

This is the Idaho Department of Fish and Game's (Department) response to comments generated by the Independent Science Review Panel (ISRP) for Project ID: 33001.

The ISRP reviewers requested responses on three main issues:

- 1.) The ISRP suggested that the proposal would be stronger and more comprehensive if Yellowstone cutthroat and redband trout sampling and associated genetic analysis was expanded to cover the entire Upper Snake and Middle Snake Provinces.**
- 2.) The ISRP suggested that we collaborate with the Department sponsor for Project ID: 199800200 (Native Salmonid Assessment Project) to describe how the anticipated genetic, abundance, life history, and habitat data will be used to identify conservation management units and to provide some idea of how these units could be linked together into a protection and recovery plan.**
- 3.) The ISRP reviewers wanted to know why our budget summaries did not show any cost sharing.**

The answers to these requests follow:

- 1.) In response to the request to include samples of Yellowstone cutthroat and redband trout outside of Idaho:**

We agree with the reviewers that the strength of our data set, and subsequent analysis could be improved if Yellowstone cutthroat and redband trout samples from outside the immediate state boundaries of Idaho were included in the experimental design. As management decisions are made, it makes logical sense to approach this process from a watershed perspective and not ignore population segments managed by adjacent state agencies. The following review summarizes the status of Yellowstone cutthroat and redband trout sampling that has been conducted outside of the state of Idaho that are available to incorporate in the study design for our proposal.

Yellowstone cutthroat trout

As cited in the proposal, over 200 samples of Yellowstone cutthroat trout from six locations in Yellowstone Lake, Wyoming and over 100 samples of Yellowstone cutthroat

trout (fine-spotted form) from the Jackson National Fish Hatchery have been collected. Additionally, the Department's Native Salmonid Assessment project (Project ID: 199800200) has sampled for Yellowstone cutthroat trout in the Goose Creek, Raft River, and Teton sub-basins in Utah, Nevada, and Wyoming (Table 1). The Department has also secured 285 samples of Yellowstone cutthroat trout from the Salt River drainage in Wyoming in cooperation with the University of Wyoming (Jason Burckhart-307-766-6313) and the Wyoming Game and Fish Department. The Department has also reached an agreement with U.S. Forest Service (James Capurso, Forest Fisheries Biologist, Caribou-Targhee National Forest, (208) 557-5780), to obtain samples of Yellowstone cutthroat from the Sinks Drainages of Southeastern Idaho.

Redband trout

In addition to the inventory of redband trout samples identified in our proposal, the Department's Native Salmonid Assessment project (Project ID: 199800200) will be expanding sampling efforts in 2002 and 2003 to include populations within Salmon Falls, the Jarbidge River, the Bruneau River and the Owyhee River. While much of this effort will be directed at Idaho waters, additional emphasis will be placed on collecting headwater samples in Nevada and Oregon. We have also developed an agreement with the Burns Paiute Tribe of Oregon (Steve M. Namitz (541) 573-1375) to provide additional redband trout samples from several locations within the Malheur basin in summer 2002. This agreement includes the collection of samples from Beulah Reservoir, Warm Springs Reservoir, mainstem Malheur River, Northfork Malheur River, and Juntura. In addition to the above, we have access to the University of Idaho's reference collection of redband trout including samples from the Kootenai River basin, the upper Columbia River basin and from several internal basins of southern Oregon.

- 2.) In the response to the request that in conjunction with Proposal #199800200, project sponsors should describe how the anticipated data (genetic, abundance, life history, and habitat) will be used to identify conservation management units and provide some idea of how these units could be linked together into a protection and recovery plan for Yellowstone cutthroat trout or redband trout in the upper Snake River system:**

We agree with the reviewers regarding the importance of the connection between abundance, life history, habitat, and genetic data generated by these two projects (199800200 and 33001) in the identification of conservation management units (CMUs) that can be incorporated into protection and recovery plans for Yellowstone cutthroat trout and redband trout in the middle and upper Snake River provinces. In this response, we first discuss the type and significance of the information provided by each project, we then describe how information from both projects are essential to the process of identifying CMUs.

Abundance is an important factor in species conservation because, all else being equal, small populations are at greater risk of extinction than larger populations. This is primarily true because small populations are more vulnerable to environmental variation, demographic stochasticity, catastrophes, and inbreeding depression, as well as other hazards. Thus, knowledge of the size of a population is critically important in establishing CMUs.

Life history is a related parameter because the ability of nearby populations to infuse new genetic material to an existing population (migration), the age at first maturity, fecundity, and other life history characteristics mediate the influence population size has on a population's risk of extinction. For example, if two isolated populations each consisting of 1000 individuals that on average live 20 years, and the age at first maturity differs between populations so that one population matures earlier while the other matures later, the ability of adults to produce offspring and replace themselves would not be equal between populations. Thus, life history and absolute population size (N) both influence effective population size (N_e). Habitat is also important because, no matter how much effort is put forth to recover populations, recovery will be hindered or prevented if adequate habitat is not present for the target species to occupy. In addition, watershed functions affect patterns in stream habitat, which in turn affect the attributes of fish populations (Isaak 2001). Thus, knowledge of site-specific conditions as well as watershed-level characteristics can both elucidate patterns of fish distribution and abundance and provide information that improvement and recovery plans can target.

Genetic data produced from project 33001 is inextricably linked to both population and habitat information provided by project 199800200 and could be used in the process

of identifying conservation management units in two ways. First, genetic identification of non-introgressed populations will allow the prioritization of those populations for conservation and preservation efforts. A description of this prioritization process, which the State of Idaho currently includes in their management plan for cutthroat trout, is explained in the document *Cutthroat Trout Management: A Position Paper, Genetic Considerations Associated with cutthroat trout management* (UDWR 2000; <http://www.nr.utah.gov/dwr/PDF/cuttpos.PDF>). This document, developed by the states of Colorado, Idaho, Montana, Nevada, New Mexico, Utah, and Wyoming, describes two conservation management components; core conservation populations and conservation populations. Core conservation populations include genetically pure populations (>99% pure, no detected introgression). The primary management goal for core conservation populations is to facilitate long-term persistence of each subspecies in a genetically pure condition, and secondarily may serve as a source of gametes for any future introductions and re-introductions through transplantation and brood stock development. Core populations would be used only to maintain genetic variation and combat the negative consequences of inbreeding depression, and only after gene flow rates and an understanding of ecological differences among populations is gained (Storfer 1999). Core populations themselves would not be the targets of translocations unless inbreeding depression, genetic drift, or other factors put the population in jeopardy. The primary management goal for conservation populations is to preserve and conserve unique ecological and behavioral characteristics of the subspecies that exist on a population-by-population basis. These populations in general will have introgression rates of less than 10%, unless unique ecological, genetic, or behavioral attributes warrant protection despite higher rates of introgression. Conservation populations may be targeted for conversion to core conservation population status by eradication and reintroduction or genetic replacement.

The process of identifying non-introgressed populations will also allow us to test a historical stocking database. Statistically significant correlation between the Idaho historical stocking database and observed introgressive hybridization could be used as a predictive tool to identify areas where introgression is unlikely and already limited conservation resources could be directed. Moreover, to investigate genetic diversity and

genetic population structure, populations that are free from rainbow trout introgression are essential since introgressed populations will confound genetic diversity estimates.

The second way in which we believe that genetic data produced from project 33001 should be used in the process of identifying conservation management units, is that an investigation of population structure in these non-introgressed areas should identify, from a genetic standpoint, a hierarchical level at which groups of populations can be grouped and managed together for conservation and management purposes (Allendorf and Leary 1988; Gyllensten 1985).

The first steps in the process of defining CMU's should include describing overall genetic variation within populations of these species throughout the basins. Likewise, total genetic diversity present within these two species across their respective geographic ranges which fall within these provinces and how that variation is partitioned is also important. Understanding population structure of a species is obviously an important step in making decisions regarding the scale at which populations should be managed in order to maintain the natural genetic diversity within a species (Ryman et al. 1995; Wenburg et al. 1999). For example, recent analysis of population structure within coastal cutthroat trout and bull trout populations led researchers to conclude that the best way to conserve the total genetic diversity present within these species (and to ensure their long-term survival) is to manage them as independent populations at the level of individual creeks and streams. (Wenburg and Bentzen 2001; Kanda and Allendorf 2001). It is unlikely that we will see a similar type of population structure in Yellowstone cutthroat trout. In fact, previous research on genetic population structure of Yellowstone cutthroat trout in the Yellowstone River drainage, suggested that most of the total genetic variation detected was contained within local populations (96.1%), and very little was due to differences observed among populations (3.9%) (Leary et al. 1989). This led the researchers to suggest, "Conservation of the genetic diversity of Yellowstone cutthroat, therefore, may effectively be accomplished by ensuring the existence of only a few populations." They added importantly, "From other perspectives, however, this may not constitute a wise management policy."

Project 33001 will examine genetic population structure in Yellowstone cutthroat trout and redband trout over much of their geographic ranges (the entire Middle and

Upper Snake River Provinces). For Yellowstone cutthroat this entails sampling multiple locations from multiple streams within ten major drainages within the Snake River Basin above Shoshone Falls up to Henrys Lake, ID. For redband trout this entails sampling multiple locations from multiple streams within ten major drainages within the middle Snake River Basin from Shoshone Falls downstream to Hells Canyon Dam, ID.

The Idaho Department of Fish and Game and the University of Idaho have already begun this process in a pilot study, examining 40 Yellowstone cutthroat trout populations throughout the upper Snake River basin above Shoshone Falls (see proposal) and examining 10 redband trout populations within the Bruneau River drainage. We are expanding this pilot study by selecting four additional sample locations (two from locations known to have been stocked with rainbow trout and two from unstocked areas according to the database) from each of the ten major drainages identified for each species. This work will allow us to test for a lack of independence and statistically significant correlation between the historical stocking database in predicting hybridization and observed introgression levels. The additional sample locations are necessary to provide sufficient statistical power to assess the stocking database as well as provide additional populations free of rainbow trout introgression to examine genetic population structure at various levels. Within drainages, we wish to sample and analyze non-introgressed populations that exhibit the diversity of life histories, behavior or morphological adaptations present in the drainage. We also wish to include, if possible, populations isolated above natural barriers. The molecular and statistical procedures for assessing genetic variation and genetic population structure are described in detail within project proposal 33001.

Information from both projects will address these types of questions: 1) how large are populations (both N and N_e); 2) how functional is the habitat for these populations? 3) how does life history influence effective population size and how does it compare to other populations; 4) how do site-specific to watershed-level environmental conditions (e.g., reach-scale habitat, hydrologic geomorphology, upland characteristics, land use, etc.) affect population strengths and weaknesses; 5) how interconnected are populations; 6) how genetically pure are populations; and, 7) how is genetic diversity partitioned throughout these populations? Most importantly, information from both projects need to

be used together in the development CMUs.

The necessity of using all available information from both projects (population abundance, habitat, genetics) becomes apparent as we start to examine the work completed thus far by project 199800200 on Yellowstone cutthroat trout populations and begin to consider the identification and prioritization of conservation management units. For example, project 199800200 has to date sampled 57 locations in the Willow Creek drainage, and has observed Yellowstone cutthroat trout at 19 locations. At these 19 locations, a total of 467 Yellowstone cutthroat trout were captured. Based on the length of stream sampled and the number of fish bearing stream kilometers in the Willow Creek drainage, it appears that many thousands of cutthroat trout inhabit the Willow Creek drainage; IDFG (2000) estimated the Willow Creek drainage contained about 47,000 Yellowstone cutthroat trout. Seven of these locations have been genetically analyzed thus far and have been demonstrated to be non-introgressed (University of Idaho, IDFG, unpublished data). Further genetic information from project 33001 on population structure of sampled locations within the drainage could have extremely important implications on how we assign a conservation management unit. If genetic analyses indicate very little genetic differences among sample locations within the Willow Creek drainage (e.g. $F_{ST} < 0.05$), this would support management of the entire Willow Creek drainage as a “conservation management unit”. Alternatively, if genetic analyses indicate 19 genetically distinct populations within the drainage, management action would obviously differ significantly from the first scenario. The opinion regarding the Willow Creek drainage as one population or many, would have significant impact on population abundance estimates, viability estimates, how we view habitat protection within the drainage, fishing regulations, and so forth. This description of two extreme scenarios, illustrates the point that synergistically, both projects add more to the process of designating conservation management units, and the protection and preservation of these species throughout the middle and upper Snake River Provinces, than either would provide alone.

The Department is currently in the process of developing conservation/management plans for both Yellowstone cutthroat and redband trout (G. LaBar, IDFG, personal communication; D. Schill, IDFG, personal communication). Information generated by

projects 33001 and 199800200 will be incorporated into these plans. Combined with life history, presence/absence, population dynamics, and habitat information that has been or is presently being collected, the Department will be well positioned to make important decisions about future management of endemic trout species within the middle and upper Snake River basins (including headwater systems in adjacent states).

3.) In response to the question as to why our budget summaries did not show any cost sharing:

We were remiss in not identifying the work that has taken place that without which, we be hard pressed to accomplish our stated objectives. All costs associated with tissue sample collection (both equipment and labor) for this project have been paid for (or listed under their current budgets) by agencies cooperating to provide samples (e.g., the Bureau of Land Management, U.S. Forest Service, the Wyoming Game and Fish Department, the Burns Paiute Tribe of Oregon, and the Idaho Department of Fish and Game). Additionally, without the support of the University of Idaho and their facilities at the Hagerman Fish Culture Experiment Station, our proposed costs would be considerably higher. The University of Idaho is providing laboratory equipment, data analysis software, office support, and clerical support for this cooperative effort. In addition to the above, Idaho Department of Fish and Game license and Dingle-Johnson funds have been used to construct a new genetics laboratory located at the Department's Eagle Fish Hatchery/Fish Health complex. When completed in the spring of 2002, this facility will be the primary location for the analysis of samples associated with this project. Costs expended in fiscal year 2002 for the development of this facility are anticipated to be approximately \$80,000. A considerable portion of the labor was provided internally by the Department. And finally, the Department is currently preparing management and conservation plans for Yellowstone cutthroat and redband trout. These efforts are being funded with internal Department funds as well. When complete, these plans will serve as guiding documents for the management of these species. Naturally, they will incorporate findings generated from Project ID: 33001

References

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Table1. Location of Yellowstone cutthroat trout sample locations from non-Idaho waters.

SUBBASIN	Streamname	Streamsite	SUBBASIN	Streamname	Streamsite
Goose Creek	Birch Creek	Lower (UTAH)	Raft River	Johnson Creek	Lower (UTAH)
Goose Creek	Birch Creek	Upper (UTAH)	Raft River	Johnson Creek	Upper (UTAH)
Goose Creek	Bluff Creek	Lower (NEVADA)	Raft River	Left Fork Johnson Creek	Only (UTAH)
Goose Creek	Bluff Creek	Upper (NEVADA)	Raft River	Left Fork Johnson Creek	Upper (UTAH)
Goose Creek	Cedar Mountain Draw	Lower (NEVADA)	Raft River	Mahogany Creek	Only (UTAH)
Goose Creek	Cedar Mountain Draw	Upper (NEVADA)	Raft River	North Junction Creek	Lower (UTAH)
Goose Creek	Dry Gulch	Lower (NEVADA)	Raft River	Raft River	Lower (UTAH)
Goose Creek	Goose Creek	Upper (NEVADA)	Raft River	Raft River	Upper (UTAH)
Goose Creek	Goose Creek	Upper-middle (NEVADA)	Raft River	Rosevere Fork of Clear Creek	Only (UTAH)
Goose Creek	Hardesty Creek	Lowest (NEVADA)	Raft River	Sawmill Canyon Fork of One Mile Creek	Upper (UTAH)
Goose Creek	Hardesty Creek	Upper (UTAH)	Raft River	South Fork Junction Creek	Lower (UTAH)
Goose Creek	Little Goose Creek	Upper (NEVADA)	Raft River	South Fork Junction Creek	Middle (UTAH)
Goose	Pole Creek	Only (UTAH)	Raft River	Wildcat Creek	Lower (UTAH)

Creek					
Goose Creek	Trout Creek	Only (NEVADA)	Raft River	Wildcat Creek	Upper (UTAH)
Raft River	Basin Creek	Lower (UTAH)	Raft River	Wildcat Creek	Upper (UTAH)
Raft River	Basin Creek	Middle (UTAH)	TETON RIVER	Moose Creek	Wyoming
Raft River	Basin Creek	Upper (UTAH)	TETON RIVER	North Fork Badger Creek	Wyoming