

RFS# 003

**Pedigree Approach to Determine Reproductive Success of Natural and Hatchery
Origin Spring/Summer Chinook Salmon Spawners in Johnson Creek, Idaho**

Submitted by:

Rick Orme
William Young
Chris Beasley

Nez Perce Tribe
Department of Fisheries Recourses
125 S Mission
PO Box 1942
McCall, Idaho
Ph. (208) 634-5290
Fax. (208) 634-4097
Email. RickO@nezperce.org
Email. BillY@nezperce.org
Email. ChrisB@nezperce.org

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BPA Request For Studies

Addressing
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Project Summary

We propose to address RPA 182 using microsatellite based parentage assignment and exclusion analyses to test for survival, productivity, and behavioral differences by life stage (parr, presmolt, smolt, and adult) for all possible crosses of naturally spawning wild, natural, and supplementation (hatchery fish) -origin spring/summer chinook salmon in Johnson Creek. A cooperative effort with the ongoing Johnson Creek Artificial Propagation and Enhancement Project (BPA project 9604300), utilizing their existing infrastructure and ongoing intensive sampling efforts, will allow for a cost effective determination of the reproductive success between all potential cross types (natural x natural, natural x supplementation, and supplementation x supplementation) for six complete F₂ brood years and three complete F₃ brood years by 2011. We will test for significant differences in the adult F₂ and F₃ generations between cross types for both proportional differences and family size differences. In addition, through the use of an existing juvenile screw trap, we will test for significant differences in relative proportion, family size, as well as biological and behavioral traits of all potential cross type at key life stages. We will use the observed data to define the Johnson Creek population according to the Viable Salmonid Population criteria; population size, population growth rate, and diversity. Finally, we will evaluate the current Johnson Creek Supplementation Project relative to its goals and objectives and make recommendation to enhance benefits or reduce risks for the current or for future supplementation efforts.

Data on reproductive success from the current "state of the art" supplementation program in Johnson Creek (using only wild/natural fish for eggs, acclimated releases, established matting protocols, availability of cryopreserved semen, etc.) will be invaluable to current and future management of ESA listed stocks. Such future artificial production projects have already been initiated with the National Marine Fisheries Service 2001 BiOp, which calls for the development of safety-net programs for stocks at high risks of extinction in the near term. This proposed project will develop reproductive success results from naturally spawning supplementation fish as early as 2003 from F₂ juvenile samples and from a complete brood year of F₂ adults in 2006. Results from F₃ juveniles will be obtained as early as 2005 and a complete brood year of F₃ adults in 2009. These timely results will greatly enhance safety-net project planning and implementation.

Introduction

Artificial propagation programs are one measure to attempt to enhance populations and increase natural production in Snake River tributaries. The National Marine Fisheries Service (NMFS) draft recovery plan (NMFS 1995) states that "supplementation programs should be initiated and/or continued for populations identified as being at imminent risk of extinction, facing severe inbreeding depression, or facing demographic risks". The NMFS restated this need in the 2002 BiOp (NMFS 2001) in section 9.6.4.3 which calls for safety-net programs to intervene with artificial production for stocks with high demographic risk of extinction.

The Johnson Creek summer chinook salmon (*Oncorhynchus tshawytscha*) population has experienced significant decline in population numbers over the past five decades. Escapement levels in Johnson Creek have declined from a recorded high of 486 redds in 1960 to a low of five redds observed in 1995. Due to critically low abundance of chinook salmon in Johnson Creek, the Nez Perce Tribe (NPT), through funding provided by the Bonneville Power Administration (BPA), initiated the development of an artificial propagation enhancement project (JCAPE) for Johnson Creek in 1998. This decision resulted from a number of factors including: increased emphasis on wild/natural production and stock recovery; consultation and requirements resulting from listing of Snake River chinook populations as threatened under the ESA; and preferred strategies for use of artificial propagation identified in *Wy-Kan-Ush-Mi Wa-Kush-Wit, Spirit of the Salmon* (CRITFC 1996).

The goal of the JCAPE project is to provide for the maintenance of genetic variability and demographic stability of the Johnson Creek spawning aggregate until such time as the factors responsible for the initial decline are addressed allowing recovery. The supplementation project began in 1998 with the collection and spawning of wild Johnson Creek chinook salmon. The JCAPE project is currently rearing up to 100,000 smolts annually and is expected to continue for a minimum of 4-5 generations (20-25 years).

The monitoring and evaluation (M&E) activities associated with the JCAPE project currently measure juvenile survival, smolt to adult returns (SAR), migration timing, age/size structure, abundance, adult to adult return, genetic diversity (allele frequency), and fecundity for hatchery and natural origin juveniles and adults. The JCAPE M&E program has established baseline information on the Johnson Creek chinook salmon spawning aggregate prior to supplementation, and will use these data as well as ongoing M&E to improve the effectiveness of supplementation within Johnson Creek.

The progeny of the first egg take were released into Johnson Creek in the spring of 2000 and the first supplementation fish returned at age three (jack) and four in 2001 and 2002. While age five fish have yet to return, the supplementation effort has succeeded in increasing adult returns to Johnson Creek. This observed increase in the number of spawning adults is a critical first step in a successful supplementation project. However, the JCAPE M&E project is unable to determine production by cross type among naturally spawning adults and must rely on other metrics for evaluation. These metrics are limited to total juvenile production, juvenile survival to Lower Granite Dam, adult-to-adult returns, age/size structure, and migration timing. These metrics are heavily influenced by environmental factors, limiting the value of these measures in determining the actual impact of supplementation. This project will provide more definitive methods to evaluate the potential long-term benefits or risks of a supplementation project.

Methods for detecting high levels of molecular variation in populations of plants and animals have made it possible to develop detailed understanding of mating systems (Avise, 1994). Using molecular markers to determine kinship and parentage can reveal population structuring, mating strategies and family structure essential for obtaining precise estimates of number of breeding individuals and effective population sizes

(Bentzen et al. 2001; Taggart et al. 2001). The power to detect these parameters comes from the ability to assign progeny and adults to only those individuals that successfully reproduce as opposed to measuring only the absolute number of progeny or adults produced. Thus, molecular markers and parentage analysis can determine the success or failure of specific segments of the breeding population. Here we propose to use microsatellite-based parentage assignment and exclusion analyses to determine the reproductive success of wild, natural, and supplementation origin spring/summer chinook salmon in Johnson Creek. Doing so will inform management decisions regarding supplementation by quantitatively evaluating the long and short-term effects of supplementation on production and productivity.

Johnson Creek provides an ideal setting for this study for the following reasons:

- 1) The JCAPE program is a small-scale supplementation program using state-of-the-art supplementation technology, hence providing a unique opportunity to examine the results of current artificial propagation technology. Funding this proposal will not only directly address RPA 182, it will improve the monitoring and evaluation program currently in place in Johnson Creek.
- 2) Hatchery-reared supplementation fish only spend one year in captivity then are released to complete their life cycle. No supplementation fish are used as brood stock in subsequent years. Analyzing the survival and reproductive fitness of these fish will enable us to examine the consequences of a single generation of hatchery rearing and determine the impact of these fish on the production and productivity of a naturally spawning population.
- 3) Adults and juveniles have been exhaustively sampled for DNA since the JCAPE program was initiated in 1998, hence allowing a retrospective analysis, limiting the timeframe necessary for F_3 evaluations. F_2 juvenile productivity results can be obtained as early as 2003 (complete brood year adult data in 2006) and F_3 juvenile productivity results can be obtained as early as 2005 (complete brood year adult data in 2009).
- 4) The existing monitoring and evaluation project provides substantial cost-sharing through operation of an existing weir and rotary screw trap.
- 5) Mark-recapture data have shown that nearly 100% of the returning adults can be sampled either at the weir or during carcass surveys, allowing a nearly complete census of adults that could potentially contribute to spawning.
- 6) We can monitor the effects of supplementation beginning with the first returning adults from supplementation efforts in a wild/natural system with minimal prior hatchery influence.

Project Overview

During the course of this study we will address RPA 182, enhance evaluation of the current supplementation project, and provide recommendations for improvements to current and future supplementation projects by addressing the following questions and uncertainties.

- 1) Are naturally spawning F1 adult supplementation fish as effective as wild fish in returning F2 adults and do differences (if observed) persist into the F3 generation?

The reproductive success of supplementation fish is a key uncertainty in supplementation efforts. Reproductive success is broadly defined by the number of offspring produced per spawner which is influenced by: changes in average fecundity of the stock, pre-spawning mortality, large and small scale spawning distribution (homing or selection of quality spawning substrate), spawning effectiveness (mate acquisition, redd digging capability, spawning timing, and egg retention), and survival of progeny of hatchery-reared fish across significant life history stages (egg-to-fry, fry-to-presmolt, presmolt-to-smolt, and smolt-to-adult). Other studies have shown a decrease in the overall reproductive success of hatchery fish after only a few generations of artificial propagation (ISAB 2002). However, it is uncertain whether the current methodologies used (egg take from wild/natural adults) will result in reduced reproductive success of supplementation adults or if a “hatchery” effect takes several generations to develop.

By employing a DNA microsatellite based pedigree or parentage analysis, progeny can be attributed to specific parents and in turn to particular cross types such as natural x natural, natural x supplementation, and supplementation x supplementation. The limitation to this method is that a large majority of spawning adults must be sampled which may be logistically impossible or cost prohibitive for some streams. Since 2001, M&E efforts have determined that the Johnson Creek adult weir is nearly 99% efficient at capturing all migrating adults. In addition, carcass surveys have a recovery rate of 50-60%, enabling samples to be collected from fish missed at the weir and from fish spawning below the weir. Generally, fewer than 10% of the fish spawn below the weir so we are confident that we can sample greater than 90% of the adult spawners at the weir or through carcass surveys. It is anticipated that total adult returns (natural and supplementation) would be approximately 500 each year.

- 2) Can differences in reproductive success be attributed to;
 - a. A specific life stage
 - b. Biological factor (condition factor)
 - c. Behavior trait (migration timing difference)

Differences in reproductive success may result from a sudden failure at a particular life stage or increased mortality through all life stages. Reproductive differences may be attributed to biological characteristics such as growth rate and condition factor, or from a behavioral attribute such as juvenile or adult migration timing. Determining at what life stage failure occurs and the likely cause of the failure is critical in establishing management options for current or future supplementation efforts.

By utilizing the existing JCAPE monitoring and evaluation project we will be able to monitor biological and behavioral attributes of all potential cross types at key life history stages. In addition to the adult tissue samples taken at the JCAPE weir, we propose to

take tissue samples from juveniles trapped, measured, weighed, and PIT tagged by the JCAPE project screw trap during the summer-fall period (parr and pre-smolts) and during the spring (smolts). Analysis of the tissue samples will allow an estimation of the proportion and family size of different cross types in the summer-fall and spring period. In addition, biological and behavioral attributes can be measured for each individual sample and attributed to different cross types. By taking and analyzing tissue samples from PIT tagged juveniles at the Johnson Creek screw trap, we will be able to extend the analysis to the lower Snake River. Samples taken from PIT tagged fish will be associated with a specific individual PIT tag. Detections of these PIT tags in the lower river system will allow for the survival of different cross types from Johnson Creek to the lower river system to be estimated.

- 3) What are the impacts to the population from spawning supplementation fish in terms of;
 - a. Population size
 - b. Population growth rate
 - c. Diversity
 - d. Goals and objectives of the supplementation project

The Viable Salmonid Population (VSP) (McElhany et al. 2000) outlined four population parameters that should be used to evaluate the status of a population. Here, we will focus our efforts on three of the four parameters; population size, population growth rate, and diversity. The fourth parameter, spatial structure, will not be evaluated as we are focusing on a single spawning aggregate. The pedigree analysis in conjunction with biological information collected at the JCAPE M&E weir, will allow for an annual quantitative measure of several population parameters (population size, population growth rate, and diversity) in the overall population and within different cross types. These population parameters will also enable adaptive management of the JCAPE program, allowing the optimization of brood stock size, release numbers, and adult returns of wild/natural and supplementation fish to increase both population size and genetic diversity.

Time Line—We propose to initiate this study with the Johnson Creek 2001 brood year and continue through 2011 (Table 1). This study will provide six complete F_2 brood years and three complete F_3 brood years. 2001 represents the first brood year for wild x wild and wild x supplementation crosses (no supplementation x supplementation crosses are possible, because all supplementation fish were jacks). Juveniles resulting from the first wild x supplementation crosses will migrate in 2002-2003. Tissue samples of smolts from the 2001 brood year are currently being collected. Results from the complete 2001 F_2 brood year (age 3, 4, and 5) will be available in 2006 while results from the first complete F_3 returns (brood year 2004) will be available in 2009. Juvenile tissue samples will be collected through 2006.

NEPA Requirements—The current JCAPE section 10 permit (BPA project 9604300) allows for the handling of ESA listed fish and the collection of all necessary tissue samples. No additional permitting will be required for this proposed project.

Project Area—Johnson Creek flows primarily in a northward direction and joins the East Fork South Fork Salmon River (EFSFSR) near the town of Yellowpine, Idaho. The Johnson Creek watershed encompasses approximately 213 sq. miles and is characterized by gentle to steep slopes that are moderately to strongly dissected by streams. The watershed includes U-shaped glacial troughs and other high elevational (6,000 feet +), steep granitic mountain slopes. Soils range from shallow to deep and have cobbly, coarse textured subsoils. Elevations range from 4,500 to 8,500 feet (mean 7,170 feet). Mean annual precipitation varies from between 15 and 58 inches. Most of this precipitation falls in the form of snow from October through April. Runoff is characterized by high flows in the spring followed by a decreasing hydrograph with the lowest flows typically in early fall through late winter. Mean annual air temperatures range from 33.4° to 39.1° F. Summer temperatures can reach near 100 at the lowest elevations, while winter lows are often well below zero. Vegetative cover ranges from dense to open stands of mixed conifers and grassy meadow complexes. Vegetative growth in much of the watershed is restricted by the cold climate (USFS 1995).

This proposed project will rely on existing facilities, operations, and data collections currently being conducted by the JCAPE project. The following is a brief description of ongoing activities and methods associated with the JCAPE project.

Adult trapping - Adult salmon trapping activities occur in Johnson Creek approximately five miles above the confluence of the EFSFSR. A picket style weir, consisting of a guide fence and an in-stream trap box is installed as soon as water flows are low enough (approximately 700 cfs) and is operated through mid September. Fish are anesthetized then visually and electronically scanned for tags and marks, fork length and mid eye to hyperle length (MEH) are recorded, a sequentially numbered opercle tag is applied, and a paper punch sample of tissue is taken from the caudal fin for genetic analysis. Fish are then released above the weir to spawn naturally.

Brood Stock Collection and Spawning - Wild adult chinook salmon are retained for brood stock representative of the age/size of the run and run timing. Age class determination is based on length frequency data from South Fork Salmon River (SFSR). Adult salmon are held at the SFSR facility and are typically spawned two (2) days a week, from mid August through the first week of September. The JCAPE Hatchery Genetic Management Plan (NPT and PRRG 2001) details a spawning matrix that maximizes the potential of each mating in case of poor returns or low male to female ratios. Cryopreserved semen is also available for use when there are low numbers of males and to maximize genetic material for spawning.

Acclimation and Release - Johnson Creek smolts are transported back to Johnson Creek for release at the end of March or the beginning of April depending on weather and road conditions. Smolts are released into a side channel of Johnson Creek where they are temporarily acclimated before release. The acclimation site is located seven (7) river miles above the confluence of Johnson Creek and the EFSFSR.

Juvenile Collection - Emigration studies in Johnson Creek are conducted with an emigrant rotary screw trap, manufactured by E.G. Solutions Inc., Corvallis, Oregon. The trap is located approximately seven kilometers above the confluence of Johnson Creek (rkm 522.303215.060.024) and the East Fork South Fork Salmon River. The screw trap is operated in Johnson Creek during three trapping seasons; summer season (July 1 to August 31, 1998), fall season (September 1 to December 31, 1998), and spring season (January 1 to June 30, 1999). The three trapping seasons are also categorized into three life history stages. Fish captured during the summer season are considered to be parr, fish captured during the fall season are considered presmolts, and fish captured during the spring season are considered smolts. However, high flows, ice conditions, repairs, maintenance and adjustments kept us from operating continuously during all seasons and life history stages.

PIT Tagging - Chinook salmon exhibit several emigration life history strategies with movement in the summer, fall, and following spring of the year. PIT tag technology is used to mark and monitor a group from each life stage. Nearly all captured juvenile chinook are PIT tagged for estimating life stage specific trap efficiency, emigration estimates, survival to Lower Granite Dam, emigration timing, and travel times to Lower Granite, Little Goose, Lower Monumental, McNary, John Day and Bonneville Dams.

Redd and Carcass Surveys - Spawning ground surveys are conducted according to standardized protocol developed by the Nez Perce Tribe. Multiple pass spawning ground surveys are conducted between August and September in Johnson Creek to determine: the start, peak and end of the spawning period, enumerate redds, determine live:dead fish ratios, determine relative abundance of spawners, determine annual and trend indexes, and enumerate total escapement of adult chinook salmon. Carcasses are recovered and checked for marks, tags and radio transmitters. Fork length and mid-eye hypural length are taken and scales and otoliths are removed from all carcasses. A portion of the caudal fin is removed and placed in labeled vials of alcohol for genetic analysis. Fish are slit open to verify sex and determine spawning success (percent spawned). Tails are then cut off to prevent duplicate sampling. A population estimate is calculated using a mark-recapture study. Adult chinook salmon captured at the adult weir are marked with a operculum disk tag and operculum punch and released upstream. Subsequent carcass recovery surveys are conducted upstream of the adult weir in order to determine the ratio of marked to unmarked fish. The carcass surveys are conducted before, during and after the last adult chinook salmon is trapped and released to insure all carcasses have an equal opportunity for recovery.

Objectives and Methods

Parentage analysis provides a wealth of information on the studied population. In addition to collecting information on the reproductive success of natural spawning supplementation fish, other information such as the reproductive success of jacks, number of males spawning with an individual female, actual number of breeders, age determination of all spawners, variation in family size, etc. are also available. The following objectives and tasks are a general outline for assessing reproductive success of

wild and supplementation fish spawning naturally. However, it is the intention of the authors to assess and report other information available from a parentage analysis. If this proposed project is selected for funding, a more detailed study plan can be provided if requested.

Objective 1. Measure the relative and absolute reproductive success of all potential cross types in the F₂ and F₃ generation.

Parentage analysis will begin with the 2001 brood year, the first year that supplementation return and continue through 2011 resulting in six complete F₂ brood years and three complete F₃ brood years. Tissue samples will be collected from all adults at the Johnson Creek weir (which includes all brood stock fish) by the JCAPE project. The JCAPE project has collected and stored 1,540 adult samples from the 2001 brood year and 1,220 adult samples for the 2002 brood year. However, we anticipate an annual collection of approximately 500 adult samples (natural and supplementation) as 2001 and 2002 represented extremely high return years. The Johnson Creek weir is extremely efficient at collecting most all adult salmon with efficiency estimate of nearly 99% for 2001 and 2002. In addition, carcass surveys are also relatively efficient with recovery rates of 56% to 63%. Carcass surveys are critical in collecting tissue samples from fish missed at and below the weir. In the event that the Johnson Creek weir is put in late, additional carcass surveys will be conducted to collect missed fish.

Tissue samples will be assayed for variation at 12 microsatellite loci. The resulting genotypes will be used to assign individuals to adults sampled in the previous generation. Assignments will be conducted using both exclusionary criteria (Comparez 5.0, J.B. Taggart, Queens University) and probabilistic approaches that explore the likelihood of each possible parentage assignment and establish statistical criteria for accepting the true parent (Cervus 2.0, Marshall et al. 1998). Analyzing all spawning individuals in a population makes collecting tissue from closely related individuals, including full sibs, unavoidable and this decreases the success of parentage assignment tests (Olsen, et al. 2001). However, theoretical and empirical results indicate that this will not be a problem using 12 microsatellite loci (Waits et al. 2001).

Regardless of the specific program used to perform parentage analyses, assignment errors can result from a lack of adequate resolution (*i.e.*, lack of ability to discriminate between potential parents) and genotyping errors (*i.e.*, laboratory or data management error). CERVUS (Marshall *et al.* 1998) uses a simulation package to address the first source of error by estimating the level of assignment confidence that can be expected based on the suite of microsatellite loci selected for assay. Genotyping errors are unpredictable, generally undetectable, and hence contribute an unknown amount of error to parentage analyses. To address genotyping errors, we intend to annually sample 60 hatchery origin juveniles. Following assay, a CERVUS parentage analysis will be implemented using the hatchery origin juvenile samples and all adults sampled at the Johnson Creek weir (both those collected as brood stock and those passed above the weir for natural spawning). Juveniles assigned to adults not retained for brood stock will therefore represent mistaken assignments. If the proportion of erroneous assignments exceeds that expected based on

the assignment resolution calculated by CERVUS simulations, we will attribute the increased error to laboratory or data management mistakes. Error attributed to both sources will be used to gauge the confidence that can be placed in parentage assignments.

Analysis of Data

Random mating—The proportion of wild x wild, wild x supplementation, and supplementation x supplementation crosses in the F1 generation will be calculated assuming random mating of wild and supplementation adults. Under the assumption of random mating, it is assumed that all fish contribute equally, all families are of equal size, and all cross types have equal probability of returning as adults. The expected proportion of cross types depends upon the number of wild and supplementation adult and the sex ratio of each type. The proportion of cross types will be calculated with and without jacks. We will test for deviations from assortative mating using juvenile tissue samples collected at the rotary screw trap and from adults sampled at the Johnson Creek weir in the next generation.

Relative Reproductive Success— We will test for differences in adult to adult survival by cross type in the F2 and F3 generation by comparing the observed proportion of adult cross types returning to Johnson Creek versus the expected proportion of cross types based on adult escapement the previous generation. Differences in proportion will be tested using a G test (Sokal and Rohlf 2001). This will test if cross types have an equal probability of surviving to the next time period. Pooling multiple brood years will increase sample size and provide additional statistical power to detect smaller differences if they occur.

Absolute Reproductive Success— We will also test for differences in reproductive success in the F₂ and F₃ generations using the mean number of progeny per parent. With an ideal population of size N, all parents have an equal expectation of being the parents of any progeny individual, assuming that gametes are drawn randomly from all breeding individuals (Hedrick 2000). With this assumption, the distribution of the number of progeny (gametes) per parent approaches the Poisson distribution when N is large. A non-random (non-Poisson) distribution of progeny per parent indicates genetic or environmental factors influenced breeding success. Comparing the differences between wild and supplementation distributions will indicate that one group was more or less successful. Pooling multiple brood years will increase sample size provide additional statistical power to detect smaller differences if they occur.

Trend Analysis—Regression analysis will be used to test for relationships between observed values of cross type proportions, family size, and biological and behavioral attributes within and among years to detect trends.

Objective 2. Determine in what life stage reproductive differences occur and if there are biological or behavioral traits associated with reproductive differences among cross types.

By utilizing the existing JCAPE monitoring and evaluation project we will be able to monitor the relative success and biological and behavioral attributes of all potential cross types at key life history stages. We propose to take tissue samples from juveniles currently being trapped, measured, weighed, and PIT tagged by the existing JCAPE project during the summer-fall period (parr and pre-smolts) and during the spring (smolts). We will collect and analyze 1,000 tissue samples from the PIT tagged summer-fall fish (parr and pre-smolts) and 1,000 tissue samples from the PIT tagged spring fish (smolts). By taking and analyzing tissue samples from PIT tagged juveniles at the Johnson Creek screw trap, we will be able to extend cross type analyses to the lower Snake River. Samples taken from PIT tagged fish will be associated with a specific individual PIT tag. Detections of these PIT tags in the lower river system will allow for the survival of different cross types from Johnson Creek to the lower river system to be estimated. Based on four years of survival and detection rates, we anticipate detecting approximately 300 summer-fall and 600 spring PIT tagged fish at and below Lower Granite Dam. Juvenile tissue samples will be collected at the Johnson Creek weir starting in 2003 with the 2002 brood year and continue through 2006 (Table 1).

Equal survival of double marked fish—We will assess potential survival differences between PIT tagged fish and tissue sampled PIT tagged fish. We hypothesize that survival of tissue sampled fish is the same as PIT tagged only fish to the Lower Snake River. Using unique detections at and below Lower Granite Dam as the survival metric, a sample size of 1,000 tissue sampled fish and 3000 or more PIT tagged only fish will allow for the detection of a 10% change in survival of PIT tagged and tissue sampled summer-fall fish versus PIT tagged only (30% survival to LGR) and a 6% survival difference in tissue sampled spring fish versus PIT tagged only fish (50% survival to LGR)(z-test). Regression analysis from pooling multiple brood years will provide a means of detecting and evaluating smaller survival differences if they occur. If significant differences are found, we will take tissue samples from non-PIT tagged fish and eliminate PIT tagged fish from future analysis.

Analysis of the tissue samples will be identical to the adults as explained under objective 1 which will allow for the proportion and family size of different cross types to be determined in the summer-fall period, during spring smolt migrations, and from PIT tag detections at and below Lower Granite Dam. We will not separate parr and pre-smolts into separate groups because of the relatively short time period between the groups during which differences can occur. Biological and behavioral attributes (condition factor, migration timing) as observed at the screw trap and from PIT tag detections will be assigned to individual samples and grouped according to cross type.

Pair wise comparison will be made to determine if differences exist between the proportion of cross types and family size of cross types at each life history stage, identical to adult comparisons in Objective 1. Comparisons will be made from F1 adults to juvenile stages (summer-fall, spring, and at and below Lower Granite Dam), juvenile stages to F2 adults, and between juvenile life stages. Pair wise comparisons of biological and behavioral attributes will also be made between different cross types by life stage.

Trend analysis within and among years will provide additional methods to detect significant differences. Trend analysis will be used to test for relationships between observed values of cross type proportions, family size, and biological and behavioral attributes within and among years.

Objective 3. Evaluate the effects the reproductive success of supplementation fish (or lack of reproductive success) has on Johnson Creek chinook population parameters as defined by the VSP.

The VSP (McElhany et al. 2000) outlined four population parameters that should be used to evaluate the status of a population. Here, we will focus our efforts on three of the four parameters; population size, population growth rate, and diversity. The fourth parameter, spatial structure, will not be evaluated as we are focusing this study to a single spawning group. Population size is the numeric abundance of a population, which determines the effective population size and potential level of inbreeding. Population growth rate is a measure of population change and is measured as adult-to-adult return rate. While diversity includes measures of genetic diversity and the range of biological and behavioral attributes such as fecundity, size at age, run timing, and age structure.

The pedigree analysis in conjunction with biological information collected at the JCAPE M&E weir, will allow for an annual quantitative measure of population parameters (population size, population growth rate, and diversity) in the overall population and within different cross types. The observed population parameters will be compared to estimates of population parameters in the absence of supplementation to evaluate change due to supplementation efforts.

Population parameters in the absence of supplementation will be estimated using a model to be developed in conjunction with population modelers at CRITFC. The developed model will use the observed annual population size (number of spawners, effective population size), population growth rate (adult-to-adult return), and diversity (allele frequency, run timing, age structure, fecundity, and return size) of wild x wild crosses. These values and the variation in these values will be expanded by the expected number of spawners in the population in the absence of supplementation, in effect adding the number of fish used for brood stock to the observed number of natural spawners in the stream. Out put of the model in the absence of supplementation will include an expected value and confidence measure of population size (number of spawners and effective population size), population growth rate, and diversity (allele frequency).

Objective 4. Evaluate the success of the JCAPE supplementation project and make recommendations for improvements in the current and for future supplementation projects.

The population model to be developed for objective 3 will be a valuable tool in exploring scenarios that may maximize benefits and reduce risks. For example, given the number of females used in the brood stock and supplementation return rate, the model can be

used to determine the optimal number of supplementation fish that could spawn with wild fish to maximize genetic diversity or effective population size. Such scenarios will be explored in an effort to optimize brood stock size, juvenile release numbers, and hatchery origin adult escapement. Results of the modeling exercise will be presented and recommendation made to the JACPE supplementation project.

Budget Estimate

This proposed project relies heavily on the existing JAPCE project activities. We will rely on the JCAPE project for the collection of adult tissue samples and for juvenile trapping and PIT tagging operations.

Adult Samples—We anticipate approximately 500 adult tissue samples will be analyzed annually. The number will likely vary depending upon juvenile production, migration survival, and ocean conditions. Current estimates for DNA analysis is approximately \$45 per sample for an annual estimated cost of \$22,500. In addition the project would require funds for office materials and supplies (computer and computer programs, office supplies, phone, etc.) at an estimated annual cost of \$5,000. The project would also require a Project Biologist (to be named) at 0.5 FTE at an annual cost of \$35,000. Administrative costs of personnel and supplies (22.6%) would be approximately \$9,000. Total estimated annual operating cost for the adult samples (2003-2011) is estimated at \$71,500 (Table 2).

In addition to the adult annual cost, an additional 2,760 adult samples collected in 2001 and 2002 would need to be analyzed at an estimated one time cost of \$124,000. These samples would be analyzed during 2003 and 2004 (Table 2).

Juvenile Samples—Estimated annual cost of tissue analysis for the juveniles is \$90,000 (2,000 samples at \$45/sample). The JACPE project does not currently collect juvenile tissue samples at the rate required by this proposal, therefore the proposed project would need funds for personal and materials to collect additional samples. The estimated cost of materials and supplies is \$5,000. Personnel costs are estimated at \$75,000 for two seasonal technicians and 0.5 FTE Project Biologist (to be named). Administrative costs of personnel and supplies (22.6%) would be approximately \$18,000. Total estimated annual cost (2003-2006) of the juvenile analysis is \$188,000 (Table 2).

Cost Sharing—The JACPE project currently has \$16,000 budgeted annually for genetic analysis of 4 loci. These funds would be used to run a portion of the samples collected in the proposed project. This will reduce the needed funds for the proposed project by \$16,000 (Table 2).

Total estimated annual cost of the project for the adult and juvenile analysis is \$259,500. With cost sharing from the JACPE project in genetic analysis, the estimated annual cost of the proposed project is \$243,500. In addition, a one time sum of \$124,000 would be needed to run samples collected in 2001 and 2002.

Funding Options—The estimated budget was separated for the adult and juvenile portions so different options could be evaluated if funds are limited. If funds are limited, only the adult portion could be funded which would provide for the most critical aspects of the proposal, reproductive success as measured in the F₂ and F₃ adults. If additional funds are available, the adult portion and the juvenile tissue sample collections could be funded. This option would provide for the collection and storage of juvenile samples which could be analyzed at a later date if reproductive differences are found in the F₂ and F₃ adults.

Table 1. Time line of the proposed project and expected number of samples collected and analyzed.

Year or Brood Year	Adult Samples	Parr and Pre Smolt Samples	Smolt Samples	Total Number of Samples	Complete F2 Returns	Complete F3 Returns
2001	1540	400	400	2340		
2002	1220	1000	1000	3220		
2003	500	1000	1000	2500		
2004	500	1000	1000	2500		
2005	500	1000	1000	2500		
2006	500	1000	1000	2500	BY 01	
2007	500			500	BY 02	
2008	500			500	BY 03	
2009	500			500	BY 04	BY 04
2010	500			500	BY 05	BY 05
2011	500			500	BY 06	BY 06

Table 2. Estimated project budget from 2003 through 2011.

Year	Direct Cost Share from JCAPE	Adult Samples and Supplies	Samples from 2001 & 2002	Personal and Fringe	Overhead (Personnel and Supplies)	Project Total for Adult Analysis	Juvenile Samples and Supplies	Personnel and Fringe	Overhead (Personnel and Supplies)	Project Total for Juvenile Analysis	Project Total
2003	(\$16,000)	\$27,500	\$62,000	\$35,000	\$9,000	\$117,500	\$95,000	\$75,000	\$18,000	\$188,000	\$305,500
2004	(\$16,000)	\$27,500	\$62,000	\$35,000	\$9,000	\$117,500	\$95,000	\$75,000	\$18,000	\$188,000	\$305,500
2005	(\$16,000)	\$27,500		\$35,000	\$9,000	\$55,500	\$95,000	\$75,000	\$18,000	\$188,000	\$243,500
2006	(\$16,000)	\$27,500		\$35,000	\$9,000	\$55,500	\$95,000	\$75,000	\$18,000	\$188,000	\$243,500
2007	(\$16,000)	\$27,500		\$35,000	\$9,000	\$55,500		\$35,000	\$9,000	\$44,000	\$99,500
2008	(\$16,000)	\$27,500		\$35,000	\$9,000	\$55,500		\$35,000	\$9,000	\$44,000	\$99,500
2009	(\$16,000)	\$27,500		\$35,000	\$9,000	\$55,500		\$35,000	\$9,000	\$44,000	\$99,500
2010	(\$16,000)	\$27,500		\$35,000	\$9,000	\$55,500		\$35,000	\$9,000	\$44,000	\$99,500
2011	(\$16,000)	\$27,500		\$35,000	\$9,000	\$55,500		\$35,000	\$9,000	\$44,000	\$99,500
Total	(\$144,000)	\$247,500	\$124,000	\$315,000	\$81,000	\$623,500	\$380,000	\$475,000	\$117,000	\$972,000	\$1,595,500

References

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- CRITFC (Columbia River Intertribal Fish Commission). 1996. *Wy-Kan-Ush-Me Wa-Kush-Wit, Spirit of the Salmon*. The Columbia River Anadromous Fish Restoration Plan of the Nez Perce, Umatilla, Warm Springs, and Yakima Tribes. Two Volumes. Columbia River Intertribal Fish Commission. Portland, OR.
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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. Commer., NOAA Tech. Memo. NMFS_NWFSC-42, 156 p.
- NMFS (National Marine Fisheries Service). 1995. Summary: Proposed recovery plan for Snake River salmon. U. S. Department of Commerce, National Oceanic and Atmospheric Administration, Portland, Oregon.
- NPT (Nez Perce Tribe) and PRRG (Production and Restoration Research Group). 2001. Johnson Creek Artificial Propagation Enhancement Hatchery and Genetic Management Plan. Nez Perce Tribe McCall Field Office, McCall, Idaho.
- Olsen JB, Busack C, Britt J, Bentzen P. 2001. The aunt and uncle effect: an empirical evaluation of the confounding influence of full sibs of parents on pedigree reconstruction. *J. Hered.* 92(3):243-247.
- Sokal, R.R and F. J. Rohlf. 2001. *Biometry: The Principles and Practice of Statistics in Biological Research*. W.H. Freeman and Company, New York.
- Taggart, J.B., I.S. McLaren, D.W. Hay, J.H. Webb and A.F. Youngson. 2001. Spawning success in Atlantic salmon (*Salmo salar*): a long-term DNA profiling-based study conducted in a natural stream. *Mol. Ecol.* 10(11):1047-1060.

USFS. Cascade and Krassel Ranger District (USDA). 1995. Upper South Fork Salmon River and Johnson Creek Watershed Analysis. Boise and Payette National Forest.

Waits LP, Luikart G, Taberlet P. 2001. Estimating the probability of identity among genotypes in natural populations: cautions and guidelines. *Mol. Ecol.* 10(1):249-56.

Key Personnel

William P. Young, Ph.D.

William Young's responsibilities will include project administration, hiring appropriate personnel, assisting in project design and data analyses, report and manuscript preparation, and presentation of results at technical and scientific meetings.

EDUCATION

1996 Ph. D. Washington State University - Zoology

1991 M.S. Michigan State University - Fisheries and Wildlife

1988 B.S. Pennsylvania State University – Biology, Genetics emphasis

PROFESSIONAL EXPERIENCE

Project Leader: 2002-present. Nez Perce Tribe, Department of Natural Resources Management. Salmonid Gamete Preservation in the Snake River Basin. Supervise field collection of chinook salmon and steelhead gametes; research techniques aimed at increasing the fertility of cryopreserved sperm; draft budgets and write reports; supervise the operation of the germplasm repository.

Affiliate Associate Professor, University of Idaho: 2003-present.

Postdoctoral Fellow: 1997-2002. Northern Arizona University.

Research: Molecular genetics of adaptive hybridization in *Populus* species; Molecular analysis of sex chromosome differentiation in rainbow trout; Genetic mapping, quantitative genetics and QTL analysis in soybean; Serial analysis of gene expression (SAGE) in soybeans; nuclear and mitochondrial DNA analysis of rainbow and coastal cutthroat trout interspecific hybridization.

Research Associate: 1996-1997. Washington State University.

Research: Genetic mapping in rainbow trout using AFLP, RFLP, microsatellite and RAPD markers; genetics of temperature adaptation in rainbow trout.

Research Assistant: 1991-1996. Department of Zoology, Washington State University.

Research: Genetic mapping in rainbow trout; Investigation of the correlation between fluctuating asymmetry and inbreeding in rainbow trout; DNA fingerprinting in salmonid fishes.

Research assistant: 1988-1991. Department of Fisheries and Wildlife, Michigan State University.

Research: Investigation of triploid chinook salmon survival in the Great Lakes; cold and warm water fish culture; Ploidy induction.

OTHER ACTIVITIES

Member of the genetic recovery team for bull trout in the lower Clark Fork River, ID, June, 2000.

Reviewer: Canadian Journal of Fisheries and Aquatic Sciences
Journal of Heredity
Journal of Fish Biology
Biotropica
USDA-NRI
Jeffress Research Grant

Professional Memberships: American Fisheries Society, Genetic Section

PUBLICATIONS

Whitham, TG, WP Young, GD Martinsen, CA Gehring, JA Schweitzer, SM Shuster, GM Wimp, DG Fischer, JK. Bailey, RL Lindroth, S Woolbright, and CR Kuske. 2003. Community Genetics: A Consequence of the Extended Phenotype. *Ecology* 84:559-573.

Nichols KM, Young WP, Danzmann RG, Robison BD, Rexroad C, Noakes M, Phillips RB, Bentzen P, Spies I, Knudsen K, Allendorf FW, Cunningham BM, Brunelli J, Zhang H, Ristow S, Drew R, Brown KH, Wheeler PA, Thorgaard GH. 2003. A consolidated linkage map for rainbow trout (*Oncorhynchus mykiss*). *Anim Genet.* Apr;34(2):102-115.

Thorgaard, G.H., P.A. Wheeler, W.P. Young, B.D. Robison and S.S. Ristow, 2003. Genetic analysis of complex traits using clonal rainbow trout lines. In: *Aquatic Genomics: Steps Toward a Great Future*. N. Shimizu, T. Aoki, I. Hirono and F. Takashima, eds. Springer, Tokyo, pp. 395-398.

Young, WP, CO Ostberg, P Keim and GH Thorgaard. 2001. Genetic analysis of hybridization and introgression between anadromous rainbow and coastal cutthroat trout. *Molecular Ecology*, 10:921-930.

Young, WP, J Schupp and P Keim. 1999. DNA methylation and AFLP marker distribution in the soybean genome. *Theor. Appl. Genet.* 99:758-790.

Hansen, JD, P Strassburger, GH Thorgaard, WP Young and L Du Pasquier. 1999. Expression, linkage and polymorphism of MHC related genes in rainbow trout, *Oncorhynchus mykiss*. *J. Immunology.* 163:774-786.

Young, WP, PW Wheeler, V Coryell, P Keim, and GH Thorgaard. 1998 A detailed genetic linkage map of rainbow trout produced using doubled haploid lines. *Genetics*:148(2) 839-850.

- Young, WP, PW Wheeler, RD Fields and GH Thorgaard. 1996. DNA fingerprinting confirms isogenicity of androgenetically-derived rainbow trout lines. *J. of Heredity* 87:77-81.
- Young, WP, PW Wheeler and GH Thorgaard. 1995. Asymmetry and variability of meristic characters and spotting in isogenic lines of Rainbow trout. *Aquaculture* 137:67-76
- Westmaas, AR, WP Young and D Garling. 1991. Induction of polyploids in bluegill and chinook salmon. *Proceedings of the North Central Aquaculture Conference*. Kalamazoo, MI.
- Thorgaard, GH, PA Wheeler, B Robison and WP Young. *In review*. Possible approaches for genetic analysis of temperature adaptations in redband trout. *Proceedings of the 1997 Redband Conference*.

INVITED SPEAKER

- Young, WP, CO Ostberg, P Keim and GH Thorgaard. Analysis of hybridization and introgression between rainbow trout and coastal cutthroat trout using AFLP markers. *Symposium: The use of genetic analysis in the conservation and management of wildlife species*. Annual Wildlife Society Meeting. Austin, TX Sept. 7-12, 1999.
- Young, WP and GH Thorgaard. Preliminary genetic analysis of the sex chromosomes in rainbow trout. *Aquaculture Workshop. Plant and Animal Genome Conference VIII*. San Diego, CA Jan. 9-12, 2000

Key Personnel Cont.

Chris A. Beasley

Chris Beasley's responsibilities will include assisting in project design and data analyses, will aid in report and manuscript preparation, and presentation of results at technical and scientific meetings.

Professional Preparation

1997 M.S., Zoology, North Carolina State University

1995 B.S., Systematics and Ecology, University of Kansas

Appointments

2002-Present Project Leader, Nez Perce Tribe, McCall, Idaho

Lead technical representative for the Nez Perce Tribe project entitled "Salmon Supplementation Studies in Idaho Rivers." Responsibilities include data management and analysis aimed at testing the effects of supplementation on short-term production and long-term productivity of naturally spawning aggregates of spring/summer chinook salmon.

1998-2002 Fisheries Scientist, Columbia River Inter-Tribal Fish Commission,
Portland, Oregon.

Specializing in genetic and ecological risk analysis as applied to artificial propagation programs under the Endangered Species Act. Responsibilities include: analysis and interpretation of genetic data; statistical analysis of biological data; designing and optimizing conservation hatcheries; report writing; publication; and presentation of data at national and international meetings.

Publications

Beasley, C.A., R. Sharma, and A.J. Talbot. *In Preparation*. Variance and inbreeding effective population size of declining salmonid population in the presence and absence of a conservation hatchery program.

Beasley, C.A., and J.E. Hightower. 2000. Effects of a low-head dam on the distribution and characteristics of spawning habitat used by striped bass and American shad. *Transactions of the American Fisheries Society*. 129: 1316-1330.

Beasley, C.A., A. Talbot, D.R. Hatch, and A. Ritchie. 2000. Johnson Creek artificial propagation and enhancement project (JCAPE) benefit risk analysis. Prepared for the Nez Perce Tribe.

Beasley, C.A. 2000. Hatchery and genetic management plan for the Johnson Creek artificial propagation enhancement program. Prepared for the Nez Perce Tribe.

Beasley, C.A., A. Talbot, D.R. Hatch, and M. Wishnie. 1999. Nez Perce tribal hatchery benefit risk analysis. Prepared for the Nez Perce Tribe.

Collaborators & Other Affiliations

- Columbia River Inter-Tribal Fish Commission (current)
- University of Idaho (current)
- Confederated Tribes of the Umatilla Indian Reservation (current)
- Confederated Tribes of the Warm Springs Reservation of Oregon (current)
- Confederated Tribes and Bands of the Yakama Indian Nation (current)

Key Personnel Cont.

Rick W. Orme

Rick Orme's responsibilities will include assisting in project design and data analyses, will aid in report and manuscript preparation, and presentation of results at technical and scientific meetings.

EDUCATION:

Utah State University, Logan, Utah, 84321
MS in Aquatic Ecology, June 1998

Utah State University, Logan, Utah, 84321
BS Fisheries and Wildlife Management, June 1994

Dixie College, St. George, Utah, 84770
Associate of Science, June 1991

EMPLOYMENT HISTORY:

June 1999 to present
Project Leader
Department of Fisheries Resources
Nez Perce Tribe, McCall, Idaho, 83638

June 1998 through May 1999
Research Associate
Utah Cooperative Fisheries and Wildlife Research Unit,
Utah State University, Logan, Utah, 83421

January 1995 to June 1998
Research Assistant
Utah Cooperative Fisheries and Wildlife Research Unit,
Utah State University, Logan, Utah, 83421

PUBLICATIONS:

Professional Journal:

Spawning and fry production of adfluvial Bear Lake strain cutthroat trout in the Strawberry basin. NAJFM. Co-author.

In preparation:

Early life history strategies of adfluvial cutthroat trout: growth, survival, and migration patterns during stream residence. TAFS. Co-author.

An assessment of post-stocking predation and handling/acclimation mortality of cutthroat trout in Bear Lake, Utah-Idaho. TAFS. Author.

Annual reports:

An assessment of post-stocking predation and handling/acclimation mortality of cutthroat trout in Bear Lake, Utah-Idaho. 1999. Author.

Reservoir fluctuations and implications on non-game fish species. 1999. Co-author.

Production and survival of Strawberry Reservoir salmonids: Final report. 1999. Co-author.

Spawning and recruitment of Strawberry Reservoir salmonids: Final report. 1997. Author.

Production and survival of Strawberry Reservoir salmonids. 1997. Co-author.

Spawning and recruitment of Strawberry Reservoir salmonids. 1996. Author.

Key Personnel Cont.

Jason Vogel

Jason Vogel's responsibilities will include aiding and assisting the project in the supervision and collection of adult and juvenile tissue samples from the Johnson Creek weir, the Johnson Creek screw trap, and from carcass surveys.

EDUCATION

3/98 Masters of Science in Fisheries, Utah State University, Logan, Utah
5/95 Bachelors of Science in Fishery Resources, University of Idaho, Moscow
12/92 Associates in Arts and Science, College of Southern Idaho, Twin Falls

TECHNICAL EXPERIENCE

Project Leader, Nez Perce Tribe, McCall, ID, Apr 1998 – Present.

Project: Johnson Creek Artificial Propagation Enhancement Monitoring & Evaluation Project

Graduate Research Assistant, Utah State University, Logan, UT, Oct 1995 – Mar 1998.

Project: Development of a visual foraging model for salmonid predators.

Field Technician, University of Idaho, Moscow, ID, May 1994 – Sep 1994, May 1995 – Sep 1995.

Project: Food web study and species interactions on Lower Granite Reservoir.

Biological Assistant, Oregon Department of Fish & Wildlife, LaGrande, OR, Mar 1995 – May 1995.

Project: Anadromous smolt monitoring on the Grande Ronde River.

Laboratory Technician, University of Idaho, Moscow, ID, Dec 1994 – Mar 1995.

Project: Lab portion of food web study of Lower Granite Reservoir.

Teaching Assistant, University of Idaho, Moscow, ID, Aug 1994 – Dec 1994.

Project: Instructed laboratory sessions for a 400-level Ichthyology course.

Biological Aid, Idaho Department of Fish and Game, Nampa, ID, May 1993 – Aug 1993.

Project: Movements and habitat utilization of bull trout in the Rapid River system.

Biological Aid, Idaho Department of Fish and Game, Riggins, ID, May 1992 – Aug 1992
May 1991 – Aug 1991, Apr 1990 – Nov 1990

Project: Idaho Power Chinook Salmon Hatchery.

Duties: project implementation, management and coordination, budget preparation and management, contract and subcontract preparation and management, report writing, personnel supervision, tribal representation in meetings with IDFG, NMFS, BPA, NPPC, CBFWA, and private consultants, data base management, data analysis, computer modeling, public speaking and presentations, and proposal development.

Skills: project management, database management, proposal writing, data analysis, report writing, data presenting, screw trap coordination and implementation, PIT tagging, spawning adult salmonids, fish culture activities, surgical implantation of ultrasonic and radio transmitters, ultrasonic and radio tracking fish, field data collection and laboratory

analysis of fresh water benthic macroinvertebrates and fish, boat electrofishing, backpack electrofishing, seining, gill netting, adult weirs and traps, hook and line, transect stream survey methodology, snorkel, redd surveys, life history research, diet analysis, database analysis, fish handling and identification, boat operation and maintenance, teaching ichthyology labs, hydroacoustics, and scuba research diving.

PUBLICATIONS/REPORTS

Vogel, J.L. and D.D. Nelson. 2001 Draft. Monitoring and evaluation activities of brood year 1997 juvenile and calendar year 1998 adult fishes in Johnson Creek. Annual Progress Report. Nez Perce Tribe, Department of Fisheries Resource Management. McCall, ID.

Vogel, J.L. and D.D. Nelson. 2001a Draft. Monitoring and evaluation activities of brood year 1998 juvenile and calendar year 1999 adult fishes in Johnson Creek. Annual Progress Report. Nez Perce Tribe, Department of Fisheries Resource Management. McCall, ID.

Vogel, J. and J. Hesse 2000. Monitoring and evaluation plan for Johnson Creek artificial propagation and enhancement program. Nez Perce Tribe. Department of Fisheries Resource Management. McCall, ID.

Vogel, J. and J. Hesse 2000. Johnson Creek Artificial Propagation and Enhancement of Spring/Summer Chinook Salmon Conceptual Monitoring and Evaluation Plan. Nez Perce Tribe. Department of Fisheries Resource Management. McCall, ID.

Nelson, D.D., and J. L. Vogel. 2000 Draft. Monitoring and evaluation activities of juvenile and adult fishes in Johnson Creek. Annual Progress Report. Nez Perce Tribe, Department of Fisheries Resource Management. McCall, ID.

Vogel, J.L. and D.A. Beauchamp. 1999. Effects of light, prey size, and turbidity, on reaction distances of lake trout (*Salvelinus namaycush*) to salmonid prey. *Can. J. Fish. Aquat. Sci.* 56:1293-1297.

Key Personnel Cont.

Paul A. Kucera

Paul Kucera's is responsible for the administration of all research related projects for the Nez Perce Tribe. Paul will assist in project administration, hiring appropriate personnel, assisting in project design and data analyses, report and manuscript preparation, and presentation of results at technical and scientific meetings.

EDUCATION: Bachelor of Science. 1975.
Utah State University.
Major: Fisheries Management.

Graduate Studies - MS
University of Idaho 1984-1987
Major: Fisheries Management.

PROFESSIONAL EXPERIENCE:

1992-present Senior Fisheries Biologist, Acting Fisheries Program Manager, and currently as Director of Biological Services with the Nez Perce Tribe Department of Fisheries Resources Management. Responsible for research projects, Department program direction and administration of the Fisheries Research Division.

1988-1991 Senior Fisheries Biologist with the Nez Perce Tribe Fisheries Department. Adult salmon population status monitoring and LSRCP hatchery evaluation studies in major river subbasins in the Snake River.

1987-1988 Acting Fisheries Program Manager with the Nez Perce Tribe Fisheries Department. Responsible for fisheries program management and direction.

1984-1986 Senior Fisheries Biologist with the Nez Perce Tribe Fisheries Department. Conducted research on juvenile steelhead trout life history characteristics and abundance in relation to physical habitat parameters on five streams.

1982-1983 Project fisheries biologist with the Nez Perce Tribe Fisheries Department. Responsible for conduct of a physical and biological inventory of streams on the reservation proper with emphasis on anadromous salmonids.

1978-1980 Fisheries biologist with the Colville Confederated Tribes Fish and Wildlife Department. Developed fishery management programs for the Colville Tribe on their 1.3 million acre reservation and the 1.7 million acre ceded area.

1975-1978 Fisheries research biologist with W.F. Sigler and Associates, Environmental Consulting Firm. Ecological and fish life history research on 110,000 acre Pyramid Lake, Nevada.

Unique Abilities:

Certified Fisheries Scientist - AFS
Experienced with Endangered Species Act and management of listed fish species.
Ecological and fish life history research on anadromous and resident fish species.
Population dynamics experience on Snake River Pacific salmon.
Management experience with resident and anadromous species.
Snake River water rights adjudication experience.
Familiar with Columbia River basin fisheries management issues.
Certified SCUBA diver - NAUI

Publications

Kucera, P.A. and M.L. Blenden. 1993. Chinook salmon spawning ground survey in Big Creek and tributary streams of the South Fork Salmon River, Idaho - 1991. Nez Perce Tribe Department of Fisheries Resources Management, Lapwai, Idaho. 42 pp.

Kucera, P.A. and M.L. Blenden. 1998. Summary report of 1997 project activities relating to threatened chinook salmon populations listed under the Endangered Species Act. Nez Perce Tribe Department of Fisheries Resources Management, Lapwai, Idaho.

Kucera, P.A. 1998. Nez Perce Tribe vision of the future for chinook salmon management in the South Fork Salmon River. Pages 177-185 *in* Proceedings of the Lower Snake River Compensation Plan Status Review Symposium. February 3-5, 1998. U.S. Fish and Wildlife Service, Boise, Idaho.

Kucera, P.A. and M.L. Blenden. 1998. Emigration of hatchery and natural chinook salmon from the Imnaha River. Pages 141-153 *in* Proceedings of the Lower Snake River Compensation Plan Status Review Symposium. February 3-5, 1998. U.S. Fish and Wildlife Service, Boise, Idaho.

Kucera, P.A. and M.L. Blenden. 1999. Chinook salmon spawning ground survey in Big Creek and tributary streams of the South Fork Salmon River, Idaho, 1992-1995. Assessment of the status of salmon spawning aggregates in the Middle Fork Salmon River and South Fork Salmon River. Technical Report 99-7. Nez Perce Tribe Department of Fisheries Resources Management, Lapwai, Idaho.

Armstrong, R. and P.A. Kucera. 2000. Salmonid Gamete Preservation in the Snake Basin, 1999. Annual Report to Bonneville Power Administration, Portland OR, Contract 97-AM30423, Project 97-038-00, and U.S. Fish and Wildlife Service, Cooperative Agreement No. 141109J003. Nez Perce Tribe Department of Fisheries Resources Management, Lapwai, Idaho.

Faurot, D. and P. A. Kucera. 1999. Escapement monitoring of adult chinook salmon in the Secesh River, Idaho, 1997. Annual Report to the Bonneville Power Administration. Nez Perce Tribe Department of Fisheries Resources Management. McCall, Idaho.

Faurot, D., P. A. Kucera and J. Hesse. 2000. Escapement monitoring of adult chinook salmon in the Secesh River and Lake Creek, Idaho, 1998. Annual Report to the Bonneville Power Administration. Nez Perce Tribe Department of Fisheries Resources Management. McCall, Idaho.

Faurot, D. and P.A. Kucera. 2001. Adult chinook salmon abundance monitoring in the Secesh River and Lake Creek, Idaho, 1999. Annual report to Bonneville Power Administration. Nez Perce Tribe Department of Fisheries Resources Management. Lapwai, ID.

Faurot, D. and P.A. Kucera. In prep. Adult chinook salmon abundance monitoring in the Secesh River and Lake Creek, Idaho, 2000. Annual report to Bonneville Power Administration. Nez Perce Tribe Department of Fisheries Resources Management. Lapwai, ID.

