

Response to ISRP Review of FY2003 Proposals
Snake River Native Salmonid Assessment - Project # 199800200

Below are specific responses to each individual concern raised by ISRP for this project.

ISRP would like to see assurances that data generated from this project will be compatible with other efforts in the region. Aquatic habitat data collection procedures should be consistent with recommendations in Johnson et al. (2001).

Our data collection procedures are entirely compatible with the recommendations in Johnson et al. (2001). Below is a bibliography of sampling protocols used to refine the sampling methodology adopted for the Native Salmonid Assessment project. References with a bold X indicate protocols either directly found in or that were precursory drafts of subsequent protocols listed in Johnson et al. (2001) for consistent use across the region. Only 7 of the 17 protocols listed below were not included in Johnson et al. (2001). It should be noted that five of the publications, as well as Johnson et al. (2001), were not available until after our data collection procedures had been established, and initiated with the 1999 field season.

X Bain, M.B., and N.J. Stevenson, editors. 1999. Aquatic habitat assessment: common methods. American Fisheries Society, Bethesda, MD.

Bonar, S. A., M. Divens, and B. Bolding. 1997. Methods for sampling the distribution and abundance of bull trout and dolly varden. Washington Department of Fish and Wildlife, Olympia, WA.

X Harrelson, C. C., C. L. Rawlins, and J. P. Potyondy. 1994. Stream channel reference sites: an illustrated guide to field technique. Gen. Tech. Rep. RM-245. Fort Collins, CO. U.S. Forest Service, Rocky Mountain Forest and Range Experiment Station. 61 p.

Hawkins, C., and 10 others. 1993. A hierarchical approach to classifying stream habitat features. Fisheries 18(6):3-12.

Hillman, T., and W. Platts. 1993. Survey plan to detect the presence of bull trout. Report of Don Chapman consultants to the Intermountain Forest Industry Association, Coeur d'Alene, Idaho.

X Idaho Division of Environmental Quality (IDEQ). 1998. Beneficial Use Reconnaissance Project. Workplan for wadable streams.

- Idaho Department of Fish and Game (IDFG). 1994. Standard stream survey. Internal document, Boise, ID.
- Kauffman, P., P. Levine, E. Robison, C. Seeliger, and D. Peck. 1999. Quantifying physical habitat in wadeable streams. EPA/620/R-99/003. U.S. Environmental Protection Agency, Washington, D.C.
- King County Department of Natural Resources. 2000. Literature review and recommended sampling protocol for bull trout in King County. Seattle, WA.
- X Moore, K., K. Jones, and J. Dambacher. 1996. Aquatic inventory project: methods for stream habitat surveys. Research and Development Section, Oregon Department of Fish and Wildlife, Corvallis, OR.
- X Overton, C., S. Wollrab, B. Roberts, and M. Radko. 1997. R1/R4 (Northern/Intermountain Regions) fish and fish habitat standard inventory procedures handbook. U.S. Forest Service, Ogden, UT. Gen. Tech. Rep. INT-GTR-346.
- X Peterson, J. J. Dunhan, P. Howell, R. Thurow, and S. Bonar. 2001. Draft protocol for determining bull trout presence. Western Division of the American Fisheries Society.
- X Platts, W., W. Megahan, and G. Minshall. 1983. Methods for evaluating stream, riparian, and biotic conditions. U.S. Forest Service, Ogden, UT. Gen. Tech. Rep. INT-138.
- X Rosgen, D.L. 1994. A classification of natural rivers. *Catena* 11:169-199.
- Smelser, M. G., and J. C. Schmidt. 1998. An assessment methodology for determining historical changes in mountain streams. Gen. Tech. Rep. RMRS-GTR-6. Fort Collins, CO. U.S. Forest Service, Rocky Mountain Range Station. 29 p.
- X USDA Forest Service. 1997. Version 9.7 Stream Inventory Handbook: Level I & II. USDA Forest Service, Pacific Northwest Region. Portland, OR. 84 p.
- X Zaroban, D. W. 1999. Protocol for placement and retrieval of temperature data loggers in Idaho streams. Idaho Division of Environmental Quality. Boise, ID.

In conjunction with Proposal #33001, 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. Would the data be useful to identify core or source populations from which recovery actions could be expanded or would sets of populations be protected in refuge-type units such as subbasin level watersheds that might be managed under special or restrictive regulations?

We agree with the reviewers regarding the importance of the connection between abundance, life history, habitat, and genetic data generated by these two projects (9800200 and 33001) in the identification of conservation management units (CMUs) that can then be incorporated into protection and recovery plans. 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 true primarily because small populations are more vulnerable to environmental variation, demographic stochasticity, catastrophes, and inbreeding depression, as well as other processes. 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 (through 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 consist of 1000 individuals that on the average live 20 years, and age at first maturity differs between populations so that one population matures earlier while the other matures much 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 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 (e.g., 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 9800200 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 genetic prioritization process, which the state of Idaho currently includes in their management plan for cutthroat trout, is described 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>). In summary, this document, developed by the states of Colorado, Idaho, Montana, Nevada, New Mexico, Utah, and Wyoming, describes two components for cutthroat trout management; 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 second way in which we believe that genetic data 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, the hierarchical level at which groups of populations can be grouped and managed together for conservation and

management purposes. A more complete description of genetic processes can be found in the ISRP Response from Project #33001.

Taken together, 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 (i.e., reach-scale habitat, hydrologic geomorphology, upland characteristics, land use, etc.) affect population strengths and weaknesses; 5) how interconnected are the populations; 6) how genetically pure are populations; 7) how is genetic diversity partitioned throughout these populations. Most importantly, information from both projects need to be used together in the development of 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 9800200 on Yellowstone cutthroat populations and begin to consider the identification and prioritization of conservation management units. For example, project 9800200 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 (i.e. $F_{ST} < 0.05$), 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.

IDFG 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 9800200 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.

References

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- Isaak, D.J. 2001. A landscape ecological view of trout populations across a Rocky Mountain watershed. Ph.D. Dissertation, University of Wyoming, Laramie.
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- Storfer, A. 1999. Gene flow and endangered species translocations: a topic revisited. *Biological Conservation* 87:173-180.
- UDWR (Utah Division of Wildlife Resources). 2000. Cutthroat trout management: a position paper. Salt Lake City, UT.