Monitor and Evaluate the Genetic Characteristics of Supplemented Salmon and Steelhead

Progress Report

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Summary

This progress report offers a summary of genetic monitoring and evaluation research related to artificial propagation of Chinook salmon and steelhead in the Snake River basin. Our principal goal has been to characterize the relative (and net) reproductive success of hatchery fish spawning in the wild in multiple sub-basins. We address a critical uncertainty identified in essentially all tribal, state, and federal recovery planning efforts. Beyond simple description of those patterns of differential reproductive success, we seek to understand the biotic and abiotic factors that contribute to our observations, including genetic and environmental elements, and the real time effects of hatchery reform.

We adopt two fundamentally different approaches that capture processes operating at different geographic scales. Our tier 2 design monitors changes in gene frequency through time in hatchery and wild populations. These studies monitor spatial and temporal genetic change over broad river basins and sub-basins. Tier 3 studies, by contrast, are able to construct pedigrees in naturally spawning populations that include hatchery and wild fish. We can then use actual matings to infer the fitness of hatchery versus wild individuals, based on the numbers of offspring we observe in our progeny samples. We get extraordinary detail from the tier 3 studies but only for a single river system. Thus, tier 2 studies provide breadth of information, whereas tier 3 studies offer unparalleled depth of insight for single discrete systems.

We exceeded our goals in almost all areas for both tier 2 and tier 3 studies, and, where we did not, we offer an explanation of why, and what future action will be taken (Lessons Learned). All subcontracts were let as expected, providing smolt trapping, tissue sampling, genotyping, and analysis. Our inter-laboratory standardization efforts with tribal, state, and federal agencies were highly successful in this period. These standardization activities have been an on-going element of this study, beginning with WDFW's forays into DNA markers in the late 1990s and continuing and becoming more formalized with the initiation of the newer genetics laboratories (CRITFC, USFWS, and IDFG).

This report is intended to document success in achieving collection and genotyping goals. Data analyses, presentation, and publication are keeping pace with data collection; however, detailed results are not presented at this time. A complete and comprehensive analysis and description of results will be provided in published manuscripts and in the 2009 annual report (the culmination of the current 3-year rolling review cycle). In the first section of this report, we present accomplishments related to individual projects within this genetic monitoring program. Subsequent to the standard reporting categories, we provide a **Specific Obligations** section that lists accomplishments exactly as the deliverables are presented in the Pisces Statement of Work. This approach results in a small amount of redundancy, but we try to minimize obvious cases. The goal is to provide our accomplishments in a format that is easily compared to the Work-Element-driven format of Pisces, yet also provide a narrative that shows continuity with the individual studies that make up this research program.

Accomplishments and Challenges

Genetic data standardization

Stevan Phelps Allele Nomenclature (SPAN) Project

- Submitted Snake River steelhead tissue samples for a multi-laboratory genetic baseline data standardization effort for steelhead (n=21).
- Collected genotype data for steelhead standardization project (n=96, 1 locus & n=96, 13 loci).
- Provided additional Snake River genotype data and re-scored genotype data for potential steelhead cutthroat hybrid individuals (n=48, 12 loci).

Genetic Analysis of Pacific Salmonids (GAPS)

- Continued participation in the coast-wide GAPS genetic standardization effort for Chinook salmon
- Principal facilitation of international, inter-laboratory genetic data standardization and compilation.

Snake River basin steelhead tier 2 gene frequency monitoring (conventional M&E)

- Submitted a draft manuscript summarizing the relationships between hatchery and wild steelhead populations in the Snake River Basin.
- Analyzed genotype data for a second manuscript comparing naturally-produced steelhead populations that have received hatchery smolts to wild populations that have received few hatchery smolts.
- Genotyped two populations in the Salmon River Basin, error checked and compiled data for analysis (n=50 individuals).

Little Sheep Creek steelhead tier 3 reproductive success project

- Collected non-lethal tissue samples for all anadromous adults passed over the weir in 2007,
- Smolts, parr, and resident adults collected in 2007 were preserved in ethanol and deposited into the Conservation Biology Division's Tissue Archive N ≈ 750).
- Genotyped and analyzed 2002 Little Sheep samples (1,700 individuals, 15 loci). Currently analyzing 5-year dataset (years 1999-2003) for publication.
- First pass genotyping (no re-runs) for 2004 samples (1,265 individuals, 15 loci) and a subset of 2005 samples (650 run for 15 loci)
- Extracted DNA for 1,200 additional 2005 samples.

Salmon River Chinook tier 2 gene frequency monitoring (conventional M&E)

- Completed data collection on Salmon River Chinook fine scale population hierarchy project. Began analysis of data and paper writing
- Analyzed data for Salmon Evolution workshop, isolation-by-distance and genetically effective population size.

Northeast Oregon Captive Chinook tier 3 reproductive success project

- Genotyping completed for parr smolts and returning adults to Lostine River and Catherine Creek (captive brood stock programs).
- Pedigree analysis completed for multiple oral and poster presentations this year.

Marker development, Single Nucleotide Polymorphisms (SNPs)

- Continued activities in SNP development were partly thwarted by difficulty coordinating with other laboratories to avoid duplication of effort and independent “discovery” of the same genetic variation.

Analytical and theoretical development

- We continue to apply our newly developed methods of estimating genetic effective population size (Waples 2006), however there are no significant theoretical developments to report in this performance cycle.

Projected and Actual Costs

Overall project is on budget with no categorical deviation greater than 5% from original budget

Map of Study sites

Figure 1. Study sites for Snake River genetic monitoring, hatchery programs in yellow boxes, Chinook salmon pedigree sites in white boxes.

Category

Monitoring and evaluation research

Lessons Learned

We did not budget sufficient time to meet all our hopes for publication. We participated as coauthors in several unexpected manuscripts, but we did not do as well in meeting our goals for first authored papers. Of two papers planned for submission, only one was successfully completed. The other is still in progress. We're proud of our collaborative accomplishments, but we recognize the importance of getting our own results published quickly in peer-reviewed literature. Our first obligation is to inform the comanagers of our preliminary findings. However, without peer-review, research results will not obtain sufficient credibility and buy-in from comanagers and the research community.

Specific Obligations

In this section we identify success in meeting specific deliverables, as laid out in the Statement of Work for the FY2008 performance period. The text passages describing the deliverables are retained from the Pisces SOW and re-iterated here (enclosed in square brackets).

ESA Permitting and reporting

- [-Take report submitted to NMFS Protected Species (Chinook and steelhead).
- Take report submitted to USFWS (bull trout).
- Annual notification of field activities (NMFS Protected Resources).]

Federal permits and consultations were kept current in this performance period. We also obtained state permits as required, and notified authorities about our field collection activities. As far as we know, our project remains fully NEPA compliant.

Analysis and interpretation of genetic, phenotypic, ecological, life-history, and other data

- [-Calculate population genetic metrics and parameter estimates (e.g., inbreeding coefficients, average heterozygosity, genetic distance, average relatedness, effective number of breeders).
- Describe geographic structure of population genetic variation by using multivariate statistical analyses such as agglomerative clustering and ordination.
- Document relative reproductive success among multiple treatment groups of Chinook salmon in Lostine River, Catherine Creek, and Grande Ronde River and steelhead in Little Sheep Creek.
- Coordinate research with other labs (phone, email, and data sharing), standardize data, and develop/implement new genetic markers.]

New data were analyzed along with previously available results and presented at numerous local, regional, and international meetings (please see ***Distribution among comanagers of results from genetic research on hatchery supplementation***). Additional analyses have already appeared or are slated for publication in peer-reviewed literature.

A complete reporting of all results and analysis is scheduled for 2009, the conclusion of the rolling review cycle.

Salmon and steelhead tissue sampling and data collection

[-Tier 2 sampling: Approximately 1,200 Chinook and 500 steelhead tissue samples will be collected for gene frequency monitoring.

-Tier 3 sampling: About 4,000 samples will be collected to determine reproductive success by pedigree analysis.

-Tier 2 microsatellite genotyping: 2,020 individual fish samples will be processed for gene-frequency monitoring.

-Tier 3 microsatellite genotyping: 4,300 samples will be processed for pedigree studies.

-SNP marker development: Survey for DNA sequence variation approximately 96 Chinook salmon individuals.

-EST-linked microsatellite development: 600 Chinook and steelhead will be surveyed for adaptive variation.]

Tissue sampling and genotyping accomplishments were fully successful and are described above organized by study. SNP marker development and analysis of EST-linked microsatellite are proceeding more slowly. Those difficulties are described in Lessons Learned.

- Combined efforts of our own field expeditions and those of our collaborators and colleagues were fully successful in meeting or exceeding our tissue sampling goals for this year.
- More than 10,000 fish were genotyped for this project in 2007, far surpassing our expectations (~7000).
- In contrast to very successful routine genotyping, our SNP development efforts continue to lag. A principal difficulty is effectively coordinating with other laboratories. Early SNP development was happening so rapidly that it was difficult to avoid duplicating effort and independent discoveries of the same variable SNPs. Given that state of flux, we tempered our expectations for SNPs and focused effort elsewhere (e.g., trying to catch up on genotyping archived samples from previous years).
- Collaborated with ODFW biologists to develop a study of potential hatchery domestication in the Imnaha River. Selected tissue samples were identified to fill the experimental design. DNAs were purified and genotyped for neutral microsatellite markers. Those putatively neutral genotypic data will be used as a benchmark against which we will compare results for EST-linked microsatellites, as those become available.

Distribution among comanagers of results from genetic research on hatchery supplementation

[4 - 5 presentations in response to invitations or requests.]

More than nine presentations were delivered to comanagers and biologists at various forums in the 2007 performance cycle.

- Does supplementation work? Analysis of long-term effects of hatchery releases on Snake River Basin steelhead populations, at the NWFSC Science Symposium in Seattle, Washington, December 2006. Described the level of introgression between hatchery and naturally produced steelhead populations in the Snake River Basin.
- Pedigrees in captive broodstock populations provide insight into reproductive success and evolutionary processes in ESA-listed Chinook salmon populations - Poster presentation at Evolutionary Changes and Salmon conference, Seattle WA December 2006.
- Captive broodstock and reproductive success in northeast Oregon - Poster presentation at center wide research symposium, Seattle WA, December 2006.
- Pedigrees in captive broodstock populations provide insight into reproductive success in Chinook salmon populations. Presentation delivered at Chinook Captive Broodstock Technical Oversight Committee, Hagerman ID, November 2006.
- Attended and presented work at 3 additional bi-monthly Captive Broodstock Technical Oversight Committee meetings.
- Broodstocking and genetic effects of artificial propagation, CCRIFC-sponsored workshop for reintroduction of salmon and steelhead to the upper Columbia River. Spokane, Washington, February 2007 (invited workshop participant).
- Genetic effects of Wallowa River steelhead straying into the Deschutes River, Lower Snake River Compensation Plan cooperators meeting. Boise, April 2007 (invited oral presentation).
- The GAPS consortium facilitates inter-laboratory standardization of salmon genetic data. American Fisheries Society. Tacoma, June 2007 (session co-chair, oral presentation).
- The ecological genetics of marine stewardship in the face of climate change. American Meteorological Society Online Ocean Studies Course, Implementation Workshop. Seattle, June 2007 (invited oral presentation).

Publication of peer-reviewed scientific publications

[2 completed manuscripts, one describing population genetics of natural Snake River steelhead, and one Steelhead reproductive success manuscript.]

Five publications and manuscript submissions were supported in part by this genetic monitoring project in FY2007:

Moran, P., D.J. Teel, E.S. LaHood, J. Drake, and S. Kalinowski. 2006. Standardizing multi-laboratory microsatellite data in Pacific salmon: An historical view of the future. *Ecol. Freshwater Fish* 15:597–605.

- Seeb, L.W., A. Antonovich, M.A. Banks, T.D. Beacham, M.R. Bellinger, M. Campbell, N.A. Decovich, J.C. Garza, C.M. Guthrie III, P. Moran, S.R. Narum, J.J. Stephenson, K.J. Supernault, D.J. Teel, W.D. Templin, J.K. Wenburg, S.F. Young, C.T. Smith. 2007. Development of a standardized DNA database for Chinook salmon. Fisheries *in press*.
- Narum, S.R., D. Hatch, A.J. Talbot, P. Moran, and M.S. Powell. 2007. Conservation of iteroparous salmonids in complex mating systems and influence on effective population size. J. Fish Biol. *in press*.
- Narum, S.R., M. Banks, T. Beacham, R. Bellinger, M. Campbell, J. DeKoning, A. Elz, C. Guthrie, C. Kozfkay, K. Miller, P. Moran, R. Phillips, L. Seeb, C. Smith, K. Warheit, S. Young, and J.C. Garza. 2008. Differentiating Chinook salmon populations at broad and fine geographic scales with microsatellites and SNPs. Molec. Ecol. *submitted*.
- Paquin, M.M., J.M. Myers, H. Pollard, R.W. Carmichael, and P. Moran. Steelhead hatchery legacy? Hatchery and wild population genetic structure in the Snake River Basin. Cons. Genet. *submitted*.

Contracting, billing and administrative logistics

[Third-party labor and smolt trapping sub-contracts let (Frank Orth and Oregon Department of Fish and Wildlife).]

All third party sub-contracts were let as expected. Delivery of all products was on time and within budget. No unexpected difficulties or costs were encountered.