BPA RFS Proposal #12

Evaluating relative reproductive success of natural- and hatchery-origin Snake River fall chinook spawners upstream of Lower Granite Dam

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ISRP comments applicable to all proposals for RPA #182

Concern/Question 1- Interpretation of studies where the extant population has a long history of potential interbreeding with hatchery fish; 'Is it enough just to compare fitness of HxW and HxH crosses with fitness of WxW in the same stream when the fitness of the WxW may be changing because of the supplementation or straying?'

Our Response:

Our study population of upper Snake River fall chinook does have a history of potential interbreeding with hatchery fish, and often, most of these fish originated from Lyons Ferry Hatchery (LFH; see Table 2 of Proposal). Current management activities for the Snake River fall chinook ESU include use of LFH fish for adult and juvenile supplementation. We think it is likely that the wild Snake River fall chinook population does include a proportion of hatchery origin genes, and that possibly it has experienced changes in reproductive success as a result. Because this situation is not likely to change in the near future we do not expect pure wild origin fish to be easily identifiable and readily available for an accurate study of comparative fitness. We are, however, proposing to estimate relative reproductive success of hatchery and wild components at the population level.

Our study is not designed to do pedigree-based assignments of hatchery or wild origin parents to naturally produced offspring, thus we will not compare fitness of offspring from particular crosses. We expect to evaluate relative reproductive success through assessment of genetic change and estimates of admixture in natural-origin fish in a time series of annual samples. We have data on annual proportions of wild and hatchery fish that could participate in spawning upstream of Lower Granite Dam (LGD). Of course these census values are not measures of actual spawners, and it is possible that the number of successful breeders may be as low as 30% of the census count (as reviewed in McElhaney et al. 2000), with hatchery and wild proportions unknown. Assuming the hatchery population has diverged sufficiently from the wild population (e.g. hatchery has not incorporated wild fish since 1990), genetic analyses will provide an estimate of the annual proportional contribution of hatchery gene pools to naturally-produced offspring. Proportional genetic contributions, coupled with census data, should allow an estimation of relative reproductive success.

For example, comparing annual genetic profiles and admixture proportion estimates to hatchery and wild adult proportions at LGD will show the degree to which genetic contributors differ from potential spawner proportions. Thus, if hatchery-origin fish compose 50% of potential spawners and their genetic contribution to natural offspring is estimated at 10%, we can infer that wild fish were 180% more likely to contribute their genes than expected (given random mating and equal sex ratios); conversely, hatchery fish realized only 20% of their potential. We will be able to assess genetic characteristics among offspring broodyears with very low to high proportions of potential naturally spawning hatchery fish and track subsequent genetic contributions of natural broodyears. This time series of proportional genetic contributions of the hatchery population should allow us to estimate average relative reproductive success of hatchery and wild populations.

If we find that reproductive success of hatchery and wild fish appears similar, we might conclude that any actual fitness differences are not large enough to detect with our analytical approach. However, if fitness is similar we should expect population abundance to increase as the number of hatchery-origin fish spawning with the wild population increases (e.g. due to intentional releases), and density-dependent factors are not an issue. We may be able to evaluate this using run reconstruction analyses of escapement data. If natural population size was actually declining during the time hatchery fish abundance had been increasing, a study result of fitness similarity might be in question or possibly the naturally spawning population was undergoing fitness declines due to hatchery fish interbreeding prior to the study period.

Concern/Question 2- studies do not include control streams with only WxW crosses (and no history of previous interbreeding with hatchery-origin fish) for comparisons with treatment streams in order to assess effects of out-of-basin factors on population growth rate and other demographic parameters crucial for interpreting population-level impacts

Our Response:

We agree that our study would benefit from a comparison of genetic change through time in a control population, that is, one of similar size and biological attributes and without hatchery fish influence. At this time we are not aware of a such a population that has a similar time series of tissue samples available. We can investigate the potential for this as necessary. We address how our study may contribute to assessing differential reproductive success effects on parameters such as growth rate ('lambda') in the next section (proposal-specific comments).

Concern/Question 3- quality control in data/database management and sampling protocols for genetic studies

Our Response:

The WDFW Genetics Lab and Conservation Biology Unit has a long history of maintaining large, standardized genetic data sets as well as developing and adhering to data collection quality control protocols (e.g. Shaklee and Phelps 1990). Sampling protocols for Lyons Ferry Hatchery broodstocks, adult fall chinook at LGD, and naturally produced Snake River juveniles were developed with appropriate statistical designs and have been followed routinely by WDFW Snake River Lab, University of Idaho, USFWS-Dworshak Office, and USGS staffs. These groups also are well-experienced in maintaining annual and historical series of data records. Sampling protocols and results for Snake River juveniles have been published in peer-reviewed papers (Connor et al. 1998; Marshall et al. 2000; Connor et al. 2002). A. Marshall has been responsible for contributing and maintaining standardized chinook salmon coast-wide Genetic Stock Identification (GSI) data sets for WDFW for over ten years (e.g. see Teel et al. 1999). We will apply similar standards and computerized procedures to our collection of DNA microsatellite data and maintenance of resulting datasets.

ISRP comments on Proposal 12

ISRP recommendation:

"Qualified funding of Phase 1, pending adequate revision. Genetic divergence should be demonstrated and the utility of the mixture analysis approach should be convincingly demonstrated.

Do not fund Phase 2 at this point, pending successful demonstration of the approach.

The applicants do not address evaluation criteria two and three in the RFS. This limits the utility and applicability of the research. This work is in a priority ESU and the project could be done in a relatively short time because the tissue samples are already collected."

The ISRP determination on whether our study addressed three RFS questions:

1) Are there statistically significant differences in the reproductive success between natural-origin and hatchery-origin fish when measured at the second generation (F2)? Do F1 progeny with HxW parents differ from F1 progeny with HxH parents in the production of F2 progeny?

ISRP conclusion: Yes

Our response:

We believe our long-term study plan will address the first question of the above couplet. However, because we are not conducting pedigree analyses to determine parentage of individuals, we will not be able to address differences in reproductive success of HxW and HxH F1 progeny.

2) What are possible hypotheses to explain this difference? For example, can the difference be attributed to reduced genetic fitness of hatchery-origin compared to natural-origin fish? Are differences more significant during any specific life history stages?

ISRP conclusion: No

Our Response:

Phase 1 of our study is designed to determine whether enough genetic differentiation exists between hatchery broodstocks and wild origin fish to allow estimation of hatchery fish contributions to naturally produced offspring. Our Phase 1 hypothesis is:

H_O: Genetic variation among wild and hatchery origin spawner components is large enough to allow accurate estimates of relative contributions to natural production of Snake River fall chinook.

If we do find adequate differentiation, we will estimate, for example, hatchery and wild proportional contributions to naturally produced age-0 juveniles, and to unmarked returning adults sampled at LGD. If we find differences in F2 generational reproductive success of hatchery and wild origin fish, we can imagine several hypotheses may explain the differences. If hatchery fish show relatively poorer success, a plausible hypothesis would be that LFH-origin fish have spent enough generations in culture that domestication effects limit their success in natural reproduction and subsequent survival. Also, there may be out-of-basin hatchery fish participating in natural spawning that might experience reduced reproductive success due to poor adaptation to Snake River conditions in addition to domestication effects.

If wild fish show relatively poorer success, a plausible hypothesis would be that the wild population has experienced such large declines in abundance over a long enough period of time that genetic diversity has diminished enough to limit their reproductive success and survival.

Continuing our analyses through Phase 2 of the study should allow us to evaluate success at the subyearling and returning adult stages for at least several broodyears of natural production.

3) What is the likely effect of any difference, in terms of population growth, population recovery, and genetic diversity/fitness in subsequent generations according to the Viable Salmonid Population (VSP) criteria?

ISRP conclusion: No

Our Response:

Phase 1 of our proposal is focused on developing the genetic basis and analytical tools that may allow us to estimate relative reproductive success of hatchery and natural origin fall chinook salmon. We expect that implementing Phase 2 would allow us to further quantify any differences in reproductive success. These values would be used to assess effects on population growth rate ('lambda'), recovery, and subsequent genetic diversity. For example, if we estimated that hatchery fish contributed 30% less than expected to natural progeny, and we assumed this came at a loss to wild fish productivity, we would expect population growth to be negatively effected by certain wild and hatchery fish ratios on spawning grounds. Assuming recovery criteria for the wild fall chinook population involve VSP abundance thresholds and positive growth rate trends, proportion and abundance of hatchery-origin fish would need to be managed if their poorer reproductive success caused growth rate declines. We will be able to compare genetic diversity over time in wild production broodyears and among broodyears that vary in level of hatchery fish interbreeding, and thus assess whether any negative changes are due to interbreeding.

The ISRP determined that our study sufficiently addressed all criteria for selecting among well-designed and responsive proposals except for the following:

Criterion to address:

-The degree to which the study is designed (or is capable of being extended) to address whether and to what extent any difference in reproductive success of hatchery spawners persists in subsequent generations (beyond F2)

Our response:

We will not know our ability to detect persistence of differences in reproductive success until we complete Phase 1. We think if capabilities do exist we will be able to sample and evaluate generations subsequent to F2s. A Phase 2 proposal would address this issue to its full extent.

The ISRP had specific comments and questions that we address below.

1) Why can't pedigree data be collected?

Our response:

To handle enough fish at LGD for a direct pedigree approach, the adult trapping facility would need extensive and costly construction of new facilities. Instead, we propose other genetic methodologies such as admixture analysis and assignment tests in lieu of pedigree analysis. Given the nature of mainstem spawning habitat used by Snake River fall chinook, we think our approach to determining relative reproductive success of hatchery and natural origin fall chinook salmon is plausible.

The Snake River is a very large basin with only one adult collection facility operating at LGD. The trap was originally built to trap a small percentage of steelhead for composition estimates. In 1990, the trap was used to collect all wire-tagged fall chinook in order to extract stray or unknown origin fall chinook from the Snake River, determine run composition at LGD by hauling them to LFH for CWT analysis, and supplement LFH when it was broodstock limited.

With increases in returns of all salmonids to LGD, it has become essential that trapping of wire-tagged fish at LGR Dam be reduced to a sub-sampling regime. In 2001, the staff at LGD sub-sampled wire-tagged fish by turning on their wire detectors every other hour during daytime operation (7am to 5pm). Night trapping allowed 100% of the wire tagged fish to be caught. In 2002, because of large steelhead and fall chinook numbers, the detectors were turned on every third hour during daytime operation. Even with this protocol it was necessary to turn the detectors off for additional days because the trap holding vessels were full. At those times, all fish were allowed to pass the trap, and thus the dam.

Currently, wire-tagged fall chinook and 3% of the steelhead run are targeted at the LGD adult trap. If untagged fish were included, such as for our study, space available for fall chinook would decrease. In 2002, the staff at LGD operated the adult trap at the fullest extent possible, handling approximately 13% of the run (~31,000 fish, fall chinook + steelhead), well under what would be needed for a pedigree analysis.

2) How will the applicants know if the observed genetic divergence is adequate to estimate differences in relative reproductive success?

Our response:

We will approach this issue in several ways. We have not had the opportunity to evaluate microsatellite data from populations within this ESU, or between this ESU and other Columbia Basin ESUs, and without the knowledge of baseline levels of differentiation, we can only speculate what values of typical estimators such as Fst, theta, or genetic distance might be effective. Most published studies using assignment methodologies and admixture methods report population differentiation values that provided accurate mixture proportions or presence of mixed individuals. We will use data from published studies to gauge population differentiation in our study samples.

Once we acquire data from the samples, we will calculate basic genetic population descriptive statistics that will provide an overview of genetic divergence, as well as indications of mixed gene pools. We expect to use some of the sample data to conduct simulation analyses to test how well admixture and assignment methodologies perform. Analyzing the natural population sample data as a time series of allele frequencies from a single, reproductively isolated population (without divergent hatchery fish interbreeding) will allow a comparison of outcomes with the genetic variability parameters expected in such a population.

We can also "self-test" population samples known to be, or presumed to be from independent, reproductively isolated units to see how well individuals assign back to their population of origin, relative to other populations that show a range of genetic divergence from it. In this way, we can determine what amount and type of divergence at the loci under study will provide accuracy for measuring contributions from LFH to the natural population. In general, we expect tests and analyses with sample data to show us if we can compute acceptable probabilities regarding true LFH broodstocks contributions or admixture proportions in annual or broodyear natural origin fish.

3) How will the applicants estimate relative reproductive success of hatchery and natural origin spawners? Details?

Our response:

Two estimators are key to our understanding of relative reproductive success of hatchery and natural origin spawners. First, we need accurate counts and proportions of hatchery (LFH and unknown origin) and wild origin fish crossing LGD, and thus being potential natural spawners upstream. Second, genetic divergence between or among potential spawning groups must be large enough to permit accurate estimation of the proportional contributions of each to annual production. It is the comparison of proportions at LGD and proportions within natural offspring that provides a gauge of relative reproductive success.

Estimates of the origin of fall chinook fish at LGD have been calculated annually and with consistent methods for many years. Only recently have the calculations become more

complicated due to the presence of unmarked LFH fish allowed upstream. The greatest uncertainty however lies in the relationship between fish passage proportions and the origins of fish that actually spawn. For our study we will have to assume the proportions remain the same. Fall chinook carcass surveys in the mainstem Snake River generally have not been successful at mark sampling adequate numbers of fish. We will try to utilize spawning ground survey data available to compare proportions with the dam counts.

The nature of genetic data analyses for our pilot study are described briefly above. Assuming we find adequate divergence between hatchery and wild broodstocks, we will employ several methods to estimate hatchery contributions, such as those described by Hansen et al. (2001) in their study of admixture and stocking impacts in wild brown trout populations. For example, the computer program of Pritchard et al. (2000) can be used to calculate admixture coefficients for individuals. The proportion of admixed (hatchery and wild) and "pure" hatchery origin individuals in a sample of natural origin fish provides an estimate of the proportion of hatchery parents. Programs for specifically testing admixture, such as Long (1991), estimate the proportion of genes from each source population. Use of assignment approaches, such as those of Rannala and Mountain (1997) and Cornuet et al. (1999) may also provide estimates of the proportion of natural origin individuals resulting from reproductive success by hatchery fish. All tests results will be compared for consistency. Similar proportions calculated by all methods may increase our confidence in results.

BPA/NOAA Fisheries H/H Subgroup comments on Proposal 12

Comments on all proposals

1) Proposals need to identify Principal Investigator (PI)

Our response:

Each of the three applicants listed on the title page will act as PI.

2) Additional references for Principal Investigators

Our response:

Non-BPA references for A. Marshall, D. Milks and M. Schuck are provided below.

Rawding, D., S. Phelps, A. Marshall and C.W. Hopley. 1999. Genetic stock identification of steelhead in the Columbia River Zone 6 fishery and at Bonneville Dam. 1997 annual report to NOAA/NMFS Northwest Fisheries Science Center, Seattle, WA NOAA Contract No. 50ABNF700089.

Marshall A. R., C. Smith, R. Brix, W. Dammers, J. Hymer, and L. LaVoy. 1995. Genetic diversity units and major ancestral lineages for chinook salmon in Washington. In C. Busack

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Utter, F. M., D. Chapman, and A. Marshall. 1995. Genetic population structure and history of chinook salmon of the Upper Columbia River. Am. Fish. Soc. Symp. 17:149-165.

Milks, D., M. Varney. 2003. Lower Snake River Compensation Plan, Lyons Ferry Hatchery Evaluation Program, fall chinook salmon, 2000 annual report. Washington Department of Fish and Wildlife Fish Program Report # FPA03-04 to U.S. Fish and Wildlife Service, Boise, ID.

Milks, D., M. Varney. 2000. Lower Snake River Compensation Plan, Lyons Ferry Hatchery Evaluation Program, fall chinook salmon, 1998 and 1999 annual report. Washington Department of Fish and Wildlife Fish Program Report # FPA00-21 to U.S. Fish and Wildlife Service, Boise, ID.

Schuck, M.L., J. D. Bumgarner. 2001. Touchet River instream habitat alteration projects, 2000 habitat evaluation surveys, 2000 progress report. Washington Department of Fish and Wildlife contract #35090082 to Columbia Conservation District, Dayton, WA.

Martin, S., M. Schuck, J. Bumgarner, J. Dedloff, and A. Viola. 2000. Lyons Ferry Hatchery Evaluation Trout Report, 1997-1998 annual report. Washington Department of Fish and Wildlife Fish Program Report # FPA00-11 to U.S. Fish and Wildlife Service, Boise, ID.

Schuck, M., A.E. Viola, J. Bumgarner, and J. Dedloff. 1998. Lyons Ferry Trout Evaluation Study, 1996-1997 annual report. Washington Department of Fish and Wildlife Hatchery report #H98-10 to U.S. Fish and Wildlife Service, Boise, ID.

Viola, A.E., and M.L. Schuck. 1997. A method to reduce the abundance of residual hatchery steelhead in rivers. North American Journal of Fisheries Management: 15(2) 488-493.

BPA references for A. Marshall, D. Milks and M. Schuck are provided below:

Connor, W.P., A.R. Marshall, T.C. Bjornn, and H.L. Burge. 2001. Growth and long range-dispersal by wild subyearling spring and summer chinook salmon in the Snake River Basin. Transactions of the American Fisheries Society 130:1070-1076.

Connor, W.P., T.C. Bjornn, H.L. Burge, A.R. Marshall, H.L. Blankenship, R.K. Steinhorst, and K.F. Tiffan. 2001. Early life history attributes and run composition of PIT-tagged wild subyearling chinook salmon recaptured after migrating downstream past Lower Granite Dam. Northwest Science 75(3): 254-261.

Marshall A. R. 1996. Genetic analysis of 1993-94 Idaho chinook salmon baseline collections and a multi-year comparative analysis. Appendix A in D. Nemeth and five coauthors. Idaho Supplementation Studies. Annual Report 1994 (Contract No. DE-BI 79-89 BP01466) to Bonneville Power Administration, Portland, OR.

Blankenship, H.L., L. LaVoy, C. Knudsen, A. Marshall, D. Thompson, and J. Sneva. 1993. Stock identification of Snake River fall chinook salmon. In H.L. Blankenship and G. Mendel, eds. Upstream passage, spawning, and stock identification of fall chinook salmon in the Snake River, 1992. Annual Report 92-93 (Contract No. DE-BI 79-92 BP60415) to Bonneville Power Administration, Portland, OR.

Mendel, G. and D. Milks. 1997. Upstream passage and spawning of fall chinook salmon in the Snake River. In Blankenship and Mendel, editors. Upstream passage, spawning, and stock identification of fall chinook salmon in the Snake River, 1992 and 1993. Project 92-046. Final report to Bonneville Power Administration, Portland, OR.

BPA implemented projects: Mark Schuck is currently the principal investigator for BPA project # 2002-053-000 (Assess Salmonids in the Asotin Creek). In addition, Mark served as Co-Project leader for BPA funded project of Bull Trout in SE Washington (Project #9005300-Reports DOE/BP 17758-1 & DOE/BP 17758-2). Successfully implemented LSRCP funded monitoring and evaluation studies for Lyons Ferry Complex Program for 20 years.

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Comments specific to Proposal 12

Comment: Respond to the ISRP's questions and comments.

Our response:

We have done so above.

Literature Cited:

Connor, W.P., H.L. Burge and D.L. Bennett. 1998. Detection of subyearling chinook salmon at a Snake River dam: implications for summer flow augmentation. North American Journal of Fisheries Management 18: 530-536.

Connor, W.P., H.L. Burge, R. Waitt and T.C. Bjornn. 2002. Juvenile life history of wild fall chinook salmon in the Snake and Clearwater rivers. North American Journal of Fisheries Management 22: 703-712.

Cornuet, J.-M, S. Piry, G. Luikart, A. Estoup, and M. Solignac. 1999. New methods of employing multilocus genotypes to select or exclude populations of origin of individuals. Genetics 153: 1989-2000.

Hansen M.M., E.E. Nielsen, D. Bekkevold and K.D. Mensberg. 2001. Admixture analysis and stocking impact assessment in brown trout (*Salmo trutta*), estimated with incomplete baseline data. Canadian Journal of Fisheries and Aquatic Sciences 58: 1853-1860.

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McElhany, P., M.H. Ruckelshaus, M.J. Ford, T.C. Wainwright and E.P. Bjorkstedt. 2000. Viable salmonid populations and the recovery of evolutionarily significant units. U.S. Dept. Commerce, NOAA Tech. Memo. NMFS-NWFSC-42, 156 p.

Pritchard, J.K., M. Stephens, and P. Donnelly. 2000. Inference of population structure using multilocus genotype data. Genetics 155: 945-959.

Rannala B., and J.L Mountain. 1997. Detecting immigration by using multilocus genotypes. Proc. Natl. Acad. Sci. USA 98:9197-9201.

Shaklee, J.B and S.R. Phelps. 1990. Operation of a large-scale, multi-agency program for genetic stock identification. American Fisheries Society Symposium 7: 817-830.

Teel, D.J., P.A. Crane, C.M. Guthrie, A.R. Marshall, D.M. VanDoornik, W.D. Templin, N.V. Varnavskaya, and L.W. Seeb. 1999. Comprehensive allozyme database discriminates chinook salmon around the Pacific Rim. North Pacific Anadromous Fish Commission Document 440. Alaska Department of Fish and Game, Division of Commercial Fisheries, Anchorage, Alaska.