
**Guidance to Develop Alternatives for Determining
the Relative Reproductive Success and Effects on Natural-Origin
Fish of Hatchery-Origin Snake River Fall Chinook Salmon**

Final

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Purpose

This guidance document was developed by a large group of scientists (see cover page) representing numerous organizations and agencies to assist the Action Agencies (BOR, BPA, USACE) in meeting the Federal Columbia River Power System (FCRPS) Biological Opinion (BiOp) Reasonable and Prudent Alternatives (RPAs) 64 and 65 as they relate to Snake River fall Chinook salmon. The purpose of this document is to provide guidance to BPA and NPCC that will allow them to develop a targeted solicitation to fulfill the requirements of FCRPS RPAs 64 and 65.

1.0 Introduction

RPAs 64 and 65 of the 2008 FCRPS BiOp call for determining the relative reproductive success (RRS) and effects on productivity of hatchery origin Snake River fall Chinook salmon (SRFCS) on naturally produced SRFCS. The specific language of the RPAs is (text bolded for emphasis):

Investigate Hatchery Critical Uncertainties (RPA 64)

RPA 64.1 -- Continue to estimate the relative reproductive success (RSS) of hatchery – origin salmon and steelhead compared to reproductive success of their natural-origin counterparts for ESA-listed spring/summer Chinook population in the Upper Grande Ronde, Lostine River, and Catherine Creek; listed spring Chinook in the Wenatchee River; and listed steelhead in the Hood River. Continue to fund the ongoing RRS feasibility study for Snake River fall Chinook to completion in 2009 (Initiate in FY 2007-2009 Projects).

RPA 64.2 -- Determine if properly designed intervention programs using artificial production make a net positive contribution to recovery of listed populations (Initiate in FY 2007-2009 Projects).

RPA 64.3 -- In collaboration with the other entities responsible for steelhead mitigation in the Methow River, BPA will fund a new RSS study for ESA-listed steelhead in the Methow River. BPA will also fund a new RSS study for listed fall Chinook in the Snake River. NOAA Fisheries will provide technical assistance to the Action Agencies in development of conceptual study designs suitable for use by the Action Agencies in obtaining a contractor to implement the new studies (Initiate in FY 2007-2009 Projects).

Investigate Hatchery Critical Uncertainties (RPA 65)

RPA 65.1 -- In the mainstem Snake River above the Lower Granite Dam, estimate the effectiveness/fitness in nature of hatchery-origin fall Chinook salmon from federally funded Snake River hatchery programs relative to natural origin Snake River fall Chinook.

RPA 65.2 -- Estimate fall Chinook hatchery program affects on the productivity of the fall Chinook salmon ESU.

RPA 65.3 -- NOAA Fisheries will provide technical assistance to the Action Agencies in development of conceptual study designs suitable for use by the Action Agencies in obtaining a contractor to implement new studies.

Beginning in fall 2008 and continuing into 2010, workgroups were organized by the Action Agencies, NOAA Fisheries, and the NPCC to develop recommendations for implementing research, monitoring, and evaluation (RM&E) for the 2008 FCRPS BiOp. The workgroups first looked through existing work, trying to determine if gaps existing in implementing the RPAs that related to RM&E. In relationship to RPAs 64 (that relate to SRFCS) and 65, the *hatchery and harvest* workgroup recommended:

. . . working with appropriate stakeholders to identify the intent of RPAs 64 and 65 in relationship to Snake River fall Chinook salmon and identify methods to meet the intent.

In addition, as mentioned in RPA 65.3, NOAA Fisheries is obligated to provide technical assistance to the Action Agencies to develop the conceptual study designs. Based on these recommendations and NOAA's obligation, a workshop was developed to begin the process of determining how to address the RPAs. The Snake River Fall Chinook Hatchery Effects Workgroup met on April 27, 2010 in Lewiston, ID (please see Appendix A for a list of the participants), and met by conference call several times through August 2010. This document is a result of the workgroup's efforts to develop methodologies to address relative reproductive success (RRS) of SRFCS produced by hatchery programs and the effect of those hatchery programs on the productivity of naturally produced SRFCS.

1.1 Intent of RPAs

RPAs 64 (portions that relate to SRFCS) and 65 were added to the FCRPS BiOp to address concerns from NOAA Fisheries about the proportion of hatchery-origin SRFCS returning in recent years. The estimated proportion of hatchery origin fish passing Lower Granite Dam usually exceeds 80-85% of the total run. In addition, while the total run increased dramatically over the last 10 years, the number of natural-origin fish has remained relatively constant since the early 2000s (Figure 1). Current estimates of natural-origin SRFCS are approximately 2,900, which is slightly lower than the minimum abundance viability threshold suggested by the Interior Columbia Technical Recovery Team (ICTRT). The increase in total abundance of hatchery- and natural-origin SRFCS is attributed to an expanded hatchery program, reduced harvest rates after ESA listing, and favorable ocean conditions. The relatively stable increased abundance of natural-origin adults may be an indication of habitat limitations.

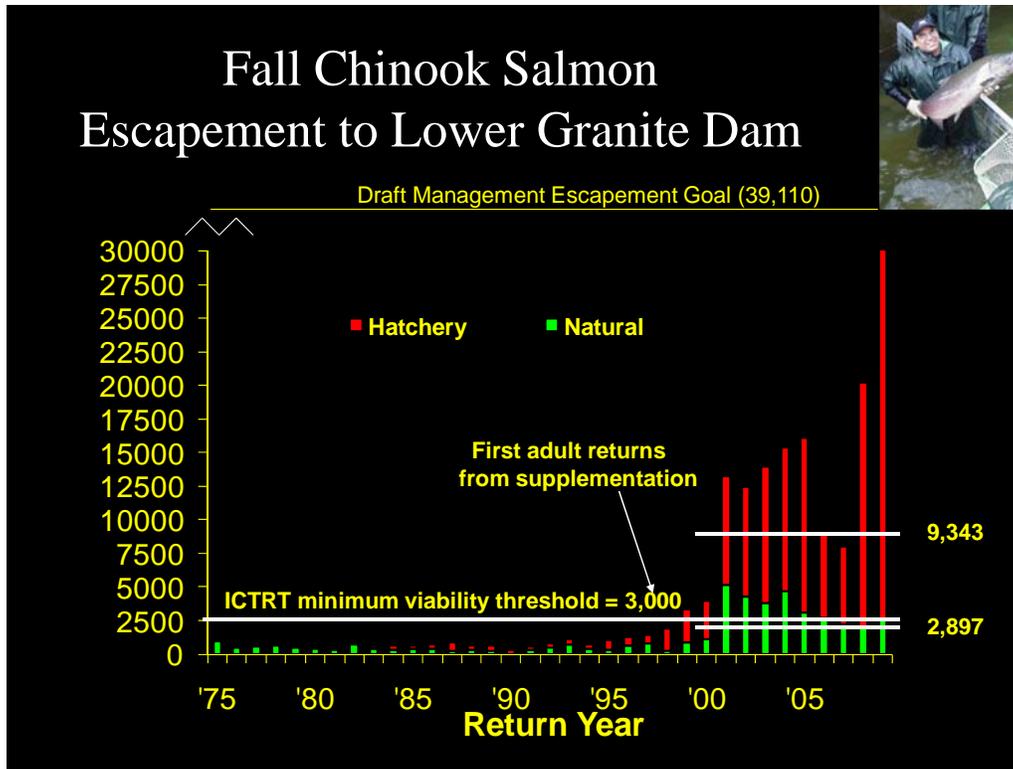


Figure 1. Snake River fall Chinook salmon escapement past Lower Granite Dam, 1975-2009 (Jay Hesse, personal communication).

The Lower Snake fall Chinook population is the only extant population in the Snake River fall Chinook ESU. As such, understanding the status of natural production within this population is critically important to NOAA Fisheries in its attempt to provide guidance for recovery of the ESU. Two critical uncertainties make this understanding problematical. One is the reproductive success, relative to naturally produced fish, of hatchery-origin fish on the spawning grounds. The second is the effect of hatchery production on natural production, either through density dependent mechanisms, or through loss of intrinsic fitness due to domestication. There are several logistical challenges to either type of research (Table 1), and it was in recognition of this that the RPAs were written as they were, with specific language about guidance toward developing these research efforts. This report documents the discussion of that workgroup and summarizes their recommendations on developing a targeted solicitation to meet the RPAs.

Table 1. Technical issues related to implementing hatchery effects research for Snake River fall Chinook salmon.

Issue	Description	Potential Action	Comment
<i>Adults</i>			
LGD Trapping Rate	Trapping is not to exceed 20% of the total run (recently it has been closer to 10%) High steelhead numbers (lately > 200,000) are	Increase trapping rate	This sampling rate limits the number of genetically "known" adults reaching the spawning grounds. For natural-origin broodstock (NOB), no

Issue	Description	Potential Action	Comment
	passing at the same time as fall Chinook. This situation results in handling too many steelhead which increases incidental take.		more than 20% of the run can be extracted.
LGD Trap	Trap limited to 800 (1,000 max) fish per day because of holding space and sampling time	Extra crew and shifts	Limits the number of genetically “known” adults reaching the spawning grounds.
Fall Chinook run size	Adult abundance returning to and passing upstream of Lower Granite Dam (LGD) is estimated via run-reconstruction. Estimate is partitioned by hatchery:natural composition and age structure. Recent run size over LGD > 30,000 fish, with < 10% natural-origin fish.		Even if trapping rate could be increased, cost and lab capacities may preclude sample analysis.
Carcass recovery	Limited to tributaries (e.g., Clearwater R.) since mainstem SR too large.		Attempts to recover carcasses and immediately post-spawn live adults in Snake R. has had limited success, and these would NOT be a random sample of parents
Identification of hatchery-origin fish	24% of hatchery production is not marked Scale reading is an inaccurate measure. Natural and hatchery populations are very similar genetically	Increase external marking, increase use of alternative marking (oxytetracycline, thermal otolith, parental-based tagging).	Sampling at locations other than spawning grounds and broodstock needs to be non-lethal. This issue has policy implications
Hatchery adult fidelity to release location	Hatchery juveniles are released at 11 locations from three separate programs: 5 locations in Snake, 5 in Clearwater, and one below LGD (Lyons Ferry).		USFWS research shows 15% of Clearwater fish ended up spawning in other areas in comparison to 20% for Snake fish
Juveniles			
Estimating juvenile production	Non-operation of fish bypass traps during the late fall-winter period limits ability to enumerate migrants during that time of year	Evaluate migration of Clearwater origin migrants (believed to be late-running) with active tags Note: this action will increase our understanding of the need to operate the	

Issue	Description	Potential Action	Comment
	Smolt trapping not possible in reservoirs except for limited shoreline areas	fish bypass systems on the mainstem Snake and Columbia rivers by knowing the magnitude and timing of off-season migration. Evaluate feasibility of operating fish bypass systems during current off-season.	
Hatchery Production	The <i>U.S. vs. Oregon</i> 2008-2017 Management Agreement targets release of 5,828,000 hatchery produced fall Chinook salmon (900,000 yearling and 4,928,000 sub-yearling).		All but 2.4 M (1.4 M NPT and 1 M IPC), and of this hatchery production is associated with LSRCP mitigation program.

2.0 Goals and Objectives

The workgroup first decided to identify a goal and objectives to help guide discussion and technical work. The sub-objectives are work points that subgroups developed. Below is the full outline of goals and objectives. Detailed discussion of each sub-objective follows the outline:

Goal Statement

Determine what short- and long-term effects the Snake River fall Chinook salmon hatchery program has on the viability of the natural population, while respecting mitigation and other priority management objectives.

Objectives

1. Assess relative reproductive success of naturally spawning hatchery fish in the wild
 - a. Determine feasibility of “grandparent” pedigree study design.
 - b. Determine if it is feasible to use a controlled environment to measure RRS.
 - c. Determine if there are sites in the natural environment that can be used to conduct a RRS study.
 - d. Determine the feasibility of a surrogate population approach.

- e. Evaluate the use of effective population size and effective number of annual breeders (N_b) to census size (N) ratio (N_b/N) to evaluate relative productivity.
 - f. Determine if there are loci under selection that can be used to detect genetic differences between hatchery-origin fish (HOF) and natural-origin fish (NOF), due to different selection regimes in hatchery and natural environments..
2. Assess the impact of the hatchery program on the short- and long-term productivity of SRFCS
- a. Evaluate the feasibility of developing and fitting a spawner recruit model that estimates effects of the proportion of hatchery-origin spawners (pHOS) and spawner density on spawner productivity
 - i. Develop the data requirements for the model
 - ii. Determine if additional populations would increase the robustness of the analysis
 - 1. Determine if there are reference populations for SR fall Chinook salmon
 - 2. Determine if another population can be used as a surrogate for SR fall Chinook salmon.
 - b. Describe what improvements are needed to improve run reconstruction.
 - c. Determine genetic basis for traits that might be affected by hatcheries (e.g., juvenile growth rate, age at maturity).

2.1 Detailed discussion and suggested approaches

Relative Reproductive Success Study Design

In the Columbia Basin pedigree-based relative reproductive success (RRS) studies have been or are being conducted on steelhead and Chinook salmon. These studies require a rigorous study design. Ideally the conditions for an effective RRS study include:

- a) Hatchery and natural populations are both large enough that existence of many close relatives do not confound parentage analysis (aunt and uncle effect) but not so large as to make parentage analysis intractable
- b) Ability to take non-lethal genetic samples (e.g., fin clips) from 100% of the potential spawners each year,
- c) Ability to with ~100% accuracy distinguish hatchery-origin from natural-origin fish when they return as adults
- d) Ability to collect biological information (sex, age, size, weight, run or spawn timing, disease status, etc) from each potential spawner
- e) Ability to collect a random sample of enough progeny from each brood year (as fry, parr, smolts, and/or returning adults) to provide adequate statistical power
- f) Ability to reliably genotype each potential parent for multiple genetic markers and to determine parentage of each offspring

Valuable results can still be obtained without completely achieving all these conditions, but care must be taken to avoid potential biases. For example, if some random fraction of potential parents cannot be sampled, power will be reduced, but, depending on other factors, could be sufficient to achieve an accurate estimate of RRS. However, if the fraction of potential spawners that cannot be sampled is not representative of the population as a whole, results could be biased. Similarly, if H or W origin cannot be determined for some potential parents power will suffer when these fish are excluded, but if some fish are misclassified as HOF when they actually are NOF (or vice versa), the resulting estimates can be biased and misleading.

As can be seen from Table 1, constraints, such as those on sampling and determining fish origin, mean that it is practically impossible to conduct an effective RRS study on hatchery and wild SRFCS. Therefore, the workgroup considered several alternatives.

1.a. Determine feasibility of “grandparent” pedigree study design

A “normal” pedigree-based parentage analysis of RRS is not possible for Snake River fall Chinook salmon, because a) only a small portion of the potential spawning population can be sampled, and b) the portion that is sampled is currently used for hatchery broodstock. However, there is an opportunity to obtain samples from all hatchery broodstock. Conceptually, therefore,

it may be possible to estimate the relative reproductive success of naturally spawning hatchery and wild-born fish by assigning grandparents to natural-origin progeny. If we can estimate whether a sampled natural-origin fish had 0 to 4 hatchery grandparents, we could in theory obtain an estimate of the relative fitness of hatchery and wild parent groups that produced the sampled fish.

There are several unknowns that would need to be overcome in order to make such an approach feasible:

- 1) The number of genetic loci used in the study. Currently, parentage studies typically use either microsatellite or single nucleotide polymorphism (SNP) markers. Power analysis would be required to demonstrate that assignment of individuals to specific grandparents could be accomplished with realistic numbers of loci.
- 2) Statistical methods of grandparentage analysis would need to be developed and validated. Currently, parentage analysis is typically conducted using either pairwise likelihood or exclusion approaches (e.g., Kalinowski *et al.*, 2007) or whole sample likelihood approaches (e.g., Wang 2009). There are no generally available computer programs that implement grandparentage analysis, so a statistically valid approach would need to be developed and implemented.

Even if a sufficient number of loci are scored to make the analysis tractable, a grandparentage-based study design will have some limitations compared to a standard parentage analysis. In particular, although grandparentage analysis can conceptually provide information on hatchery fish relative reproductive success, it would not be possible to include parental traits (such as age or size) as co-factors in the analysis to help explain variation in fitness. In addition, the high fraction of hatchery origin fish in the system will complicate the analysis. Assuming random mating, the expected proportion of W x W matings is equal to the square of the proportion of wild fish. In the Snake River fall Chinook salmon population, some estimates indicate that wild fish make up only ~17% of the natural spawners, so WxW crosses may make up only 3% of the sample progeny if mating is random.

1.b. Determine if it is feasible to use a controlled environment to measure RRS

The grandparentage approach just presented is a “whole population” approach. Another approach would be to do a typical single-generation study in a controlled environment with a small number of fish, such as the work of Berejikian *et al.* (2001) and Schroder *et al.* (2008). Such work, however, is always open to criticism because spawning dynamics in an experimental environment such as a spawning channel may be quite different than in the natural environment. This is especially true of fall Chinook, which typically spawn in large streams that are difficult to duplicate experimentally. Thus the results from work of this sort may have limited applicability.

1.c. Determine if there are sites in the natural environment that can be used to conduct a controlled RRS study

Another approach is the subpopulation approach, where the pedigree analysis is carried out on a portion of the population. A sub-group considered various areas within the range of SRFCs spawning against several criteria, shown in the table below:

Criteria	Snake River Population	Snake River Mainstem	Clearwater	Grande Ronde	Salmon	Imnaha
Similar Habitat structure to SR population area	Yes	No	No	No	No	No
Able to collect carcasses	No	No	Yes	No	No	No
Able to trap adults	Yes (<20%)	No	No	Maybe	No	Yes
Adequate amount of natural origin adults	Yes	Yes	Yes	No	No	No
Able to estimate hatchery natural:composition	Yes	No	Yes	No	No	No
Able to sample tissue from >75% of escapement	No	No	No	No	No	No

The sub-group basically determined that they did not believe that a pedigree study could be carried out in any of the locations they considered. In addition, they also had concerns that, even if a study could be performed, the results may not be transferable to the main SRFCS population because of potential life history and habitat differences.

1.d. Determine the feasibility of a surrogate population approach

This approach bypasses the challenges of the SRFCS situation by using another population. The concept has some value in that all RRS studies of Chinook salmon to date have dealt with spring-run populations with obligate stream-type juvenile life histories. There is reason to believe that ocean-type, subyearling-outmigrant, Chinook salmon, of which SRFCS are an example, undergo less domestication in hatchery environments (if they are released as subyearlings) than stream-type fish (RIST 2009), so it may be misleading to apply existing spring-run Chinook salmon study data to SRFCS. Therefore a subgroup considered other ocean-type populations on which RRS studies might be conducted, including Deschutes, Klamath, Lower Columbia Tule, Wenatchee summer-run, and Hanford Reach (mainstem Columbia River) populations. In general, the sub-group remained concerned that RRS study results would not be easily transferred because of unique habitat conditions within the Snake River basin.

1.e. Evaluate the use of effective population size and N_b to N (N_b/N) to evaluate relative productivity

Another approach considered was a non-pedigree approach. Some interesting parallels exist between the concepts of RRS and effective population size (N_e). RRS studies evaluate the degree to which different groups of individuals (typically, HOF vs NOF) have different mean reproductive success. Similarly, the ratio of effective size to census size (N_e/N) is an index of

the degree to which different individuals within a population have different expected reproductive success. This suggests that evaluating how the ratio N_e/N changes with the pHOS might provide insights into RRS of hatchery fish. Some practical considerations regarding implementation of this idea are:

1. For Pacific salmon, the relevant population parameters are the number of spawners (N) and the effective number of breeders (N_b) per year.
2. N and pHOS can be estimated from counts at Lower Granite Dam, although pHOS estimates currently are not very reliable.
3. N_b can be estimated for individual years from juvenile samples using either single-sample or two-sample (temporal) methods based on genetic data. The most reliable estimates are obtained from samples taken from a single cohort (e.g., age-0 juveniles or adults that have been aged and sorted by birth year). With mixed-age samples it is difficult to match the estimate of effective size to N in a particular year.
4. The CV of a genetic estimate of N_b is an increasing function of N . As a consequence, without a great deal of data it is difficult to get a precise estimate if true N_b is about 1000 or larger. Most published estimates of N_b/N for salmon are in the range 0.1-0.4, and in recent years the number of fish passing Lower Granite Dam has been in the tens of thousands. This suggests precision might be limited in applying this method to SRFCS.
5. Empirical data for salmon show that estimated N_b/N is inversely related to N . A possible biological explanation for this result is that competition for mates and/or spawning sites increases as N gets large, which means that some individuals that might be successful at low density do not manage to produce any offspring. This density factor would have to be controlled for before any conclusions about RRS could be drawn from estimates of N_b/N .
6. Even ignoring density effects, the relationship between N_b/N is complex and can depend on factors that are difficult to estimate, including the variance among individuals in reproductive success.

These factors indicate that, at a minimum, it would be very challenging to extract useful information about RRS using this method. However, it might be possible to include estimates of N_b/N along with other such as N , RRS, and pHOS in models such as that described in sub-objective 2.a (see below).

1.f. Determine if there are loci under selection that can be used to detect genetic differences between HOF and NOF, due to different selection regimes in hatchery and natural environments.

Another approach considered by the workgroup is based on genetic differences between natural-origin and hatchery-origin fish that would be reflected as relative reproductive success. Artificial production subjects salmon to different selective forces than those experienced by wild-born and reared individuals, which may differentially alter the frequencies of heritable genetic diversity. A trait may increase in frequency within a hatchery environment (relative to wild) if it provides a direct advantage to fitness within the hatchery, and conversely, may decrease if it provides a

direct advantage to fitness in natural environments. The expectation would be that hatchery and wild populations would diverge at genetic loci under directional selection. The frequency of a heritable trait may also change within a hatchery environment (relative to wild) due to relaxed selective constraints. Hatchery and natural-origin Snake River fall Chinook salmon are known to be genetically similar at neutral genetic loci, so investigating genetic diversity influenced by directional selection may provide a means to differentiate hatchery and natural-origin populations, and be informative for evaluating RRS. This targeted-gene approach would likely focus on genetic loci known to be subject to selection, such as those coding for growth regulation, immune response, or reproductive development proteins.

An alternative approach to investigate potential selective forces operating within the hatchery environment is the use of genome scans. This approach would look for statistical associations between treatment groups (e.g., hatchery and wild) and genetic variation at loci distributed throughout the genome. Genome scans would likely employ on the order of thousands of genetic loci. Traits expected to differ between treatment groups would not be defined *a priori*, but rather statistical inference would direct investigations toward informative genomic regions. Genetic variation between HOF and NOF resolved with this method could be used to evaluate RRS. Research of this type is important for achieving the understanding of selective forces that we need to fully evaluate domestication selection risks, but this research in itself will not directly estimate relative reproductive success. Also, this approach assumes the differences in performance that determine relative reproductive success are genetically based, and it is possible that a large portion of any performance difference is phenotypic, not genotypic.

1.g. Evaluating the effect of the SRFCS hatchery programs on the short- and long-term productivity of natural spawners

Many of the same features that make RRS studies of SRFCS difficult to accomplish also complicate approaches to studies of other effects of the hatchery programs. Here the subgroup explored one approach aimed directly at the problem and two others that aid in the development of insights about hatchery impacts, but cannot be expected to directly provide the information to resolve uncertainties.

2.a. Evaluate the feasibility of developing and fitting a spawner recruit model that estimates the effects of pHOS and spawner density on spawner productivity

Conceptually, it is possible to estimate the effects of hatchery fish on wild population abundance or productive by developing a model that includes parameters of interest, such as hatchery fish reproductive success or competition between hatchery and wild fish, and estimating these parameters from population data. For example, Buhle et al. (2009) used population abundance and hatchery fraction data for coho salmon on the Oregon coast to estimate the effects of changing hatchery fish abundance levels on wild population productivity. Recently, the Recovery Implementation Science Team reviewed several such studies (Table 4 of their report, available at http://www.nwfsc.noaa.gov/tr/puget_docs/hatchery_report_april92009.pdf). One advantage of these approaches is that they can be applied retrospectively to data that were

collected for another purpose. Such approaches are also useful for obtaining an estimate of the overall ongoing impacts from the presence of hatchery fish. One important limitation of such approaches, particularly when applied retrospectively, is an inability to strongly infer causation. In addition, such approaches also typically provide little insight into the biological mechanisms underlying their estimates, and at least as applied to date have not been able to strongly distinguish between ongoing and cumulative effects. Nonetheless, such model fitting approaches seem worth exploring for evaluating the effects of hatchery origin spawners on wild Snake River fall Chinook salmon abundance and productivity.

Issues to consider before implementing such an approach include:

- 1) A model will need to be developed that both contains parameters of interest and is tractable to fit with either existing data or data that can be feasibly collected.
- 2) An appropriate experimental design will need to be developed and implemented. It will be necessary to ensure that a model appropriate to the experimental design is used. For example, if managers do not believe that accurate prospective control of pHOS is possible, then it will clearly be necessary to use a model that allows for random variation in this parameter. It is also important to define the factors of interest that will influence the parameters needed in the model. For example, if the relationship between pHOS and natural productivity is of interest, it will not be possible to learn anything useful about this relationship if pHOS does not vary sufficiently.
- 3) It will be important to evaluate whether useful information can be gained through an experimental design that focuses solely on the Snake River fall Chinook salmon population, or whether inclusion of data from other populations will be necessary. If including data from other population is determined to be useful, then these populations will need to be identified and the appropriate monitoring or data collection implemented.

Some exploration of the number of years of monitoring required to obtain parameter estimates of sufficient precision will important. It will also be useful to evaluate whether data collected previously from the population(s) can be included in the analysis.

2.b. Determine if another population can be used as a surrogate for SR fall Chinook

This approach received only limited consideration. Similar to the approach considered in the relative reproductive success section, the basic idea is that if the research is intractable with this particular population, conduct the research on a population that is sufficiently similar to permit the results to be credibly applied to SRFCS. No such population could be identified. Even if it could, applicability of the results would be problematic, as the intent of the RPA 65 is clearly to resolve uncertainties about SRFCS, not other populations that are similar to it.

2b. Describe what improvements are needed to improve run reconstruction.

There was much discussion in the workgroup about the shortcomings of SRFCS run reconstruction in that it creates uncertainty about both hatchery- and natural production. Run reconstruction for SRFCS use estimates from a multitude of data types to determine numbers and origins of fish returning to Lower Granite Dam. The main uncertainties are accurately differentiating natural- from hatchery-origin fish in the unmarked/untagged returns and the precision of the estimated return. PIT tags and scales are used to identify natural-origin fish. The PIT tagged fish were seined as juveniles and provide an accurate identifier of natural-origin fish when they return. Unfortunately less than 20 of those fish return each year. Scales have been an accurate identifier of natural-origin fish in the past but in recent years they have proven less accurate because of similarities in growth patterns between small subyearling hatchery and natural-origin fish. Unfortunately, scales are all we presently have to use. Until all hatchery fish are marked/tagged in some manner (marked/tagged/otolith marked/tetracycline marked), the accuracy and precision of the estimates of natural-origin fish will be suspect.

The estimate of total numbers of fish is not precise. Natural-origin fish tend to arrive early in the season, oftentimes when the trap is not running. During that time of year the water is too warm to safely handle the fish, so the trap is closed. In addition the trap is closed later in the season because of low numbers of fish. During those times, window counts of Chinook salmon are used to estimate the numbers, lengths, and clips of the fish passing the dam. Discrepancies between estimates of fish passing the counting window and estimates derived from trapping data often occur in numbers of fish in each size category by clip. These discrepancies may occur because fish are not accurately identified or tallied at the fish counter window or the true sample rate may vary from the expected sample rate.

Improved run reconstruction in itself will not yield direct information on the impact of the hatchery programs on natural productivity, but is rather a key step needed to understanding this issue.

2c. Determine genetic basis for traits that might be affected by hatcheries

As in the case of RRS studies, the workgroup considered a basic genetic approach to this research need. If hatchery supplementation has long-term effects on fitness/productivity of a natural population, the most plausible mechanism is via selective pressures that differ between natural and hatchery environments. But different selective regimes are not enough: the trait(s) under selection must be heritable so that genetic changes can be transmitted across generations. A recent review found a large number of published studies that documented a genetic basis for a wide range of traits in salmonids, including many that might be expected to be under differential selection in hatchery and wild environments (e.g., size, fecundity, growth rate, age at smolting and at maturity). However, results can vary considerably by species and location, and no such studies specific to Snake River fall Chinook salmon have been published.

Heritability studies examine the correlations between trait expression in parents and offspring. A variety of experimental designs can be adopted, but in every case it is essential to be able to 1) identify individual parents by sex and obtain estimates for the desired trait(s), and 2) measure the same traits in offspring and match offspring to parents. Step 2 can be accomplished by rearing each family separately until the families can be uniquely marked, or by parentage analysis using

genetic markers. Given various logistical challenges, as well as ESA permitting and *U.S. v Oregon* issues that constrain many aspects of experimental design, the parentage analysis approach is probably more feasible for SRFCS. Each of the two hatchery programs (Lyons Ferry and Nez Perce Tribal Hatchery) has more than enough returning adults to provide estimates of heritability with precision that is comparable to or higher than most published estimates. Although heritability information can be obtained using the current mating designs (pairwise matings), some additional benefits can be realized if at least some factorial matings (which create both full-sib and half-sib families) can be implemented.

Although identifying key traits that have an underlying genetic basis in Snake River fall Chinook salmon would provide valuable information into potential mechanisms for fitness effects related to hatchery domestication, demonstrating that such traits are heritable will not by itself allow one to quantify the effects on fitness. Therefore, this type of study should be viewed as a key step in addressing issues related to long-term hatchery effects on fitness rather than a comprehensive answer to this challenging problem. This approach is also limited in that it only considers genetic factors contributing to the impact; ecological factors also may be involved

3.0 Conclusion

1. Based on logistical, technical, and process constraints, a pedigree-based parentage analysis to estimate RRS is not feasible for SRFCS. A promising alternative at this point appears to be a grandparental study design, but a number of details need to be worked out. Approaches such as using controlled spawning areas or surrogate populations appear far less attractive. Other approaches yielding useful but less direct RRS information are possible.
2. Evaluating the effect of the hatchery programs on natural SRFCS productivity is very challenging, and the challenge is exacerbated by inadequacies in run reconstruction. The only approach the workgroup recognized as most appropriate was a model-fitting approach similar to that of Buhle et al. (2009). Again, however, a number of feasibility and statistical power details need to be worked out. The option of using a surrogate population is highly undesirable. Other approaches yielding useful but less direct information are possible.

The information presented above should not be considered the final word in approaches to address RPAs 64 and 65; there may be novel approaches that did not occur to the workgroup. However, this information was developed by a large group of scientists with considerable expertise in these research areas, so any other approach prospective researchers might propose should be carefully scrutinized. Because of biological and management constraints, this is a difficult population in which to explore RRS and hatchery fish effects on natural productivity. We urge the Action Agencies that any targeted solicitation stipulates that proposals be fully developed in terms of feasibility and experimental power.

4.0 References

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Appendix A. List of participants in the April 27 workshop.

Name	Organization
Bill Arnsberg	NPT
Craig Busack	NOAA Fisheries
Matthew Campbell	IDFG
Rich Carmichael	ODFW
Billy Conner	USFWS
Tom Cooney	NOAA Fisheries
Ron Costello	BPA
Scott Everett	NPT
Peter Galbreath	CRITFC
Jay Hesse	NPT
Damon Holzer	NOAA Fisheries
Becky Johnson	NPT
Dave Johnson	NPT
Anne Marshall	WDFW
Glen Mendel	WDFW
Debbie Milks	WDFW
Chuck Peven	Facilitator, BPA
Andy Pierce	CRITFC/UI
Stuart Rosenberger	IPC
Bill Schrader	IDFG
Mark Schuck	WDFW
Maureen Small	WDFW
Gene Shippentower	CTUIR (by phone)
Dave Venditti	IDFG
Robin Waples	NOAA Fisheries
Bill Young	NPT
Steve Yundt	USFWS