**Lower Rogue Report October 2022**

**Reviewers’ comments**

**Peter Stevens comments in bold:**

**Science Bulletin text is in italics**

* **Was curious about distinction between Information Reports and Science Bulletin? Is it merely semantic? Why is the previous Information Report being re-done as a Science Bulletin?**
  + Good question. It is my understanding that ODFW, specifically Tom Friesen, spent quite a bit of time updating the agency’s policy and process for reporting and the outcome was this new Science Bulletin format. Emails were sent out in January 2020 outlining the new policy and process. Let me know if you’d like me to forward you that information.
  + The previous Information Report is not being re-done as a Science Bulletin. This Science Bulletin focuses on a second year of sampling (2020) and the results. The previous Information Report focused on 2019 sampling and results.
  + There was no indication that we would be analyzing samples from two consecutive years, so we wrote up the first year of results. I believe that was very beneficial for a variety of reasons that I won’t delve into here but would be happy to discuss if you are interested.
* **Seeing now that this is a follow-up/mash-up of two previous and one follow-up study, do we have enough for a manuscript? I like internal reports and all but they rarely see light of day, even internally, and this has some useful results.**
  + Sampling was conducted opportunistically by ODFW and others. While the information is quite valuable, there are limitations to the study design that would likely make it difficult to publish a peer-reviewed paper. We could potentially revisit this possibility now that we have two years of data in hand. If we go that route, these reports and bulletins would serve as the foundation for a paper so it is valuable exercise.
  + As for seeing the light of day, I am working hard to change that. See this paper which cites two of the previous Information Reports <https://doi.org/10.1093/jhered/esab069> Though the links are broken and ODFW is still working to repair them.
  + Given the timing of the petitions, the NOAA review process and issues that needed to be resolved between ODFW and previous collaborators, we had to opt for reports vs. a peer-reviewed paper so that they could be cited in the peer-reviewed paper.
* ***Spring Chinook salmon in the lower river are defined as those adult Chinook salmon that enter freshwater during the period from February through mid-July, and pass Huntley Park (river mile 8) by Julian Day 252 (September 9 during non-leap years).* Would this new genetic information provide the opportunity to update this definition to one more biologically relevant based on genetic markers? Could still be index to timing for ease of "field ID" but might be useful in management docs to have a more rigorous definition since it is now available.**
  + Note, based on Dan Van Dyke’s comment, we have removed the phrase “and pass Huntley Park (river mile 8) by Julian Day 252 (September 9 during non-leap years).”
  + Yes, genetic information can be used to improve our understanding of spring Chinook salmon in this system. Based on results illustrated in Figure 5, the last homozygous spring Chinook salmon was detected on July 15 while the first homozygous fall Chinook salmon was detected on June 3. Heterozygous fish were detected April 29 – September 2. I’ll defer to the managers as to how best to incorporate the genetic information and possibly update the definition.
* ***For example, O’Malley et al. (2020a) successfully genotyped 158 Chinook salmon caught in the Lower Rogue River fishery from March 19 to July 8 in 2019 and reported that the majority (~84%) of the naturally produced homozygous spring Chinook salmon were captured prior June 1.* Information Report says May 20-something, I think. Why the change? Just more conservative or implementable number?**
  + The statement that is being referenced can be found in the Discussion section of the previous Information Report (O’Malley *et al.* (2020a): *Based on Greb1L SNP1, the majority of naturally produced homozygous spring Chinook salmon (83.8%; 98 out of 119 fish) genotyped in this study were captured during the period when retention of unmarked Chinook salmon was prohibited (Mar 1-Jun 1). Thus, the current angling regulations are protective of the early run life history genetics.*
* **Volunteer angler, creel and seine samples were caught successively but at distinct and separate times. Does that introduce any caveats/bias? Two are fishery dependent and one is fishery independent. Any chance different life histories bite better? Little Devil's advocate here.**
  + Yes, all good points and reasons why it would likely be difficult to publish these results in a peer-reviewed paper.
* **Text above indicates no overlap in sampling dates between creel and seine. However, this figure shows overlap. X-axis scale and figure caption indicates these are "Sampling Weeks" NOT "Sampling Dates" as labelled. If that is the case, might want to change x-axis label just to clarify.**
  + No dates overlap between Creel and Seine sampling, but the end of the Creel sampling period and the beginning of the Seine sampling period overlap when the data is binned by week as it is in the figure. For example, July 19 is a Creel Survey day and July 21 is a Seine day, both fall in the interval between July 15 and July 22.
  + The caption was not revised, but the x-axis label was revised to “Week”
* ***Based on greb1L SNP1, the majority of naturally produced homozygous spring Chinook salmon (82%; 41 out of 50 fish) genotyped in this study were captured during the period when retention of unmarked Chinook salmon was prohibited (April 5-May 31).* Thought results said a total of 49 homozygous ChS.**
  + Yes, 49 individuals were homozygous spring when focusing on the two *greb1l* SNPs but 50 individuals were homozygous spring when focusing only on *greb1l* SNP1.
  + *Of the remaining 209 samples, 49 samples were genotyped homozygous spring, 35 samples were genotyped heterozygous, 121 samples were genotyped homozygous fall and four samples had discordant genotypes across the two greb1l SNPs.*
  + *Focusing only on greb1l SNP1, 50 individuals were homozygous spring, 37 were heterozygous, and 122 were homozygous fall*
* ***The majority of naturally produced Chinook salmon collected at Huntley Park from July 21 to Sept 30 were homozygous fall Chinook salmon (91%; 120 out of 132 fish). The remaining fish were heterozygous at greb1L SNP1.* Are heterozygous fish still important as a potential reservoir of "spring" timing alleles (or fall for that matter though they seem less an issue here)? Possibly an important management consideration if we're looking to maintain the genetic potential to adapt to changing conditions and/or rebuild from catastrophic events.**
  + Yes, heterozygous fish are still important as a potential reservoir of "spring" timing alleles.
  + We included a sentence in the Discussion to emphasize this point.
* ***Despite a highwater event in April of 2019, anglers collected samples from 107 Chinook salmon caught in the Lower Rogue River from March 19 to May 31. In 2020, only 47 angler-caught samples were collected from Chinook salmon in the Lower Rogue River from April 5 to May 26.* Think this is its own separate thought but requires a little more text to explain importance. This was due to overall lower run size? Wild Fire? Lower/hot water? Etc?**
  + As Dan Van Dyke pointed out, “fishery success in the lower river is associated with higher river flows. When I look at the graphs of flow (added to the end of this document) it not surprising to me that more fish were caught in 2019 than in the lower flow year of 2020, regardless of the 2019 flood. I think there is data on this in the ChS completion report if you are interested. Definitely not critical for this paper.”
  + Based on Dan’s comment, we have removed this point from the Discussion.
* ***In both years, more than 80% of the fish sampled prior to June 1 were homozygous spring Chinook salmon based on greb1L SNP1. It is important to note that in 2019 and 2020, homozygous spring Chinook salmon represented about one third the total catch after this sample period. In 2019, 36.5% (19 out of 52 fish) of the naturally produced Chinook salmon sampled between June 1 and July 8 were homozygous spring. Similarly in 2020, 38.1% (8 out of 21 fish) of the naturally produced Chinook salmon sampled between June 2 and July 8 were homozygous spring.***

**I struggled a bit with this whole paragraph. When I read it closely, I realized it was referencing what proportion of the total fish homozygous spring Chinook represented pre/post June 1 in both years (denominator was total spring chinook within each period). However, my brain really wanted to read it as the proportion of homozygous spring chinook caught pre/post June 1 (denominator was total homozygous spring Chinook caught across whole sampling season). This latter way was more intuitive to me.**

**I think the fisheries manager part of my brain was more concerned with where I set the guideline to escape enough homozygous spring Chinook than what proportion of the overall catch the represent by time period. If that is a critical insight, perhaps explain why/how? I might be dense on this one.**

* + Xx
* ***In both years, more than 80% of the fish sampled prior to June 1 were homozygous spring Chinook salmon based on greb1L SNP1. It is important to note that in 2019 and 2020, homozygous spring Chinook salmon represented about one third the total catch after this sample period. In 2019, 36.5% (19 out of 52 fish) of the naturally produced Chinook salmon sampled between June 1 and July 8 were homozygous spring. Similarly in 2020, 38.1% (8 out of 21 fish) of the naturally produced Chinook salmon sampled between June 2 and July 8 were homozygous spring.* These dates and the ones below for 2020 are different and seem a little arbitrary (though they might not be). Could you just say "following June 1" instead. That would be clearer and simpler assuming it is also accurate in both locations.** 
  + The paragraph has been revised to hopefully improve clarity: *In both years, more than 80% of the fish sampled prior to June 1 were homozygous spring Chinook salmon based on greb1L SNP1. It is important to note that in 2019, 36.5% (19 out of 52 fish) of the naturally produced Chinook salmon sampled from June 1 to July 8, the last day of sample collection, were homozygous spring. Similarly in 2020, 38.1% (8 out of 21 fish) of the naturally produced Chinook salmon sampled during the same period were homozygous spring.*

**Marc Johnson’s comments in bold:**

**Science Bulletin text is in italics**

* ***ODFW’s management strategy for the spring Chinook salmon fishery in the Lower Rogue River is to protect wild early run “spring” Chinook salmon while providing harvest opportunity on hatchery (i.e. adipose fin removed) spring Chinook salmon.* (or natural origin) Accidental omission? Otherwise, I'm confused by this sentence.**
  + Revised to “natural-origin”
* **These adult run timing genetic markers provide a useful tool to evaluate the effectiveness of management actions ~~with respect to the metrics described in the Rogue Spring Chinook Salmon Conservation Plan~~ intended to….[describe the intent of relevant management actions, to give meaning here].**
  + The text was not revised to address this comment.
* ***O’Malley et al. (2020b) also used the adult run timing markers to evaluate the spatial and temporal patterns of “early” and “late” run alleles across the entire spawning period for Chinook salmon in the Upper Rogue River (river mile 125.5-157)…*Consider using all metric - map of figure 1 already in km. Same comment for Figure 3 caption.**
  + x
* ***In this additive scenario, particular attention might be paid to escapement of spring associated alleles per se rather than genotypic class of individuals.* Is this a suggestion? If so, I suggest more direct language be used.**
  + The text has been revised:

However, a potential disconnect between sampling date and migration timing due to the possibility of individuals holding in the lower river before sampling reduces our confidence in this estimate (Waples et al. 2022).

Under an additive model, we could pay particular attention to escapement of spring associated alleles themselves rather than genotypic class (i.e. – homozygous v. heterozygous) of individuals. From this perspective, half of all spring-associated alleles at greb1L SNP1 in the dataset are observed by the third week of May and 80% of all spring associated alleles are observed by the third week of June.

**Dan Van Dyke’s comments in bold**

**Science Bulletin text is in italics**

* **As a result of improved returns of spring Chinook salmon following plan adoption, however, ODFW proposed a framework for providing additional fishery opportunities if population abundance continues to increase, even if abundance is below desired status.**
  + **Most recent returns have declined in line with poor ocean conditions (just barely dropped into conservation status this year). Our ChS are thought to be the rogue fish with the most northerly distribution in the ocean, so these fish may have experienced lower productivity than other Rogue runs. The wording I used above may be better.**
  + The text has been revised as Dan suggested.
* *Briefly, we filtered genotypes on the basis of missingness, sample duplication and the individual fuzziness index (IFI), which estimates the amount of cross-contamination in a given individual.*
  + **Really? These are real terms?**
  + Yes
* ***Based on greb1L SNP1, the majority of naturally produced homozygous spring Chinook salmon (82%; 41 out of 50 fish) genotyped in this study…*** **Fyi—pg 1 states approx. 84%**
  + The statement on page 1 refers to samples collected in 2019. The statement above refers to samples collected in 2020.
* **For what it’s worth, fishery success in the lower river is associated with higher river flows. When I look at the graphs of flow (added to the end of this document) it not surprising to me that more fish were caught in 2019 than in the lower flow year of 2020, regardless of the 2019 flood. I think there is data on this in the ChS completion report if you are interested. Definitely not critical for this paper.**
  + The statements regarding flow and catch have been removed from the Discussion.
* *Based on greb1L SNP1, the majority of naturally produced homozygous spring Chinook salmon (82%; 41 out of 50 fish) genotyped in this study were captured during the period when retention of unmarked Chinook salmon was prohibited (April 5-May 31). The remaining nine homozygous spring Chinook salmon were captured between June 2 and July 19. During this same period, 19 heterozygous and 2 homozygous fall fish were caught by anglers or sampled at the cleaning station. The majority of naturally produced Chinook salmon collected at Huntley Park from July 21 to Sept 30 were homozygous fall Chinook salmon (91%; 120 out of 132 fish). The remaining fish were heterozygous at greb1L SNP1.*

*Despite a highwater event in April of 2019, anglers collected samples from 107 Chinook salmon caught in the Lower Rogue River from March 19 to May 31. In 2020, only 47 angler-caught samples were collected from Chinook salmon in the Lower Rogue River from April 5 to May 26. In both years, more than 80% of the fish sampled prior to June 1 were homozygous spring Chinook salmon based on greb1L SNP1. It is important to note that in 2019 and 2020, homozygous spring Chinook salmon represented about one third the total catch after this sample period. In 2019, 36.5% (19 out of 52 fish) of the naturally produced Chinook salmon sampled between June 1 and July 8 were homozygous spring. Similarly in 2020, 38.1% (8 out of 21 fish) of the naturally produced Chinook salmon sampled between June 2 and July 8 were homozygous spring.*

* + **In the paragraph above, the 2020 data are reported for the period June 1-July 19—9 chs, 19 hets, 2 chf. Not a big deal, and I don’t remember whether July 8 vs July 19 relates to one of the methods used, but I noticed the difference—I thought ChS were just under 30%, not 38%. Caused me to look at the numbers in detail.**
  + I am not sure I understand this comment since the 2020 data are reported above for the period of June 2 – July 19.
  + In 2019, the last day a fish was captured was on July 8th.
  + The paragraph has been revised to:

*Based on greb1L SNP1, the majority of naturally produced homozygous spring Chinook salmon (82%; 41 out of 50 fish) genotyped in this study were captured during the period when retention of unmarked Chinook salmon was prohibited (April 5-May 31). The remaining nine homozygous spring Chinook salmon were captured between June 2 and July 19. During this same period, 19 heterozygous and 2 homozygous fall fish were caught by anglers or sampled at the cleaning station. The majority of naturally produced Chinook salmon collected at Huntley Park from July 21 to Sept 30 were homozygous fall Chinook salmon (91%; 120 out of 132 fish). The remaining fish were heterozygous at greb1L SNP1.*

*In both years, more than 80% of the fish sampled prior to June 1 were homozygous spring Chinook salmon based on greb1L SNP1. It is important to note that in 2019, 36.5% (19 out of 52 fish) of the naturally produced Chinook salmon sampled from June 1 to July 8, the last day of sample collection, were homozygous spring. Similarly in 2020, 38.1% (8 out of 21 fish) of the naturally produced Chinook salmon sampled during the same period were homozygous spring.*

* *From this perspective, half of all spring associated alleles at greb1L SNP1 in the dataset are observed by the third week of May and 80% of all spring associated alleles are observed by the third week of June.*
  + **80% of spring alleles found in homozygous and hets are observed by the third week of June?**
* **General: So that spring allele comment is interesting. For instance, more protective angling regulations that might be used when the population is in conservation status or facing uncertain river conditions could use that 3rd week in June date—wild harvest opportunity is delayed until the last week in June.**

**I know this is obvious, but just thought I would reiterate—the objective of our spring chinook plan is to achieve a healthy population that can sustain desired status levels of abundance and provide additional opportunity to harvest wild fish, with an emphasis on restoring the early run component of the population. Early run ChS experienced the most significant decline following dam construction and operation. These fish return early, contribute very well to the fishery in the river, tend to larger, and migrate the farthest distance upstream.**

**During plan development, ODFW estimated that harvest rates on early run fish were not sustainable. The angling regulation format was intended to protect early run fish from direct harvest, while encouraging more fishing pressure on late run Chs (harvested at much lower rates than early run fish at plan adoption).**

**This focus on early run fish was prescient—early run is almost synonymous with homozygous. My point is simply that we don’t at this time manage to protect all homozygous or all spring alleles. I know you know this, but thought it might be good add here as a comment.**

* + The text has been revised to incorporate the points above.



