

Memorandum

To: Wells, Rocky Reach, and Rock Island HCPs Hatchery Committees and Priest Rapids Coordinating Committee Hatchery Subcommittee Date: October 16, 2019

From: Tracy Hillman, HCP Hatchery Committees Chairman and PRCC Hatchery Subcommittee Facilitator

cc: Larissa Rohrbach, Anchor QEA, LLC

Re: Final Minutes of the September 18, 2019 HCP Hatchery Committees and PRCC Hatchery Subcommittee Meetings

The Wells, Rocky Reach, and Rock Island Hydroelectric Projects Habitat Conservation Plans (HCPs) Hatchery Committees (HCs) and Priest Rapids Coordinating Committee Hatchery Subcommittee (PRCC HSC) meetings were held in Wenatchee, Washington, on Wednesday, September 18, 2019, from 9:00 a.m. to 2:30 p.m. Attendees are listed in Attachment A to these meeting minutes.

Action Item Summary

Joint HCP-HCs and PRCC HSC

- Mike Tonseth will coordinate with Andrew Murdoch (Washington Department of Fish and Wildlife [WDFW]) to present pre-spawn mortality modeling results for spring Chinook salmon at an upcoming HCP-HC meeting (Item I-A). *(Note: this item is going.)*
- Kirk Truscott will discuss with Colville Confederated Tribes (CCT) biologists whether elemental signature analysis could differentiate natural-origin Okanogan spring Chinook salmon from other natural-origin Chinook salmon during broodstock collection at Wells Dam for Methow Fish Hatchery programs (Item I-A). *(Note: this item is ongoing.)*
- Brett Farman will discuss with Charlene Hurst (NMFS) and Tonseth the potential use of a multi-population model for estimating proportionate natural influence (PNI) for the Nason and Chiwawa spring Chinook salmon programs (Item I-A). *(Note: this item is ongoing.)*
- Greg Mackey will distribute a white paper reviewing broodstock composition and mating strategies for conservation programs, focusing on spring Chinook salmon at the Methow Hatchery (Item I-A). *(Note: this item is ongoing.)*
- Larissa Rohrbach will add HCP Policy Committee guidance on policy-level issues to the HCP-HC Meeting Protocols (version dated May 15, 2019; Item I-A).
- Tonseth will distribute a suggested drafting plan for the Broodstock Collection Protocols (BCPs) assigning specific members to address topics for discussion; Tracy Hillman will determine

whether there is a need for an additional conference call in early October to discuss research needs to address given topics (Item II-B).

- Catherine Willard will coordinate with other HCP-HC and PRCC HSC members to draft separate sets of genetic monitoring hypotheses that are specific for the individual hatchery programs to monitor for changes in population genetics over time (Item II-C).

PRCC Hatchery Subcommittee

- PRCC HSC representatives will submit a list of minimum data or information needs for making a decision on the White River spring Chinook salmon hatchery program to Tracy Hillman (Item I-A). (*Note: This item is ongoing.*)
- Brett Farman will ask Craig Busack (National Marine Fisheries Service [NMFS]) to participate in PRCC HSC process for identifying data needs and making a decision on the White River spring Chinook salmon hatchery program (Item I-A).

Decision Summary

- The Wells HCP-HC voted to concur that there is sufficient capacity at Wells Fish Hatchery for WDFW's additional production of subyearling Chinook salmon for southern resident orca prey, without compromising the existing, on-station HCP programs, confirmed via an email by Larissa Rohrbach on September 11, 2019 (Item I-A).
- The Rock Island and Rocky Reach HCP-HCs voted to approve the *Relative Reproductive Success Study Extension SOA Memorandum* in today's meeting (Item II-A).
- The HCP-HCs and PRCC HSC voted to approve the *Broodstock Collection Protocols Development Timeline Statement of Agreement* in today's meeting (Item II-B).
- The Wells HCP-HC voted to approve Douglas PUD's 2019 Egg Treatment Study Plan in today's meeting (Item III-A).
- The Rock Island and Rocky Reach HCP-HCs voted to approve Chelan PUD's 2020 Draft Monitoring and Evaluation Implementation Plan in today's meeting (Item IV-A).

Agreements

- The HCP-HCs and PRCC HSC agreed to describe the alternative method of equivalence testing in the narrative in the genetic monitoring objectives of the PUDs' Monitoring and Evaluation Plan (M&E Plan).

Review Items

- Larissa Rohrbach sent an email to the Wells HCP-HC on September 16, 2019, notifying them that Douglas PUD's draft 2018 Monitoring and Evaluation Report for the Wells and Methow programs is available for 60-day review with edits due by Friday November 15, 2019 (Item I-A).

- Rohrbach sent an email to the Wells HCP-HC on September 20, 2019, requesting a vote by email to indicate agreement with Douglas PUD that releasing surplus fish from the Methow Safety-Net and Columbia Safety-Net Programs into a non-anadromous lake will not prevent the HCP steelhead programs from meeting the target production.

Finalized Documents

- The Monitoring and Evaluation of the Chelan and Grant County PUDs Hatchery Programs 2018 Annual Report was distributed via email by Larissa Rohrbach on September 16, 2019.
- The Rock Island and Rocky Reach HCP-HCs-approved *Relative Reproductive Success Study Extension SOA Memorandum* was distributed via email by Rohrbach on September 23, 2019 (Item II-A).
- The Rock Island and Rocky Reach HCP-HCs-approved *Broodstock Collection Protocols Development Timeline Statement of Agreement* was distributed via email by Rohrbach on September 23, 2019 (Item II-B).
- The Wells HCP-HC-approved *Broodstock Collection Protocols Development Timeline Statement of Agreement* was distributed via email by Rohrbach on September 23, 2019 (Item II-B).
- The Wells HCP-HC-approved *2019 Egg Treatment Study Plan* was distributed via email by Rohrbach on September 23, 2019 (Item III-A).

I. Welcome

A. Review Agenda, Review Last Meeting Action Items, and Approve the August 21, 2019 Meeting Minutes (Tracy Hillman)

Tracy Hillman welcomed the HCP-HCs and PRCC HSC and reviewed safety procedures on safe egress and first aid, should an emergency occur during the meeting.

Hillman asked for any additions or changes to the revised agenda (distributed via email by Larissa Rohrbach on September 17, 2019). The HCP-HCs and PRCC HSC members voted to approve the revised agenda.

The HCP-HCs and PRCC HSC representatives reviewed the revised meeting minutes. Rohrbach said there were some revisions that the representatives then reviewed. Additional revisions were made in the meeting. The HCP-HCs and PRCC HSC members approved the meeting minutes as revised.

Action items from the HCP-HCs and PRCC HSC meeting on August 21, 2019, were reviewed, and follow-up discussions were addressed (*note: italicized text below corresponds to agenda items from the meetings on August 21, 2019*):

Joint HCP-HCs and PRCC HSC

- Mike Tonseth will coordinate with Andrew Murdoch (WDFW) to present pre-spawn mortality modeling results for spring Chinook salmon at an upcoming HCP-HC meeting (Item I-A). *Tonseth said this item is ongoing. Tonseth said pre-spawn mortality has been estimated for females but not yet for males. Todd Pearsons asked if this topic is going to be discussed by Jeff Jorgensen in the September 25, 2019 PRCC meeting. Keely Murdoch said Jorgensen gave a presentation to the Regional Technical Team (RTT) last week that will probably be similar to what will be presented to the PRCC. Tracy Hillman said that in the RTT meeting, Jorgensen did note that model results were sensitive to pre-spawn mortality. Murdoch said Jorgensen compared the Wenatchee populations with others, particularly Willamette River spring Chinook, and he said the pre-spawn mortality observed in the Wenatchee River is not atypical compared to other basins. Pearsons asked if pre-spawn mortality estimates are needed for the long-term need to discuss changes to conservation program sizing. Murdoch said yes, pre-spawn mortality is needed for the crude back-casting she has done to work on conservation program sizing. It was suggested that the life-cycle model could be used to inform a new model to forecast sizing of the conservation programs. Murdoch said she believed that early estimates of pre-spawn mortality included in program-size back-casting are too low; the data that were used were from the original Wenatchee spring Chinook management plan that was written early in the process of collecting pre-spawn mortality data. Tonseth said he did not know if pre-spawn mortality information would be passed to Jorgensen for inclusion in the Wenatchee life-cycle model.*
- Kirk Truscott will discuss with Colville Confederated Tribes (CCT) biologists whether elemental signature analysis could differentiate natural-origin Okanogan spring Chinook salmon from other natural-origin Chinook salmon during broodstock collection at Wells Dam for Methow Fish Hatchery programs (Item I-A). *Truscott said this item is ongoing.*
- Brett Farman will discuss with Charlene Hurst and Tonseth the potential use of a multi-population model for estimating PNI for the Nason and Chiwawa spring Chinook salmon programs (Item I-A). *Farman said this item is ongoing.*
- Hillman and Larissa Rohrbach will add review of the BCPs to the September meeting agenda to help the HCP-HCs and PRCC HSC identify co-authors and opportunities to discuss major revisions in advance of 2020 deadlines (Item II-F). *This item will be discussed in today's meeting. This item is complete.*
- Greg Mackey will distribute a white paper reviewing broodstock composition and mating strategies for conservation programs, focusing on spring Chinook salmon at the Methow Hatchery (Item I-A).

Mackey said this item is ongoing. Mackey said the paper is complete and will be distributed after the meeting. He will give a presentation on this topic in today's meeting.

- Rohrbach will add HCP Policy Committee guidance on policy-level issues to the HCP-HC Meeting Protocols (version dated May 15, 2019; Item I-A).

Hillman said this item is ongoing, pending finalization of the HCP Policy Committee meeting minutes. He said the draft meeting minutes were distributed a few days ago asking for a couple of weeks for meeting attendees to review.

- Catherine Willard will update the genetics section of the *Monitoring and Evaluation Plan for PUD Hatchery Programs (Update to the 2017 Plan)* to reflect revisions that were suggested in the August 21, 2019 meeting (Item II-D).

Willard sent an updated version to the HCP-HCs and PRCC HSC as distributed by Rohrbach on September 17, 2019. This topic will be discussed in today's meeting. This item is complete.

PRCC Hatchery Subcommittee

- HSC representatives will submit a list of minimum data or information needs for making a decision on the White River spring Chinook salmon hatchery program to Tracy Hillman (Item I-A).

Hillman said this item is ongoing.

- Brett Farman will ask Craig Busack (NMFS) to participate in the Wenatchee Basin life-cycle modeling discussion at the PRCC meeting on September 25, 2019, at Wanapum Dam, Washington (Item V-B).

Farman said neither he nor Busack will be able to participate in the September 25, 2019 PRCC meeting due to an internal conflicting meeting. Hillman asked if Busack will be able to re-engage with the HSC. Farman said he will discuss this with Busack on Friday. This item is complete.

II. Joint HCP-HCs and PRCC HSC

A. DECISION: Relative Reproductive Success Study Extension SOA Memorandum Update

Mike Tonseth said Catherine Willard provided suggested edits to the section on ESA Take and Permitting via email between meetings. Tonseth said Willard's changes were incorporated for clarity but no substantive changes were made to the plan from the previous version.

Todd Pearsons said it seems like there was concern about the adult sampling rate at Tumwater Dam and how that sampling rate may affect the PUD programs. Pearsons said for example the Relative Reproductive Success (RRS) Study Plan is written for a 100% sample rate of returning natural-origin adults, and the PUDs don't need a 100% sample rate and may only need to sample 3 to 4 days per week, which could be a source of conflict. Tonseth said the permit allows a 100% sample rate.

Tonseth said he does not see the connection to the PUD programs. Pearsons asked whether this SOA summarizes what is ongoing in the RRS Study. Pearsons said he thought the sampling rate was intended to collect a representative subsample versus a 100% sample, at least during the main portion of the adult spring Chinook sample run.

Tonseth said the goal of the study has always been to sample up to 100% of the natural-origin adults based on the assumption that a larger sample size would provide better data. Tonseth said they recognize that sampling all adults is not always possible. For instance, achieving an 80% sample rate is acceptable. Tonseth said the focus of the RRS Study extension memorandum is natural-origin adults; the hatchery-origin adults are not part of this memorandum.

Pearsons asked whether it is necessary to have 80% to 100% of the offspring of the RRS Study fish genetically typed back to the parents. Pearsons said he thought this would be analogous to sampling the smolts at the smolt trap; to capture a subsample of the total population. Tonseth said it is correct that the intent is to collect an adequate number of genetic samples from the progeny of the parents who are the focus of the RRS Study analysis. Tonseth said the smolt trap is only capable of sampling a portion of the river and smolts at one time, whereas at Tumwater Dam they have the ability to sample nearly all fish.

To clarify, Willard asked whether the original RRS study plan did state the goal was to sample 100% and the reason for this revised SOA was to extend the duration of the study? Tonseth said yes, and to ensure the focus of the study was on natural-origin adults.

Hillman asked Pearsons whether his question was to clarify management goals or to determine potential effects of RRS Study sampling on PUD programs? Pearsons said clarity should be provided in the SOA revisions that the goal is to sample 80% to 100% or a representative sample of the natural-origin returns. Pearsons said when a study requires 100% sampling or a relative subsample, it has been communicated in committee in the past.

Hillman suggested adding a sentence to the Proposed Action stating the permit allows for sampling up to 100% of adults. Pearsons suggested adding a sentence about the intent, not just what is allowed. Tonseth said the intent is to sample 100% of the population, if possible. Bill Gale suggested adding a sentence that reads, for example, "the goal of the study is to sample the maximum amount of the natural-origin population as possible, up to 100% of adult fish passing over Tumwater Dam."

Hillman called for a vote of the Rock Island and Rocky Reach HCP-HCs and PRCC HSC to approve the revised *RRS Extension SOA Memorandum*, including the revisions suggested in today's meeting. All members of the Rock Island and Rocky Reach HCP-HCs and PRCC HSC voted to approve the memorandum.

Tonseth said he will finalize the *RRS Study Extension SOA Memorandum* by including today's revisions and distribute it to the HCP-HCs and PRCC HSC (Attachment B).

B. DECISION: Broodstock Collection Protocols Development

Broodstock Collection Protocols Timeline SOA

Mike Tonseth said there are no major revisions to the Annual BCP timeline SOA compared to the version distributed last month.

Bill Gale suggested adding some language that the committees will re-evaluate the effectiveness of the new timeline on a given date and determine if changes are necessary. Tonseth said he did not include specific dates in this SOA because he was trying to avoid having to develop multiple SOAs over several years. Greg Mackey asked Gale what direction he thinks the schedule could shift? Gale said given how complicated developing the BCPs has become over the past years, he is suggesting adding flexibility in the future and a point for deciding that changes to a given topic may not be made in time for that year's BCP. Gale and Mackey agreed one check-in date should be stated in the SOA and the BSP schedule would be evaluated on an as needed basis only, after the first year.. Tracy Hillman added language to the draft SOA in the meeting to allow for the schedule to be re-evaluated in August 2020.

Tonseth said there is a need to develop several versions of this SOA for each of the HCP-HCs and the PRCC HSC. Hillman will send the revisions made to the BSP timeline SOA in today's meeting to Tonseth. Tonseth will then develop three SOAs, one for each committee (Attachment C).

The HCP-HCs and PRCC HSC voted to approve the generic version with the knowledge that it will be used as a template for developing three separate SOAs for the different committees.

Tasks and Co-Authors

Tracy Hillman asked for a review of the BCP drafting plan to assign people to lead discussions and to draft revisions on specific topics. Mike Tonseth said he will distribute a suggested BCP topics assignment list next week for all to consider. Bill Gale asked if a conference call should be scheduled to review the list between meetings. Todd Pearsons suggested discussing the list in the October meeting. Hillman said he will determine whether there is a need for an additional conference call after Tonseth sends the draft list.

Greg Mackey said he is prepared to give a presentation on establishing ranges around broodstock collection targets in October.

Gale said Michael Humling (USFWS) is available to help Tonseth develop the content on out-planting surplus Methow spring Chinook. Mackey said Douglas PUD would be happy to help with that topic.

Catherine Willard said she is waiting for data to be able to discuss the sources for Chiwawa spring Chinook topic. Discussion of this topic will be moved to the November meeting.

Hillman said Kirk Truscott's task on elemental signature analysis to differentiate Okanogan spring Chinook from other stocks is not relevant to this year's BCP but progress should be made this year to prepare for collecting samples in subsequent years.

Keely Murdoch said the Yakama Nation typically provides the Coho broodstock collection plan as an appendix.

C. Genetics Updates to the Monitoring and Evaluation Plan for PUD Hatchery Programs

Catherine Willard said two additions were made to the PUDs' Monitoring and Evaluation Plan (M&E Plan) based on feedback from geneticists and discussions in last month's meeting. [1) adding hypotheses for tests of equivalence and 2) analyzing hatchery-origin fish in addition to natural-origin fish.]

Equivalence Testing

Catherine Willard said hypotheses were added based on an equivalence testing approach. These hypotheses are in addition to the standard null-hypothesis testing approaches. Equivalence testing was recommended by the Independent Scientific Advisory Board and the writers of the original M&E Plan. Changes were made to the M&E Plan by Willard and Tracy Hillman.

Willard said she discussed the M&E updates with Todd Seamons, WDFW geneticist, and Christian Smith, USFWS geneticist, to receive the geneticists' perspective on determining important effect sizes. Willard read from an email response provided by Seamons. Seamons wrote that to his knowledge there is no existing deterministic biological meaning for effect sizes for these genetic metrics; there is solid evidence for increasing genetic diversity but no evidence for determining the importance of the size of the difference between stocks or populations. Seamons wrote that knowledge of genomes is insufficient to determine the importance of the genetic differences. Bill Gale said Christian Smith's response was very similar. Hillman said the topic of how much genetic difference between hatchery and natural-origin fish is significant in terms of the recovery of the stocks has been discussed for many years. Gale said, simplistically, the M&E Plan will have to determine a value for deciding what is significant. Hillman said at this time, the M&E Plan allows simple statistics to determine if there is a difference between hatchery and natural-origin fish, noting that statistical significance may have nothing to do with biological or management importance. He indicated the Committees should try to determine a difference that is biologically important. Hillman said, however, it is difficult for managers to make a decision on effect size if geneticists can't decide what is a significant genetic difference.

Greg Mackey said when geneticists make a phylogenetic tree, they use a clustering algorithm. The main clustering algorithm is a bootstrap support tool to estimate the of the phylogenetic groups in the tree and also the [genetic] distance between clusters, which gives information on the confidence of how far apart different groups are [similar to effect size and statistical support]. Mackey said the post-hoc interpretation of these results is analogous to what managers have to use to identify what difference is important to the fish and program goals.

Kirk Truscott said re-occurring assessments should show the trend in assessments to look for greater and greater divergence over time. Truscott said managers also need to know the effective population size for interpretation, to decide whether effects are from hatchery influence, or are natural.

Hillman asked if a departure from the genetic baseline is observed, whether that is really a bad thing. He said it is possible that the baseline is not the ideal state because of past hatchery effects on the population. Hillman said the equivalence-test hypotheses were included in the M&E Plan for use in the future, when we have information on biological significance.

Mackey said for some metrics, we know what is a good or bad direction, e.g., it is always negative for a population when effective population size goes down. Mackey said causes for linkage disequilibrium or allele frequency shifts may be variable and not necessarily a negative impact of the hatchery population. Todd Pearsons said losing alleles is a bad thing generally. Mackey said, yes, generally an overall loss of allelic diversity would be bad, but if some alleles are lost and some are gained over time, it's hard to say whether it's bad for the program or not. Gale asked if low allelic diversity is necessarily a bad thing? Hillman said no, in his recollection of discussions with geneticists during the writing of the recovery plans, some loss of alleles happens when a population becomes locally adapted. Gale said perhaps at the scale of evolutionarily significant unit (ESU), there should be greater allelic diversity but at the local population scale, specialization would be better.

Tom Kahler asked if there is a different metric that should be used [besides allelic diversity]. Truscott said the ultimate goal is to evaluate whether the hatchery program is having a good or bad effect on the natural population. Truscott said the Committees should consider multiple aspects of a program (e.g., genetics, stray rate, productivity) to answer this question. Mackey said analyses should look for evidence for retention of genetic diversity, but also for evidence of homogenization across subpopulations from genes introduced by another subpopulation. Pearsons said there has now been a lot of review [of genetic monitoring objectives in the M&E Plan] and still there is a lot of uncertainty around the utility of the sampling and data. Pearsons agrees that it's hard to interpret the genetics data by itself, for instance (an extreme example), a population may have a very high proportion of hatchery origin spawners (pHOS) present on spawning grounds, but if the fish are not effective spawners there may be no genetic impact. You would not know this unless you looked at all the data together. Willard said once this document is updated, it can be reviewed in the future to

add new metrics. Pearsons suggested adding some details to note whether it's possible to establish a prescriptive effect size. Hillman said the standard statistical effect sizes can be included, but they may not be biologically relevant; he suggested including these but adding information that the biological relevance should be reviewed in the future. Pearsons said he is fine with editing the document either way. Willard noted that in Seamons' email, he said he would not be comfortable prescribing an effect size unless it was in a publication and peer reviewed.

All agreed decisions would not be made based on one metric. Hillman said the M&E Plan was written with this in mind. Pearsons said the problem may be that the HCP-HC and PRCC HSC programs are pushing the envelope on using data from long-term genetic monitoring.

Hillman said the monitoring questions are written such that we need to demonstrate no difference between hatchery and natural-origin fish. Equivalence testing is set up to evaluate these kinds of questions. Currently, however, the hypotheses are written to demonstrate differences. We can never prove the null hypotheses to be true. Therefore, we added additional hypotheses that allow equivalence testing even though we have not yet identified important biological differences.

Hillman asked if the Committees want to retain the edits, keeping in mind the plan will change after the completion of the Comprehensive Report and the Before-After-Control-Impact analyses. Pearsons asked if we could resolve the equivalency testing issue with a note stating there is no pre-determined effect size or take these equivalency hypotheses out completely. Hillman said the original M&E Plan included this language and we can add it back into the M&E Plan.

Gale said he sees value in leaving the equivalency hypotheses in the report, using the standard statistical approaches for testing but noting that it is unknown whether statistical differences are biologically meaningful. Gale said doing the analysis may provide information that could be used in the future. Hillman said standard thresholds identified in statistical text books could be used; for instance, the probability of a small difference could be 5%, a medium difference could be 10%, and a large difference could be 20%. Pearsons suggested performing a power analysis, given the data and the amount of variability, to identify the percent difference that can be detected without using predetermined thresholds of importance. Mackey agreed and said that a power analysis answers whether the test is able to detect a difference that could be large enough to be biologically meaningful (e.g., 10%).

All Members agreed to leave the alternative method of equivalence testing in the genetic monitoring objectives of the M&E Plan. Mackey said he would like the explanation [of effect size] in the main body of the text instead of just a footnote. Hillman said he would add text in the introductory sections pointing the reader to the nature of the interpretation.

Hillman said adding hypotheses to support equivalency tests makes sense for several other objectives of the M&E Plan that do not have specific targets (in addition to the genetic monitoring objectives). Pearsons said this may be a larger process for generating biologically significant effect sizes for other metrics and he needs more time to think about including effect size for all the objectives in the entire M&E Plan. Hillman suggested writing the hypotheses generically, since an equivalence test would not be appropriate for all metrics. Hillman said this was done originally but was later eliminated. Pearsons said general hypotheses make the decision-making of biological significance more difficult because more interpretation is needed. Pearsons said relevant effects sizes for objectives could also be informed by the comprehensive report after the end of next year.

Inclusion of Hatchery-Origin Fish in Genetic Monitoring

Tracy Hillman said the second question is about allelic frequency and whether it is appropriate to test hatchery-origin fish in addition to natural-origin fish. Todd Pearsons presented slides prepared by Grant PUD to expand on the discussion (Attachment D).

Slide 2: Pearsons said the focus is on integrated programs with a conservation component and a safety-net component. Integrated programs attempt to facilitate gene flow between natural-origin and hatchery-origin fish. Safety-net programs are one-generation removed from conservation programs and [ideally] don't spawn in nature; safety-net program fish are kept separate from the conservation program fish unless a population bottleneck occurs. Pearsons said this is because programs are willing to take more genetic risk if population abundance falls below a certain level. It's highly unlikely that there are any true wild fish over time.

Slide 3: A diagram shows the likelihood of having completely wild fish by descent (i.e., no hatchery ancestry) over seven generations of conducting an integrated hatchery program. The diagram showed Wild, Hatchery, and Safety-net fish. Safety-net fish are a "dead end" and not used in the integrated program typically. The Chiwawa spring Chinook program is on approximately the fifth generation. The intent of the figure is to show that when there is a high degree of mixing between natural-origin and hatchery-origin fish, it is difficult to discern genetic differences between the two groups. Pearsons said recent events [low natural-origin returns requiring the use of safety-net fish in broodstock] suggest the use of the safety-net fish may be different in the future. Keely Murdoch said this figure doesn't show what proportion of the natural-origin fish are going into the hatchery broodstock, which in some years is a lot lower than targets. Pearsons said yes, the diagram assumes equal reproductive success of hatchery and wild fish. Kirk Truscott said this also assumes the hatchery-origin and natural-origin fish occupy the same habitat and we know that's not true. Truscott said the level of mixing can be variable. For instance, a high proportion of hatchery-origin fish spawn next to the hatchery or acclimation facility. Murdoch asked if a different approach would

be taken for integrated and segregated programs. Pearsons said yes, the sampling could be different for integrated and segregated programs.

Greg Mackey said that in programs using all wild fish in broodstock, there is no hatchery lineage to test in that population. Mackey said the genetic samples would come from wild fish that could be the offspring of hatchery fish, except they would be influenced by only one generation of hatchery effects; there's no long-term hatchery lineage. Pearsons agreed and said that is at the heart of the discussion. If you were to compare hatchery and natural-origin fish, you are only comparing the effect of one generation, not six or seven generations of hatchery rearing. Tom Kahler said when it comes time to sample, one would ask "what are the hatchery fish?"

Slide 4: Pearsons said natural-origin fish are a good integrator of previous spawnings between hatchery- and natural-origin fish and reproductive success resulting from processes in nature. Pearsons said, for instance, in the Chiwawa many of those fish are not passing on genes to the next generation due to environmental conditions. He said integration of datasets on productivity with genetic analysis would inform decisions about the health of the natural-origin population. The Independent Scientific Advisory Board identified that the hypotheses were not necessarily structured to focus on the natural-origin population and so were inconsistent with the goal stated in the text.

Slide 5: Pearsons said programs are actively trying to minimize genetic differences between natural-origin and hatchery-origin fish (see Slide 5 of Attachment B for specific methods). Pearsons said early identification of divergence between hatchery-origin and natural-origin fish is addressed by monitoring PNI, stray rates, and other phenotypic measures. He asked, even if differences were detected, would it matter if it wasn't reflected in the population at large? For example, one may detect a genetic difference between hatchery-origin and natural-origin fish that are one generation removed, but all other metrics indicate the population is healthy and the natural-origin population sample does not indicate a problem. Truscott agreed these are good questions. The original perspective on genetic analysis of hatchery-origin fish was on how to sample, which analyses maximize the ability to assess a change caused by hatchery effects on the natural population, and to provide management options though we don't know what those management options would be. Truscott said a difference in genetics of hatchery and natural-origin fish may be an early indicator of a potential issue later. If the samples are not collected until decades later, the opportunity to make management changes [to limit or prevent adverse effects on natural-origin fish] may be lost. Truscott said the effort needed to collect additional hatchery-origin samples is relatively small and could be done as a preventative measure. Truscott said, for instance, proportion of natural origin fish in the broodstock (pNOB) is below the program targets and we don't know whether this is posing a demographic risk. Bill Gale said there is a limited ability to control safety-net fish spawning. For instance, in the Methow River, there is not a good barrier (like Tumwater Dam) to control their

passage. Pearsons suggested running the samples from the natural-origin baseline and contemporary natural-origin fish, and if no difference is detected then do not analyze the hatchery-origin fish. On the other hand, if a difference is detected it would be important to know if the difference was due to the hatchery. Pearsons said he supports a stepwise approach that may tell you the effect of the hatchery. Pearsons said the change may also be due to some other impact like a founder effect [in the broodstock for a given year].

Catherine Willard asked how big the difference would need to be between the natural-origin baseline and contemporary natural-origin fish. Pearsons said at this time the intent would be to test the null hypothesis and see if there is a difference. Truscott said it would still be a retrospective analysis on causation every 10 years to provide the confidence that there is no difference between the conservation programs or, alternatively, trigger an analysis of the program practices.

Slide 6: Pearsons said the alternative perspective is to ask whether it is worth investing in something that has limited utility on making management decisions for the program. Pearsons said if there are two completely separate lineages as in other programs, divergence in the genetic identities could be determined to be a result of gene flow over multiple generations.

Slide 7: Pearsons said in the outcomes of the last genetic assessment when hatchery and natural-origin samples were collected, there were no significant differences between hatchery and natural-origin fish. Pearsons said analyzing the hatchery-origin samples didn't add a lot to the discussion or work as an early warning system. Truscott said if there was no difference between hatchery and natural-origin fish, managers would be satisfied with the outcome of the hatchery programs from the genetic perspective. Willard said the previous sampling was a mixture of hatchery and natural-origin fish that may not be representative of the ideal statistical comparison. Hillman said the results from past genetic analyses are in the back of the annual report, which was finalized last week.

Slide 8, Conclusions: The first conclusion states, *"Unless significant differences are detected between baseline and contemporary natural-origin samples, there may be little benefit of running hatchery-origin genetic samples to address genetic M&E objectives."* Pearsons said Grant PUD supports a proposal to follow a stepwise approach. The second conclusion states, *"In cases where differences [between baseline and contemporary natural-origin samples] exist, then it may be worthwhile to run hatchery samples to help evaluate the mechanism of change."* Pearsons said segregated hatchery programs will be monitored differently.

Gale asked whether these samples have already been collected and analyzed for Parentage-Based Tagging (PBT) by CRITFC. Gale said the genotypes have been run and SNP data are available for these programs, perhaps it's just a matter of performing the analyses. Willard said yes, for some but not all populations. Pearsons said natural-origin samples are available for Upper Columbia fall

Chinook, if the Committees chose to run hatchery-origin samples, the samples are probably available.

Kahler said for Methow spring Chinook it would not be obvious what the hatchery-origin fish would be. Would they be hatchery-origin fish sampled on the spawning grounds? Hatchery-origin fish that return to the hatchery? Hatchery-origin fish used in broodstock? Gale said it would include all of those.

It was agreed that sampling of upper Columbia programs for PBT analysis is somewhat comprehensive already for the Chinook and steelhead programs. In the past there has been open sharing of data between CRITFC and USFWS geneticists, and there may be opportunities to analyze data that are already available. Hillman suggested coordinating with geneticists to determine whether samples are available. Pearsons suggested making a decision now about the genetic analysis approach and then determining whether samples are already available. Gale said it will save time to identify where sampling has already been done.

Hillman asked members for their individual perspectives on the need to analyze hatchery-origin fish genetically. Gale said the question of which fish to test as hatchery-origin fish is a major one but tends to agree that the analysis of hatchery-origin fish should go forward. Murdoch said she supports analyzing hatchery-origin fish when it informs the programs. Mike Tonseth supported analysis of hatchery-origin fish for some programs, but not all. For instance, it may not be necessary for segregated programs, nor non-conservation programs. Tonseth said the Wenatchee steelhead program should be analyzed to determine if there has been an influence because of the inclusion out of basin (Wells stock) fish in the broodstock historically. Brett Farman agreed that collecting more information from hatchery-origin fish in the near-term may prevent long-term genetic impacts. Mackey said he does not see the value of including hatchery-origin fish that are only one generation separated from the natural-origin parents and said it's complicated because the different programs have different bounds around including natural-origin fish in the broodstock. Mackey said we already have a better dataset on Methow steelhead for a long-term trend analysis using the Twisp RRS study data with 10 years of detailed data available, and there is a valuable long-term data set for analysis of spring Chinook in Methow using microsatellites. Willard said she understands the problems at hand regarding genetic distance resulting from only one generation of hatchery rearing and discerning which fish to test; however, if SNPs are already available, she agreed the samples could be analyzed.

Gale asked if the timing is aligned for analysis of the Methow and the Wenatchee fish? Mackey and Willard said yes, the timing of this analysis is now aligned. Gale said USFWS would like to do similar analyses and follow the same timeline so the outcomes and reporting are aligned for the entire Upper Columbia. He requested to be kept informed on the timeline for analysis.

Hillman summarized that there is a need to discern which programs should be analyzed, what would be compared for each type of program, and whether samples already exist.. Willard said for next year's HCP-HCs Comprehensive Report, collecting new samples is not possible, as that would have to occur now.

Pearsons asked Tonseth whether he was suggesting analyzing listed programs and not analyzing the unlisted programs. Tonseth said yes. Gale said for segregated programs, if the question is whether hatchery-origin fish differ from the natural-origin fish, the answer is yes. Willard said the question is different for segregated programs. Pearsons said the most relevant question is whether or how the hatchery-origin fish are affecting the natural-origin fish. Mackey said there can be multiple causes for differences in the genetics and it's difficult to identify those causes after the fact in order to make management decisions.

Hillman asked if the plan is to analyze the samples that have already been collected and use those to determine genetic differences over time? Truscott said yes, the original intent of genetic analyses was to track changes over time. Truscott said monitoring PNI using the multi-population model was undertaken because it was suspected there were differences between the hatchery-origin and natural-origin fish.

Mackey said the difference is that genetic monitoring evaluates neutral markers and doesn't inform the phenotypic changes between groups that are the result of selection. For instance, traits under selection can change while neutral markers show no change. Conversely, neutral markers may show a shift while traits under selection have remained stable. Truscott asked if this analysis would help us make a different decision about pNOB or pHOS or stray rate targets? Mackey said no, because the PNI concept is concerned with fitness traits that are under selection, but if there were major shifts in neutral allele frequency observed between groups you might be concerned that selective traits were also changing. Or, the neutral marker frequencies may shift while the trait under selection has not changed. The PNI concept is not (directly) concerned with neutral markers. It is focused on traits that are under selection.

Pearsons proposed incorporating the samples that were already analyzed by CRITFC. Willard agreed that this could be done for the Chiwawa spring Chinook program. Pearsons proposed keeping the hypotheses in the M&E Plan focused on natural-origin fish; however, the narrative could report on comparisons to hatchery-origin fish.

Tonseth said there is one disclaimer. DNA is collected on all broodstock except for summer Chinook (Methow and Wenatchee). There is no hatchery-origin lineage for those programs because they are achieving their pNOB targets of 1 and no samples are taken on hatchery-origin fish. Tonseth said natural-origin fish are identified as unclipped without wire tags and origin is confirmed by scale

analysis. Gale asked whether hatchery fish returning to Wells Dam for instance, are being bio-sampled. Tonseth said yes, samples are taken to confirm run composition, but the only biological samples taken are scales. Gale said for fish returning to USFWS facilities, they are collecting biological samples.

Hillman suggested following Pearsons' suggestion to delete the hypotheses on sampling hatchery-origin fish for programs in which genetics of hatchery-origin fish is not needed. Thus, the evaluation of hatchery-origin fish would be program specific. Hillman pointed out the section of the M&E Plan, which indicates that hatchery and natural-origin fish from "all programs" will be evaluated for genetics. Gale suggested editing it to say, "all integrated programs." Truscott asked what the nexus would be for genetic sampling if not included in this plan? Truscott asked if the comparison to hatchery-origin fish could begin with the 2017/2018 brood. Willard said yes. Truscott said there were samples collected for the Chief Joseph Hatchery Program that could be included with the Methow summer Chinook analysis. Pearsons agreed there is a need for coordinating the inclusion of all samples. Gale said if only natural-origin fish are included, USFWS would only contribute the samples from steelhead captured in winter and spring for broodstock; if hatchery-origin fish are included, it expands the scope to other programs.

Hillman recorded a placeholder in the target species or populations section of the M&E Plan to focus the hatchery-origin analysis on specific program types. Mackey said he needs time to map out what the relevant programs are and what samples are available. Pearsons asked how the Committees could complete this in time to discern what samples need to be sent for analysis. Hillman said the discussion so far indicates that segregated and unlisted programs would be excluded. Gale said he still questions whether segregated programs should be excluded. He said it may be useful to track whether the contemporary segregated broodstock is similar to or different from the natural-origin baseline and whether the population genetics are shifting over time. Willard said she agrees with Gale and there is a whole set of other questions for segregated programs. Gale said he would rather get this correct rather than rush these revisions and have a report that does not answer the questions at hand.

Pearsons asked whether there is support for moving the completion date for the genetics portion of the comprehensive plan? Kahler said the programs are ready to get started with analyses and it may not require a lot of time to determine which samples are analyzed.

Hillman said this may require identifying and categorizing the different hatchery programs within the M&E Plan and then writing specific hypotheses for each program category. Hillman suggested members craft specific hypotheses for each program category. Willard volunteered to coordinate with other members to develop a draft set of hypotheses for the various programs.

D. Alternative Broodstock Composition and Mating Strategies

Greg Mackey gave a presentation entitled, "*Review of Hatchery Broodstock and Mating Practices for Conservation Programs.*"

Mackey said in previous years a problem originated when encountering limitations on broodstock availability and asking whether jacks should be included in the broodstock. He said the answer to this question became a more comprehensive review of advancements in thinking about broodstock selection and mating strategies.

Slide 2: Mackey reviewed the purpose of conservation programs, which are the following:

- Conserve and rebuild populations
- Minimize negative ecological impacts
- Conserve diversity
- Minimize negative genetic impacts

Slide 3: Mackey said problems have been encountered if the ideal conditions are not met and problems must be worked around; artificial selection is inevitable when fish are propagated in hatcheries.

Slide 4, 5: Mackey identified key factors that contribute to artificial selection in broodstock collection and interaction with fisheries.

Slide 6: Mackey presented data showing the proportion of PIT-tagged Methow spring Chinook lost between Bonneville and McNary dams. Mackey said the data show larger (older) fish are being removed by the fishery, potentially changing the age structure of the populations. Bill Gale asked if jacks are being lost to fisheries, noting that the gill-net fishery is selecting older fish but are jacks kept in the recreational fishery? Mackey said these are spring chinook and there is not a recreational fishery on them that might remove jacks.

Slide 7: Mackey showed that Wells summer Chinook fecundity is on a downward trend in both the wild and hatchery fish and suggested it may be an effect of hatcheries, fisheries, or both. Mackey said he and Mike Tonseth have discussed whether this could be a factor of reduction in size or age at return.

Slide 8: Mackey reviewed published literature on jack contributions to a spawning population. Gale said information from a study by NMFS with steelhead using the Winthrop spawning channel could inform this work. Results are in a Bonneville Power Administration report. Tonseth said the Wenatchee RRS Study data could be leveraged. Mackey agreed getting the best available data to make decisions on incorporation of jacks into the broodstock would be good.

Slides 9 & 10: Mackey provided an example of the potential method for prescribing the contribution by jacks in a broodstock by multiplying jack rate by the typical rate of offspring produced by jacks in the natural environment.

Slide 11: Mackey presented a figure showing the complexities of steelhead mating systems in nature.

Slide 12: Mackey said genetic analysis done to determine if fish deformities observed in Twisp River spring Chinook were isolated to a small number of parents, suggesting a genetic family effect. He said the results showed there did not appear to be a tight connection to a genetic issue. However, in an extension of the original study, Sewell Young (WDFW) found that the Twisp River, a tiny population and a tiny program, has lower rates of homozygosity compared to all Snake River subpopulations. Mackey said small programs are often assumed to carry more genetic risk than large programs, but the population status may not be as bad as is often assumed.

Slide 13: Mackey summarized a large body of literature on strategies for broodstock management.

Slide 14: Mackey said the first general strategy, which he calls the genetically benign approach, seeks to use sufficient numbers of fish to minimize genetic drift and domestication, wild fish in the broodstock (though not necessarily a pNOB of 1), and randomized broodstock selection and spawning to minimize artificial selection.

Slide 15: Mackey said the second general strategy, which he calls emulating natural processes approach, seeks to actively counter artificial selection in hatcheries and fisheries for younger age at maturity, and to emulate mate choice in nature.

Slides 16–19: Mackey presented several other aspects of broodstock management including reviews of the following:

- Typical hatchery mating processes versus typical wild mate choices
- Production of early maturing males increases with use of wild broodstock
- Minimizing kinship
- Equalizing family sizes
- Various potential mating schemes
- Studies showing that humans do not do a great job of “randomly” selecting broodstock

Slides 20: Mackey described the current broodstock collection methods at Methow Hatchery:

- Broodstock collection is (somewhat) random
- Mating follows a 2x2 matrix with males used as backup reciprocally
- Culling only done to control bacterial kidney disease; not to control family size

Tonseth said jacks are not targeted because a size cutoff is used to differentiate age 3 and age 4 males, though some are inadvertently included in the broodstock at rates that could be similar to background levels. Mackey said he and Charlie Snow (WDFW) looked at the Methow spring Chinook data and did not think this was happening. Tonseth said it may be more common in the summer Chinook.

Slide 21: Mackey presented a possible path forward for the Methow Hatchery spring Chinook program, specifically, with several suggestions for consideration:

- Continue to collect brood at random to the best of our abilities
- Continue to use factorial mating protocols with backup males
- Include jacks at a rate they occur in the wild and fertilize eggs from one female at a percent observed in the wild (e.g. 20% of one female's eggs). Todd Pearsons said in some places the practitioners would add milt from one male (jack) in a small area of the mixing container [representative of the typical contribution from jacks on the spawning ground], allow it to fertilize, then mix in milt from full-size males to the rest of the container.
- Ensure time intervals between primary and back-up fertilization to minimize sperm competition
- Follow the model developed by Hankin to preferentially mate females with males that are larger to drive the population toward older age at maturity and larger individuals; however, its unknown the extent to which this can be applied in smaller programs because some fish ripen on different days resulting a numerous smaller spawns than fewer larger ones.
- Use genotypes to avoid close relatedness in matings

Gale said experience suggests that hatchery managers may resist changes because they tend to follow the protocols that provide them the best eye-up rates. Mackey said he talked to Brandon Kilmer (Douglas PUD Methow Hatchery Supervisor) and would work closely with hatchery staff. Mackey said staff at the Methow Hatchery are open to ways to improve.

Pearsons asked how the effects could be measured, for instance, could you select for some trait other than size like the Hankin model? Mackey said they were unaware of any other way to spawn fish together by a phenotype. Pearsons said there are some other patterns informed by the RRS Study work. Mackey said yes, the risk is it would cause really uneven family sizes, magnified by the hatchery process, and potentially exacerbate a Raiman-Laikre effect. Mackey said he would like to try a lot of different things but a constant challenge is balancing the need to stabilize spawning practices while trying to implement something new.

Gale asked if anyone has studied the difference in progeny produced in a spawning channel versus typical controlled hatchery spawning. Mackey said he is not familiar with any such study. Gale said

the Winthrop spawning channel produced a significant number of offspring in one study, more than he expected from a relatively small area.

Mackey suggested they would be trying some of this novel approach in the Methow Hatchery program. Gale said there has been a swing toward asking if the genetically benign approach recommended by the Hatchery Scientific Review Group (HSRG) is still the best path forward.

Hillman suggested Committees members share Mackey's review with hatchery managers to start informing them of a desire to improve broodstock selection and mating processes, and to bring them along in the discussion.

Mackey will send the literature review to Larissa Rohrbach for distribution.

E. National Marine Fisheries Service Consultation Update

Brett Farman provided one update. Farman said the permits that Emi (Kondo) Melton (NMFS) had reviewed (the unlisted summer and fall Chinook bundle and steelhead) were sent out for countersignature by WDFW and the PUDs.

III. Wells HC

F. DECISION: 2019 Egg Treatment Study Plan

Greg Mackey reminded the Wells Committee of the components of the draft 2019 Egg Treatment Study that were reviewed in the August 21, 2019 meeting. Mackey said he addressed comments provided by Mike Tonseth regarding oversights or areas that were not written clearly. He said the main goals are to reduce *Saprolegnia* infection and to reduce formalin use at the hatchery. The test carried out at Methow Hatchery in 2018 showed that plain water worked as well as other treatments; however, the eggs may not have been exposed to *Saprolegnia* fungus in the water supply at levels that cause infection. He reminded the Committee that the 2019 study includes a new treatment introduced using elemental copper ions that has worked in other trout hatcheries.

Mackey said he added a table that helped define the treatment groups and their ultimate fate. Mackey said they will try to reduce family effects on the study results by pooling eggs and dividing them into separate groups. He also clarified that 50 eggs from each treatment group tray will be retained and grown to the fry stage to observe latent effects of the treatments.

Study eggs could be surplus to the Wells Hatchery program and made available for other programs, or could be included in the Wells Hatchery production if needed to meet program targets. Fish treated with elemental copper cannot be released due to FDA regulations. Betsy Bamberger inquired with Ecology and FDA to determine rules for releasing fish from copper treated eggs but it was decided that the fish grown from copper treated eggs would not be released. Mackey said he added

a column titled "Available for Transfer" to Table 1 that indicates whether eyed eggs at that stage should be available for transfer to other programs or used in the Wells Hatchery program if treated with formalin, water or salt. Keely Murdoch asked if the copper-treated eggs are the only fish that could not be transferred. Mackey said yes, that was their determination at this time.

The Wells HC voted to approve Douglas PUD's draft *Control of Saprolegnia sp. Growth on Summer Chinook (Oncorhynchus tshawytscha) Eggs, Experimental Protocol – Pilot Study* as final.

IV. Rock Island/Rocky Reach HCs

A. Draft 2020 Monitoring and Evaluation Implementation Plan

Catherine Willard said no additional feedback on Chelan PUD's *Draft 2020 Monitoring and Evaluation Implementation Plan* was received after last month's meeting. Willard added Objective 7 to Table 5 as recommended in the last meeting. Hillman asked if there were any additional edits or comments; there were none.

The Rock Island and Rocky Reach HCs voted to approve Chelan PUD's *Draft 2020 Monitoring and Evaluation Implementation Plan* as final.

V. PRCC HSC

A. Approve the August 21, 2019 Meeting Minutes, Committee Updates, and Meeting Summary Review (Todd Pearsons)

The PRCC HSC representatives approved the August 21, 2019 meeting minutes as revised.

Tracy Hillman reminded the committees that they are invited to attend the PRCC meeting on September 25, 2019, when Jeff Jorgensen will present aspects of his Wenatchee spring Chinook life-cycle model and respond to questions from the PRCC and PRCC HSC. Keely Murdoch confirmed the meeting is scheduled for 10 a.m. at Wanapum Dam and usually outside presenters are scheduled for the beginning of the day. Hillman said he has requested that a call-in number be provided as well.

Hillman asked whether discussion of any other administrative business was necessary.

Todd Pearsons said the King of the Reach fishing derby will occur on October 25 through 27 [for the collection of Priest Rapids Hatchery Fall Chinook Salmon]. Pearsons said Grant PUD limited entries to 100 boats and the limit was reached in the first week after registration was open.

Tonseth said he has identified an additional topic for the PRCC HSC that should be considered during development of the BCPs. Tonseth said WDFW is still interested in reducing the reliance on the Priest Rapids Dam Off-Ladder Adult Fish Trap for collecting broodstock for the Priest Rapids

Hatchery Fall Chinook Program. Tonseth said WDFW is working toward determining whether enough broodstock could be collected by other means, such as in the King of the Reach derby.

No other business was discussed. Hillman adjourned the meeting.

VI. Administration

A. Next Meetings

The next HCP-HCs and PRCC HSC meetings are October 16, 2019, November 20, 2019, and December 18, 2019, at Grant PUD in Wenatchee, Washington.

VII. List of Attachments

Attachment A List of Attendees

Attachment B Rationale for using natural-origin fish for genetics monitoring in hatchery conservation programs

Attachment C Review of Hatchery Broodstock and Mating Practices for Conservation Programs

Attachment D Relative Reproductive Success Study Extension SOA memorandum

Attachment E Broodstock Collection Procotols Development Timeline SOA Revised

Attachment F *Control of Saprolegnia sp. Growth on Summer Chinook (Oncorhynchus tshawytscha) Eggs, Experimental Protocol – Pilot Study, 2019*

**Attachment A
List of Attendees**

Name	Organization
Tracy Hillman	BioAnalysts, Inc.
Larissa Rohrbach	Anchor QEA, LLC
Ian Adams	Chelan PUD
Catherine Willard*	Chelan PUD
Kirk Truscott*‡	Colville Confederated Tribes
Greg Mackey*	Douglas PUD
Tom Kahler*	Douglas PUD
Todd Pearsons	Grant PUD
Deanne Pavlik-Kunkel	Grant PUD
Brett Farman*‡°	National Marine Fisheries Service
Bill Gale*‡	U.S. Fish and Wildlife Service
Mike Tonseth*‡	Washington Department of Fish and Wildlife
Keely Murdoch*‡	Yakama Nation

Notes:

- * Denotes HCP-HC member or alternate
- ‡ Denotes PRCC HSC member or alternate
- ° Joined by phone