year** | **Source\*\*\*** | **Sex** | **N** | **TLF** | **SD** | **Range** |
| 2007 | Hatchery Outplant | F | 318 | 0.89 | 1.49 | 0 - 11 |
| 2007 | Hatchery Outplant | M | 427 | 0.72 | 1.56 | 0 - 17 |
| 2008 | Hatchery Outplant | F | 288 | 0.8 | 1.46 | 0 - 12 |
| 2008 | Hatchery Outplant | M | 585 | 0.4 | 1.03 | 0 - 9 |
| 2009 | Hatchery Outplant | F | 603 | 0.16 | 0.47 | 0 - 4 |
| 2009 | Hatchery Outplant | M | 780 | 0.13 | 0.43 | 0 - 3 |
| 2010 | Cougar Trap | F | 62 | 0.23 | 0.61 | 0 - 3 |
| 2010 | Cougar Trap | M | 189 | 0.27 | 0.66 | 0 - 4 |
| 2010 | Hatchery Outplant | F | 201 | 0.29 | 0.74 | 0 - 5 |
| 2010 | Hatchery Outplant | M | 295 | 0.13 | 0.53 | 0 - 6 |
| 2011 | Cougar Trap | F | 150 | 0.66 | 1.3 | 0 - 7 |
| 2011 | Cougar Trap | M | 235 | 0.79 | 1.67 | 0 - 9 |
| 2011 | Hatchery Outplant | F | 170 | 0.78 | 1.59 | 0 - 9 |
| 2011 | Hatchery Outplant | M | 170 | 0.29 | 0.73 | 0 - 4 |
| 2012 | Cougar Trap | F | 191 | 0.4 | 0.76 | 0 - 5 |
| 2012 | Cougar Trap | M | 326 | 0.36 | 0.78 | 0 - 5 |
| 2012 | Hatchery Outplant | F | 248 | 0.25 | 0.58 | 0 - 3 |
| 2012 | Hatchery Outplant | M | 182 | 0.18 | 0.46 | 0 - 2 |
| 2013 | Cougar Trap | F | 86 | 0.69 | 1.2 | 0 - 6 |
| 2013 | Cougar Trap | M | 101 | 0.8 | 1.38 | 0 - 8 |
| 2013 | Hatchery Outplant | F | 239 | 0.29 | 0.71 | 0 - 5 |
| 2013 | Hatchery Outplant | M | 201 | 0.22 | 0.57 | 0 - 3 |
| 2014 | Cougar Trap | F | 59 | 0.24 | 0.75 | 0 - 4 |
| 2014 | Cougar Trap | M | 94 | 0.3 | 0.73 | 0 - 3 |
| 2014 | Hatchery Outplant | F | 327 | 0.14 | 0.45 | 0 - 3 |
| 2014 | Hatchery Outplant | M | 159 | 0.23 | 0.54 | 0 - 3 |
| 2015\* | Cougar Trap | F | 53 | 0.28 | 0.91 | 0 - 6 |
| 2015\* | Cougar Trap | M | 101 | 0.29 | 0.55 | 0 - 3 |
| 2015\* | Hatchery Outplant | F | 412 | 0.12 | 0.35 | 0 - 2 |
| 2015\* | Hatchery Outplant | M | 188 | 0.17 | 0.51 | 0 - 4 |
| 2016\*\* | Cougar Trap | F | 86 | 0.33 | 0.58 | 0 - 2 |
| 2016\*\* | Cougar Trap | M | 156 | 0.42 | 1 | 0 - 8 |
| 2016\*\* | Hatchery Outplant | F | 315 | 0.31 | 0.66 | 0 - 5 |
| 2016\*\* | Hatchery Outplant | M | 144 | 0.42 | 0.93 | 0 - 6 |
| 2017\*\* | Cougar Trap | F | 45 | 0 | 0 | 0 - 0 |
| 2017\*\* | Cougar Trap | M | 112 | 0 | 0 | 0 - 0 |
| 2017\*\* | Hatchery Outplant | F | 325 | 0 | 0 | 0 - 0 |
| 2017\*\* | Hatchery Outplant | M | 123 | 0 | 0 | 0 - 0 |

**Table 6c:** Average TLF and standard deviation per parent year, source and sex.

\* Note that 2015 estimates do not include potential year 6 offspring. However we expect these offspring to contribute very little to TLF (< 2%)

\*\* Note that 2016 and 2017 offspring do not include potential year 5 and 6 offspring, and potential year 4 5 and 6 offspring, which are expected to substantially contribute to TLF for these parents years

*\*\*\** Note that there are 5 individuals sampled during spawning ground surveys above the dam and 12 precocial males sampled above the dam that were included as candidate parents. None had an offspring assigned to them and they are not presented in this table

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Year** | **Sex** | **TLF HOR** | **TLF NOR** | **SD HOR** | **SD NOR** | **Range HOR** | **Range HOR** |
| 2007 | F | 0.89 |  | 1.49 |  | 0 - 11 |  |
| 2007 | M | 0.72 |  | 1.56 |  | 0 - 17 |  |
| 2008 | F | 0.8 |  | 1.46 |  | 0 - 12 |  |
| 2008 | M | 0.4 |  | 1.03 |  | 0 - 9 |  |
| 2009 | F | 0.16 |  | 0.47 |  | 0 - 4 |  |
| 2009 | M | 0.13 |  | 0.43 |  | 0 - 3 |  |
| 2010 | F | 0.29 | 0.25 | 0.73 | 0.63 | 0 - 5 | 0 - 3 |
| 2010 | M | 0.13 | 0.29 | 0.52 | 0.69 | 0 - 6 | 0 - 4 |
| 2011 | F | 0.76 | 0.68 | 1.57 | 1.33 | 0 - 9 | 0 - 7 |
| 2011 | M | 0.27 | 0.86 | 0.69 | 1.74 | 0 - 4 | 0 - 9 |
| 2012 | F | 0.25 | 0.41 | 0.58 | 0.77 | 0 - 3 | 0 - 5 |
| 2012 | M | 0.18 | 0.37 | 0.46 | 0.78 | 0 - 2 | 0 - 5 |
| 2013 | F | 0.28 | 0.75 | 0.7 | 1.25 | 0 - 5 | 0 - 6 |
| 2013 | M | 0.21 | 0.85 | 0.56 | 1.41 | 0 - 3 | 0 - 8 |
| 2014 | F | 0.14 | 0.27 | 0.45 | 0.79 | 0 - 3 | 0 - 4 |
| 2014 | M | 0.23 | 0.3 | 0.57 | 0.72 | 0 - 3 | 0 - 3 |
| 2015\* | F | 0.12 | 0.31 | 0.35 | 0.95 | 0 - 2 | 0 - 6 |
| 2015\* | M | 0.17 | 0.31 | 0.5 | 0.58 | 0 - 4 | 0 - 3 |
| 2016\*\* | F | 0.3 | 0.39 | 0.64 | 0.63 | 0 - 5 | 0 - 2 |
| 2016\*\* | M | 0.35 | 0.54 | 0.84 | 1.16 | 0 - 6 | 0 - 8 |
| 2017\*\* | F | 0 | 0 | 0 | 0 | 0 - 0 | 0 - 0 |
| 2017\*\* | M | 0 | 0 | 0 | 0 | 0 - 0 | 0 - 0 |

**Table 6d:** Average TLF and standard deviation per parent year, sex and origin.

\* Note that 2015 estimates do not include potential year 6 offspring. However we expect these offspring to contribute very little to TLF (< 2%)

\*\* Note that 2016 and 2017 offspring do not include potential year 5 and 6 offspring, and potential year 4 5 and 6 offspring, which are expected to substantially contribute to TLF for these parents years

Chart, line chart

Description automatically generated

**Figure 6:** Total lifetime fitness from 2007 to 2015, by sex and parent source

\* Note that 2015 estimates do not include potential year 6 offspring. However we expect these offspring to contribute very little to TLF (~2%)

*Cohort Replacement Rate*

Cohort replacement rate results paragraph. Max, min, never reaches one. Refers to table 7.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Year** | ***noffspring*** | ***ncandidate parents*** | ***nfemale candidate parents*** | ***nfemale candidate parents*** | **CRR** | **CRRF** | **CRRM** |
| 2007 | 331 | 745 | 318 | 427 | 0.44 | 0.36 | 0.43 |
| 2008 | 247 | 873 | 288 | 585 | 0.28 | 0.30 | 0.26 |
| 2009 | 114 | 1383 | 603 | 780 | 0.08 | 0.06 | 0.08 |
| 2010 | 94 | 747 | 263 | 484 | 0.13 | 0.12 | 0.11 |
| 2011 | 284 | 725 | 320 | 405 | 0.39 | 0.34 | 0.32 |
| 2012 | 171 | 947 | 439 | 508 | 0.18 | 0.11 | 0.19 |
| 2013 | 151 | 627 | 325 | 302 | 0.24 | 0.14 | 0.26 |
| 2014 | 73 | 652 | 386 | 266 | 0.11 | 0.08 | 0.11 |
| 2015\* | 69 | 754 | 465 | 289 | 0.09 | 0.06 | 0.12 |
| 2016\*\* | 135 | 705 | 403 | 302 | 0.19 | 0.10 | 0.29 |
| 2017\*\* | 0 | 605 | 370 | 235 | 0.00 | 0.00 | 0.00 |

**Table 7:** Cohort Replacement Rate (CRR) per parent year. CRR is defined as the number of spawners produced by a spawner estimated as number offspring successfully assigned to at least one parent in a given year (noffspring), divided by the number of candidate parents (ncandidate parents) in that year. We also present CRRF: the number female offspring successfully assigned to at least one female parent in a given year, divided by the number of female candidate parents (ncandidate parents) in that year. CRRM is the equivalent values for males.  
\* Note that 2015 estimates do not include potential year 6 offspring. However we expect these offspring to contribute very little to TLF (~2%)  
\*\* Note that 2016 and 2017 offspring do not include potential year 5 and 6 offspring, and potential year 4 5 and 6 offspring, which are expected to substantially contribute to TLF for these parents years

*Effective Number of Breeders*

Nb results paragraph. Briefly explains in the beginning what an Nb larger and smaller than the number of successful candidate parents might mean, highlights year where this comparison is larger, smaller or the same. Refers to table 8.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Year** | ***ncand*** | *nsuccess* | ***noffspring*** | ***Nb*** | **CIlower** | **CIupper** | **Nb nsuccess ratio** |
| 2007 | 745 | 261 | 331 | 265.5 | 222.7 | 322.8 | 1.02 |
| 2008 | 873 | 229 | 247 | 247.5 | 203.7 | 308.8 | 1.08 |
| 2009 | 1383 | 156 | 114 | 368.6 | 228.1 | 848.6 | 2.36 |
| 2010 | 747 | 105 | 94 | 169.8 | 116.6 | 288 | 1.62 |
| 2011 | 725 | 209 | 284 | 220.1 | 181.7 | 272.7 | 1.05 |
| 2012 | 947 | 206 | 171 | 297.2 | 216.5 | 451.4 | 1.44 |
| 2013 | 627 | 152 | 151 | 139.8 | 104.3 | 199.7 | 0.92 |
| 2014 | 652 | 90 | 73 | 167.5 | 104.7 | 361.6 | 1.86 |
| 2015\* | 754 | 103 | 69 | 211.9 | 122.1 | 627.5 | 2.06 |

**Table 8:** Effective number of breeders (*Nb*) per parent year as estimated by NeEstimator v2.1. Number of candidate parents (*ncand*) is the number of salmon released above the Cougar Dam in a given year that were sampled, and successfully genotyped, *nsuccess* is the number of candidate parents with one or more offspring in the pedigree. *noffspring* is the number of offspring assigned to candidate parents released above the dam that parent year. Upper and lower 95% confidence intervals based on jack-knife are provided. Finally the Nb : *nsucces* ratio is the Nb estimate divided by the number of successful breeders.

Predictors of Fitness

*GLMM Results*

*HOR/NOR Fitness Effects*

**Discussion**

Main Findings

1. Main findings presented in same order as objectives
2. Main Finding 2
3. Main Finding 3
4. Main Finding 4
5. Main Finding 5
6. Main Finding 6
7. Main Finding 7

Assignment Rates

Discussion of any important results from the assignments. Including discussion of the rate of NOR immigrants arriving at the trap.

Predictors of Fitness

Discussion paragraphs about the what drives variation in fitness among individuals, including environmental/release strategy variables and origin.

Demography

Discussion of whether or not the population is reaching replacement.

Conclusion

Example conclusion from 2016 report: We have consistently found that Chinook are not replacing themselves above Cougar Dam when only HOR Chinook were reintroduced. These results may suggest the need for improved juvenile survival

through Cougar Dam. However, we have not evaluated CRR in years that both HOR and NOR Chinook have been reintroduced. These years may have higher CRR because we have found higher mean RS estimates among NOR Chinook in 2010 and 2011. However, we caution relying on the use of results made with RS estimates too heavily, because our results suggest that RS does not explain 74.3% of the variation in TLF. In this report, we also found that the LSDR method was effective at limiting the number of non-Cougar adult returns transported above Cougar Dam, and we recommend that managers continue to use this method. Results from adult-adult pedigrees in future years will provide valuable information regarding CRR rates and TLF estimates between HOR and NOR.

**References**

Harrison HB, Saenz‐Agudelo P, Planes S, Jones GP, Berumen ML (2013) Relative accuracy of three common methods of parentage analysis in natural populations. Molecular ecology, 22, 1158-1170.

APPENDIX A: ASSIGNMENT POWER

This appendix will hold all the tables describing allele frequencies and variation, marker information content, non-exclusion probabilities, expected false parentages, and estimated genotype error rates for each offspring year and their set of candidate parents. I plan to generally follow the approach to presenting these values as Evans 2016, with a few changes. Most importantly, I will estimate a worst case scenario NEP, which assumes each parent offspring pair is evaluated at only the 7 markers with the largest (i.e. least powerful) NEPs.