



**POPULATION STUDIES OF REDBAND TROUT:  
GENETIC INVESTIGATION OF  
POPULATION STRUCTURE**

**FY2005 Final Report**



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**IDFG Report Number 06-40  
October 2006**

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**To**

**U.S. Department of the Interior  
Bureau of Land Management  
Lower Snake River Ecosystem  
Boise District Office  
3948 Development Avenue  
Boise, ID 83705**

**Contract #DLF040559**

**IDFG Report Number 06-40  
October 2006**

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## INTRODUCTION

Idaho Department of Fish and Game (IDFG) and the Bureau of Land Management (BLM) have both identified redband trout *Oncorhynchus mykiss gairdneri*, residing in arid southwest Idaho basins, as a sensitive subspecies. These populations of redband trout in Idaho were proposed for listing under the Endangered Species Act (ESA) during the mid-1990s, but the petition was not found to be warranted at that time (USFWS 1995). The original petition that involved Idaho fish did not distinguish between desert redband trout and other interior forms, including steelhead. Strong interest in the preservation and status of these populations in Idaho remains among environmental groups, and the potential for a future petition submittal remains high. As a group, populations of redband trout residing in Idaho desert basins are one of the least studied Idaho salmonids (Schill et al. 2002). Although population inventories have been conducted in select drainages (e.g., Allen et al. 1996; Zoellick 1999; Zoellick et al. 2005; Zoellick and Cade 2006), basic life history and population dynamics information is lacking for most populations. Knowledge of suspected spawning areas and associated habitat currently only exists for a few streams (B. Zoellick, BLM, personal communication). Furthermore, knowledge of movement patterns is not well known.

Genetic analyses are a complimentary method to demographic and ecological studies, which can provide relevant information regarding movement patterns and population persistence. Genetic diversity levels can be good indicators of population health and evolutionary adaptability (Primmer et al. 2003; Reed & Frankham 2003; Borrell et al. 2004). Low levels of variability are seen as limiting a species' ability to respond to short-term and long-term demographic and environmental changes and are often a consequence of inbreeding or genetic drift in small populations. Diversity may be gained through mutation or gene flow from a neighboring population, and the balance between gene flow and genetic drift is important to the maintenance of genetic diversity in small populations. In addition, the level of genetic exchange between populations can provide information regarding the potential for recolonization of extirpated populations (Fraser et al. 2004) and can replace tagging studies in some cases (Berry et al. 2004).

An understanding of the relationship between genetic structure and environment can help develop predictions for how genetic variation is partitioned and be an important step in defining practical units for management. Whiteley et al. (2004) outlines three ways in which genetic structure may be predicted: 1) physical template of stream network, 2) distance, and 3) patch size. Population structure may mirror the physical template of the system where branching patterns dictate levels of genetic differentiation (Meffe and Vrijenhoek 1988). This pattern allows for delineation of population units based upon stream networks. Secondly, population structure may mirror geographic distance where dispersal abilities are constrained in salmonids leading to increased genetic differentiation with increasing geographic distance. In this instance, dispersal distance can dictate the delineation of management units. Thirdly, population structure may correspond to patch size, whereas the presence and absence of suitable habitat dictate levels of genetic differentiation. In this scenario, unsuitable habitat would serve as a barrier to migration and lead to increased genetic differentiation. The scale for differentiation would then be dependent upon the amount of suitable habitat. This scenario is likely the most difficult to generalize across landscapes since it is highly dependent upon migration barriers and measurable habitat features.

In this study, we analyze 13 microsatellite loci to understand the patterns of genetic differentiation among 38 sample locations in the Owyhee, Bruneau, and Salmon Falls drainages in southern Idaho. This report is a final document of our findings.

## **OBJECTIVES**

1. To evaluate levels and patterns of genetic diversity and genetic differentiation among desert redband populations,
2. To evaluate intraspecific hybridization among native redband trout and hatchery-origin rainbow trout, and
3. To compare these results to other *O. mykiss* population genetic studies.

## **METHODS**

### **Sampling and DNA Extraction**

During 2001-2005, IDFG personnel collected 3,000 redband trout fin clips from 150 sample sites in the upper Snake River basin. For this report, 1,256 fin clips were analyzed from 38 sample locations. Sample sizes and locations of each sample site are presented in Table 1 and Figure 1. Samples were stored in 100%, nondenatured ethanol until DNA extraction. DNA was extracted using a salt-chloroform method described by Paragamian et al. (1999).

### **Microsatellite Amplification**

Thirteen polymorphic microsatellite loci were amplified: Oki23 (Genbank Accession #AF272822), Ssa289 (McConnell et al. 1995), Omy1011 (P. Bentzen, unpublished), Oke4 (P. Bentzen, unpublished), Ssa408 (Cairney et al. 2000), Ssa407 (Cairney et al. 2000), Ots4 (Banks et al. 1999), Oneu8 (Scribner et al. 1996), Ogo1a (Olsen et al. 1998), Omy27 (Heath et al. 2001), Ogo4 (Olsen et al. 1998), Omy325 (O'Connell et al. 1997), and Oneu14 (Scribner et al. 1996), using fluorescently labeled primers. PCR reaction conditions and cycling profiles are available from the authors upon request. PCR products were separated electrophoretically using an ABI 3100 automated sequencer (Applied Biosystems) platform. PCR products from multiplex 1 (Oki23, Ssa289, Omy1011, Oke4, Ssa408, Ssa407) were electrophoresed together. PCR products from multiplex 2 (Ots4, Oneu8, Ogo1a, Omy27) were electrophoresed together, and PCR products from multiplex 3 (Ogo4, Omy325, Oneu14) were electrophoresed together. Fragments were sized against GS500 ROX size standard (Applied Biosystems) using GeneMapper® 3.5 software (Applied Biosystems).

### **Statistical Analyses**

Each population was tested for Hardy-Weinberg equilibrium and linkage disequilibrium using Genepop on the Web (Raymond and Rousset 1995). A sequential Bonferroni correction was used to adjust significance for multiple comparisons (see Rice 1989). An alpha value of 0.05 was chosen for statistical significance for all analyses.

Genetic diversity was measured by the number of alleles per locus ( $A$ ) and expected heterozygosity ( $H_e$ ) using FSTAT version 2.9.3 (Goudet 2001). Pairwise  $F_{ST}$  estimates (Weir and Cockerham 1984) were generated using Arlequin 2.0 with significance based upon a permutation process. A sequential Bonferroni correction was used to adjust significance for multiple, simultaneous comparisons (see Rice 1989). The following guidelines (Hartl and Clark 1997) were used to interpret  $F_{ST}$  estimates:

$F_{ST} = 0.00$  to  $0.05$  indicates little genetic differentiation.

$F_{ST} = 0.05$  to  $0.15$  indicates moderate genetic differentiation.

$F_{ST} = 0.15$  to  $0.25$  indicates great genetic differentiation.

$F_{ST} > 0.25$  indicates very great genetic differentiation.

In this study, smaller  $F_{ST}$  estimates ( $< 0.05$ ) indicated that populations were connected or partially connected while  $F_{ST}$  estimates higher than  $0.05$  indicated that these populations were more isolated. An unrooted neighbor-joining (NJ) tree using Cavalli-Sforza and Edward's (1967) chord distance ( $D_{ce}$ ) was used to display the clustering relationship among populations using the software Populations 1.2.14 (Langella 2001) and TreeView (Page 1996). The relationship between gene flow ( $F_{ST}$ ) and geographic distance was investigated with a Mantel test (Mantel 1967). Geographic distance was measured in kilometers following stream networks for each pair of sampling locations using a program written for ArcView 3.2. A regression of  $F_{ST}$  to logarithm of geographic distance for all population pairs within drainages was conducted with Genepop on the Web.

Samples from hatchery sources were also analyzed (Table 1) to evaluate intraspecific hybridization. We first compared alleles within the hatchery reference populations to sample locations with no stocking history to identify diagnostic hatchery alleles. A diagnostic hatchery allele would be an allele present within any of the hatchery populations and not present within any of the sample locations with no stocking history. We verified that an allele was truly diagnostic if it was then present in sample locations with a stocking history. An unrooted NJ tree was also used to depict hybridized populations. We would expect that if there had been a recent or large impact of hatchery stocking, then allele frequencies would be similar between impacted populations and their hatchery source and these populations would cluster with one another. These two methods take into account population-level allele frequencies to assess intraspecific hybridization. We also used a Maximum-Likelihood Assignment Test, which takes into account genotype frequencies at the individual level. The program GeneClass 2.0 was used to evaluate whether an individual was a hybrid. The likelihood ratio of drawing a genotype from the population of sampling origin ( $L_h$ ) over the likelihood of observing the genotype in any of the sampled hatchery populations ( $L_{max}$ ) was computed using the program GeneClass 2.0, and an alpha level of  $0.05$  was used for significance. Hybrid fish would be those with a higher likelihood of belonging to a hatchery population than the population within which it was sampled.

## RESULTS

### Hardy-Weinberg and Linkage Disequilibrium

Tests for Hardy-Weinberg equilibrium revealed that genotypes were in expected proportions, except for 77 of the 507 tests. While these results are higher than expected by chance (25 tests expected from Type I error of  $0.05$ ), none of the tests was associated with a

particular locus and no more than four tests were rejected per population except for the following populations (Wickahoney Creek: 5 loci rejected; Cottonwood Creek: 6 loci rejected; Shack Creek: 5 loci rejected; Jump Creek (1127): 5 loci rejected). A total of 2,921 tests for linkage disequilibrium were performed, and 405 of the tests were rejected at  $\alpha = 0.05$ , which also was higher than expected by chance (146 expected from Type I error of 0.05). None of the tests clustered around a particular locus pair or population. Therefore, there doesn't appear to be any problems with physical linkage of loci or deviations from Hardy-Weinberg expectations.

### **Genetic Diversity**

The number of alleles per locus ranged from seven alleles (Ogo1a) to 27 alleles (Omy325). Genetic diversity varied widely within populations (Table 1). Expected heterozygosity ranged from 0.48 in Crab Creek to 0.80 in Jarbidge River, and allelic richness ranged from 3.2 alleles in Jump Creek (1127) to 10.8 alleles in Jarbidge River.

### **Genetic Differentiation and Gene Flow**

An overall  $F_{ST}$  value of 0.135 (95% CI 0.129 to 0.141), indicated significant population differentiation within all of the drainages. In the Bruneau River drainage,  $F_{ST}$  values ranged from 0.01 for Deer Creek (1333) and Deer Creek (1335) to 0.28 for Little Jacks Creek and Crab Creek (Table 2a). All  $F_{ST}$  values were greater than 0.05 except for Duncan Creek ('02) and Duncan Creek ('03), and all of the following populations with one another: Bruneau Creek, MF Willow Creek, Willow Creek (1240), Willow Creek (1253), Deer Creek (1333 and 1335), and Jarbidge Creek. All of the comparisons were greater than 0.05 in the Salmon Falls drainage except for Cottonwood, North Fork Salmon Falls, Middle Fork Shoshone, and North Fork Salmon Falls creeks (Table 2b). The only Snake River comparison, with an  $F_{ST}$  larger than 0.05, was Dive Creek and Bennett Creek (Table 2c). In the Owyhee River basin, all of the pairwise comparisons were greater than 0.05 except for Jordan Creek (1294) with Jordan Creek (1298) and Williams Creek (1281) with Williams Creek (1282) and Williams Creek (1506; Table 2d).

Mantel tests for isolation by distance failed to reject the null hypothesis of no association between genetic and geographic (fluvial) distance in all of the drainages ( $P > 0.05$ ). An examination of genetic distance against fluvial distance revealed that populations in the Bruneau River drainage were less differentiated at shorter distances, but overall there was no significant relationship between genetic distance and geographic distance in this drainage (Figure 2). The predominant pattern observed in all of the sampled drainages was large genetic distances among pairwise comparisons regardless of fluvial distance.

Drainage-wide differences in genetic variation were depicted with a neighbor-joining tree using Cavalli-Sforza and Edward's (1967) chord distance (Figure 3). All of the populations clustered with other populations from the same river drainage except for Jarbidge River, North Fork Owyhee River, unnamed tributary of Owyhee River, McMullen Creek, Upper Cedar Creek, Bruneau River, and Salmon Falls Creek.

### **Intraspecific Hybridization**

In total, 218 alleles were screened at the 13 loci. This yielded 17 (<1%) potentially diagnostic "hatchery" alleles spread over nine of the 13 microsatellite loci. The frequency of 14

of these alleles was less than 5% within the hatchery populations. We evaluated whether any of these 17 “hatchery” alleles were present within populations with a stocking history. None of the 17 alleles was present within any of the populations with a stocking history. Therefore, we were unable to assess the impacts of stocking using diagnostic alleles given the similarity among hatchery-origin and native redband trout. A NJ tree was constructed and revealed that one of the populations, Salmon Falls Creek, appeared to be impacted by stocking. However, this population-level method for intraspecific hybridization was not very conclusive for the other populations that did not cluster with the hatchery reference populations. The maximum-likelihood assignment test did not assign any individuals from any of the populations with a stocking history to the hatchery reference populations, including Salmon Falls Creek, which appeared to cluster with the hatchery reference populations.

## DISCUSSION

Our results indicated that redband trout were highly structured within these drainages. Both the  $F_{ST}$  estimates and Mantel Test indicated that genetic drift was strongly affecting the majority of the sample locations. If gene flow was more influential than genetic drift in any of these drainages, than the scatter plots in Figure 2 would reveal a positive, monotonic relationship between genetic distance and fluvial distance with the scatter increasing outward from narrow at the origin of the plot to wider at further distances of separation. In the Owyhee River, Salmon Falls River, and Snake River drainages, high  $F_{ST}$  estimates were observed across all fluvial distances, indicating that genetic drift was more influential than gene flow. In the Bruneau River drainage, some of the populations were less differentiated than populations separated by similar distances in other drainages. However, these results should be taken with caution as low pairwise  $F_{ST}$  estimates were observed for pairs separated by 100 to 200 km as well as less than 35 km. This is likely an artifact of both small sample sizes for some populations ( $n = 7$  for Willow Creek and MF Willow Creek) and random genetic drift. Increasing the sample sizes for Willow Creek and MF Willow Creek will help to resolve this issue.

Significant differentiation was observed at small spatial scales unlike other *O. mykiss* (e.g., steelhead) populations. While genetic diversity estimates reported in this study were similar to those previously reported in other *O. mykiss* studies of population genetic structure (Moran 2003; Heath et al. 2001), anadromous steelhead populations appear to experience higher levels of gene flow at a larger scale. In the Clearwater River basin, low to moderate levels of genetic differentiation were reported ( $F_{ST} > 0.05$ ) for steelhead populations sampled within an entire drainage (Moran et al., unpublished data). Similar levels of genetic differentiation have been reported for steelhead populations in other areas where populations within drainages are not differentiated from one another (Heath et al. 2001; Nielsen et al. 2004). In contrast, we observed significantly higher  $F_{ST}$  estimates within a sampled drainage, indicating that drainages consisted of multiple, independent populations of redband trout. The scale of genetic differentiation was more similar to those observed for fragmented populations of inland cutthroat trout (Neville-Arsenault 2003; Wofford et al. 2005; Cegelski et al. 2006).

Historically, some of these populations consisted of an anadromous component. However, for the past century, dam construction has significantly limited and eventually blocked all upstream passage from the Snake River to these populations. In 1890, irrigation dams were constructed on the lower Bruneau River, which limited fish passage from the Snake River to the Bruneau River. In 1901, Swan Falls Dam was constructed which further blocked all steelhead passage from the Bruneau River drainage and isolated the Bruneau River drainage from the

Owyhee River drainage. In 1930, the Owyhee Dam was constructed which blocked passage from the Owyhee River drainage to the Snake River. Furthermore, between 1952 and 1967, the construction of C.J. Strike Dam and the Hells Canyon Complex additionally blocked all anadromous movement. The loss of an anadromous component is evident in the fine-scale structuring observed in this study. An anadromous life history would likely lead to gene flow at a larger regional scale as observed in the studies cited above. Whitely et al. (2006) also observed significant differentiation within both bull trout and mountain whitefish in the region upstream from Hells Canyon and downstream of Shoshone Falls. Whitely et al. (2006) suggests that similar patterns of genetic differentiation across multiple species highlights that the dams and other environmental features may be responsible for the degree of differentiation.

Genetic differentiation could be due to the following factors: life history, barriers to movement, habitat suitability, and unequal degrees of intraspecific hybridization with hatchery-origin rainbow trout. Currently, little information is available as to whether these populations are comprised of resident or migratory fish, but most likely, there is a mixture for at least some of the populations. Natal homing or ability to migrate finite distances can constrain gene flow at specific distances and lead to significant population genetic structure. For example, data from PIT-tagged fish suggest that redband trout move an average of 28 km during upstream spring spawning migrations (Schill et al. 2004). Thurow (1990) also reported movements up to 40 km in the Big Wood River, Idaho. Therefore, we may hypothesize that the scale for population differentiation corresponds with migratory abilities. Our data suggested that sample locations less than 20 km (Deer Creek [1333] and Deer Creek [1335]; Williams Creek [1282], Williams Creek [1281] and Williams Creek [1506]; Jordan Creek [1294] and Jordan Creek [1298]; and Dive Creek [1730] and Bennett Creek [1720]) are connected but that redband trout exist as partially independent or isolated populations at distances greater than 35 km. The sample locations that are partially connected in the Bruneau River drainage are Bruneau River, Jarbidge River, Deer Creek, Willow Creek, and MF Willow Creek. Therefore, there is likely some gene flow among these populations, but it is not sufficient to maintain uniform allele frequencies among populations. In the Salmon Falls drainage, Cottonwood Creek, MF Shoshone Creek, and NF Salmon Creek are less genetically differentiated and partially connected. All of the other sample locations in this study appear to be isolated.

Intermittent stream flows characterize many streams in these areas and likely contribute to the patterns of population differentiation and observed fragmentation. For example, Little Jacks Creek and Wickahoney Creek appear to be isolated due to intermittent flows in the lower parts of the streams. Furthermore, fish from Little Jacks Creek and Big Jacks Creek are probably never connected to the mainstem Snake River due to significant habitat alteration. In 2002, upstream movement of redband trout was blocked in Duncan Creek due to stream desiccation near Buncel Ford (Schill et al. 2004). While Duncan Creek was reported to be isolated in 2004, an ongoing drought in Southwestern Idaho and Northern Nevada has led to reduced connectivity among many of the sample locations within the past several years. Intermittent stream flows and drought conditions would lead to partially connected populations if in some years dispersal is possible, and in other years it is severely limited. Barriers to movement, such as waterfalls, also block upstream movement on Jump Creek and Cottonwood Creek.

Temperature also appears to be shaping the distribution and abundance of redband trout at the southern extent of its range (Li et al. 1994, Zoellick 2004) and likely influences the amount of movement between streams (Zoellick and Cade 2006). Ebersole et al. (2001) concluded that an average of 10-40% of redband trout residing within 12 northeast Oregon stream reaches were observed within thermal refugia created by substrate upwelling during

mid-afternoon periods of maximum stream temperatures. The same authors reported that abundance was inversely correlated with average maximum stream temperatures within 12 stream reaches. Many of the larger streams experience high temperatures and are unable to support viable populations of redband trout. As a result, an absence or low abundance of redband trout in large streams (e.g., North Fork Owyhee River) that serve to connect smaller tributary streams (Zoellick et al. 2005), may also lead to significant genetic differentiation at small scales. The relationship between movement and temperature was not investigated in this study but would be an interesting relationship to study. Northcote (1962) observed that upstream migrations of juvenile rainbow trout increased when temperatures exceeded 15°C and hypothesized that rapid changes in temperature induced movement. We may hypothesize that migration is favored (in connected habitats) due to the ability of fish to escape unfavorable temperature regimes. Alternatively, we may hypothesize that residency is favored because of the energetic costs involved in moving, establishing new territories, dealing with predators and disease, and adapting physiologically to new environments (Northcote 1992). Tied closely to this concept is the degree to which fish could move in unaltered environments and current stream flow conditions and habitat conditions for the sample locations in this study. If fish are unable to move due to habitat alteration and intermittent streams flows, then the persistence of populations inhabiting high temperature streams may be at risk.

Lastly, intraspecific hybridization could lead to significant differentiation within a drainage if some populations have been impacted by stocking and others have not. This may lead to similarity among hybridized populations and significant differentiation between hybridized populations and nonhybridized populations. To find diagnostic alleles, we assumed that the reference populations with no stocking history have not been impacted by stocking. If hybrid fish moved into a stream from a neighboring stream and the population with no stocking history is actually hybridized, then we would miss diagnostic alleles. The degree to which stocking of nonnatives alters native allele frequencies depends on the last year and number of years of stocking, number of fish stocked, survival of fish stocked, fitness of the hybrids, and allele frequency differences among the native populations and the stocking sources. Since the hatchery reference populations naturally share many alleles with native redband trout (and there were no diagnostic alleles), it is impossible to detect hybridization in this study unless the level of hybridization is large enough to maintain uniform allele frequencies among the hatchery reference population and the population of interest. Salmon Falls Creek has been extensively stocked with nonnative rainbow trout in the past decade with numerous hatchery strains of rainbow trout (see stocking records at <http://fishandgame.idaho.gov/apps/stocking/>), and the clustering results revealed that this population has been significantly impacted by stocking. However, the assignment test did not assign any individual fish to the hatchery populations. While Salmon Falls Creek is likely introgressed, this methodology does not allow us to quantify the level of introgressive hybridization. Therefore, we do not know what level of hybridization was detectable in this population (e.g., >10%, >20%, >50%) or the degree of hybridization (high, medium, low). The other sampled populations may be hybridized at lower levels (<10%, <20%, <50%), but the allele frequency differences may be intermediate between the hatchery reference populations and what existed in the sample location prior to stocking. This would preclude this method from working. Therefore, our methodology was unable to detect hybridization either qualitatively or quantitatively. We plan on developing and screening SNPs (single nucleotide polymorphisms) next. SNPs are widely distributed in the genome and are becoming a preferred marker for many population genetic studies (Morin et al. 2004). SNPs were also used recently to quantify introgressive hybridization between introduced rainbow trout and native rainbow trout in California (Sprowles et al. In Press).

Future work should aim at correlating habitat features and barriers to movement to increase our understanding of the processes influencing gene flow in these drainages and biological knowledge of the species in general. One possibility is to correlate flow regimes with gene flow. Since 2006 was a high water year, we may hypothesize that there is increased gene flow compared to earlier years when many streams were dewatered and determine fine-scale patterns of dispersal (e.g., dispersal distances). By also having temperature data, we could evaluate if specific life histories (e.g., residency or fluvial) are favored under certain environmental conditions and the degree to which temperature is a barrier to movement. An understanding of genetic structure within the mountain habitats may also offer an important comparison among temperature, movement (gene flow), and life history. Future work will also attempt to evaluate hybridization in these drainages using different methods. We will try to find SNP alleles that are diagnostic between hatchery strains and interior redband trout to assess hybridization with hatchery-origin rainbow trout. All of these efforts will aid with future management decisions regarding redband trout at its southern distribution.

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Table 1. Sample locations, major drainage, site number in Figure 1, and sample size (N) for redband trout populations along with genetic diversity estimates. He = average expected heterozygosity across 13 loci; A = average number of alleles across 13 loci; Rt = average allelic richness across 13 loci.

Code	Field ID	Population	Year	Drainage	Sample Size	A	He
1	1434	Big Jacks Creek	2003	Bruneau River	29	6.69	0.70
2	1251	Bruneau River	2003	Bruneau River	19	7.00	0.74
3	1727	Crab Creek	2001	Bruneau River	35	3.38	0.48
4	1333	Deer Creek	2003	Bruneau River	29	6.08	0.69
5	1335	Deer Creek	2003	Bruneau River	28	6.46	0.71
6	1742	Duncan Creek '02	2002	Bruneau River	29	5.00	0.60
	1737	Duncan Creek '03	2003	Bruneau River	44	5.92	0.63
7	1728	Jarbidge River	2004	Bruneau River	46	10.85	0.80
8	1739	Little Jacks Creek	2003	Bruneau River	63	5.69	0.57
9	1254	Middle Fork Willow Creek	2003	Bruneau River	7	5.00	0.72
10	1743	Wickahoney Creek	2002	Bruneau River	49	4.77	0.61
11	1240	Willow Creek	2003	Bruneau River	19	5.08	0.74
12	1253	Willow Creek	2003	Bruneau River	7	5.85	0.71
13	1540	Indian Creek	2003	Owyhee River	30	7.00	0.71
14	n/a	Juniper Creek	2005	Owyhee River	30	8.31	0.72
15	1298	Jordan Creek	2003	Owyhee River	29	7.92	0.74
16	1294	Jordan Creek	2003	Owyhee River	24	7.69	0.75
17	1184	North Fork Owyhee River	2003	Owyhee River	29	4.62	0.62
18	n/a	Petes Creek	2005	Owyhee River	30	7.85	0.73
19	1544	Squaw Creek	2003	Owyhee River	30	8.00	0.77
20	1584	Unnamed Trib of Owyhee River	2003	Owyhee River	28	5.62	0.67
21	1282	Williams Creek	2003	Owyhee River	27	5.62	0.68
22	1281	Williams Creek	2003	Owyhee River	29	6.15	0.69
23	1506	Williams Creek	2003	Owyhee River	29	6.46	0.72
24	1203, 1214	Cottonwood Creek	2003	Salmon Falls Creek	36	7.62	0.73
25	1224	Middle Fork Shoshone Creek	2003	Salmon Falls Creek	23	6.23	0.67
26	1197	North Fork Salmon Falls Creek	2003	Salmon Falls Creek	30	7.92	0.74
27	1731	Salmon Falls Creek	2003	Salmon Falls Creek	40	8.77	0.74
28	1470	Shack Creek	2003	Salmon Falls Creek	30	5.38	0.67
29	1155	Upper Cedar Creek	2003	Salmon Falls Creek	29	5.77	0.62
30	1720	Bennett Creek	2001	Snake River	30	6.31	0.65
31	1085	Cold Spring Creek	2002	Snake River	63	5.92	0.61
32	1730	Dive Creek	2001	Snake River	38	6.69	0.66
33	1127	Jump Creek 1127	2002	Snake River	57	3.23	0.52
34	1738	Jump Creek 1738	2001	Snake River	43	5.92	0.72
35	1735	Little Canyon 9.5	2002	Snake River	32	6.77	0.70
36	1587	McMullen Creek	2003	Snake River	27	5.85	0.65
37	1179, n/a	Shoofly Creek	2003, 2006	Snake River	30	5.46	0.60
38	1136	Sinker Creek	2002	Snake River	29	6.92	0.71
—	—	Hayspur R9	2005	Hatchery	47	7.62	0.73
—	—	Kamloops	2005	Hatchery	45	5.77	0.66
—	—	Arlee	2002	Hatchery	11	4.92	0.69
—	—	Eagle Lake	2002	Hatchery	17	5.38	0.60
—	—	Fish Lake	2002	Hatchery	15	5.31	0.68
—	—	Shasta	2002	Hatchery	12	4.31	0.58
—	—	Erwin	2002	Hatchery	17	3.85	0.59
—	—	McConaughy	2002	Hatchery	20	6.69	0.72

Table 2. Pairwise  $F_{ST}$  estimates within each drainage: a) Bruneau River drainage, b) Salmon Falls drainage, c) Snake River drainage, and d) Owyhee River drainage.

a. Bruneau River drainage:

	Big Jacks Creek	Bruneau River	Crab Creek	Deer Creek (1333)	Deer Creek (1335)	Duncan Creek '02	Duncan Creek '03	Jarbridge River	Little Jacks Creek	MF Willow Creek	Wickahoney Creek	Willow Creek (1240)
Bruneau River	0.08											
Crab Creek	0.21	0.19										
Deer Creek (1333)	0.11	0.05	0.13									
Deer Creek (1335)	0.08	0.03	0.15	0.01								
Duncan Creek '02	0.05	0.11	0.25	0.15	0.13							
Duncan Creek '03	0.07	0.11	0.25	0.14	0.11	0.03						
Jarbridge River	0.07	0.03	0.15	0.04	0.05	0.11	0.11					
Little Jacks Creek	0.12	0.16	0.28	0.19	0.19	0.17	0.16	0.15				
MF Willow Creek	0.09	0.03	0.13	0.00	0.02	0.14	0.13	0.02	0.20			
Wickahoney Creek	0.09	0.12	0.26	0.17	0.13	0.12	0.13	0.12	0.21	0.17		
Willow Creek (1240)	0.06	0.01	0.20	0.04	0.03	0.10	0.10	0.03	0.17	0.03	0.11	
Willow Creek (1253)	0.07	0.05	0.18	0.06	0.04	0.13	0.13	0.05	0.19	0.04	0.14	0.03

b. Salmon Falls drainage

	Cottonwood Creek	MF Shoshone Creek	NF Salmon Falls Creek	Salmon Falls Creek	Shack Creek
MF Shoshone Creek	0.06				
NF Salmon Falls Creek	0.01	0.04			
Salmon Falls Creek	0.13	0.16	0.11		
Shack Creek	0.05	0.11	0.05	0.16	
Upper Cedar Creek	0.11	0.15	0.13	0.19	0.14

c. Snake River drainage

	Bennett Creek	Cold Spring Creek	Dive Creek	Jump Creek (1127)	Jump Creek (1738)	Little Canyon Creek	McMullen Creek	Shoofly Creek
Cold Spring Creek	0.17							
Dive Creek	0.00	0.17						
Jump Creek (1127)	0.19	0.28	0.19					
Jump Creek (1738)	0.14	0.19	0.13	0.19				
Little Canyon Creek	0.09	0.14	0.08	0.17	0.13			
McMullen Creek	0.11	0.15	0.12	0.20	0.13	0.09		
Shoofly Creek	0.18	0.27	0.18	0.24	0.20	0.17	0.17	
Sinker Creek	0.10	0.16	0.10	0.21	0.10	0.10	0.10	0.16

d. Owyhee River drainage

	Indian Creek	Juniper Creek	Jordan Creek (1298)	Jordan Creek (1294)	N.F. Owyhee River	Petes Creek	Squaw Creek	Un-named trib. of Owyhee River	Williams Creek (1282)	Williams Creek (1281)
Juniper Creek	0.07									
Jordan Creek (1298)	0.07	0.09								
Jordan Creek (1294)	0.06	0.08	0.00							
N.F. Owyhee River	0.12	0.13	0.10	0.12						
Petes Creek	0.06	0.08	0.08	0.07	0.12					
Squaw Creek	0.05	0.03	0.07	0.06	0.09	0.05				
Un-named trib. of Owyhee River	0.08	0.08	0.10	0.09	0.09	0.08	0.05			
Williams Creek (1282)	0.09	0.11	0.11	0.09	0.15	0.12	0.08	0.12		
Williams Creek (1281)	0.09	0.11	0.11	0.09	0.14	0.12	0.07	0.12	0.01	
Williams Creek (1506)	0.06	0.09	0.08	0.06	0.14	0.10	0.06	0.11	0.02	0.02

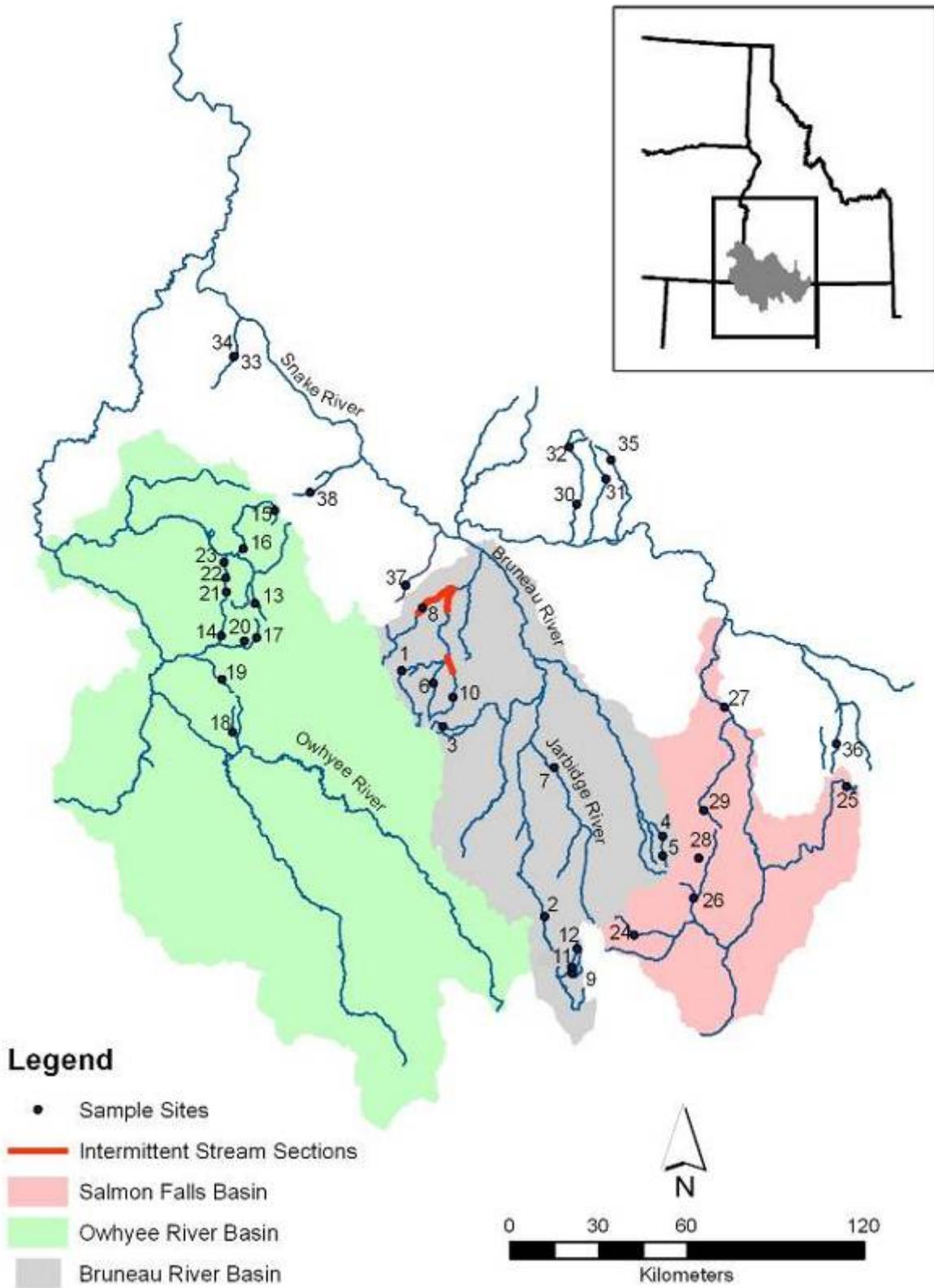


Figure 1. Map of the 38 redband trout sampling locations in Idaho and Nevada. Populations are numbered according to Table 1.

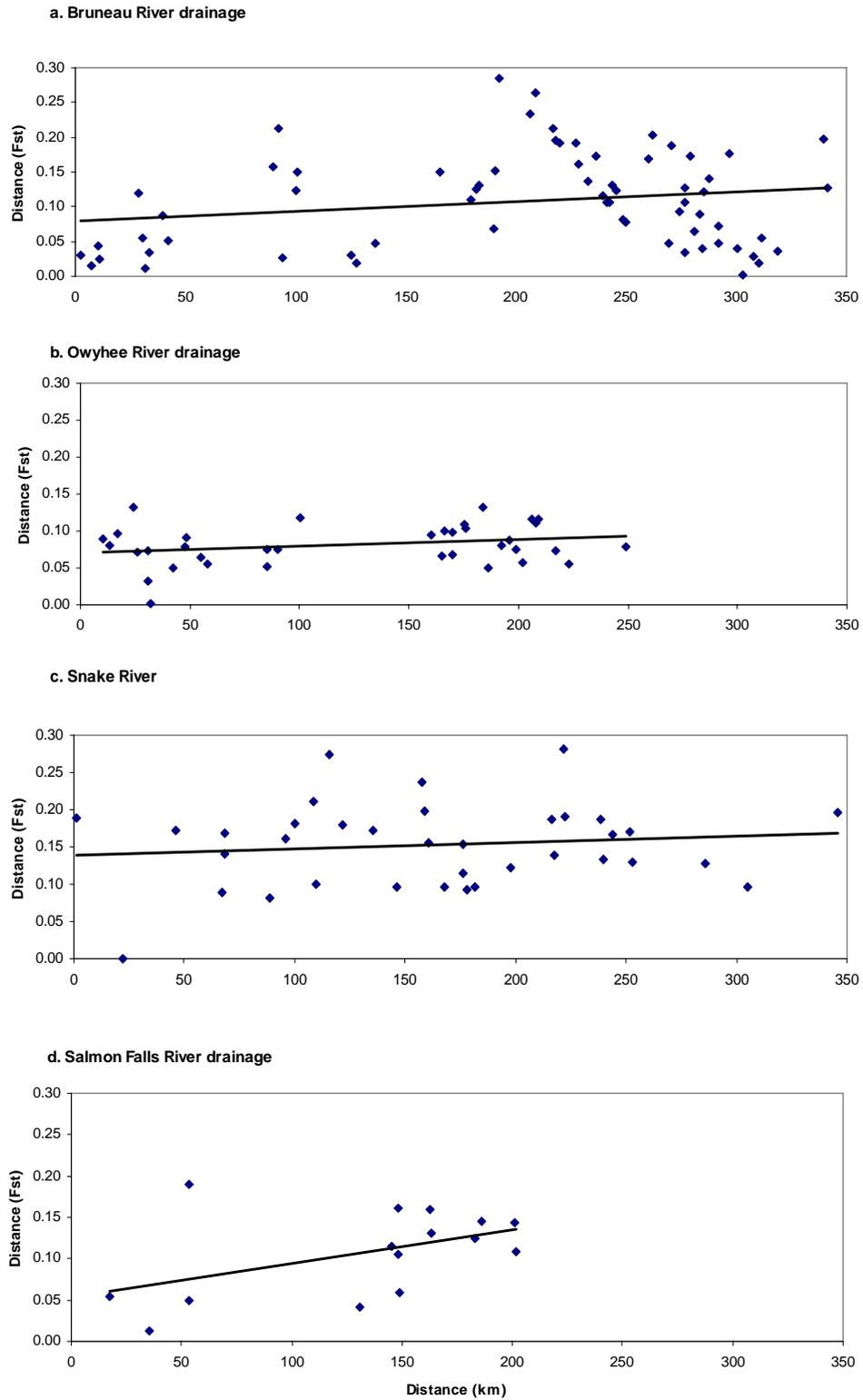


Figure 2. Scatter plots of the Mantel Test Results. Geographic distance (km) is displayed on the x-axis and genetic distance ( $F_{ST}$ ) is displayed on the y-axis for each drainage.

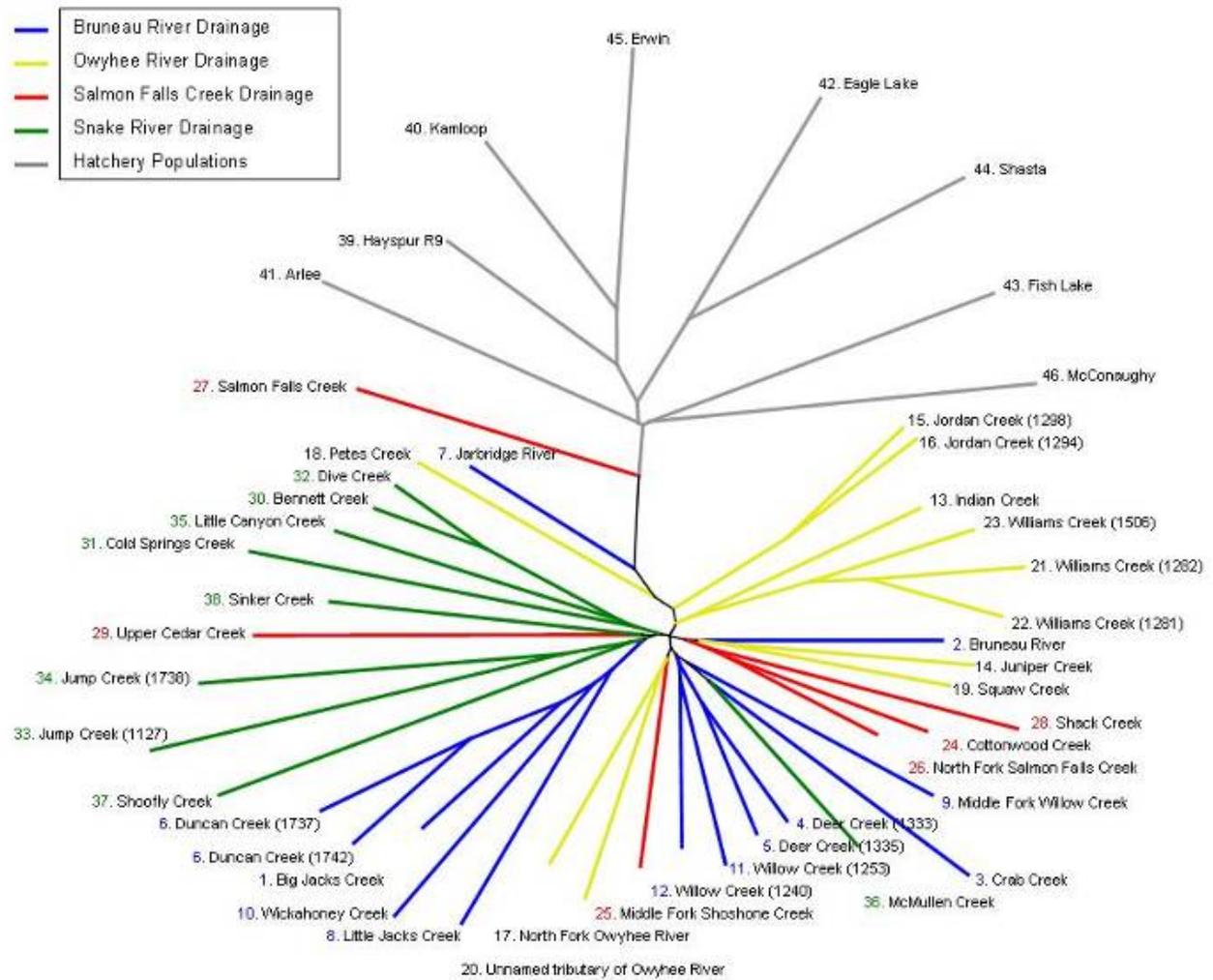


Figure 3. Neighbor-joining dendrogram (unrooted) of the genetic relationships among 38 redband trout populations and 8 hatchery reference populations based on Cavalli-Sforza and Edward's (1967) chord distance. Populations are color-coded based upon drainage location.

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