GENETIC CONSIDERATIONS FOR THE CONSERVATION AND MANAGEMENT OF YELLOWSTONE CUTTHROAT TROUT (ONCORHYNCHUS CLARKII BOUVIERI) IN YELLOWSTONE NATIONAL PARK

by

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A thesis submitted to the faculty of
Brigham Young University
in partial fulfillment of the requirements for the degree of

Master of Science

Department of Integrative Biology
Brigham Young University
December 2006

BRIGHAM YOUNG UNIVERSITY

GRADUATE COMMITTEE APPROVAL

of a thesis submitted by

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This thesis has been read by each member of the following graduate committee and by majority vote has been found to be satisfactory.

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ABSTRACT

GENETIC CONSIDERATIONS FOR THE CONSERVATION AND MANAGEMENT OF YELLOWSTONE CUTTHROAT TROUT (ONCORHYNCHUS CLARKII BOUVIERI) IN YELLOWSTONE NATIONAL PARK

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A key component to conservation is an accurate understanding of genetic subdivision within a species. Despite their ecological and economic importance, relatively little is understood about the genetic structuring of Yellowstone cutthroat trout in Yellowstone National Park. Here, we use traditional (F_{st}, R_{st}, Nm, and AMOVA) and modern (Bayesian assignment tests, coalescent theory, and nested clade analysis) analytical approaches to describe the population genetic subdivision of cutthroat trout spawning populations in Yellowstone Lake and to identify genetically distinct population segments throughout Yellowstone National Park. Evidence for restricted gene flow between spawning populations within Yellowstone Lake was detected using nested clade analysis. This is the first molecular evidence for restricted gene flow between spawning populations in Yellowstone Lake. In contrast, traditional methods such as F_{st} and R_{st} as well as the Bayesian clustering program STRUCTURE v2.0 failed to detect evidence for restricted gene flow. Across our sampling range within Yellowstone National Park, eleven genetically distinct cutthroat trout population segments were detected. These showed a general pattern of small, isolated populations with low genetic diversity in headwater streams and wide-spread, genetically diverse populations in higher-order rivers. We recommend populations be managed to maintain current levels of genetic diversity and gene flow. Based on the recent decline of and distinct morphological, behavioral, and genetic nature of cutthroat trout in Yellowstone Lake, we recommend the Yellowstone Lake spawning populations collectively be recognized as an evolutionarily significant unit.

ACKNOWLEDGEMENTS

I would like to thank Dennis Shiozawa and Paul Evans for always being willing to share their time by discussing ideas, offering suggestions, and reviewing manuscripts. Thanks also to Jerry Johnson and Keith Crandall for their helpful reviews. Special thanks to Andrew Johnson, Becky Miller, Matt Pyne, and Rebecca Scholl for assistance with sample collecting, lab work, map creation, and data analysis. Also thanks to all those who helped catalogue samples, isolate DNA, and keep the lab running. I thank Matt Campbell of the Idaho Fish and Game who kindly assisted in developing primers. I am also grateful to Dan Mahony, Todd Koel, Kerry Gunther, and Kristine Smith of the National Park Service, who were responsible for collecting tissue samples and organizing collecting trips. I also thank to Yellowstone Park Foundation for partially funding this project. Thanks also to all of my family members, who have always supported and encouraged my interest in nature and in fisheries. Finally, I would like to express my gratitude to my wife Amanda for her encouragement, patience, and unwavering support through this whole process.

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INTRODUCTION

The identification of conservation units (i.e. distinct population segments, evolutionarily significant units, stocks, etc.) within a species is critical to maintaining genetic diversity, making it an important management objective (Waples 1994; Wang et al. 2002; Reed and Frankham 2003). An important step in this process is the identification of genetically distinct populations. Preserving these populations helps maintain total genetic diversity, which reinforces the species' ability to persist over time (O'Brien et al. 1985; Allendorf and Leary 1988; Spielman et al. 2004). The loss of genetic diversity within a species increases extinction risk through an overall decreased ability to adapt to environmental change and a reduction in fitness due to increased inbreeding (Newman and Pilson 1997; Amos and Balmford 2001). In addition to contributing to total genetic diversity, genetically distinct populations are important to the evolutionary legacy of a species. These populations often occur at the periphery of a species' range, an area where the first steps in speciation (i.e. genetic divergence and local adaptation) are thought to take place (Lesica and Allendorf 1995). Conserving genetically unique populations therefore decreases the likelihood of extinction and allows for the continued evolution of the species.

The application of genetic data to conservation is evident in the management of Pacific salmon. Information regarding population genetic structure has repeatedly helped fisheries managers identify and prioritize genetically distinct populations, or stocks, in order to preserve genetic diversity (Wilson et al. 1987; Allendorf et al. 1997; Small et al. 1998; Shaklee 1999; Guthrie and Wilmot 2004; Quinn 2005; Beacham et al. 2006). Experimental evidence has shown that native salmon stocks exhibit greater survival and fitness than transplanted salmon, suggesting native stocks are adapted to local environmental conditions (Brannon and Hershberger 1984; Reisenbichler 1988; Mayama 1989) and justifying management at the population level. While a tremendous effort has been made to classify stocks of anadromous salmonids, the use of genetic data to identify conservation units in nonanadromous salmonids (e.g. inland cutthroat trout) has received less attention (Gresswell et al. 1997) despite the threatened status of many indigenous trout populations in western North America (Behnke 2002; Young 2002; Quinn 2005).

The most widely distributed non-anadromous native trout in western North American is the cutthroat trout. Behnke (2002) recognized fourteen subspecies of cutthroat trout, two of which are extinct and three of which are listed as threatened under the Endangered Species Act. Each subspecies has generally been managed as a single conservation unit. In fact, extensive analysis of population genetic structure (beyond quantifiying levels of introgression) is limited to studies on just a few subspecies, mainly coastal, westslope, Lahontan, and Yellowstone cutthroat trout outside of Yellowstone National Park (Leary et al. 1989; Wenburg et al. 1998; Nielsen and Sage 2002; May et al. 2003; Taylor et al. 2003; Young et al. 2004). The potential for classifying distinct conservation units within the cutthroat trout subspecies remains largely unexplored.

Historically, one of the most abundant subspecies of cutthroat trout has been the Yellowstone cutthroat trout (YCT), *Oncorhynchus clarkii bouvieri*. Yellowstone Lake, located in Yellowstone National Park (YNP), is home to the largest genetically pure population of cutthroat trout in the world. That population has been estimated at over one million adult fish (Behnke 2002). In the last decade, however, the population has plummeted in Yellowstone Lake due to the introductions of lake trout and whirling disease (Koel et al. 2005). YCT in the Yellowstone River watershed below Yellowstone Falls, withinYNP, are also threatened by hybridization with nonnative rainbow trout and by competition with introduced brown and brook trout (Behnke 2002; Koel et al. 2005). As a direct result of these threats, YCT are considered a sensitive species by many state and federal natural resource agencies (Young 2002). Although rejected in 2001 and 2006 (U.S. Fish and Wildlife Service 2001, 2006), the YCT was petitioned in 1998 (Biodiversity Legal Foundation et al. 1998) and 2004 (U.S. Fish and Wildlife Service 2006) for federal listing as a threatened species under the Endangered Species Act. Rejection for listing was based primarily on the healthy status of river populations of YCT (U.S. Fish and Wildlife Service 2006), although it is unknown whether or not genetically distinct populations exist within the species' range (i.e. lacustrine vs. fluvial). It is imperative to identify genetically pure (non-hybridized) and genetically distinct populations as numbers continue to decline and conservation efforts intensify.

Objectives

The objective of this study was to determine the genetic makeup of native YCT populations in YNP. This information provide data about the genetic diversification of YCT following a relatively recent invasion (8,000 to 12,000 years ago, Behnke 1992) into a glaciated alpine region. The genetic data can also be combined with ecological data to identify conservation units (Crandall et al. 2000; Pennock and Dimmick 1997). Here, we used the term 'genetically distinct population segment' to denote a population with restricted gene flow between it and surrounding populations. We used the definition of Crandall et al. (2000) for evolutionarily significant unit (ESU), which is a genetically distinct population segment that also exhibits ecological differentiation (e.g. life history and morphological characteristics); individuals from an ESU are not exchangeable with outside individuals from a genetic or ecological standpoint. Our focus was to gather information in order to identify genetically distinct populations, however life history and/or morphological information was applied when available in order to identify potential ESUs.

We tested two hypotheses with regards to YCT population structure in Yellowstone Lake and throughout YNP: (1) spawning populations of cutthroat trout within Yellowstone Lake are genetically structured because they return, or home, to their natal stream each year to spawn, and (2) YCT throughout YNP are genetically structured in association with geographical barriers. Both of these hypotheses were tested against a null hypothesis of a lack of population genetic structure throughout YNP.

The homing of YCT in Yellowstone Lake is well documented. Experimental evidence from mark-recapture studies has suggested approximately 3% of spawning fish stray from their natal stream to spawn (Ball 1955; Cope 1957; McCleave 1967). An inverse relationship between straying rate and population genetic structure has been demonstrated in Pacific salmon species (Hendry et al. 2004; Quinn 2005). Pink salmon have relatively low levels of genetic structuring and their straying rate has been estimated at 5.1% (Thedinga et al. 2000). Sockeye and chinook salmon have a higher level of genetic structuring and approximate straying rates of 1.5% (Foerster 1936) and 1.4% (Quinn and Fresh 1984), respectively. The 3% straying rate of YCT lies approximately halfway between the extremes within these salmon species, so it is reasonable to expect YCT spawning populations in Yellowstone Lake exhibit some restricted gene flow and genetic differentiation.

Additional support for genetic structuring in Yellowstone Lake is provided by studies on YCT morphological and life history traits. Bulkley (1963) detected variation between spawning populations in potentially heritable mophological traits such as spotting, number of hyoid teeth, and coloration. Behavioral differences were reported by Bowler (1975), who examined fry movement in spawning populations of outlet vs. inlet streams in Yellowstone Lake. Differences were detected in fry movement between the two populations with a greater proportion of upstream movement exhibited by fry from the outlet population than by fry from the inlet population. Most recently, Gresswell et al. (1994, 1997) documented significant differences in mean spawning time and total body length between Yellowstone Lake spawning populations. These findings suggest spawning populations in Yellowstone Lake are locally adapted and reproductively isolated by space and time.

Our second hypothesis is that geographical barriers throughout YNP have led to fragmentation and genetic structuring of YCT populations. Studies of westslope cutthroat trout have shown restricted gene flow to be associated with the presence of waterfalls (Taylor et al. 2003). Many potential barriers (i.e. waterfalls, geothermal lakes, the continental divide, etc.) exist in the park, providing a basis for the hypothesis that populations are fragmented and genetically structured.

Besides presenting a unique set of management circumstances, the post-glacial invasion of YNP by YCT provides an opportunity to use a variety of analytical techniques to test hypotheses about recently developed population genetic structure. Despite advances in software programs for analyzing genetic data, many researchers continue to rely heavily on traditional methods (i.e. F_{st}, R_{st}, Nm, and AMOVA) whose assumptions are often violated by natural populations (Pearse and Crandall 2004). Modern analytical techniques (Bayesian assignment tests, coalescent theory, and nested clade analysis) claim to have increased power to detect population genetic structure. This study compares the ability of several traditional and modern analytical techniques to describe population structure and detect restricted gene flow in a population with low levels of genetic divergence.

MATERIALS AND METHODS

Study Area

The habitat available to Yellowstone cutthroat trout (YCT) in Yellowstone National Park (YNP) has been shaped by both geologic and climatic events. Yellowstone Lake is a caldera lake formed from a volcanic explosion approximately 600,000 years ago (Good and Pierce 1996). YNP has also been repeatedly glaciated, most recently by the Pinedale glaciation, which lasted from 12,000 to 30,000 years ago (Love et al. 2003). Approximately 12,000 years ago the glaciers receded, gradually making fluvial and lacustrine habitat available for fish. YCT in YNP therefore represent a newly established population relative to their ancestors in the lower Snake River.

Between 8,000 and 12,000 years ago YCT invaded the Yellowstone River drainage via Two Ocean Pass, a marsh located at the continental divide connecting Pacific Creek and Atlantic Creek (Behnke 2002). This passage still exists today, but populations on either side are believed to be reproductively isolated from each other based on life history differences (Behnke 2002). Once across the continental divide, YCT spread throughout the Yellowstone River system and also became firmly established in Yellowstone Lake. YCT spawning has been documented in 68 of 124 tributaries to the lake (Gresswell et al. 1997). These tributaries provide a variety of temperature and flow regimes to which spawning populations could potentially adapt. As mentioned previously, an estimated 97% of YCT in Yellowstone Lake return to their natal stream each year to spawn (Ball 1955; Cope 1957; McCleave 1967). Downstream from Yellowstone Lake, genetically pure YCT populations are confined almost exclusively to small order streams where introgression with introduced rainbow trout and competition with brown and brook trout is nonexistent. The upstream migration of these non-native species is blocked by natural barriers such as Yellowstone Falls.

Since the establishment of YNP in 1872, YCT have played an important role in the local economy. The economic value of the Yellowstone Lake ecosystem has been estimated at $36 million per year based on the number of angler days on the Yellowstone River, Yellowstone Lake, and tributaries to the lake (Gresswell and Liss 1995; Varley and Schullery 1995). In addition, the economy is fueled by fish watchers, who come to observe native YCT at fishing bridge below Yellowstone Lake and at LeHardy Rapids on the Yellowstone River. It has been estimated that over a third of a million people participate in fish watching each year, which exceeds the average annual number of angler days for all of YNP (Gresswell and Liss 1995). In addition, 22 mammal and 20 bird species are known or suspected to utilize YCT as a food source (Varley and Schullery 1995), including grizzly bears, bald eagles, and pelicans (Stapp and Hayward 2002; Haroldson et al. 2005). These predators may consume as many as 300,000 cutthroat trout annually (Behnke 2002). The critical role of YCT in the economy and ecosystem justifies the exploration of their genetic makeup for purposes of conservation.

Cutthroat trout in the lake have been devastated by the recent introductions of lake trout and whirling disease (Koel et al. 2005). Lake trout were officially reported in the lake on July 30, 1994, although unofficial reports had preceded the announcement by a number of years. Lake trout do not hybridize with YCT, but are highly piscivorous and will readily eat YCT (Kaeding et al. 1996). An average lake trout consumes an estimated 41 YCT each year (Ruzycki et al. 2003). Since 1994 over 100,000 lake trout have been removed by Yellowstone biologists in an effort to curtail damage to the YCT population (Koel et al. 2005).

The second major cause for the decline in YCT numbers in Yellowstone Lake has been whirling disease. This protozoan parasite induces considerable mortality in young of the year cutthroat trout by causing cranial deformities during their early stages of development (Thompson et al. 1999). Biologists believe the disease may be largely responsible for the decline of certain spawning populations in Yellowstone Lake. For example, in Pelican Creek (a major tributary to Yellowstone Lake) YCT spawners numbered near 30,000 in 1981 (Koel et al. 2005) but in 2004 only 5 fish returned to the stream to spawn (Dan Mahoney, National Park Service, personal communication). Declines of this nature can be found in a number of streams entering the lake.

Sampling and genetic data collection

To test the hypothesis of genetic structuring in Yellowstone Lake, 300 YCT representing 10 spawning populations (or tributaries) (Table 1, Figure 1) and 30 YCT from Sedge Creek were examined. Sedge Creek, a tributary to Yellowstone Lake, has been isolated for approximately 8,000 years by a geothermal lake (Kaplinski 1991). Muscle and liver samples were taken from whole fish collected with an electroshocker and frozen at -80°C.

In order to understand the population structure of YCT throughout Yellowstone National Park (YNP), an additional 817 fin clips were obtained from seven locations in the upper Snake River watershed and 16 locations in the Yellowstone River drainage. Five of these locations were tributaries to Yellowstone Lake: Clear Creek, Yellowstone River at LeHardy Rapids, Thorofare Creek, Atlantic Creek, and Yellowstone River above Yellowstone Lake (Table 1, Figure 2). One location, Pacific Creek, is not actually in YNP but is included because it is believed to represent the invasion route for YCT from the Snake River to the Yellowstone River drainage (Behnke 2002). Fin clips were stored in 95% ethanol. All samples were accessioned into the Monte L. Bean Life Science Museum at Brigham Young University.

Because sampling occurred over a period of 18 years it is possible that a temporal change in population structure has occurred. This could potentially complicate comparisons between populations collected at different times because of the difficulty in separating temporal variation from spatial variation. Conclusions vary from previous studies on temporal change in salmonid population structure (Laikre et al. 1998; Nielsen et al. 1999; Tessier and Bernatchez 1999; Heath et al. 2002), suggesting temporal stability is dependent on the system. We failed, however, to detect significant differences (Fst values were not significantly different from zero) in haplotype or allele frequencies at locations where replicate samples were taken in 1987 and 2005 (Clear Creek, Yellowstone River at LeHardy Rapids, and Cache Creek) and therefore assumed temporal genetic stability.

DNA Extraction and PCR

DNA extraction from frozen muscle tissues was performed according to the protocol for animal tissues in the Qiagen DNeasy kit (Qiagen Inc., Valencia, CA). DNA was isolated from fin clips stored in ethanol using the pureGene DNA purification kit (Gentra Systems Inc., Minneapolis, MN).

Amplification of the NADH dehydrogenase subunit 1 and 2 genes (ND1, ND2; 2,286 base pairs) from the mitochondrial genome was performed by polymerase chain reaction (PCR) according to protocol used by Shiozawa and Evans (2001) using four sets of internal primers developed in our lab (Table 2). PCR was performed in 20 µl reactions consisting of DNA template (~100 ng), deoxyribonucleotides (0.125 mM each), primers (10 pM each), buffer (10 mM Tris-HCl, 1.5 mM $MgCl_2$, 25 mM KCl), and Taq polymerase (0.25 units). Reactions were run on an MJ Research PTC-225 Peltier TC tetrad (Bio-Rad Laboratories, Inc., Hercules, CA). PCR products were cycle sequenced using ABI Big Dye terminator protocol (Applied Biosystems, Inc., Foster City, CA) for 10 seconds at 96.0°C, 5 seconds at 50.0°C, and 4 minutes at 60.0°C for 24 cycles. The Big Dye product was cleaned with Sephadex G-50 medium (Sigma-Aldrich Co., St. Louis, MO) and electrophoresed on an ABI 3730 XL automated sequencer. Sequences were aligned and cleaned using Sequencher v4.2 (GeneCodes Corp., Ann Arbor, MI).

Early analysis of cutthroat trout population genetic structure in Yellowstone Lake using protein electrophoresis and mitochondrial DNA (mtDNA) failed to detect genetic differences between spawning populations (Shiozawa and Williams 1992). However, newly developed analytical techniques and molecular markers with higher levels of variability (e.g. microsatellites) have not yet been tried. Microsatellites have a high amount of variation due to an inherent high mutation rate (Weber and Wong 1993) and are therefore especially informative in identifying recent shifts in population structure (Hendry et al. 2000). We used six microsatellite loci to examine the partitioning of genetic variation in Yellowstone Lake and YNP (Table 3). PCR was performed in 20 μl reactions consisting of the same components as the mtDNA reactions described above. The following thermal profile was used for microsatellite amplification: initial denaturation for 2 min at 93°C, then 40 cycles for 15 sec at 93°C, 1.5 min at 60, 54, or 50°C, 1.5 min at 72°C, followed by a final 10 min extension at 72°C (Rexroad III and Palti 2003). Two multiplexes were run: (1) Ots107, Omm1036, and Fgt3, and (2) Ocl8, Ssa85, and Omm1241. In order to reduce stuttering and clarify allele peaks, a pigtail sequence of GTTTCT was added to the 5' end of Ocl8-R, Ssa85-R, and Omm1241-R. Alleles were scored and binned using Genotyper v2.5 (Perkin Elmer).

DATA ANALYSIS

Measuring introgression

Detecting genetically pure populations is a high priority for species in which hybridization with non-native species is common (Allendorf et al. 2001; May et al. 2003). Populations containing a high proportion of native genes are typically a higher priority for conservation than introgressed populations (Utah Division of Wildlife Resources 2000). To assess levels of YCT hybridization with rainbow trout in the lower Lamar River drainage we screened ten populations for the presence of rainbow trout alleles and mtDNA haplotypes (Table 4, Figure 3). This was done by amplifying two microsatellite markers (Ocl8 and Ssa85, Table 3), one nuclear marker (ITS-2, Table 2), and a portion of ND2 from the mitochondrial genome. These populations were analyzed strictly to assess introgression and were therefore not used in the analyses described below, with the exception of YCT mtDNA haplotypes from Lamar River, Lamar River across from Geyser basin, and Slough Creek section 1. Percent introgression per population was estimated by screening for rainbow trout nuclear alleles and mtDNA, which is readily distinguished from YCT mtDNA because of a relatively high sequence divergence (~8%, Allendorf et al. 1988). It should also be noted that the two microsatellite markers and ITS-2 are only able to differentiate between cutthroat trout and rainbow trout, not between cutthroat trout subspecies.

Nested clade analysis

Examination of the relationship between haplotype distribution and geographical proximity can often reveal a great deal about population history (Templeton et al. 1995). Nested clade analysis (NCA) is a tool for identifying historical processes (i.e. fragmentation, colonization, or range expansion) that have led to the current distribution of genetic variation

(Templeton et al. 1995; Templeton 1998). Here, NCA was used to test for isolation, fragmentation, and/or restricted gene flow between YCT populations against the null hypothesis of panmixia. A minimum spanning haplotype network for ND1 and 2 was created by statistical parsimony implemented in TCS v1.21 (Clement et al. 2000). Nesting categories, or clades, were assigned according to Templeton (1998). Approximate linear river distances (km) were obtained using a digital chartmeter and a 1:100,000 topographic map (Fetzner and Crandall 2003). Statistical analysis of the nested haplotype network and geographic distance was performed using GEODIS v2.5 (Posada et al. 2000) with 10,000 replications. Phylogeographical inferences were made for clades with significant clade distances (Dc, the spatial spread of the clade) and/or nested clade distances (Dn, the distance of the clade from other clades in the same nesting category) according to Templeton's inference key (2004).

Isolation by distance

The isolation by distance option (Rousset 1997) implemented in GENEPOP v3.4 (Raymond and Rousset 1995) was used to test for a correlation between river distance (km) and genetic divergence [$F_{st}/(1-F_{st})$] using 10,000 permutations. P-values were calculated by regression analysis. Linear river distances were the same as those used above in GEODIS v2.5. Pairwise F_{st} and R_{st} values were calculated using ARLEQUIN v2.0 (Schneider et al. 2000). The Sedge Creek population was already known to be fragmented and genetically distinct (Dennis Shiozawa, personal communication) and was therefore not included in this analysis.

Population Structure and Genetic Diversity

Summary statistics about the six microsatellite loci were obtained using FSTAT v2.9.3.2 (Goudet 1995). This included the number of alleles per locus and population, genetic diversity, and allelic richness per locus (corrected for sample size) and population as well as over all populations.

Departure from Hardy-Weinburg equilibrium can bias estimates of F_{st} by violating the assumptions of F-statistics (e.g. stable population size and migration-drift equilibrium; Pearse and Crandall 2004). Therefore, significant deviations from expectations under Hardy-Weinberg equilibrium were determined using the locus by locus exact test (chain length = 100,000) implemented in ARLEQUIN v2.0 (Schneider et al. 2000) for each population. Pairwise tests (chain length = 100,000) for linkage disequilibrium were also performed for each population using ARLEQUIN v2.0 (Schneider et al. 2000).

Population structure was described using F_{st} (Weir and Cockerham 1984) for mtDNA and R_{st} (Slatkin 1995) for microsatellite loci. R_{st} is generally considered a more accurate estimate for microsatellite loci because it uses the stepwise mutation model (SMM) of evolution and takes into account the mutation rate of microsatellites, which can be as high as 10^{-3} per generation (Weber and Wong 1993). F_{st} and R_{st} were calculated separately for 1) Yellowstone Lake spawning populations and 2) populations located elsewhere in YNP. Migration rates were estimated using the equation $F_{st} = 1/(4Nm + 1)$ (Wright 1951) where Nm equals the number of effective migrants per generation. The partitioning of genetic variation among and within regions and within populations was calculated by analysis of molecular variance (AMOVA) (Excoffier et al. 1992) at 10,000 permutations. Regions were initially defined by drainage: Snake River, Yellowstone River, and Lamar River. F_{st}, R_{st}, Nm, and AMOVA calculations were performed using ARLEQUIN v2.0 (Schneider et al. 2000).

Defining populations

It is likely the sampled "populations" do not reflect the actual spatial genetic subdivision of populations. While F_{st} can provide some information about the similarity of populations, the assumptions made in making this estimation (i.e. migration-drift equilibrium between populations) are biologically unrealistic and require defining populations *a priori* (Pearse and Crandall 2004). A more reasonable approach is to allow the data to define the populations before analyzing them. This method is implemented in the Bayesian clustering program STRUCTURE v2.0 (Pritchard et al. 2000). We used STRUCTURE to define the number of populations in each of the following three regions based on allelic data from six microsatellite loci: Yellowstone Lake, Snake River drainage, and Yellowstone River drainage. A burnin period of 25,000 iterations was followed by 100,000 Markov chain Monte Carlo (MCMC) repetitions. The best estimate of K (equal to the number of populations) was defined as the least negative Ln P(D) value (the natural log of the probability of the data given a particular K value) or the K value at which Ln P(D) began to stabilize.

The use of sequence data in STRUCTURE is not recommended because the program assumes each nucleotide is a separate, unlinked locus. Therefore we did not include mtDNA data in this analysis. However, any significant inconsistencies between the STRUCTURE results and mtDNA F_{st} values were taken into account as we defined our populations. These new populations, or STRUCTURE-defined populations, were considered genetically distinct population segments and used in the analyses described below for estimating effective population size and migration rates.

Migration rates and effective population size

Using F_{st} to calculate the effective number of migrants per generation (Nm) relies on assumptions that are often violated by small, isolated populations (Pearse and Crandall 2004). Coalescent-based methods for estimating effective population size and migration rates are better able to utilize all the information contained in the data and do not rely on the same assumptions. For example, traditional approaches such as Nm are unable to estimate asymmetric gene flow between two populations. We used the coalescent-based program LAMARC v2.0.2 (Kuhner et al. 2005) to estimate theta (θ) and migration rate (M) as part of our objective to determine the genetic status of YCT populations in YNP. Both of these parameters offer useful information about extinction risk and gene flow. Theta can be used to obtain an estimate of effective population size; populations with low effective population sizes may exhibit decreased fitness (Newman and Pilson 1997) and are therefore at increased risk of extinction. Migration rate estimates provide information about gene flow that can assist in the identification of distinct population segments.

The data were divided into two sets—one with the STRUCTURE-defined populations from the Snake River drainage, Yellowstone Lake, and Sedge Creek, and the second with the STRUCTURE-defined populations from the Yellowstone River drainage (including Yellowstone Lake). Thirty individuals were selected at random from each population to be included in the two data sets. The decision to divide the data into two sets and use only thirty individuals from each population was based on recommendations by Kuhner et al. (2005), who suggest a maximum of five or so populations and 20-30 individuals from each population. Any more than this and the program cannot estimate all the parameters effectively and computation time increases dramatically.

Two options for modeling sequence evolution are available in LAMARC, F84 and GTR. We used MODELTEST v3.7 (Posada and Crandall 1998) executed in PAUP* (Swofford 2000) to determine which of these two models is most likely to generate the observed patterns of our data. Base frequencies and relative mutation rates were generated in the same manner. Separate runs were performed for mtDNA and microsatellites for each of the two data sets. Under the Bayesian setting, one initial chain (mtDNA: samples = 4,000, interval = 15, burnin = 5,000; microsatellite DNA: samples = 5,000, interval = 25, burnin = 6,250) and one long chain (mtDNA: samples = 250,000, interval = 40, burnin = 100,000; microsatellite DNA: samples = 100,000, interval = 50, burnin = 100,000) were run. Ten replicate runs with different random number seeds were executed for each data set.

Effective population size (N_e for microsatellites, N_f or effective number of females for mtDNA) for each population was estimated using the equations $\theta = 4 N_e \mu$ and $\theta = 2 N_f \mu$ for microsatellite and mtDNA, respectively (θ = theta; μ = per site mutation rate) (Kuhner et al. 2005).

Migration rate (M) is equal to m/μ where m is the per-generation migration rate and μ equals the per site mutation rate. M was converted to the effective number of migrants per generation (Nm) according to the equation $Nm = M/(4\theta_{\text{recipient population}})$ (Kuhner et al. 2005). These values were then compared to Nm estimates produced by ARLEQUIN v2.0 [$F_{st} = 1/(4Nm + 1)$, Wright 1951].

We assumed a mutation rate of 10^{-3} for microsatellites and 8.33×10^{-7} for mtDNA. These approximations were chosen because the six microsatellite markers we used generally had a high number of unit repeats, which increases mutation rates (Lai and Sun 2003). The mutation rate of salmonid mtDNA has been estimated at 1/3 to 1/2 that of higher vertebrates (G.R. Smith, Museum of Zoology, University of Michigan, Ann Arbor, Michigan, pers. comm., from Billington and Hebert 1991), which have a rate of 2% per million years, or 2×10^{-6} (Brown et al. 1979). While choosing an estimate for mutation rate is debatable, knowing the actual mutation rate is not essential for comparing of effective population sizes between populations within the study area.

RESULTS

Introgression

Rainbow trout genes were detected in six out of ten populations: Slough Creek (sec. 1), Lamar River, Lamar River canyon, Lamar River at Soda Butte Creek, Lamar River across from Geyser Basin, and Pebble Creek at bridge to Soda Butte Creek (Table 4). Also, one individual with a rainbow trout haplotype was found in Heart Lake; this fish was removed from all subsequent analyses. Additionally, three westslope cutthroat trout mitochondrial haplotypes were found: one in the Yellowstone River below Yellowstone Lake, one in Slough Creek (sec. 1), and one in Lamar River. The individual from Yellowstone River below Yellowstone Lake was removed from the analysis. The presence of the rainbow trout haplotype in Heart Lake and the westslope cutthroat trout haplotype in Yellowstone River below Yellowstone Lake creates the possibility that a small number of undetected, non-native microsatellite alleles are present in the data set. This is of minimal concern, however, as very low levels of introgression have been reported to not significantly alter the results of population genetic analyses (Wenburg et al. 1998).

Nested clade analysis

A total of 943 individuals were sequenced and 86 haplotypes were detected. Sixty-five of these haplotypes were detected from the 410 individuals sequenced from the Yellowstone Lake spawning populations. The distribution of haplotypes in the Yellowstone Lake spawning populations and the YNP populations is shown in figures 4 and 5, respectively. Three dominant haplotypes were identified, two of which ('A' and 'B') occurred throughout the study area but primarily in the Yellowstone River drainage. The third ('S1') occurred exclusively in the Snake River drainage. Maximum sequence divergence between haplotypes was 0.35% (8/2286 base pairs).

The haplotype network generated with TCS indicated most haplotypes differed from one of the two dominant haplotypes ('A' and 'B') by one or two base pairs. Twenty-one one-step clades and three two-step clades were identified (Figure 6). GEODIS analysis of these clades revealed significant ($p<0.05$) within clade (D_c) and/or nested clade (D_n) distances in seven one-step clades, all three two-step clades, and the total cladogram. Using Templeton's (2004) inference key, two of these significant values (clades 1-11 and 1-15) were inconclusive due to inadequate geographical sampling. Six clades (1-4, 1-5, 1-6, 1-12, 1-20, and 2-1) showed restricted gene flow with isolation by distance. Clade 2-2 and the total cladogram exhibited restricted gene flow/dispersal but with some long distance dispersal. It should be noted that two of the significant one-step clades within clade 2-2 were from Yellowstone Lake. Finally, clade 2-3 showed past fragmentation and/or long distance colonization (Table 5).

Isolation by distance

Regression analysis of geographic river distances (km) and genetic distance [$F_{st}/(1- F_{st})$] revealed a small but significant correlation for both mtDNA and microsatellite data (Figures 7 and 8). The proportion of variation in genetic distance explained by variation in river distance was $r^2 = 0.18$, $p = 0.000000$ for mtDNA and $r^2 = 0.12$, $p = 0.000000$ for microsatellites.

Population structure and genetic diversity

Five of the six microsatellite loci amplified were highly polymorphic, with the number of alleles/locus ranging from seven to 38. The least polymorphic locus was Ssa85, for which one allele was found at very high frequencies (70-100%) in all populations except Forest Creek. With a few exceptions, genetic diversity for all loci except Ssa85 ranged from 0.6-0.95. Genetic diversity for Ssa85 was much lower, generally falling from 0.2 to 0.6. Allelic richness was as low as 1 in Sedge Creek and upper Antelope Creek and as high as 13.48 in the Yellowstone River at LeHardy Rapids (Table 6).

Significant deviations ($p<0.05$) from expectations under Hardy-Weinburg equilibrium were detected in 27 out of 174 (15.5%) possible occurrences (29 populations x 6 loci) (Table 7). This could be due to genotyping errors or the presence of null alleles, which would result in an underestimation of heterozygosity. This seems a likely explanation because observed heterozygosity was less than expected heterozygosity in all 27 detected deviations.

Linkage disequilibrium occurred for 47 out of 405 (11.6%) locus by locus pairwise comparisons ($p<0.01$). However, no two loci were linked more often than others, suggesting that the observed level of linkage disequilibrium is due to population-specific errors in identifying and scoring alleles.

Population structure as described by F_{st} (mtDNA) and R_{st} (microsatellites) was low in the pairwise population comparisons of the Yellowstone Lake spawning populations. Only 2 out of 78 possible comparisons had significant ($p<0.05$) F_{st} values while 11 out of 78 pairwise R_{st} values were significant (Tables 8 and 10). Both significant F_{st} and six of 11 significant R_{st} values occurred in comparisons with Yellowstone River at Fishing Bridge. The effective number of migrants (Nm) was generally high (after correcting for haploid and maternal inheritance of mtDNA) for nearly all pairwise population comparisons for Yellowstone Lake, ranging from 3.03 to infinity (Tables 9 and 11) with most being at or near infinity. Nm values were generally higher for pairwise estimates based on mtDNA. The overall F_{st} and R_{st} determined by AMOVA for Yellowstone Lake did not differ significantly from zero with values of 0.00576 ($p = 0.20$) and -0.00563 ($p = 0.75$), respectively.

YCT populations located throughout YNP showed a higher level of genetic structuring than those in Yellowstone Lake. Because very little evidence was detected for significant structuring in the Yellowstone Lake spawning populations, the Yellowstone Lake populations were grouped together for comparison with all other YNP populations. F_{st} and R_{st} values ranged from insignificant ($R_{st} = 0.001$ for Heart River vs. Snake River) to highly significant ($F_{st} = 0.901$ for Sedge Creek vs. Lamar River at Geyser Basin). Significant values ($p<0.01$) were found in 170 out of 190 pairwise F_{st} and 121 out of 136 pairwise R_{st} comparisons (Tables 12 and 14). Nm values calculated from F_{st} and R_{st} ranged from 0.07 to infinity and were typically below 2.50, evidence of restricted gene flow between populations (Tables 13 and 15). AMOVA indicated an overall F_{st} of 0.316 for mtDNA and an R_{st} of 0.200 for microsatellites, both significantly different from zero ($p<0.00000$). Variation among and within drainages (Snake River, Yellowstone River, Lamar River) and within populations for mtDNA was 7.47%, 24.15% and 68.39%, respectively, and 6.26%, 13.72%, and 80.03% for microsatellites. Allele frequencies for Fgt3, Ocl8, and Omm1241 are displayed respectively in figures 9, 10, and 11.

Defining populations

The STRUCTURE results indicated that the most likely number of populations (K) in the data set containing the Yellowstone Lake tributaries is two (Figures 12 and 13). One of these, Sedge Creek, is an isolated population and has been inaccessible to spawning fish from Yellowstone Lake for approximately 8,000 years (Kaplinski 1991). All other Yellowstone Lake spawning populations and upper Pelican Creek were grouped into one cluster. The second cluster, or population, consisted of the 30 individuals from Sedge Creek.

In the Snake River drainage, values for Ln P(D) began to stabilize at K= 4 (Figure 14), one cluster of which consisted of the Yellowstone Lake samples, which were included in order to verify that the Snake River populations are genetically distinct from Yellowstone Lake (past stocking from Yellowstone Lake to the Snake River drainage in YNP may have occurred in the past century, however we failed to detect any clear evidence that stocking altered the gene pool of recipient populations). This suggests an actual population size of three in the upper Snake River drainage. Clusters were composed of: 1) Heart Lake, Heart River, Sickle Creek, Pacific Creek, most of Snake River (29/41), and part of Forest Creek (7/34), 2) Crooked Creek and part of Snake River (12/41), and 3) most of Forest Creek (27/34) (Figure 15).

The Yellowstone River drainage had a least negative Ln P(D) at K = 5 (Figure 16), one of which was Yellowstone Lake. The remaining four clusters consisted of (1) Trout Creek, (2) McBride Lake and Slough Creek at confluence with Elk Tongue Creek, (3) Pebble Creek and Cache Creek, and (4) upper and lower Antelope Creek (Figure 17).

AMOVA (using ARLEQUIN v2.0) of the STRUCTURE-defined populations supports that the above designations as genetically distinct population segments represent the actual division of populations. When groups were defined as described above (with the exceptions of

Pacific Creek and Pebble Creek, which were separated based on significant F_{st} values as described below) a much higher percentage of the genetic variation was attributed among groups rather than among populations within groups as opposed to when groups were defined by drainage. This suggests populations within the STRUCTURE-defined groups are very similar from a genetic standpoint and that genetic variation is not partitioned by drainage, but rather by populations within drainages. The values were as follows for variation among groups, among populations within groups, and within populations, respectively: 30.70%, 2.24%, and 67.06% (mtDNA) and 19.85%, -0.42%, and 80.57% (microsatellites).

Migration rates and effective population size

Analysis with LAMARC was performed after the original 29 sampling locations were divided into 11 genetically distinct population segments based on the STRUCTURE results and pairwise F_{st} values for mtDNA. These populations were identical to the clusters identified by STRUCTURE but with two exceptions: Pacific Creek and Pebble Creek were separated from their STRUCTURE-assigned clusters because of highly significant F_{st} values (based on mtDNA) between those populations and others in their cluster.

Population set 1 consisted of 30 randomly selected individuals from each of the following six STRUCTURE-defined populations: Crooked Creek, Snake River (Heart Lake, Heart River, Sickle Creek, most of Snake River, and some of Forest Creek), Forest Creek, Pacific Creek, Yellowstone Lake, and Sedge Creek. Population set 2 consisted of 30 randomly selected individuals from each of the following: Trout Creek, Antelope Creek (upper and lower), Slough Creek (McBride Lake and Slough Creek at confluence with Elk Tongue Creek), Pebble Creek, Cache Creek, and Yellowstone Lake.

Effective population sizes (N_e, computed as the average of the ten replicate runs) ranged from 5.9 for Sedge Creek to 3179 for Pacific Creek (Table 16). Effective number of females (N_f) ranged from 3.3 for Sedge Creek to 802 for Yellowstone Lake (Table 16). Estimations of for N_e (which are expected to be equal to $2N_f$) were generally 4-10 times greater than N_f, likely because of inaccuracies in assuming a mutation rate. Both estimates (N_e and N_f) followed similar patterns for all populations, with the exception of Crooked Creek, which had a relatively high N_e and a low N_f. Also, Pacific Creek had the highest N_e value and only the fifth highest N_f value.

Migration rates were converted to effective number of migrants (Nm) using the equation $Nm = M/(4\theta_{\text{recipient population}})$ (Kuhner et al. 2005). Comparison of these values to Nm estimates provided by ARLEQUIN [$F_{st} = 1/(4Nm + 1)$] revealed similar patterns, although the ARLEQUIN estimates were generally four to ten times greater (Tables 17 and 18). Outliers (up to two) were identified and omitted from the data set using the curvefiles produced by LAMARC (see example in Figure 18). Nm values from LAMARC were generally less than one (the two exceptions being Pacific Creek and Trout Creek), suggesting the STRUCTURE-defined genetically distinct population segments are reproductively isolated.

DISCUSSION

Introgression

Introgression with rainbow trout appears to be highest in the lower Lamar River system, including lower Slough Creek. Unexpectedly, very little evidence for introgression was detected in the populations from upper Slough Creek, Pebble Creek, and upper Lamar River. Based on our results, it appears that introgression is very low above the confluence of the Lamar River

Soda Butte Creek. The only rainbow trout genes detected upstream from this location were in one individual from Lamar River at Soda Butte Creek (heterozygous YCT x RT at Ocl8 and Ssa85), one individual from Pebble Creek at bridge to Soda Butte Creek (heterozygous YCT x RT at Ssa85; Table 4), and one individual from Lamar River across from beyser basin (RT mtDNA; heterozygous YCT x RT at ITS-2, Ocl8, and Ssa85). Downstream from this location toward the confluence of the Lamar River with Slough Creek, however, hybridization with rainbow trout is low to moderate. The consistency of introgressed individuals between genetic markers suggests these individuals are F1 (first generation) hybrids. The non-random distribution of genes in the population suggests this is not a hybrid swarm. Rather, F1 hybrids are either failing to reproduce or only one or two generations of hybridization have taken place.

The presence of three westslope cutthroat trout haplotypes is an indication that a small number of these fish have been transferred into the Yellowstone River drainage by natural or non-natural means. Transfer by humans seems the most likely explanation. This explanation is also likely for the unexpected detection of an individual with a rainbow trout haplotype in Heart Lake, although it is possible rainbow trout have migrated up the Snake River to Heart Lake.

Population structure and gene flow: Yellowstone Lake

Genetic diversity in Yellowstone Lake as a whole was high, but variation described by F_{st} and R_{st} was generally not partitioned by spawning population. Instead, nearly all of the variation occurred between individuals within populations. The only exception was in the small number of significant F_{st} and R_{st} values detected in comparisons with Yellowstone River below Yellowstone Lake. While this may be an indication of reproductive isolation of this population, this conclusion is suspect because it is possible these results arose due to chance alone; at $p<0.05$

one in twenty comparisons will be significant due to chance alone, which is close to the proportion we observed (13/156 or 8.33%).

The most likely explanation for the majority of the variation occurring between individuals within populations is that gene flow between populations is retarding genetic divergence. This is good evidence that straying fish are successfully reproducing in locations other than their natal stream. A factor that may be important in increasing straying rates is drought. During times of drought small spawning streams may either dry up completely or do not get enough runoff to blow out sand bars built up at the mouth of the stream. Either of these situations would prevent YCT spawners from entering the stream, likely forcing them to stray to another stream to spawn. This, along with natural rates of straying, may explain much of the gene exchange between spawning populations.

Based on the AMOVA (overall F_{st}) and STRUCTURE results, no evidence was found that YCT in Yellowstone Lake are, from a genetic standpoint, anything but a panmictic population. However, these methods often fail to detect population structure under moderate levels of gene flow ($Nm \geq 5$; Waples and Gaggiotti 2006). Interestingly, evidence for rejecting the null hypothesis of panmixia in Yellowstone Lake was detected using nested clade analysis (NCA), suggesting moderate but restricted levels of gene flow between spawning populations with some reproductive isolation.

NCA provided insight about population genetic structure at a finer scale than F_{st}, R_{st}, or the Bayesian assignment program STRUCTURE v2.0. Specifically, statistically significant evidence was detected for restricted gene flow between spawning populations within Yellowstone Lake. Such evidence was not detected with other methods. This is the first case in which molecular data has indicated spawning populations in Yellowstone Lake are to some degree reproductively isolated. Moreover, this case illustrates the ability of NCA to detect population structure under conditions of restricted but ongoing gene flow, a power not available in other methods.

Restricted gene flow between Yellowstone Lake spawning populations was evident from significant GEODIS results for clade 2-2 (Figure 6). Within this clade, evidence for restricted gene flow/dispersal with some long distance dispersal was detected in Clear Creek and Flat Mountain Arm Creek & Little Thumb Campground Creek. Clade 1-10 contained seven individuals from Clear Creek, which represents 10.4% of the Clear Creek population (7/67). Six of these individuals had haplotype 'L' and one had haplotype 'C3', which is one step away from haplotype 'L'. The remaining three individuals in clade 1-10 were from other populations throughout Yellowstone Lake. By comparison, these three individuals represent just 1.0% (3/314) of the populations in Yellowstone Lake other than Clear Creek. The significantly small within clade and nested clade distances of clade 1-10 suggest some degree of reproductive isolation of the Clear Creek spawning population. The three fish from this clade found in other locations likely represent low levels of ongoing gene flow, or straying fish, from Clear Creek to other populations.

Significantly small distances were also detected in clade 1-8, which contained haplotypes 'M1' and 'U1' from Flat Mountain Arm Creek and Little Thumb Campground Creek. Interestingly, although not statistically significant, these two streams shared two other haplotypes: 'O' and 'N1'. This suggests these two streams are more likely to exchange migrants with each other than with other streams, which is not unlikely considering the close geographic proximity of these two streams to each other. Additionally, a significantly small within clade distance in clade 1-18 (within clade 2-3) indicated restricted gene flow between the Yellowstone

River below Yellowstone Lake and other spawning populations. The five individuals with haplotypes 'T' and F1' in this clade were found only in this location.

While individual spawning populations do not qualify as genetically distinct population segments, information regarding gene flow between spawning populations will allow fisheries managers to make decisions that will maintain current levels of gene flow. Although evidence for restricted gene flow was not found in all inlet streams to Yellowstone Lake, evidence in a few locations opens the door for future exploration of the population dynamics of this system through genetic analysis. Clear Creek and Yellowstone River below Yellowstone Lake (plus LeHardy Rapids) are the two locations with large sample sizes (67 and 82, respectively), suggesting the detection of population structure in other spawning populations may be a matter of increasing sample size from 30 to 70-100 in order to obtain a statistically significant representation of the rare haplotypes.

NCA allowed us to obtain more information from the data than would have been possible if we had relied solely on F-statistics. It is likely that in other studies assessing populations with low levels of genetic divergence and some degree of reproductive isolation this approach (NCA) will allow investigators to obtain a more detailed picture of the study system than using F-statistics alone.

Population structure, gene flow, and genetic diversity: Yellowstone National Park

NCA provided information about population fragmentation and restricted gene flow for a number of YCT populations located throughout YNP. Past fragmentation and/or long distance colonization was detected between the upper Snake River (including Pacific Creek) and the Yellowstone River. This is consistent with what is known about the invasion history of YCT. YCT invaded the Yellowstone River drainage from Pacific Creek via Two Ocean Pass. It is believed, however, that YCT movement across the continental divide via Two Ocean Pass is presently uncommon and that populations on either side are distinct (Behnke 2002). Our results support Behnke's (2002) contention that gene flow is restricted across the continental divide.

Evidence for past fragmentation was also found in Forest Creek within the Snake River drainage. This location represents a headwater stream with a relatively small population size. The dominant haplotype found in Forest Creek is separated from the next closest haplotype by two base pairs. This suggests the Forest Creek population has possibly been isolated from the Snake River population for as many as several thousand years. By way of comparison, Sedge Creek (all of one haplotype) of the Yellowstone basin has been isolated for ~8,000 years (Kaplinski 1991) and is also separated from all other haplotypes by two base pairs.

Within the Yellowstone River drainage, past fragmentation and/or long distance colonization was evident in Antelope Creek. The clade containing the two Antelope Creek haplotypes is likely the result of past isolation; it should be noted, however, that the presence of the 'A' haplotype (5 base pairs away from the Antelope Creek clade) in this location suggests possible recent gene flow with the nearby Lamar River where 'A' is the dominant haplotype. If so, the historical barrier to gene flow appears to no longer be impeding fish migration.

Evidence for restricted gene flow with isolation by distance was detected within the Slough Creek drainage (clades 1-4 and 1-5). This region, however, exhibited restricted gene flow with some long distance dispersal when compared to surrounding regions, such as the upper Lamar River. Unfortunately, our sampling scheme was inadequate to determine the relationship between Slough Creek and Yellowstone Lake (isolation by distance, fragmentation, or range expansion).

Population structure estimates (F_{st} and R_{st}) and STRUCTURE cluster assignment results were generally consistent with the NCA results, suggesting eleven genetically distinct population segments over the range of sampling locations (Figure 19). Four of these are isolated headwater streams (Crooked Creek, Forest Creek, Sedge Creek, and Antelope Creek) although it is possible that with more extensive sampling the range of the Antelope Creek population would expand into the Yellowstone River. Four wide-spread populations were identified in the higher-order river basins: Snake River, Yellowstone Lake basin, Lamar River/Cache Creek, and Slough Creek. These results indicate a general pattern of isolation by drainage basin (with some isolation by distance) in the larger rivers and population fragmentation in small, headwater streams. The remaining three populations, Pacific Creek, Trout Creek, and Pebble Creek, need more extensive sampling in order to determine the extent of their respective ranges.

A wide range of effective population sizes was detected, indicating some populations are likely more susceptible than others to perturbations (i.e. disease, environmental change, etc.). Of the eleven genetically distinct population segments, those isolated to small headwater streams had the lowest effective population sizes. These were Sedge Creek, Antelope Creek, and Forest Creek. The exception was Crooked Creek, which had a low N_f but a high N_e. This may be the result of the stochastic effects of genetic drift acting separately on mtDNA and microsatellite DNA. Another possibility is that male-mediated gene flow is occurring while females are not migrating. This would help sustain levels of genetic variation in nuclear genes while mtDNA, which is maternally inherited, would experience a loss of variation due to genetic drift acting on the isolated female portion of population. In any case, it is likely the Crooked Creek population has been isolated for a shorter time period than Sedge Creek, Forest Creek, and Antelope Creek because the mtDNA haplotypes in Crooked Creek (of which 91% were ‘S1’) have not diverged from the dominant Snake River haplotype ‘S1’. In contrast, Sedge Creek is dominated by the ‘I’ haplotype, which is separated by two steps from the next nearest haplotype. Estimates of effective population size were very low for Sedge Creek, indicating this population has likely been strongly affected by founder effects and/or population bottlenecks (Templeton 2005). According to Newman and Pilson (1997), these types of populations could have reduced fitness relative to populations with higher effective population sizes.

N_e for Yellowstone Lake, Snake River, and Pacific Creek reflects the relative age of these populations. Large, old source populations are generally expected to have higher effective population sizes than subsequently founded populations because of a greater time for the accumulation of mutations. As the glaciers receded 8,000 to 12,000 years ago Pacific Creek, which has the largest N_e, was the first drainage accessible to invasion by YCT. Next to be exposed was the upper Snake River drainage within YNP followed by Yellowstone Lake. The effective population sizes support this sequence of invasion by YCT.

Migration rate estimates provided information about which populations are currently exchanging genes with each other or have exchanged genes in the recent past. Although Nm values were low, Trout Creek and Yellowstone Lake as well as Snake River and Pacific Creek had a relatively high effective number of migrants between them, suggesting recent divergence or low levels of ongoing gene flow between these populations. As expected, the lowest migration rates were found in comparisons with the isolated, headwater populations. This further supports the hypothesis that these populations (Forest Creek, Sedge Creek, and Antelope Creek) have been isolated for a relatively long time period. Additionally, migration rates from headwater streams to locations downstream were very low, indicating barriers impede migration in both directions.

Migration rates generated by LAMARC and ARLEQUIN were generally consistent with each other although ARLEQUIN estimates were typically much higher (Tables 17 and 18). One discrepancy should be noted, however, in which the LAMARC estimate more accurately described the biology of the system. This occurred in the Nm estimates between Snake River and Yellowstone Lake. Using ARLEQUIN, this value was higher than the comparison between Yellowstone Lake and Pacific Creek, suggesting these two populations are more closely related than Yellowstone Lake is to Pacific Creek and that perhaps YCT invaded the Yellowstone drainage through the Snake River headwaters. There is a remote possibility that this occurred and the rivers have since changed course. It is also possible that extensive human-facilitated transferring of fish has occurred. This is very unlikely, however, as no other evidence has been detected to support either of these explanations. Conversely, LAMARC indicated higher migration rates between Pacific Creek and Yellowstone Lake than between Snake River and Yellowstone Lake. These estimations are more consistent with the hypothesized migration route of YCT, which was from Pacific Creek to the Yellowstone River. This may reflect the increased ability of coalescent-based programs such as LAMARC to accurately describe migration rates.

Identifying natural barriers to fish migration is a common objective of fisheries biologists. STRUCTURE analysis provided evidence for barriers to gene flow in the upper Snake River, Forest Creek, Antelope Creek, and Sedge Creek. The division of samples within Forest Creek and within Snake River into different clusters is due to the fact that samples were collected from multiple locations along these two streams. The collecting site farthest downstream on Forest Creek grouped with cluster 1 (Snake River), indicating a barrier to gene flow is present somewhere in the narrow canyon between this site and the remaining upstream sites. Similarly, the sampling site furthest upstream on the Snake River grouped with cluster 2

(Crooked Creek), indicating a barrier to gene flow exists somewhere between this site and those downstream. Interestingly, the Snake River barrier is also located in a narrow canyon, suggesting narrow, steep canyons may be effective barriers to migration in both directions. These results demonstrate the use of analyzing genetic data with STRUCTURE v2.0 under a continuous sampling scheme in order to locate barriers to fish migration.

Barriers to migration were also apparent in Antelope Creek and Sedge Creek. Evidence for a barrier between Antelope Creek and all downstream populations was detected. Also, a "potential barrier" between the Antelope Creek sampling sites was determined to either be ineffective in impeding migration or has not existed long enough to allow for population divergence. The identification of restricted gene flow between Sedge Creek and Yellowstone Lake is consistent with the known effectiveness of the geothermal lake as a barrier.

Conservation implications

The results of this study have specific consequences for the management and conservation of YCT in YNP. Hybridized populations are typically managed according to the level of introgression. Fish and wildlife agencies of the intermountain western states (Utah Division of Wildlife Resources 2000) proposed three categories of populations for conservation priority: (1) core conservation populations, which are >99% native cutthroat trout genes, (2) conservation populations, generally >90% native cutthroat trout genes, and (3) cutthroat trout sport fish populations, which "meet the species phenotypic expression defined by morphological and meristic characters of cutthroat trout." Under these criteria, three of the populations we assessed for hybridization fell under category 3, one population under category 2, and the remaining six populations were assigned to category 1 (Table 4).

The detection of restricted gene flow between spawning populations within Yellowstone Lake suggests populations have the potential to be locally adapted. While it has been claimed populations will not diverge due to genetic drift when Nm ≥ 1 (Slatkin 1987), the relationship between population divergence and strength of selection is still being explored (Hendry et al. 2002; Hendry 2005). Because neutral markers were used in this study, we were only able to detect changes resulting from genetic drift. It is possible genes under selective pressure (which now have two forces acting on them, selection and genetic drift) have diverged to a greater degree. Nevertheless, it appears that spawning populations within Yellowstone Lake are closely related and are either currently exchanging genes at a low level or have done so in the recent past. The potential impact of managing the Yellowstone Lake system as a single population from a genetic standpoint therefore appears to be minimal, although efforts should be made to preserve current levels of gene flow between spawning populations and maintain the natural dynamics of the system, such as selective forces that may be acting on individual spawning populations.

We identified eleven genetically distinct population segments in the area over which the study was conducted (Figure 19). Four of these were isolated populations in small, headwater streams, four were wide-spread populations located in large river basins, and the full range of the final three populations could not be defined. Management of these YCT populations should reflect the partitioning of genetic variation in order to conserve total genetic diversity. This will maximize the probability of preserving local adaptations that may be present in the population. The detection of morphological and life history differences between these populations, especially the isolated headwater populations, would meet our definition of an ESU; this work is yet to be done and provides a number of potential research opportunities.

Support for the conservation of these small, isolated populations in order preserve local adaptation is offered in the documentation of population-specific adaptations in Sedge Creek. Individuals taken from Sedge Creek to another location typically do not move up or downstream from the transplant location (Robert E. Gresswell, personal communication). It is likely this trait of staying stationary has developed due to selection against individuals who tend to move up and downstream frequently—these fish would experience increased mortality because they are more likely to stray into the uninhabitable geothermal lake located downstream. It is possible other isolated populations throughout YNP (i.e. Forest Creek, Crooked Creek, and Antelope Creek) have also become locally adapted. The conservation of these populations will allow for the continued evolution of the species.

In addition to the need for preserving local adaptation, small, isolated populations require special attention because of their increased susceptibility to environmental change. Theory predicts that small, isolated populations with lower genetic diversity and smaller effective population sizes (i.e. Forest Creek and Sedge Creek) are at greater risk than genetically diverse populations with large effective population sizes (i.e. Snake River and Trout Creek) due to decreased fitness (O'Brian et al. 1985; Newman and Pilson 1997). Fisheries managers should be aware of the potential increased risk these populations are under.

Yellowstone Lake was found to be genetically distinct from other YCT populations in YNP. This is not surprising considering that morphological differences between the Yellowstone Lake population and fluvial YCT populations have already been documented, such as a relatively high number of basibranchial teeth and gill rakers in the lake fish (Behnke 2002). Additionally, life history adaptations for an allacustrine life style, such as spawning migrations up inlet streams, are unique to YCT in Yellowstone Lake. Based on these three lines of evidence

YCT in Yellowstone Lake meet our definition for an ESU; these fish do not appear to be genetically or ecologically exchangeable with surrounding fluvial YCT populations.

CONCLUSIONS

Moderate to low levels of hybridization with rainbow trout were detected in YCT populations in the lower Lamar River system and lower Slough Creek. Very low hybridization was detected above the confluence of the Lamar River and Soda Butte Creek. Additionally, three westslope cutthroat trout haplotypes indicate the transfer of a small number of these fish into the Yellowstone River drainage.

Nested clade analysis (NCA) of YCT in Yellowstone Lake detected restricted gene flow between spawning populations. Until now this has never been documented using genetic data. Other methods, such as F-statistics and the Bayesian clustering program STRUCTURE v2.0, failed to detect population genetic subdivision, highlighting the ability of NCA to detect fine-scale levels of genetic structuring. This suggests low to moderate levels of ongoing gene flow between spawning populations but with some degree of reproductive isolation, consistent with the estimated straying rate of 3% for YCT in Yellowstone Lake.

Analysis of YCT populations located throughout YNP revealed eleven genetically distinct population segments over the study area. A general pattern of isolation by drainage basin in the larger rivers and population fragmentation in small, headwater streams was detected. Barriers to gene flow were detected and/or confirmed in several cases. The program STRUCTURE v2.0 was especially useful in this respect. We recommend the conservation of each of these populations in order to preserve the current genetic diversity of YCT in YNP and to ensure the continued evolution of the species.

Of special concern is the YCT population in Yellowstone Lake, which is genetically, morphologically, and behaviorally distinct from fluvial YCT populations and thus meet our criteria for an evolutionarily significant unit. Additionally, this population is in considerable danger due to lake trout predation and infection by whirling disease. In order to preserve this unique population, it should be treated as a separate entity with regards to conservation.

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Table 1.

Location	N	BYU #'s	GPS coordinates	Date(s) collected
Little Thumb Creek	30	90001-90030	533405E 4920448N	06/04/1987
Yellowstone River at LeHardy Rapids	66	90031-42, 90073-86, 188678-717	548901E 4939499N	06/04/1987; 06/16/2005
Clear Creek	70	90043-72, 142175-214	557304E 4924686N	06/05/1987; 06/21/2005
Pelican Creek	30	90087-90116	551035E 4934165N	06/09/1987
Flat Mountain Arm Creek	30	90147-90176	548930E 4913428N	06/11/1987
Grouse Creek	30	90177-90206	552922E 4903420N	06/12/1987
Hatchery Creek	30	90211-90240	544555E 4930727N	06/141987
Day Bed Creek	30	90241-90270	541274E 4923604N	06/15/1987
Little Thumb Campground Creek	30	90271-90300	534371E 4916913N	06/15/1987
Yellowstone River near Fishing Bridge	30	90301-90330	549054E 4934988N	08/16/1987
Thorofare Creek	27	135899-135925	573477E 4887235N	2002
Yellowstone River inlet	30	188778-188807	567817E 4904456N	2003
Atlantic Creek	16	135883-135898	568733E 4878803N	2002
Heart River	34	141886-910, 976-77, 87, 142008-13	542690E 4896673N	08/2004
Heart Lake	22	91012-91033	540756E 4900936N	08/01/1989
Sickle Creek	37	141911-46, 142014	549162E 4893279N	08/20-21/2005
Crooked Creek	38	141947-65, 142027-45	552979E 4889613N	10/03/ 2004
Snake River (upper)	41	141978-86, 141988-142007, 142015-26	543192E 4895609N	08/24/ 2004
Forest Creek	34	141841-74	532230E 4890897N	08/2005
Pacific Creek	18	136751-68	558942E 4874114N	09/17/2001
Sedge Creek	30	90361-90390	560090E 4934729N	09/03/1987
Pelican Creek (upper)	40	142100-142139	562541E 4937865N	09/08/2005
Trout Creek	50	141966-75, 142046-55, 142145-74	541504E 4942970N	09/28/2005
Antelope Creek (lower)	32	188619-50	548743E 4970563N	08/17/2000
Antelope Creek (upper)	27	188651-77	548736E 4970451N	07/052001
McBride Lake	30	90117-146	558781E 4979066N	06/10/1987

Slough Creek (sec. 1)	60	188718-77	556867E 4977881N	2002
Slough Creek at confluence with Elk Tongue Creek	46	188570-615	563213E 4982819N	10/01/ 2002
Lamar River	37	188860-96	553350E 4973748N	07-08/2002
Lamar River at Geyser Basin	30	188943-72	565919E 4965187N	07/19-29/2003
Pebble Creek	42	188808-49	569992E 4974125N	07/19-26/2001
Cache Creek	50	188983-189012, 142056-75	569130E 4964018N	08/7-12/2003

Table 2.

Gene	Primer name	Sequence (5’ to 3’)
ND1	F1	ACCAAGATTGCCTGAAAGAACGGC
ND1	R1	ACGGTTTGTTTCAGCGAGGGTAGA
ND1	F2	GGCAGTGGCACAAACCATTTCCTA
ND1	R2	AGTGGTGTAGTGGAAGCACCAAGA
ND2	F3	TGCCTGAATGCTTAAGGACCACCT
ND2	R3	ACTATAAGTGCGAAGGGTGCGAGT
ND2	F4	TTGGACTAGCACCCGTTCACTTC
ND2	R4	TGGGTTGCATTCAGAAGATGTGGG
ITS-2	5.8S	CTACGCCTGTCTGAGTGTC
ITS-2	28S	ATATGCTTAAATTCAGCGGG

Table 3.

Primer name	**Ta (°C)**	**Sequence (5' to 3')**	**Reference**
Ots107-F	54	ACAGACCAGACCTCAACA	Nelson and Beacham 1999
Ots107-R		ATAGAGACCTGAATCGGTA	
Omm1036-F	60	TGTAGCAGGTGAGAATACCCA	Genbank
Omm1036-R		CACCATCTCCATCCTAGGC	
Fgt3-F	54	CAAGAAATTTGTGGAGCGG	Sakamoto et al. 1994
Fgt3-R		GAAGCCCTGTTTGACTTTTAGC	
Ocl8-F	60	TAGTGTTCCGTGTTCGCCTG	Condrey and Bentzen 1998
Ocl8-R-pigtail		GTTTCTCACCTTCCATCTCTCATTCCAC	
Ssa85-F	50	AGGTGGGTCCTCCAAGCTAC	Wenburg and Bentzen 2001
Ssa85-R-pigtail		GTTTCTACCCGCTCCTCACTTAATC	
Omm1241-F	60	GAAGAGAGGAGGCTCACCTATCG	Rexroad III and Palti 2003
Omm1241-R-pigtail		GTTTCTCCTCTTCTTATTCTTGTGGAACCC	

Table 4.

Population	Gene	N	RT	WCT	YCT	% YCT
Slough Creek sec.1	mtDNA	23	188768, 776	188777	188718, 20, 22, 33, 36, 41, 46-49, 52, 53, 57, 58, 60, 61, 66, 67, 69, 74	87%
	ITS-2	21	188718(het), 76, 77	-	188718(het), 22, 33, 36, 41, 46-49, 52, 53, 57, 58, 60, 61, 66, 67, 69, 74	88.1%
	Ocl8	17	188718(het), 76(het), 77	-	188718(het), 22, 33, 36, 41, 46-47, 49, 53, 57, 58, 60, 61, 67, 74, 76(het)	88.2%
	Ssa85	23	188718(het), 76, 77	-	188718(het), 20, 22, 33, 36, 41, 46-49, 52, 53, 57, 58, 60, 61, 66-69, 74	89.1%
Slough Creek sec.2	mtDNA	19	-	-	188543, 44, 46-48, 50-55, 58-61, 64-67	100%
	ITS-2	0	-	-	-	-
	Ocl8	0	-	-	-	-
	Ssa85	11	-	-	188544, 46, 50-52, 54, 55, 59, 65, 66, 68	100%
Lamar River	mtDNA	35	188866-69, 74-77, 80, 81, 86	188871	188862-65, 70, 72, 73, 78, 79, 82-85, 87-96	65.7%
	ITS-2	34	188860, 61, 66-68(het), 71, 75-78(het), 79-81(het), 86(het)	-	188862-65, 68(het), 70, 72-74, 78(het), 81(het), 82-84, 86(het), 87, 89-96	64.7%
	Ocl8	34	188860, 61, 67, 69(het), 70, 71, 75-78(het), 79, 80, 86(het)	-	188862-66, 69(het), 72-74, 78(het), 82-86(het), 87, 88, 90-96	66.2%
	Ssa85	35	188860, 61, 66, 67, 68(het), 69(het), 70(het), 71, 75-78(het), 79-81(het), 86(het)	-	188862-65, 68(het), 69(het), 70(het), 72, 73, 78(het), 81(het), 82-86(het), 87, 88, 90-96	62.9%
Lamar River Canyon	mtDNA	10	188897, 188906	-	188898-905	80%
	ITS-2	10	188906	-	188897-905	90%
	Ocl8	10	188906(het)	-	188897-905, 906(het)	95%
	Ssa85	10	188897(het), 188906(het)	-	188897(het), 898-905, 906(het)	90%
Lamar River at Soda Butte Creek	mtDNA	8	-	-	188907-14	100%
	ITS-2	8	-	-	188907-14	100%
	Ocl8	8	188910(het)	-	188907-10(het), 11-14	93.8%
	Ssa85	8	188910(het)	-	188907-10(het), 11-14	93.8%
Lamar River upstream from Soda Butte Creek	mtDNA	10	-	-	188915-24	100%
	ITS-2	10	-	-	188915-24	100%
	Ocl8	8	-	-	188915-17, 19, 21-24	100%
	Ssa85	9	-	-	188915-19, 21-24	100%
Lamar River - 2 reaches	mtDNA	9	-	-	188925-31, 33-34	100%
	ITS-2	10	-	-	188925-34	100%
	Ocl8	8	-	-	188926, 28-34	100%
	Ssa85	9	-	-	188925, 26, 28-34	100%

Lamar River above Soda Butte Creek	mtDNA	7	-	-	188935-38, 40-42	100%
	ITS-2	6	-	-	188935, 36, 38, 40-42	100%
	Ocl8	6	-	-	188936-38, 40-42	100%
	Ssa85	7	-	-	188935-38, 40-42	100%
Lamar River across from Geyser Basin	mtDNA	30	188945	-	188943, 44, 46-72	96.7%
	ITS-2	28	188945(het)	-	188944, 45(het), 46-57, 59-70, 72	98.2%
	Ocl8	27	188945(het)	-	188943-45(het), 46-57, 59, 60, 62-70, 72	98.1%
	Ssa85	28	188945(het)	-	188943-45(het), 46-57, 59-60, 62-72	98.2%
Pebble Creek at bridge to Soda Butte Creek	mtDNA	10	-	-	188973-82	100%
	ITS-2	10	-	-	188973-82	100%
	Ocl8	4	-	-	188977, 78, 80, 81	100%
	Ssa85	6	188978(het)	-	188974, 75, 77, 78(het), 80, 81	91.7%

Table 5.

		Geographic distance		I-T distance			
Clade	**Haplotype/ clade**	**Dc**	**Dn**	**Dc**	**Dn**	**Chain of inference**	**Inference**
Clade 1-4	A2	7.149S	21.36S	18.43L	5.83L	1-2-3-4-No	Restricted gene flow with isolation by distance
	C2	25.58	27.19L				
Clade 1-5	Y1	18.41S	20.28S	12.26L	5.38L	1-2-3-4-No	Restricted gene flow with isolation by distance
	Z1	30.68L	25.66L				
Clade 1-6	A	79.39L	77.23L	62.99L	19.26L	1-2-3-4-No	Restricted gene flow with isolation by distance
	R	12.17S	50.41S				
	Y	5.9	48.94S				
	S2	0S	67.58				
	J	26.32S	55.62S				
	S	13.07S	53.31S				
	G1	0S	49.06S				
Clade 1-11	R1	0S	44.25S	11.6	21.76L	1-19-20-No	Inadequate geographical sampling
	M2	11.6	66.02L				
Clade 1-12	N2	0S	17.23	14.94L	2.17	1-2-3-4-No	Restricted gene flow with isolation by distance
Clade 1-15	B2	6.84S	120.21L	45.36L	1.28	1-2-3-4-5-6-7-8-No	Sampling design inadequate to discriminate between isolation by distance (short-distance movements) vs. long-distance dispersal
	C	9.2S	51.73				
Clade 1-20	J2	2.3S	2.33S	-2.3	.09L	1-2-3-4-No	Restricted gene flow with isolation by distance
	D3	0	2.42L				
Clade 2-1	Clade 1-5	23.15S	24.75S	47.49L	22.61L	1-19-20-No	Restricted gene flow with isolation by distance
	Clade 1-21	70.64L	47.36L				
Clade 2-2	Clade 1-4	25.56S	82.26	47.03L	-5.97S	1-2-3-5-6-7-Yes	Restricted gene flow/dispersal but with some long-distance dispersal
	Clade 1-8	17.68S	63.58				
	Clade 1-10	11.94S	55.09S				
	Clade 1-11	53.19	133.15L				
Clade 2-3	Clade 1-12	17.62S	120.91L	66.66L	-19.3S	1-2-3-5-15-No	Past fragmentation and/or long-distance colonization
	Clade 1-13	0S	89.87S				
	Clade 1-14	16.18S	85.19S				

	Clade 1-15	76.87S	95.7S				
	Clade 1-16	0	147.3L				
	Clade 1-17	11.2	80.55S				
	Clade 1-18	4.43S	85.26S				
	Clade 1-19	0S	112.92L				
	Clade 1-20	2.43S	130.66L				
Total Cladogram	Clade 2-1	26.24S	110.37L	-	-	1-2-3-5-6-7-Yes	Restricted gene flow/dispersal but with some long-distance dispersal
	Clade 2-2	77.26S	93.38S				
	Clade 2-3	104.85	109.87L				

Table 6.

	Little Thumb Creek				Yellowstone River at LeHardy Rapids				Clear Creek				Pelican Creek				Flat Mountain Arm Creek			
Locus	N	AR	NA	GD	N	AR	NA	GD	N	AR	NA	GD	N	AR	NA	GD	N	AR	NA	GD
Ots107	24	6.58	8	0.81	64	5.02	8	0.73	62	5.63	10	0.74	30	5.39	8	0.74	30	6.41	9	0.79
Omm1036	23	10.06	13	0.90	64	9.30	15	0.87	64	10.19	18	0.89	27	6.66	9	0.78	30	8.44	13	0.84
Fgt3	17	10.26	12	0.91	64	9.78	19	0.87	63	10.56	20	0.89	17	8.31	10	0.83	30	9.67	15	0.87
Ocl8	20	12.18	18	0.90	62	9.00	19	0.81	66	8.95	18	0.83	28	11.37	18	0.91	30	11.82	18	0.92
Ssa85	23	3.93	5	0.41	66	3.49	5	0.31	67	3.31	6	0.26	30	2.47	5	0.13	29	3.39	5	0.26
Omm1241	18	13.41	17	0.95	56	13.48	26	0.95	61	12.57	24	0.94	12	9.74	10	0.93	29	12.07	17	0.93

	Grouse Creek				Hatchery Creek				Day Bed Creek				Little Thumb Campground Creek				Yellowstone River near fishing bridge			
	N	AR	NA	GD	N	AR	NA	GD	N	AR	NA	GD	N	AR	NA	GD	N	AR	NA	GD
Ots107	26	6.58	9	0.81	23	6.87	9	0.76	24	5.69	7	0.77	29	6.32	9	0.79	26	4.71	5	0.75
Omm1036	23	9.02	13	0.85	23	7.89	10	0.84	25	11.94	17	0.93	29	9.82	15	0.88	28	7.44	11	0.80
Fgt3	24	9.08	13	0.87	22	8.69	10	0.82	24	10.43	15	0.87	29	9.60	15	0.88	25	8.30	12	0.83
Ocl8	25	9.03	13	0.82	23	9.64	15	0.83	30	9.43	13	0.84	29	10.89	16	0.88	26	11.75	15	0.93
Ssa85	29	2.76	5	0.17	24	3.55	5	0.30	30	4.17	6	0.46	29	3.32	4	0.43	26	2.90	3	0.46
Omm1241	24	11.96	15	0.94	24	12.40	18	0.94	20	11.82	15	0.93	27	11.72	19	0.91	22	13.19	20	0.94

	Thorofare Creek				Yellowstone River above Yell. Lake				Heart River				Heart Lake				Sickle Creek			
	N	AR	NA	GD	N	AR	NA	GD	N	AR	NA	GD	N	AR	NA	GD	N	AR	NA	GD
Ots107	27	5.37	7	0.72	28	5.09	7	0.73	34	7.96	9	0.86	21	10.35	13	0.91	37	7.06	10	0.81
Omm1036	27	10.13	13	0.90	30	11.08	17	0.92	32	10.24	15	0.91	21	11.02	14	0.92	37	10.64	17	0.89
Fgt3	27	10.08	15	0.90	30	8.43	14	0.83	33	9.24	13	0.88	20	10.70	14	0.90	35	11.71	18	0.92
Ocl8	18	8.69	11	0.80	28	12.04	18	0.92	29	11.15	15	0.93	21	7.30	9	0.85	36	10.72	16	0.89
Ssa85	27	2.70	4	0.21	28	2.42	4	0.14	34	2.99	3	0.59	21	3.51	4	0.61	37	3.47	4	0.53
Omm1241	22	13.24	19	0.94	28	13.20	19	0.94	30	10.77	16	0.89	14	10.73	12	0.89	37	11.00	15	0.92

	Crooked Creek				Snake River (upper)				Forest Creek				Pacific Creek				Atlantic Creek			
Locus	N	AR	NA	GD	N	AR	NA	GD	N	AR	NA	GD	N	AR	NA	GD	N	AR	NA	GD
Ots107	38	7.70	10	0.83	41	8.40	12	0.87	34	4.86	6	0.78	16	5.35	6	0.76	16	5.35	6	0.68
Omm1036	38	8.24	11	0.84	41	10.86	14	0.92	34	9.38	14	0.89	17	11.44	14	0.92	16	11.47	13	0.92
Fgt3	36	9.38	15	0.87	41	13.10	22	0.94	33	5.57	10	0.57	14	9.27	10	0.90	16	10.41	12	0.91
Ocl8	36	7.62	11	0.79	40	12.48	21	0.93	33	9.39	15	0.84	15	12.78	15	0.93	15	10.45	12	0.90
Ssa85	38	2.99	3	0.58	41	3.67	4	0.55	32	3.49	5	0.57	16	3.91	4	0.63	14	1.00	1	0.00
Omm1241	37	10.32	16	0.90	40	13.24	22	0.94	33	8.99	16	0.81	16	10.66	12	0.92	11	11.00	11	0.93

	Sedge Creek				Pelican Creek (upper)				Trout Creek				Antelope Creek (lower)				Antelope Creek (upper)			
	N	AR	NA	GD	N	AR	NA	GD	N	AR	NA	GD	N	AR	NA	GD	N	AR	NA	GD
Ots107	29	1.00	1	0.00	29	4.30	5	0.70	50	3.59	6	0.60	29	3.38	4	0.67	27	3.88	4	0.67
Omm1036	29	1.62	2	0.07	29	7.14	10	0.80	46	6.07	11	0.78	29	2.90	3	0.38	27	1.00	1	0.00
Fgt3	29	1.00	1	0.00	29	7.36	12	0.77	50	6.92	13	0.80	28	6.03	7	0.81	27	5.18	6	0.76
Ocl8	28	1.00	1	0.00	25	10.52	12	0.93	50	8.45	16	0.84	17	6.63	8	0.61	25	4.30	6	0.57
Ssa85	28	1.00	1	0.00	31	4.12	5	0.39	50	3.06	4	0.55	29	1.62	2	0.07	25	1.44	2	0.04
Omm1241	28	1.64	2	0.07	28	11.07	14	0.92	43	11.83	19	0.93	23	4.66	5	0.58	18	3.97	4	0.61

	McBride Lake				Slough Creek near confluence w/ ET Cr.				Pebble Creek				Cache Creek				Total			
	N	AR	NA	GD	N	AR	NA	GD	N	AR	NA	GD	N	AR	NA	GD	N	AR	NA	GD
Ots107	29	4.87	5	0.77	22	5.30	6	0.68	42	7.33	11	0.84	49	7.49	11	0.82	936	6.98	20	-
Omm1036	30	7.63	10	0.82	24	7.03	9	0.84	41	5.78	7	0.78	50	5.31	8	0.66	934	11.02	23	-
Fgt3	30	3.96	5	0.59	24	5.06	7	0.60	42	5.30	8	0.75	49	6.39	12	0.75	908	11.48	37	-
Ocl8	30	6.35	8	0.78	21	6.25	8	0.79	41	6.39	8	0.81	47	7.45	12	0.84	894	12.44	33	-
Ssa85	30	2.93	3	0.39	28	2.71	4	0.23	42	1.00	1	0.00	50	1.00	1	0.00	954	3.74	7	-
Omm1241	28	6.58	10	0.70	17	9.89	13	0.79	37	5.09	9	0.59	45	8.71	13	0.87	828	13.68	38	-

Table 7.

	Little Thumb Creek		Yellowstone River at LeHardy Rapids		Clear Creek		Pelican Creek		Flat Mountain Arm Creek	
Locus	H_o	H_e	H_o	H_e	H_o	H_e	H_o	H_e	H_o	H_e
Ots107	0.958	0.816	0.750	0.740	0.726	0.742	0.633	0.760	0.800	0.802
Omm1036	0.913	0.897	0.750	0.873	0.844	0.893	0.704	0.778	0.900	0.841
Fgt3	0.882	0.914	0.859	0.877	0.825	0.890	0.882	0.829	0.767	0.866
Ocl8	0.750**	0.894	0.774**	0.816	0.682*	0.830	0.821	0.915	0.933	0.923
Ssa85	0.478	0.409	0.273	0.312	0.269	0.273	0.133	0.161	0.276	0.286
Omm1241	0.944	0.948	0.929	0.946	0.918	0.938	0.500*	0.931	0.897	0.933

	Grouse Creek		Hatchery Creek		Day Bed Creek		Little Thumb Campground Creek		Yellowstone River near fishing bridge	
Locus	H_o	H_e	H_o	H_e	H_o	H_e	H_o	H_e	H_o	H_e
Ots107	0.846	0.817	0.652	0.757	0.792	0.768	0.862	0.796	0.692	0.744
Omm1036	0.957	0.855	0.739	0.854	0.840	0.931	0.931	0.880	0.821	0.801
Fgt3	0.958	0.868	0.818	0.823	0.958	0.876	0.931	0.881	0.760	0.837
Ocl8	0.760	0.820	0.870	0.828	0.800	0.842	0.862	0.887	0.769**	0.931
Ssa85	0.172	0.197	0.292	0.337	0.400	0.463	0.414	0.428	0.269**	0.481
Omm1241	0.917	0.935	0.917	0.938	0.65**	0.928	0.815*	0.906	0.909	0.937

	Thorofare Creek		Yellowstone River above Yell. Lake		Heart River		Heart Lake		Sickle Creek	
Locus	H_o	H_e	H_o	H_e	H_o	H_e	H_o	H_e	H_o	H_e
Ots107	0.778	0.737	0.679	0.731	0.882	0.868	0.952	0.908	0.919	0.816
Omm1036	0.889	0.906	0.933	0.915	0.938	0.909	0.857	0.925	0.919	0.895
Fgt3	0.889	0.901	0.967	0.836	0.818	0.885	0.950	0.905	0.886	0.815
Ocl8	0.833	0.800	0.857	0.922	0.621**	0.931	0.476**	0.853	0.861	0.889
Ssa85	0.222	0.240	0.143	0.171	0.500	0.588	0.429*	0.630	0.568	0.530
Omm1241	1.000	0.943	0.929	0.946	0.8*	0.899	0.857	0.862	0.919	0.919

	Crooked Creek		Snake River (upper)		Forest Creek		Pacific Creek		Atlantic Creek	
Locus	H_o	H_e	H_o	H_e	H_o	H_e	H_o	H_e	H_o	H_e
Ots107	0.740	0.827	0.778	0.864	0.889	0.758	0.813	0.774	0.813	0.679
Omm1036	0.760	0.856	0.917	0.929	0.815**	0.881	0.941	0.929	1.000	0.925
Fgt3	0.646**	0.884	0.917	0.928	0.500	0.475	1.000	0.899	0.813	0.917
Ocl8	0.667	0.815	0.794*	0.940	0.63**	0.787	0.933	0.926	0.733	0.906
Ssa85	0.48*	0.558	0.583	0.576	0.400	0.509	0.688	0.661	NA	NA
Omm1241	0.878**	0.910	0.943	0.945	0.731	0.767	0.938	0.921	0.818	0.931

	Sedge Creek		Pelican Creek (upper)		Trout Creek		Antelope Creek (lower)		Antelope Creek (upper)	
Locus	H_o	H_e	H_o	H_e	H_o	H_e	H_o	H_e	H_o	H_e
Ots107	NA	NA	0.793	0.718	0.640	0.595	0.655	0.666	0.667	0.672
Omm1036	0.069	0.527	0.793	0.800	0.848	0.779	0.448	0.405	NA	NA
Fgt3	NA	NA	0.724**	0.771	0.780	0.804	0.75*	0.808	0.630	0.774
Ocl8	NA	NA	0.68**	0.926	0.76*	0.846	0.647	0.611	0.520	0.596
Ssa85	NA	NA	0.452	0.418	0.500	0.553	0*	0.102	0.040	0.079
Omm1241	0.071	0.533	0.929*	0.921	0.884	0.930	0.565	0.576	0.667	0.646

	McBride Lake		Slough Creek near confluence w/ ET Cr.		Pebble Creek		Cache Creek	
Locus	H_o	H_e	H_o	H_e	H_o	H_e	H_o	H_e
Ots107	0.897	0.774	0.636	0.716	0.810	0.840	0.755	0.819
Omm1036	0.833	0.816	0.833	0.837	0.707	0.787	0.660	0.657
Fgt3	0.500	0.586	0.625	0.632	0.667*	0.756	0.633	0.757
Ocl8	0.533**	0.775	0.714	0.803	0.78**	0.813	0.809	0.847
Ssa85	0.367	0.416	0.214	0.347	NA	NA	NA	NA
Omm1241	0.623	0.694	0.824	0.793	0.595	0.594	0.778	0.874

Table 8.

	1	2	3	4	5	6	7	8	9	10	11	12
2	0.02	-										
3	-0.00	0.00	-									
4	-0.03	0.03	0.02	-								
5	0.01	0.00	0.01	0.00	-							
6	-0.03	0.02	0.01	-0.04	0.00	-						
7	-0.02	-0.01	-0.01	-0.01	-0.01	-0.02	-					
8	0.00	-0.00	-0.01	0.04	0.02	0.02	-0.01	-				
9	-0.01	-0.01	-0.01	0.01	-0.01	-0.00	-0.02	-0.02	-			
10	-0.01	**0.04**	0.04	-0.03	0.00	-0.02	0.01	**0.07**	0.03	-		
11	-0.01	0.02	0.02	-0.02	-0.00	-0.02	-0.01	0.04	0.01	-0.02	-	
12	0.01	0.06	0.07	-0.03	0.01	-0.00	0.02	0.11	0.06	-0.04	-0.03	-
13	-0.03	0.02	0.01	-0.03	-0.01	-0.03	-0.02	0.02	0.00	-0.02	-0.02	-0.02

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13. Thorofare Creek

Table 9.

	1	2	3	4	5	6	7	8	9	10	11	12
2	57.7	-										
3	inf	345.6	-									
4	inf	30.1	62.2	-								
5	143.3	317.8	92.2	381.9	-							
6	inf	46.7	162.6	inf	689.8	-						
7	inf	inf	inf	inf	inf	inf	-					
8	46.9	inf	inf	26.7	40.7	56.0	inf	-				
9	inf	inf	inf	76.1	inf	inf	inf	inf	-			
10	inf	24.0	23.7	inf	242.3	inf	150.0	14.1	29.7	-		
11	inf	40.3	46.6	inf	inf	inf	inf	23.8	79.0	inf	-	
12	82.8	15.1	14.5	inf	116.2	inf	44.4	8.5	16.5	inf	inf	-
13	inf	52.6	110.7	inf	inf	inf	inf	45.8	inf	inf	inf	inf

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Table 10.

	1	2	3	4	5	6	7	8	9	10	11	12
2	**0.04**	-										
3	0.03	**0.03**	-									
4	0.06	-0.16	-0.09	-								
5	-0.04	-0.00	**0.04**	-0.27	-							
6	0.01	-0.01	-0.00	-0.16	-0.01	-						
7	-0.04	-0.02	0.01	-0.32	-0.01	-0.03	-					
8	0.02	0.01	-0.04	0.03	-0.04	-0.03	-0.07	-				
9	0.05	-0.01	0.02	-0.33	0.04	-0.00	0.01	-0.03	-			
10	0.05	**0.03**	**0.08**	-0.11	-0.03	0.03	-0.02	**0.07**	0.04	-		
11	0.07	0.01	-0.02	-0.05	0.01	-0.02	-0.03	-0.00	-0.03	**0.11**	-	
12	0.01	0.00	0.00	-0.18	0.00	-0.02	-0.02	-0.03	-0.00	**0.04**	-0.02	-
13	-0.01	**0.02**	-0.00	-0.16	**0.04**	-0.02	0.01	-0.07	0.03	**0.07**	-0.04	-0.02

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Table 11.

	1	2	3	4	5	6	7	8	9	10	11	12
2	6.0	-										
3	9.2	8.1	-									
4	3.9	inf	inf	-								
5	inf	inf	6.0	inf	-							
6	22.0	inf	inf	inf	inf	-						
7	inf	inf	25.6	inf	inf	inf	-					
8	12.5	54.6	inf	8.0	inf	inf	inf	-				
9	4.6	inf	10.6	inf	6.2	inf	21.8	inf	-			
10	5.1	8.2	3.0	inf	inf	7.9	inf	3.5	6.4	-		
11	3.6	20.2	inf	inf	19.8	inf	inf	inf	inf	2.1	-	
12	33.4	187.8	593.3	inf	inf	inf	inf	inf	inf	5.4	inf	-
13	inf	11.0	inf	inf	6.6	inf	24.0	inf	7.6	3.3	inf	inf

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10. Yellowstone River near Fishing Bridge
11. Yellowstone River inlet
12. Atlantic Creek
13. Thorofare Creek

Table 12.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
2	0.47	-																	
3	0.05	0.76	-																
4	0.06	0.67	**0.00**	-															
5	0.14	0.72	0.14	0.11	-														
6	0.29	0.79	0.42	0.37	**0.12**	-													
7	0.19	0.64	0.27	0.24	0.24	0.37	-												
8	0.23	0.64	0.35	0.32	0.30	0.39	**0.05**	-											
9	0.16	0.65	0.25	0.22	0.21	0.34	**0.03**	**0.03**	-										
10	0.13	0.63	0.15	0.12	0.15	0.34	0.11	0.18	**0.07**	-									
11	0.21	0.90	0.14	0.11	0.30	0.61	0.47	0.57	0.49	0.29	-								
12	0.20	0.90	**0.11**	0.09	0.25	0.57	0.41	0.51	0.42	0.25	**0.00**	-							
13	0.18	0.89	**0.09**	**0.07**	0.22	0.54	0.35	0.46	0.36	0.19	**0.01**	**0.00**	-						
14	0.24	0.77	0.43	0.40	0.42	0.52	0.34	0.33	0.31	0.36	0.68	0.63	0.60	-					
15	0.09	0.64	0.25	0.24	0.28	0.40	0.24	0.24	0.21	0.24	0.51	0.46	0.43	**0.05**	-				
16	0.27	0.66	0.40	0.37	0.37	0.46	0.31	0.30	0.27	0.32	0.59	0.55	0.52	**0.01**	0.12	-			
17	0.32	0.75	0.46	0.41	0.42	0.52	0.37	0.37	0.34	0.37	0.65	0.61	0.58	0.47	0.38	0.41	-		
18	0.10	0.61	0.19	0.18	0.21	0.36	0.21	0.22	0.17	0.18	0.42	0.37	0.34	**0.05**	**0.02**	**0.07**	0.35	-	
19	0.41	0.89	0.65	0.58	0.61	0.69	0.54	0.53	0.53	0.54	0.81	0.79	0.78	**0.13**	0.33	**0.08**	0.64	0.25	-
20	0.16	0.74	0.36	0.34	0.35	0.46	0.27	0.24	0.23	0.30	0.65	0.60	0.56	0.22	**0.09**	0.26	0.42	0.15	0.53

1. Yellowstone Lake
2. Sedge Creek
3. Pelican Creek (upper)
4. Trout Creek
5. Antelope Creek (lower)
6. Antelope Creek (upper)
7. McBride Lake
8. Slough Creek at confluence with Elk Tongue Cr.
9. Slough Creek (section 1)
10. Pebble Creek
11. Cache Creek
12. Lamar River at Geyser Basin
13. Lamar River
14. Heart Lake
15. Heart River
16. Snake River
17. Forest Creek
18. Sickle Creek
19. Crooked Creek
20. Pacific Creek

Table 13.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
2	1.11	-																	
3	17.40	0.32	-																
4	14.98	0.50	294.51	-															
5	5.99	0.40	5.97	7.84	-														
6	2.44	0.26	1.41	1.74	7.26	-													
7	4.42	0.56	2.72	3.20	3.16	1.68	-												
8	3.32	0.57	1.83	2.11	2.32	1.54	20.72	-											
9	5.13	0.54	2.95	3.59	3.83	1.91	34.38	35.06	-										
10	6.68	0.58	5.83	7.47	5.67	1.95	8.05	4.48	12.82	-									
11	3.67	0.11	6.08	7.85	2.35	0.63	1.13	0.75	1.06	2.43	-								
12	4.05	0.11	8.32	10.82	3.04	0.76	1.39	0.94	1.37	2.96	358.49	-							
13	4.42	0.12	10.59	14.00	3.64	0.86	1.86	1.16	1.79	4.24	125.37	inf	-						
14	3.14	0.29	1.34	1.53	1.41	0.94	1.89	2.05	2.22	1.79	0.47	0.58	0.66	-					
15	10.22	0.56	3.08	3.14	2.53	1.51	3.13	3.14	3.79	3.13	0.94	1.16	1.33	17.78	-				
16	2.77	0.51	1.50	1.71	1.73	1.19	2.19	2.36	2.68	2.13	0.68	0.83	0.93	50.71	7.19	-			
17	2.16	0.33	1.17	1.42	1.40	0.92	1.68	1.70	1.96	1.74	0.54	0.65	0.74	1.13	1.64	1.42	-		
18	9.33	0.63	4.26	4.63	3.69	1.82	3.79	3.39	4.81	4.52	1.38	1.73	1.99	18.76	53.19	13.99	1.90	-	
19	1.45	0.13	0.54	0.72	0.63	0.45	0.84	0.89	0.88	0.84	0.23	0.26	0.29	6.78	2.04	11.64	0.57	2.95	-
20	5.35	0.35	1.82	1.99	1.83	1.20	2.68	3.13	3.39	2.37	0.53	0.68	0.80	3.56	9.76	2.88	1.37	5.58	0.90

1. Yellowstone Lake
2. Sedge Creek
3. Pelican Creek (upper)
4. Trout Creek
5. Antelope Creek (lower)
6. Antelope Creek (upper)
7. McBride Lake
8. Slough Creek at confluence with Elk Tongue Cr.
9. Slough Creek (section 1)
10. Pebble Creek
11. Cache Creek
12. Lamar River at Geyser Basin
13. Lamar River
14. Heart Lake
15. Heart River
16. Snake River
17. Forest Creek
18. Sickle Creek
19. Crooked Creek
20. Pacific Creek

Table 14.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
2	0.36	-														
3	**0.04**	0.54	-													
4	0.12	0.77	0.11	-												
5	0.22	0.61	0.22	0.30	-											
6	0.08	0.41	**0.01**	0.16	0.21	-										
7	0.09	0.42	**0.01**	0.13	0.20	**0.00**	-									
8	0.12	0.55	0.06	0.15	0.39	0.14	0.16	-								
9	**0.02**	0.51	0.14	0.22	0.31	0.15	0.16	0.15	-							
10	0.06	0.44	**0.03**	**0.06**	0.17	**0.00**	**0.00**	0.12	0.14	-						
11	0.21	0.56	0.19	0.30	0.18	0.21	0.18	0.33	0.30	0.19	-					
12	**0.03**	0.55	0.13	0.24	0.26	0.13	0.12	0.17	**0.00**	0.11	0.23	-				
13	0.19	0.57	**0.09**	**0.06**	0.16	0.20	0.21	0.28	0.26	0.15	0.18	0.24	-			
14	0.13	0.73	0.18	0.20	0.09	0.20	0.19	0.29	0.26	0.11	0.12	0.24	**0.12**	-		
15	0.17	0.42	0.22	0.45	0.21	0.13	0.12	0.33	0.23	0.15	0.21	0.18	0.32	0.37	-	
16	0.27	0.44	0.16	0.31	0.16	0.18	0.19	0.37	0.36	0.20	0.06	0.30	0.19	0.08	0.16	-
17	0.13	0.33	0.23	0.44	0.25	0.12	0.14	0.29	0.17	0.16	0.28	0.11	0.33	0.39	**0.01**	0.24

1. Yellowstone Lake
2. Sedge Creek
3. Heart Lake
4. Pacific Creek
5. Forest Creek
6. Heart River
7. Sickle Creek
8. Crooked Creek
9. Trout Creek
10. Snake River
11. Cache Creek
12. Pelican Creek (upper)
13. McBride Lake
14. Slough Creek at confluence with Elk Tongue Cr.
15. Antelope Creek (lower)
16. Pebble Creek
17. Antelope Creek (upper)

Table 15.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
2	0.4	-														
3	6.6	0.2	-													
4	1.9	0.1	2.1	-												
5	0.9	0.2	0.9	0.6	-											
6	2.8	0.4	inf	1.4	1.0	-										
7	2.5	0.4	19.3	1.6	1.0	inf	-									
8	1.9	0.2	4.3	1.4	0.4	1.6	1.4	-								
9	13.0	0.2	1.6	0.9	0.6	1.4	1.3	1.4	-							
10	3.7	0.3	inf	4.2	1.2	inf	62.7	1.8	1.6	-						
11	0.9	0.2	1.1	0.6	1.2	1.0	1.2	0.5	0.6	1.1	-					
12	7.2	0.2	1.7	0.8	0.7	1.7	1.8	1.2	103.8	2.0	0.8	-				
13	1.1	0.2	2.5	4.0	1.3	1.0	1.0	0.6	0.7	1.5	1.2	0.8	-			
14	1.6	0.1	1.1	1.0	2.6	1.0	1.1	0.6	0.7	2.0	1.9	0.8	inf	-		
15	1.3	0.4	0.9	0.3	1.0	1.8	1.8	0.5	0.8	1.4	1.0	1.2	0.5	0.4	-	
16	0.7	0.3	1.3	0.6	1.3	1.1	1.1	0.4	0.4	1.0	3.9	0.6	1.1	2.9	1.3	-
17	1.6	0.5	0.9	0.3	0.8	1.9	1.5	0.6	1.2	1.3	0.6	2.0	0.5	0.4	inf	0.8

1. Yellowstone Lake
2. Sedge Creek
3. Heart Lake
4. Pacific Creek
5. Forest Creek
6. Heart River
7. Sickle Creek
8. Crooked Creek
9. Trout Creek
10. Snake River
11. Cache Creek
12. Pelican Creek (upper)
13. McBride Lake
14. Slough Creek at confluence with Elk Tongue Cr.
15. Antelope Creek (lower)
16. Pebble Creek
17. Antelope Creek (upper)

Table 16.

		mtDNA			Microsatellites		
	Population	θ	N_f = [θ/(2μ)]	Std. dev. (N_f)	θ	N_e = [θ/(4μ)]	Std. dev. (N_e)
Pop Set #1	Crooked Cr.	0.000136	81.8	40.2	6.35	1586.90	171.20
	Forest Cr.	0.000199	119.2	26.3	1.61	403.02	62.86
	Pacific Cr.	0.000558	335.0	54.1	12.72	3179.21	625.59
	Sedge Cr.	0.00000547	3.3	6.1	0.024	5.94	4.40
	Snake R.	0.000918	551.0	79.2	11.73	2932.02	903.72
	Yellowstone Lake	0.000109	653.1	90.2	8.83	2206.36	436.15
Pop Set #2	Antelope Cr.	0.000166	99.5	34.4	1.01	252.14	25.10
	Cache Cr.	0.00045	270.2	75.0	1.85	461.54	131.24
	Pebble Cr.	0.000417	250.1	27.1	1.90	474.78	120.55
	Slough Cr.	0.000559	335.4	68.1	2.80	700.53	139.11
	Trout Cr.	0.000826	495.5	75.7	5.28	1319.18	81.27
	Yellowstone Lake	0.000134	801.5	99.0	11.27	2818.10	471.22

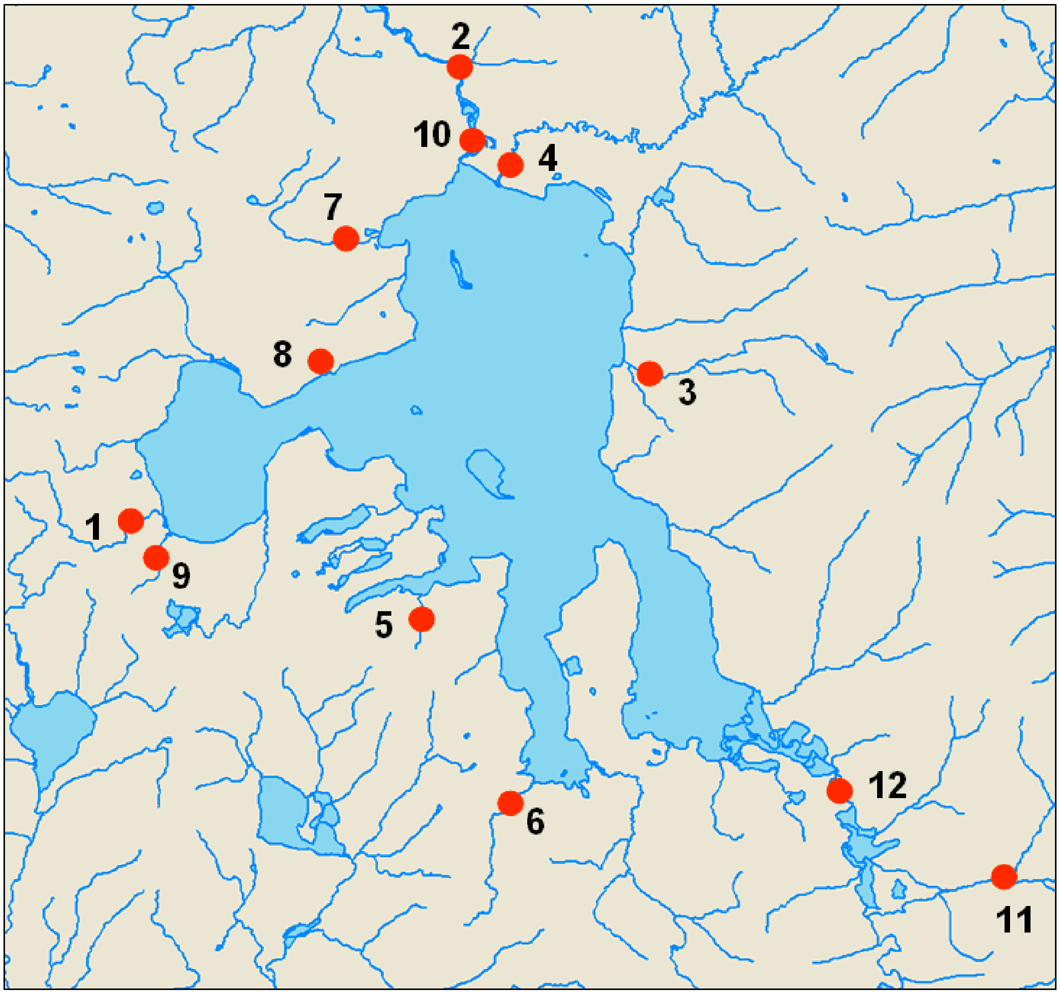
Table 17.

Population comparison	M	Std. dev.	Nm (LAMARC)	Nm (ARLEQUIN)
Snake River to Crooked Creek	0.27	0.076	0.41	1.57
Crooked Creek to Snake River	0.20	0.036	0.59	
Snake River to Forest Creek	0.15	0.037	0.06	1.08
Forest Creek to Snake River	0.04	0.009	0.12	
Snake River to Pacific Creek	0.93	0.324	2.81	2.08
Pacific Creek to Snake River	0.56	0.211	1.64	
Snake River to Yellowstone Lake	0.19	0.062	0.42	3.12
Yellowstone Lake to Snake River	0.16	0.048	0.46	
Sedge Creek to Yellowstone Lake	0.06	0.021	0.13	0.42
Yellowstone Lake to Sedge Creek	3.40	1.866	0.02	
Yellowstone Lake to Pacific Creek	0.25	0.121	0.77	0.94
Pacific Creek to Yellowstone Lake	0.15	0.074	0.34	

Table 18.

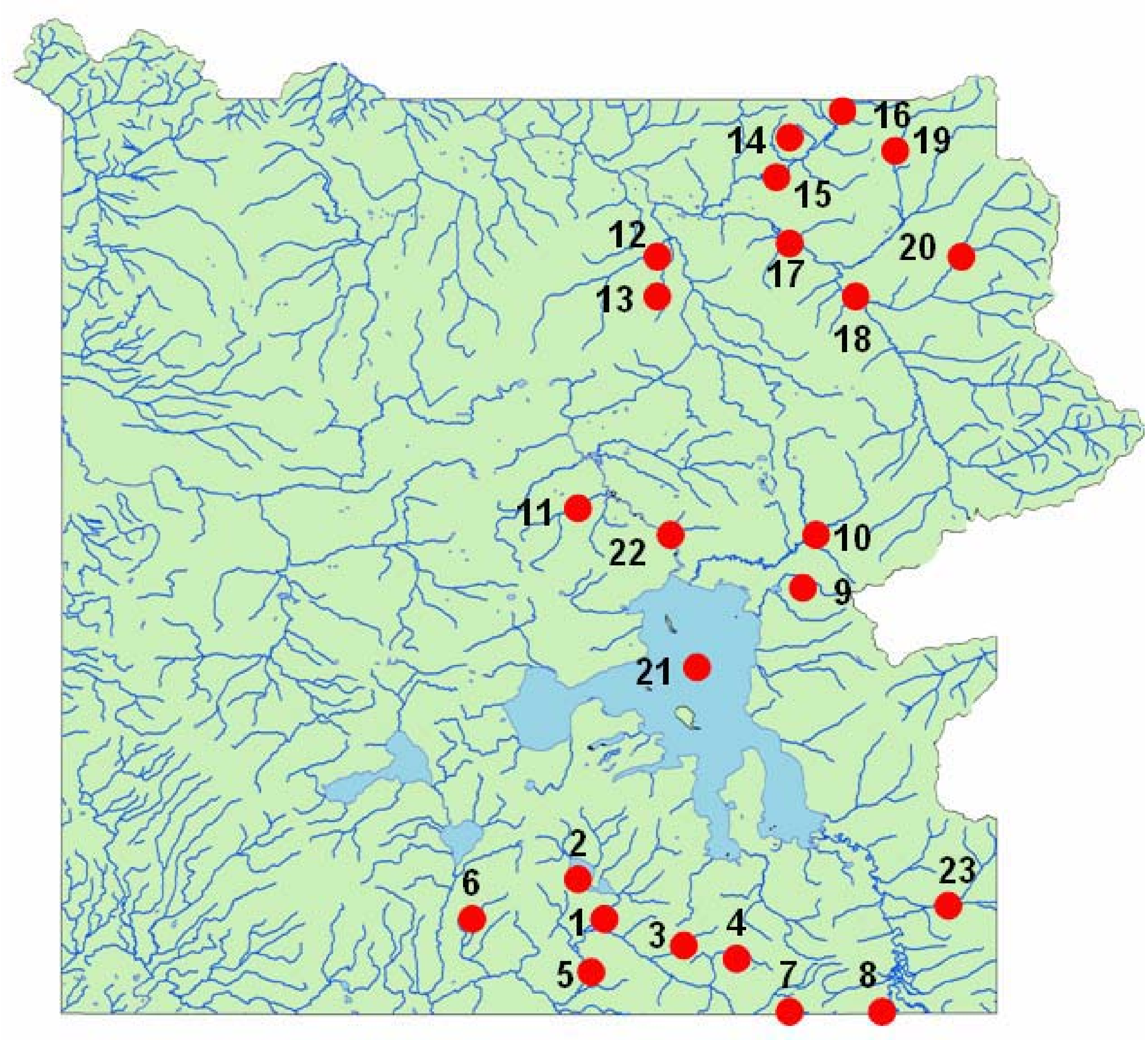
Population comparison	M	Std. dev.	Nm (LAMARC)	Nm (ARLEQUIN)
Antelope Creek to Slough Creek	0.09	0.035	0.06	0.44
Slough Creek to Antelope Creek	0.18	0.039	0.05	
Antelope Creek to Trout Creek	0.10	0.033	0.13	0.87
Trout Creek to Antelope Creek	0.33	0.074	0.09	
Antelope Creek to Yellowstone Lake	0.17	0.045	0.48	1.35
Yellowstone Lake to Antelope Creek	0.77	0.230	0.20	
Cache Creek to Pebble Creek	1.60	0.527	0.74	3.94
Pebble Creek to Cache Creek	1.05	0.159	0.61	
Cache Creek to Slough Creek	0.28	0.044	0.20	1.21
Slough Creek to Cache Creek	0.34	0.157	0.20	
Cache Creek to Yellowstone Lake	0.07	0.019	0.19	0.95
Yellowstone Lake to Cache Creek	0.20	0.199	0.12	
Pebble Creek to Slough Creek	0.37	0.176	0.26	1.17
Slough Creek to Pebble Creek	0.50	0.167	0.23	
Pebble Creek to Yellowstone Lake	0.07	0.018	0.20	0.67
Yellowstone Lake to Pebble Creek	0.25	0.069	0.12	
Slough Creek to Trout Creek	0.11	0.036	0.15	0.64
Trout Creek to Slough Creek	0.24	0.099	0.17	
Slough Creek to Yellowstone Lake	0.15	0.024	0.43	1.13
Yellowstone Lake to Slough Creek	0.28	0.123	0.20	
Trout Creek to Yellowstone Lake	0.70	0.104	1.99	12.95
Yellowstone Lake to Trout Creek	0.67	0.251	0.89	

Figure 1.



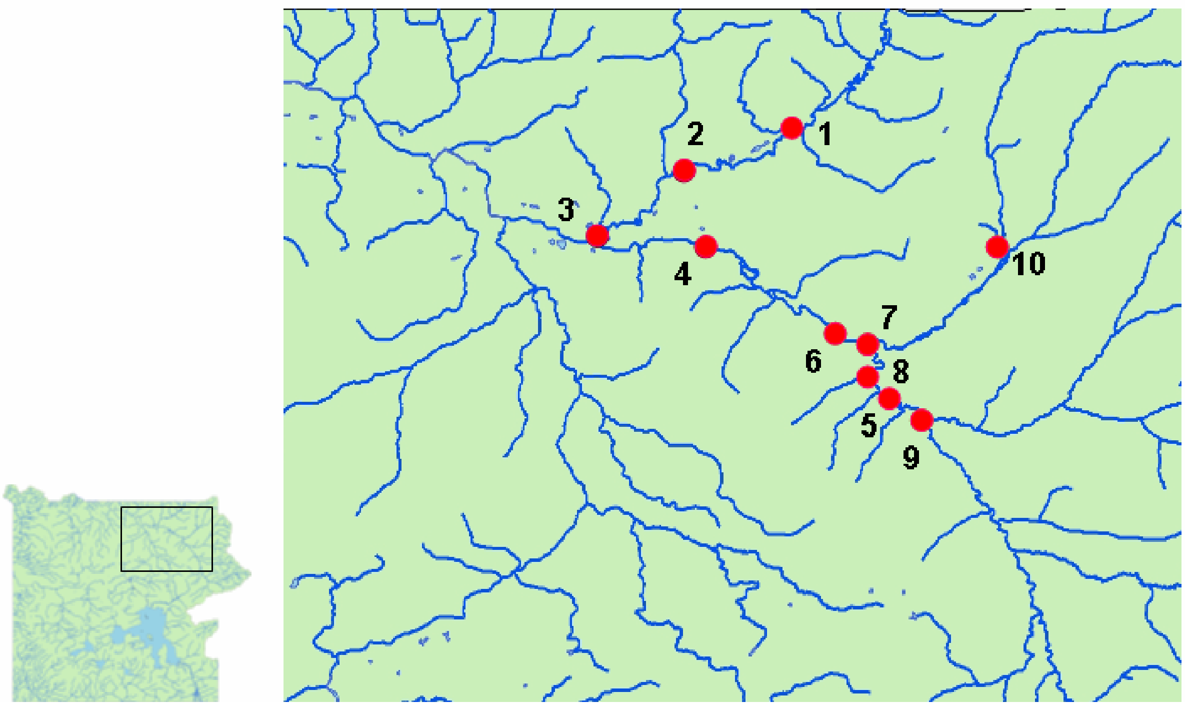
1. Little Thumb Creek
2. Yellowstone River at LeHardy Rapids
3. Clear Creek
4. Pelican Creek
5. Flat Mountain Arm Creek
6. Grouse Creek
7. Hatchery Creek
8. Day Bed Creek
9. Little Thumb Campground Creek
10. Yellowstone River near Fishing Bridge
11. Thorofare Creek
12. Yellowstone River inlet

Figure 2.



1. Heart River
2. Heart Lake
3. Sickle Creek
4. Crooked Creek
5. Snake River
6. Forest Creek
7. Pacific Creek
8. Atlantic Creek
9. Sedge Creek
10. Pelican Creek (upper)
11. Trout Creek
12. Antelope Creek (lower)
13. Antelope Creek (upper)
14. McBride Lake
15. Slough Creek (sec. 1)
16. Slough Creek at confluence with Elk Tongue Creek
17. Lamar River
18. Lamar River at Geyser Basin
19. Pebble Creek
20. Cache Creek
21. Yellowstone Lake
22. Yellowstone River at LeHardy Rapids
23. Thorofare Creek

Figure 3.



1. Slough Creek (sec. 2)
2. Slough Creek (sec. 1)
3. Lamar River
4. Lamar River canyon
5. Lamar River across from geyser basin
6. Lamar River – 2 reaches
7. Lamar River at Soda Butte Creek
8. Lamar River above Soda Butte Creek
9. Lamar River upstream from Soda Butte Creek
10. Pebble Creek at bridge to Soda Butte Creek

Figure 4.

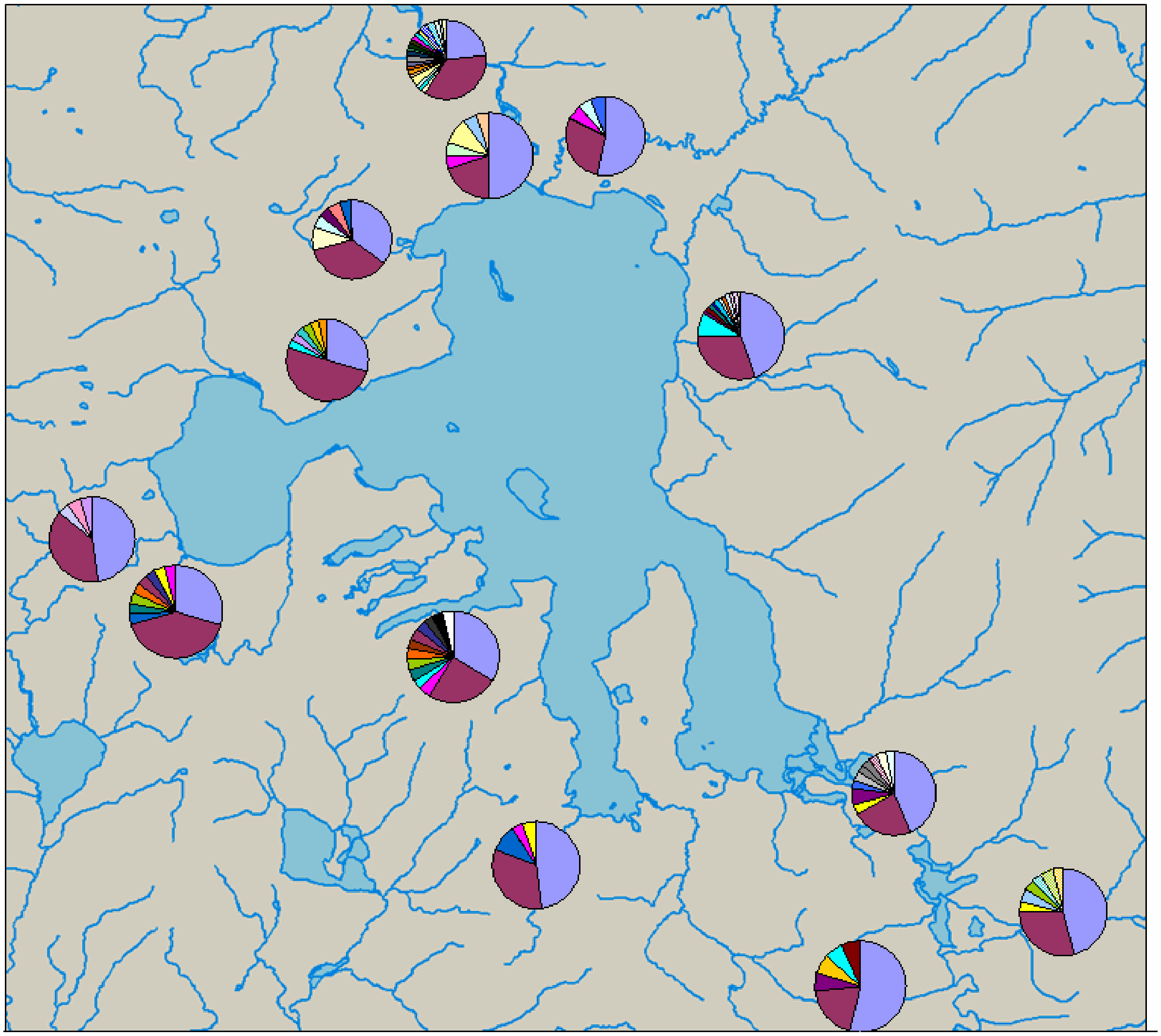


Figure 5.

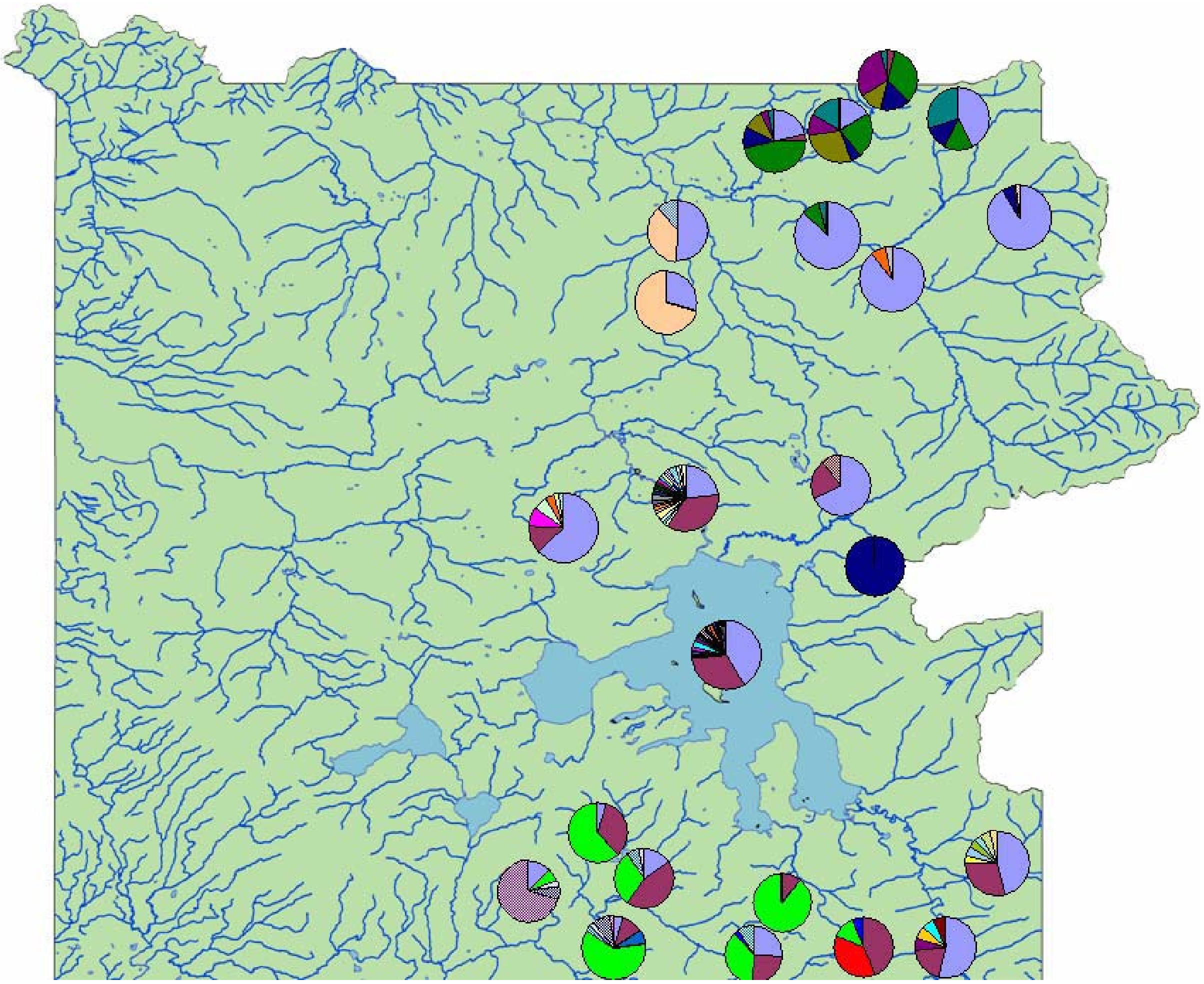
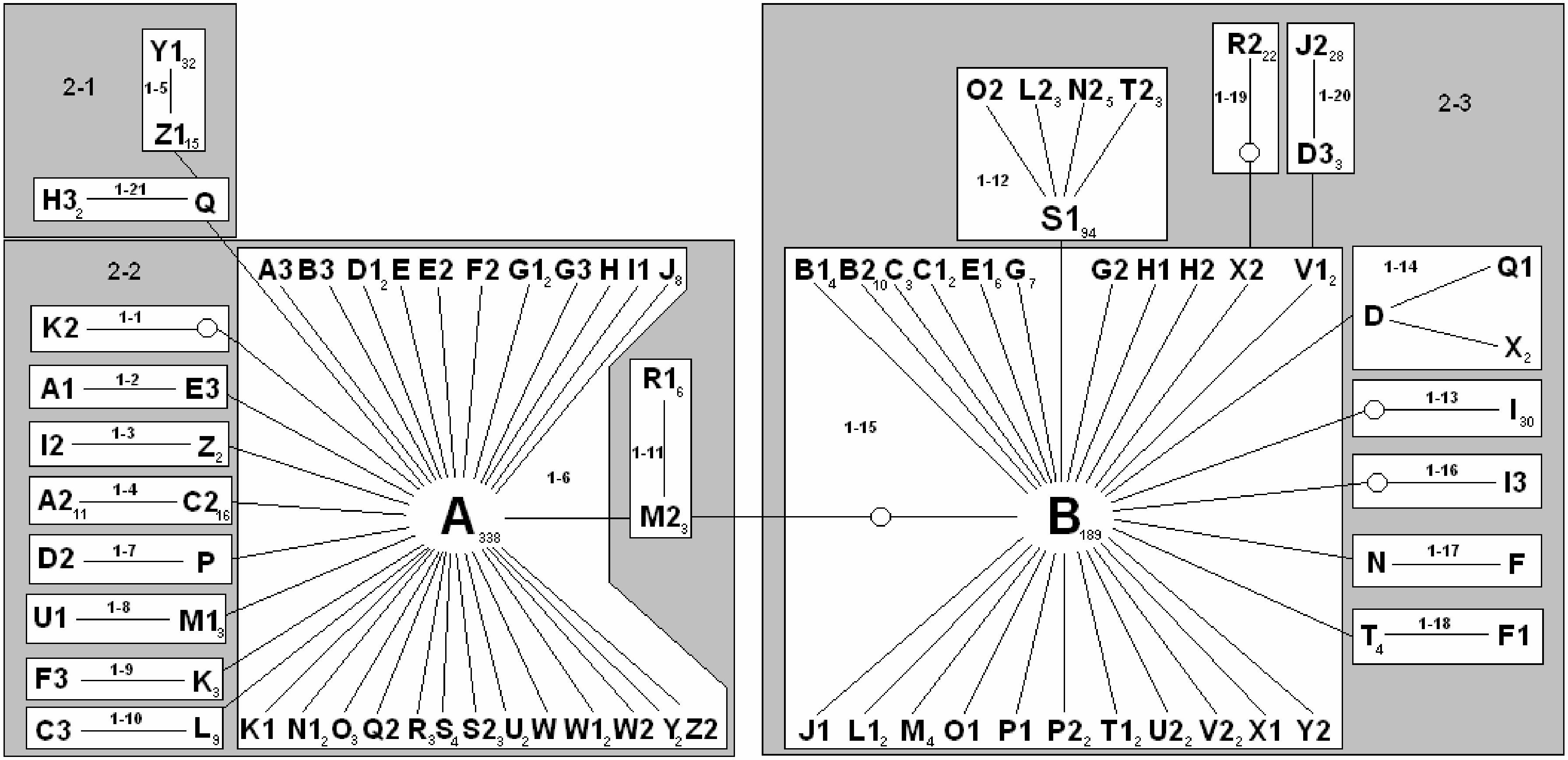


Figure 6.



2-1
$Y1_{32}$
1-5
$Z1_{15}$
$H3_{2}$
1-21
Q
2-2
K2
1-1
A1
1-2
E3
I2
1-3
Z_{2}
$A2_{11}$
1-4
$C2_{16}$
D2
1-7
P
U1
1-8
$M1_{3}$
F3
1-9
K_{3}
C3
1-10
L_{9}
A3 B3 $D1_{2}$ E E2 F2 $G1_{2}$ G3 H I1 J_{8}
1-6
A_{338}
$R1_{6}$
1-11
$M2_{3}$
K1 $N1_{2}$ O_{3} Q2 R_{3} S_{4} $S2_{3}$ U_{2} W $W1_{2}$ W2 Y_{2} Z2
2-3
O2 $L2_{3}$ $N2_{5}$ $T2_{3}$
1-12
$S1_{94}$
$R2_{22}$
1-19
$J2_{28}$
1-20
$D3_{3}$
$B1_{4}$ $B2_{10}$ C_{3} $C1_{2}$ $E1_{6}$ G_{7}
G2 H1 H2 X2 $V1_{2}$
1-15
B_{189}
J1 $L1_{2}$ M_{4} O1 P1 $P2_{2}$ $T1_{2}$ $U2_{2}$ $V2_{2}$ X1 Y2
1-14
Q1
D
X_{2}
1-13
I_{30}
1-16
I3
N
1-17
F
T_{4}
1-18
F1

Figure 7.

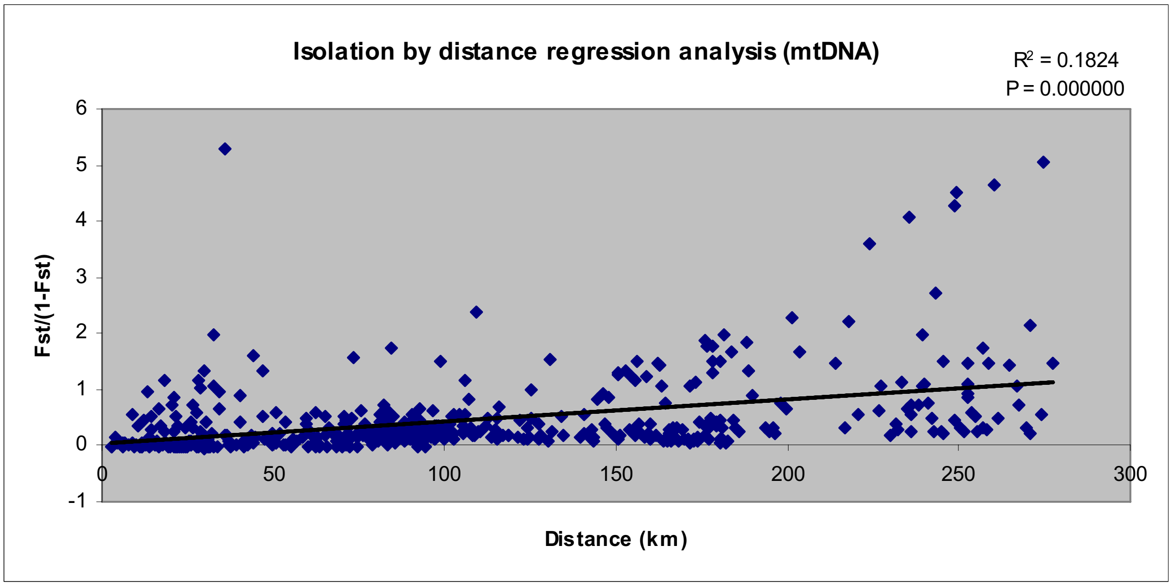

Isolation by distance regression analysis (mtDNA)
R² = 0.1824
P = 0.000000
Fst/(1-Fst)
6
5
4
3
2
1
0
-1
0
50
100
150
200
250
300
Distance (km)

Figure 8.

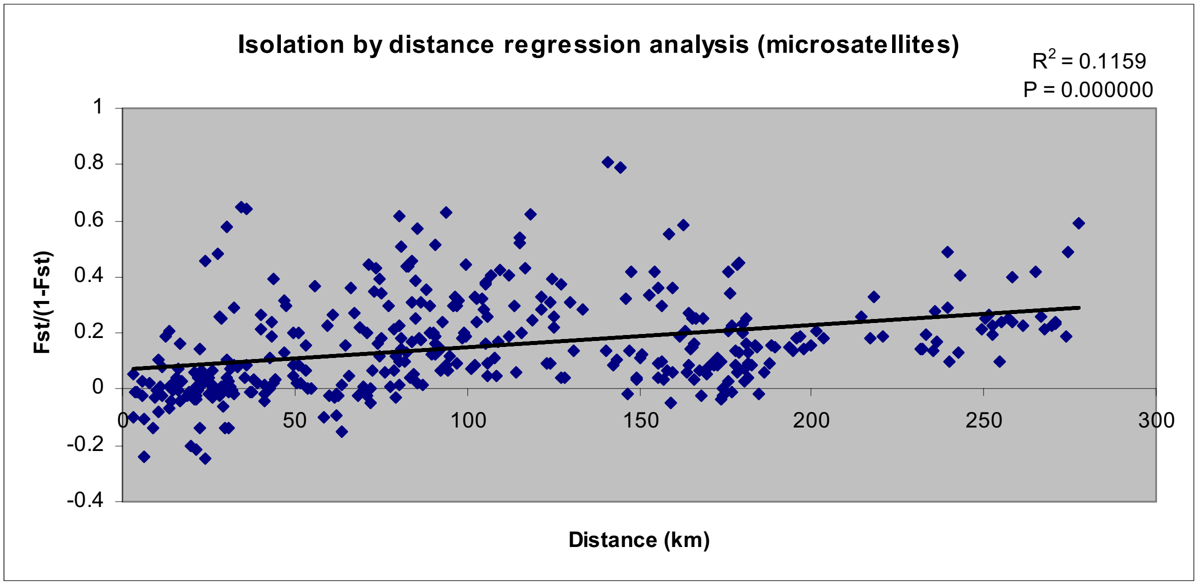

Isolation by distance regression analysis (microsatellites)
$R^2 = 0.1159$
P = 0.000000
Fst/(1-Fst)
1
0.8
0.6
0.4
0.2
0
-0.2
-0.4
0
50
100
150
200
250
300
Distance (km)

Figure 9.

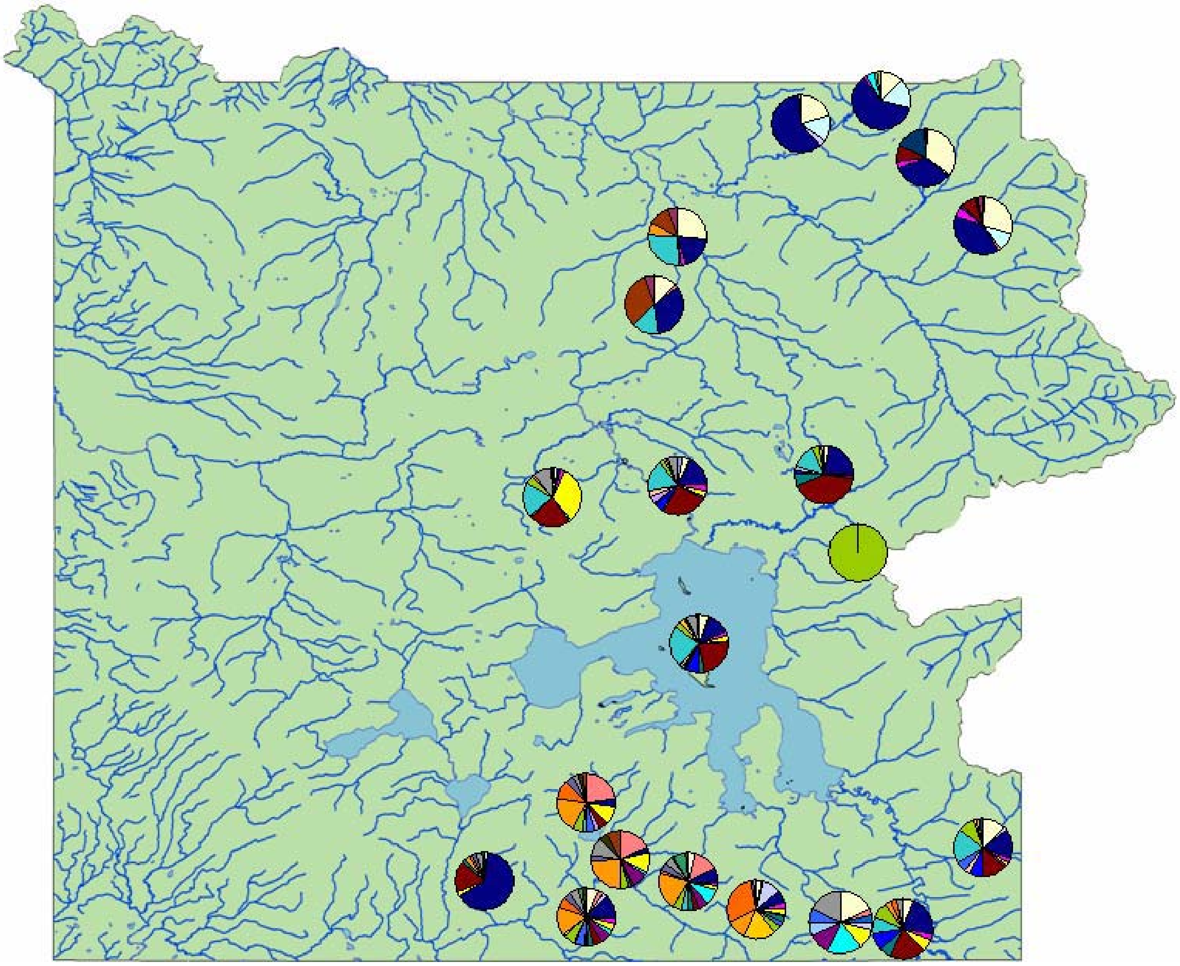


Figure 10.

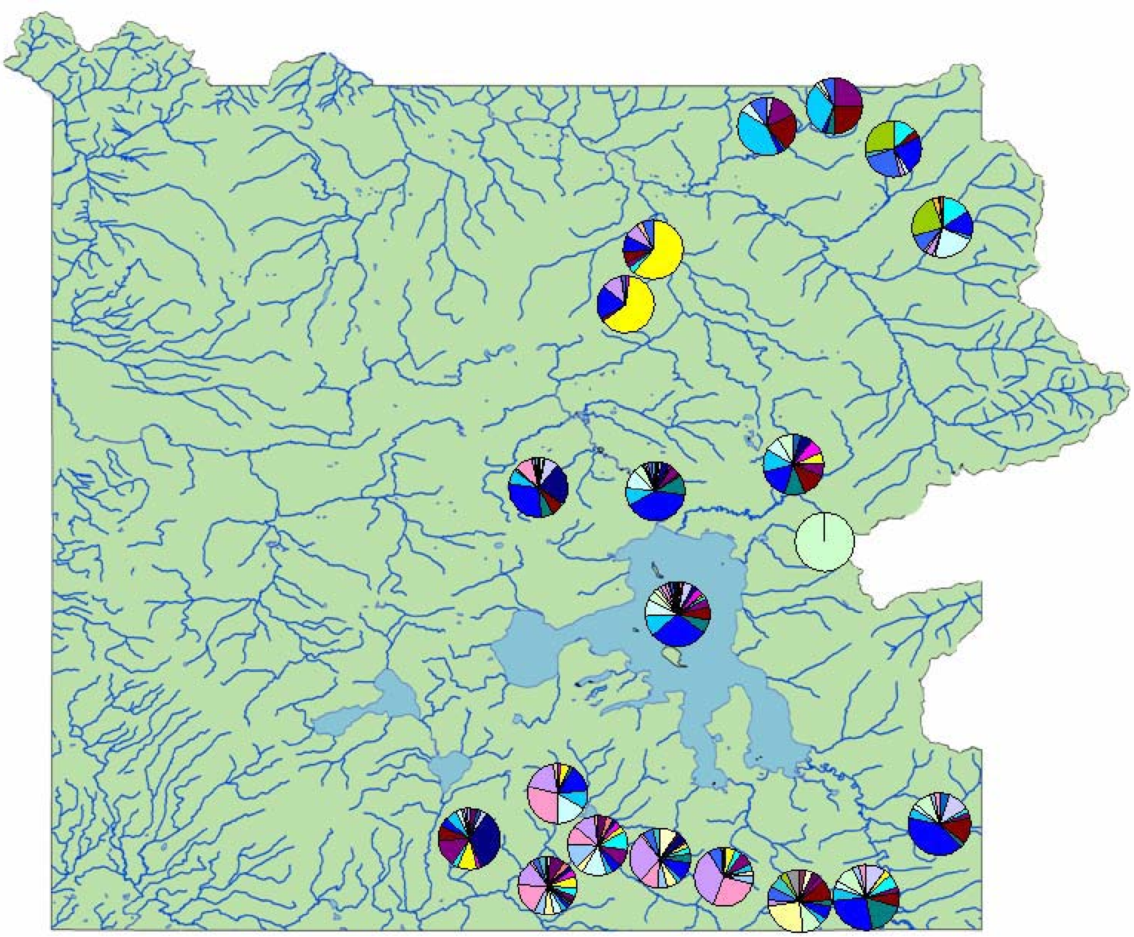


Figure 11.

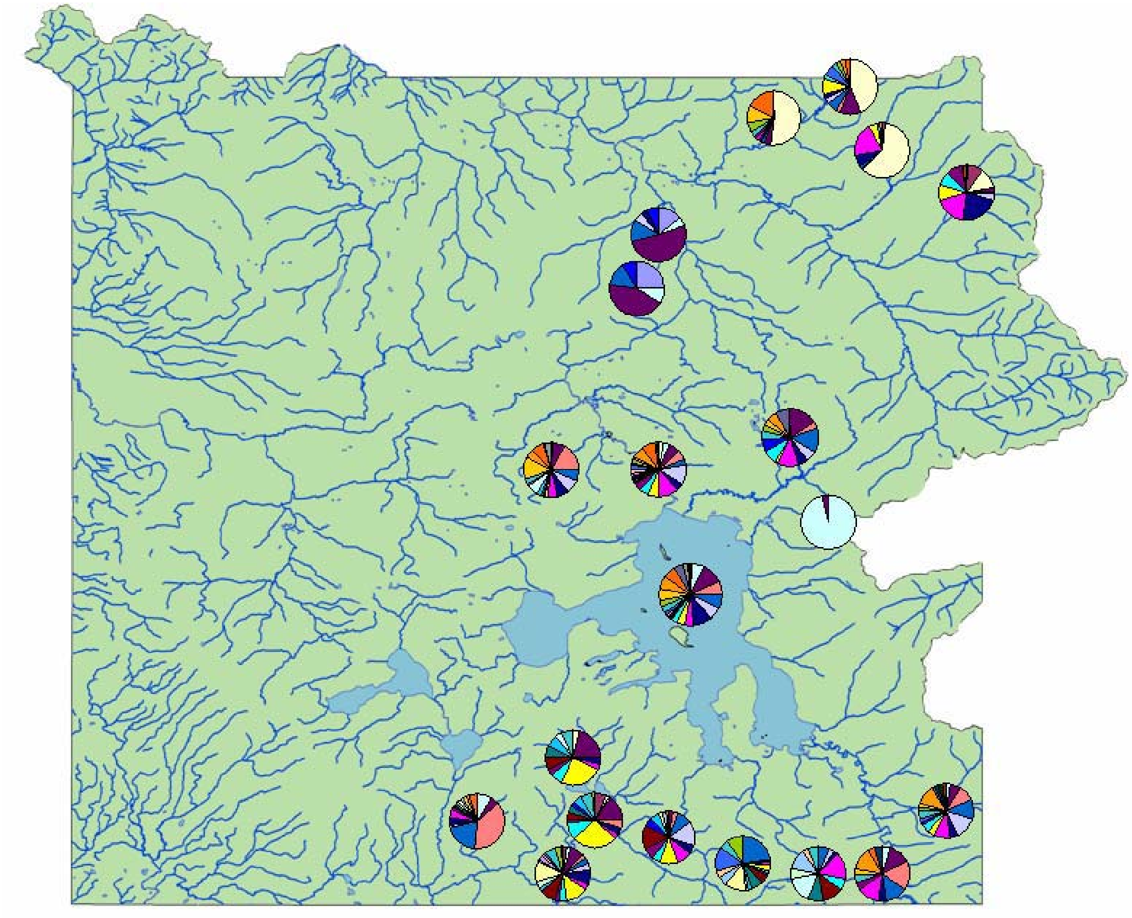


Figure 12.

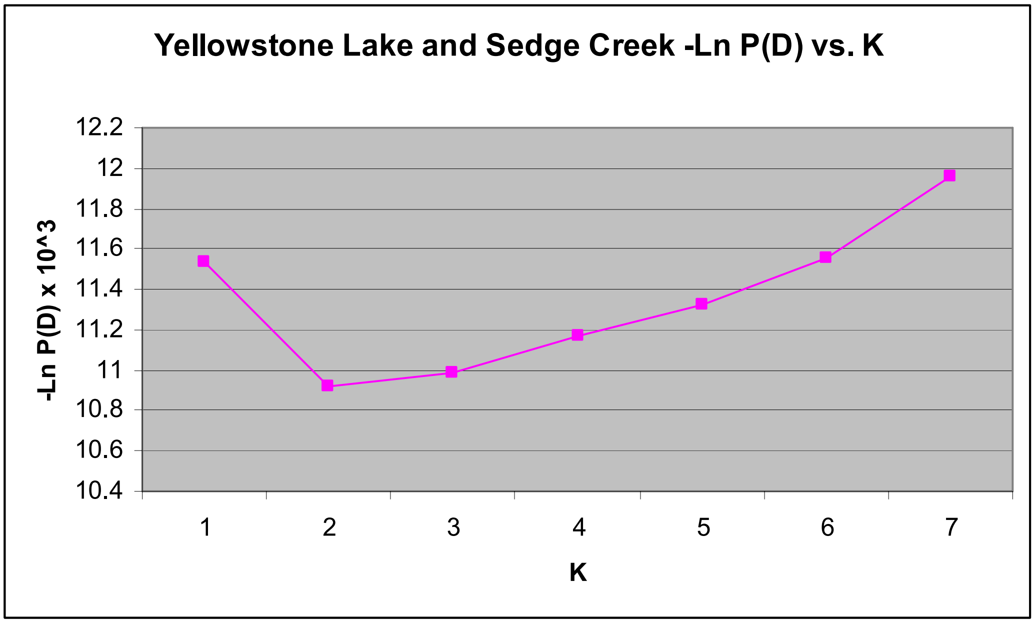

Yellowstone Lake and Sedge Creek -Ln P(D) vs. K
-Ln P(D) x 10^3
12.2
12
11.8
11.6
11.4
11.2
11
10.8
10.6
10.4
1
2
3
4
5
6
7
K

Figure 13.

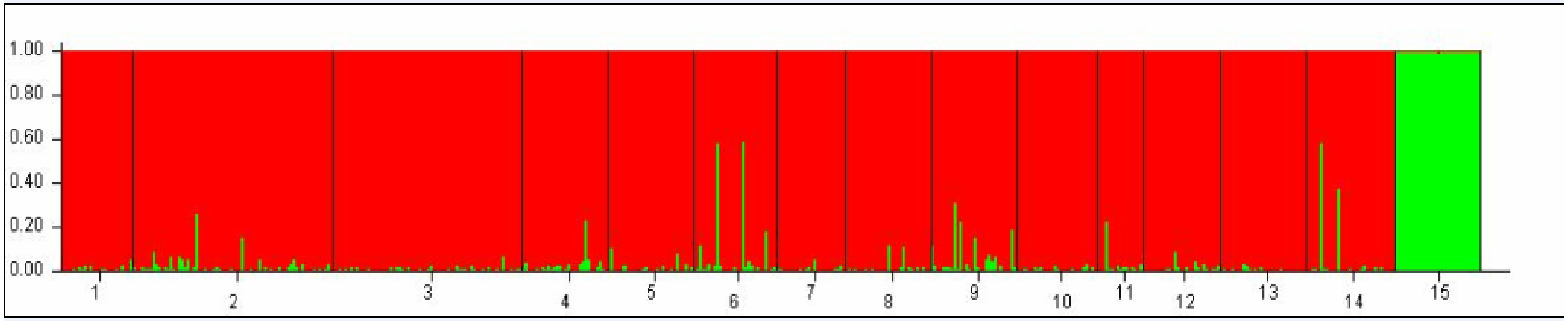


Figure 14.

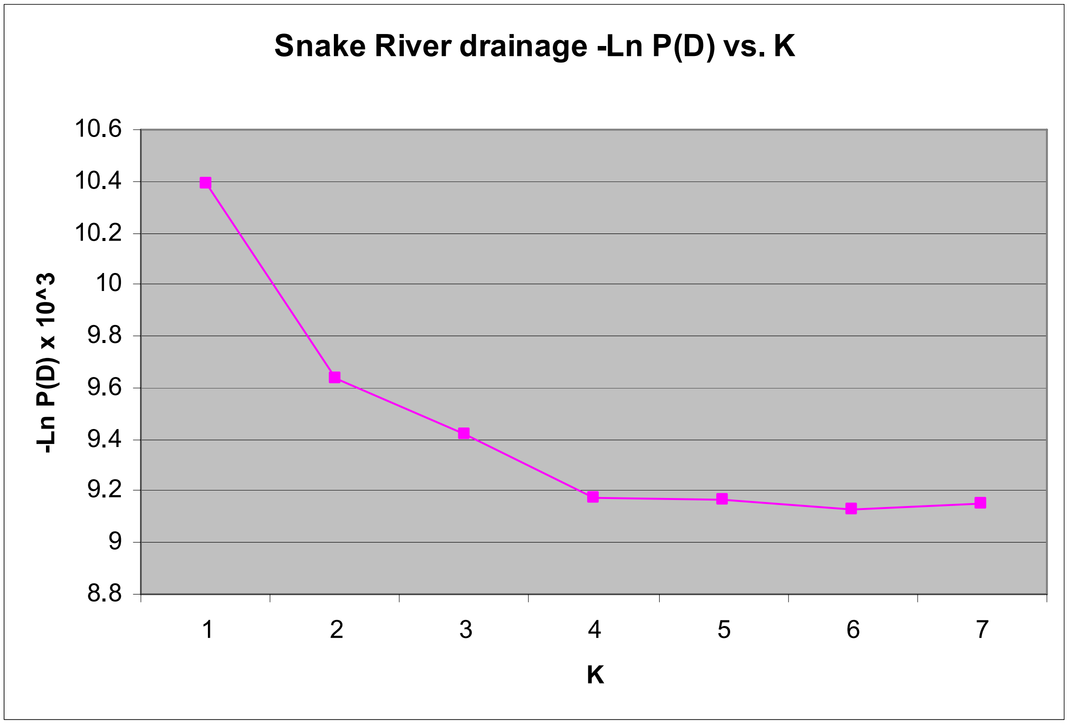

Snake River drainage -Ln P(D) vs. K
-Ln P(D) x 10^3
10.6
10.4
10.2
10
9.8
9.6
9.4
9.2
9
8.8
1
2
3
4
5
6
7
K

Figure 15.

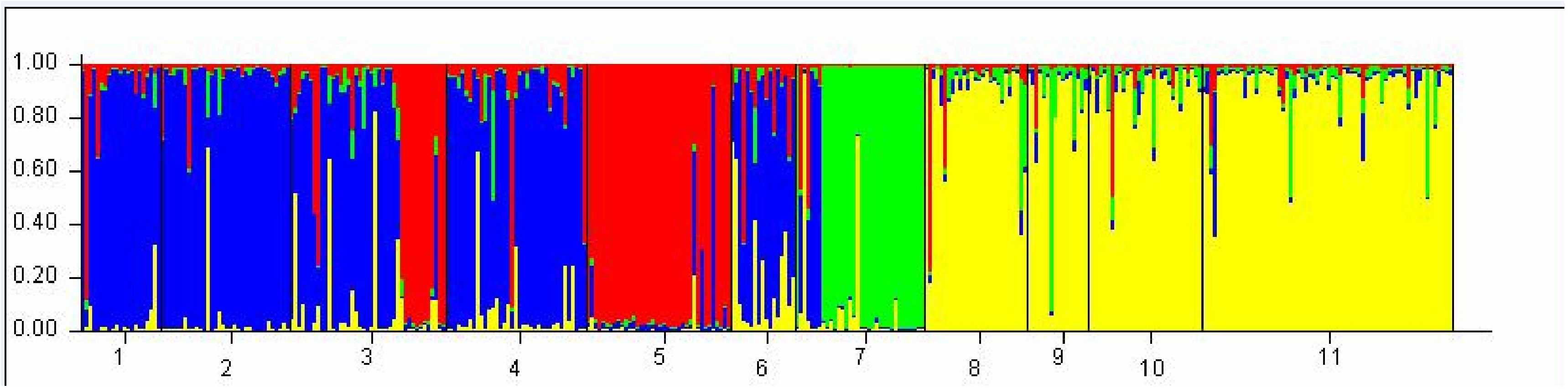


Figure 16.

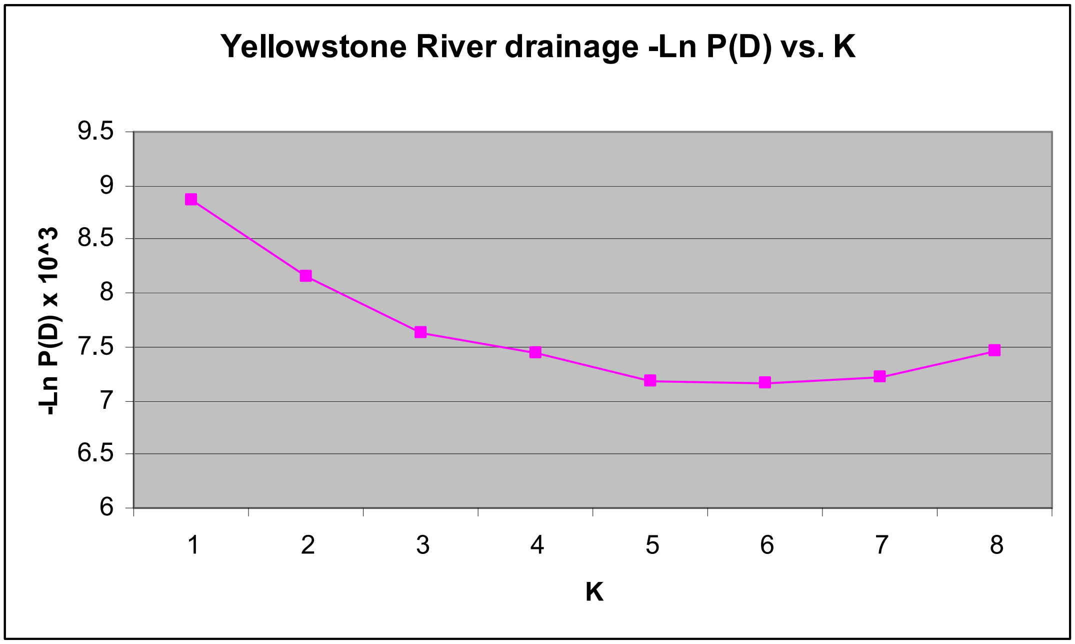

Yellowstone River drainage -Ln P(D) vs. K
-Ln P(D) x 10^3
9.5
9
8.5
8
7.5
7
6.5
6
1
2
3
4
5
6
7
8
K

Figure 17.

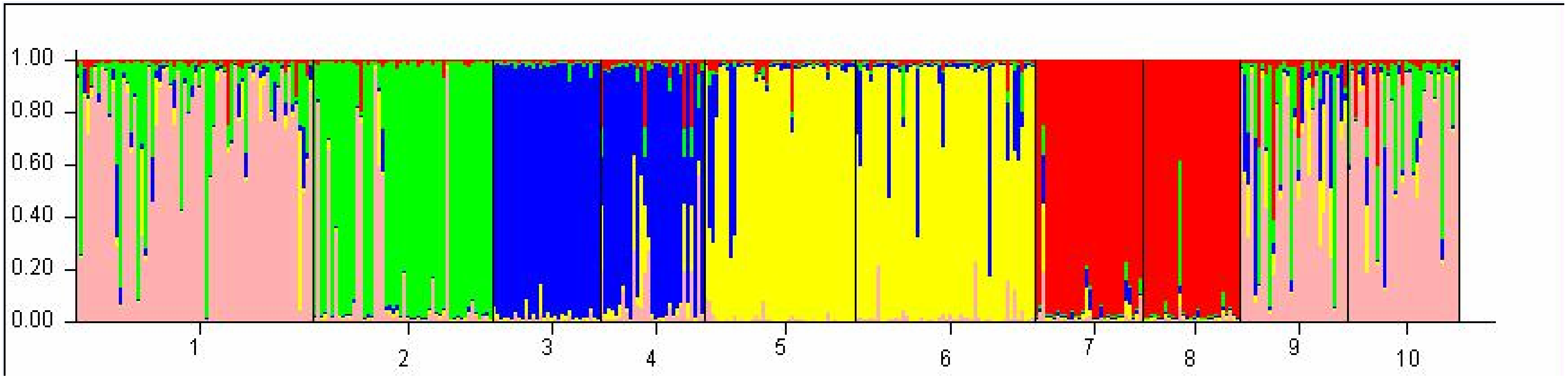


Figure 18.

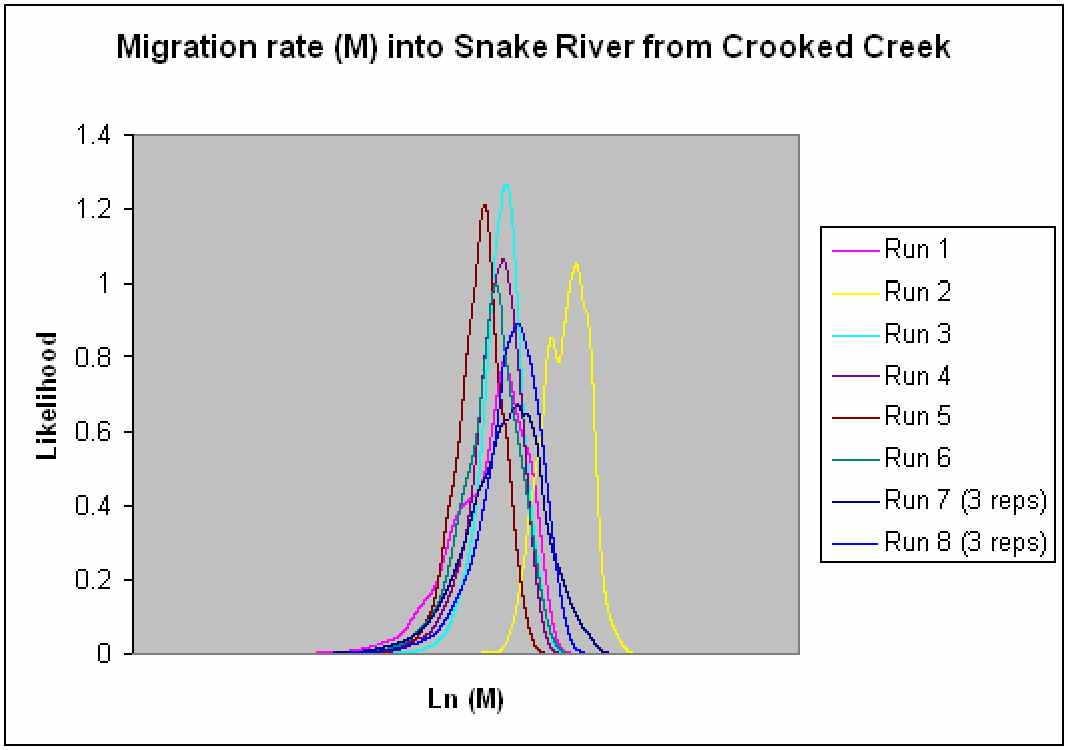
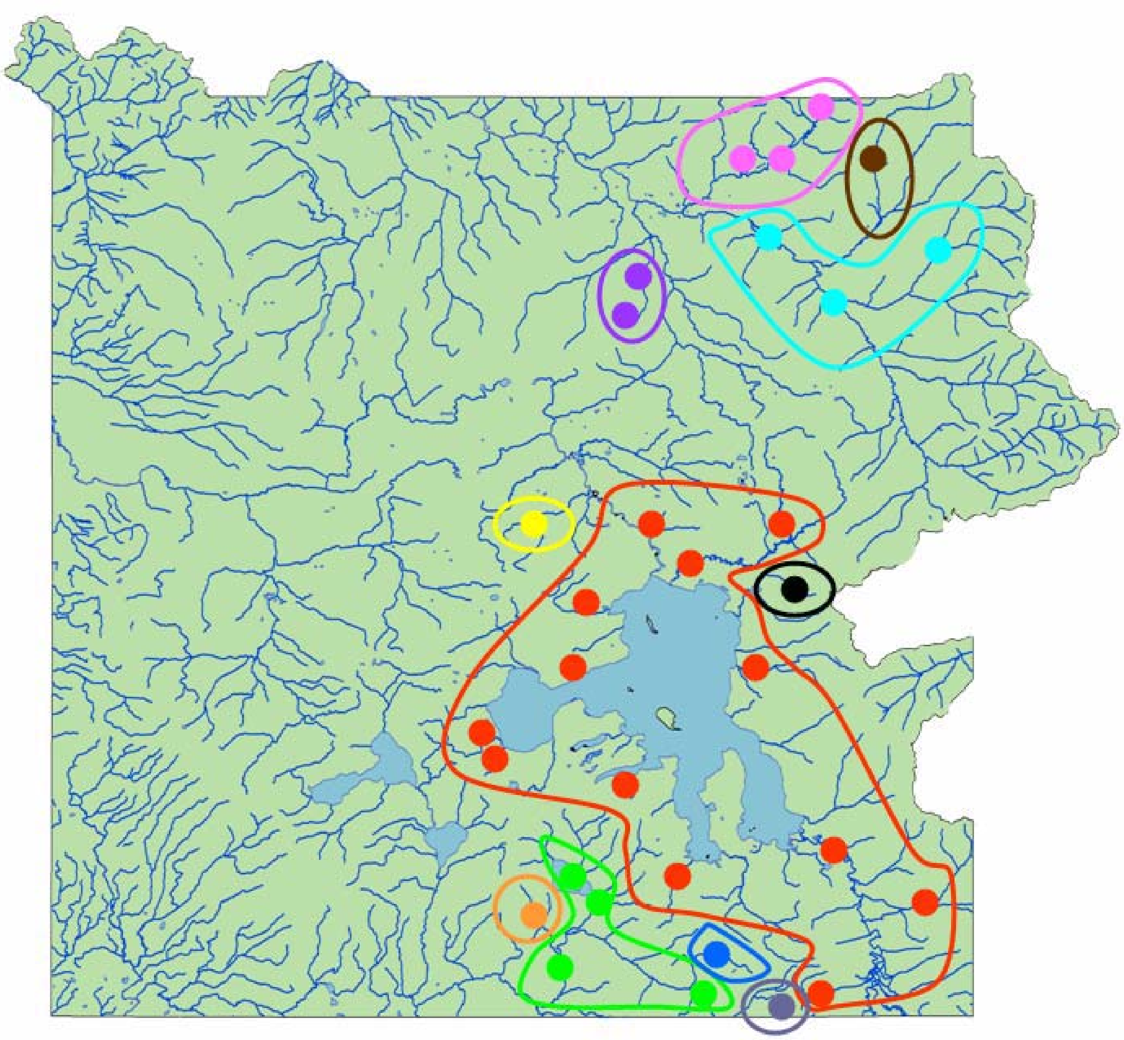

Migration rate (M) into Snake River from Crooked Creek
Likelihood
1.4
1.2
1
0.8
0.6
0.4
0.2
0
Ln (M)
Run 1
Run 2
Run 3
Run 4
Run 5
Run 6
Run 7 (3 reps)
Run 8 (3 reps)

Figure 19.



Appendix. Haplotypes and allele sizes for each individual by location. Hybrids from Lamar River, Lamar River across from geyser basin, and Slough Creek (sec. 1) are shown in Table 4 (H = haplotype, AJH = haplotype designation by Andrew Johnson, RT = rainbow trout).

Location	BYU #	H	AJH	Ots107		Omm1036		Fgt3		Ocl8		Ssa85		Omm1241	
Little Thumb Creek	90002	A	YCTyr1/sr5	167	175	212	261	201	225	175	189	117	119	254	277
	90003	B	YCTyr2/sr3	167	171	208	212	227	249	164	181	117	117	269	273
	90004	W	YCTyr56	163	171	195	203	216	229	179	191	117	117	258	269
	90005	H	YCTyr25	171	211	195	229	201	249	162	187	117	119	265	273
	90006	A	YCTyr1/sr5	155	167	195	203	249	251	177	191	117	119	187	258
	90007	B	YCTyr2/sr3	163	171	195	212	227	249	177	177	117	119	258	262
	90008	X	YCTyr57	167	175	203	254	-	-	152	183	117	119	171	258
	90009	B	YCTyr2/sr3	159	167	212	250	229	246	177	177	115	117	191	207
	90010	B	YCTyr2/sr3	163	167	208	216	246	249	173	183	117	117	183	199
	90011	B	YCTyr2/sr3	167	175	195	258	225	249	168	173	117	117	-	-
	90012	-	-	-	-	212	212	-	-	-	-	-	-	-	-
	90013	A	YCTyr1/sr5	155	167	212	269	-	-	-	-	115	117	-	-
	90014	A	YCTyr1/sr5	167	175	203	233	-	-	158	160	117	117	179	183
	90017	B	YCTyr2/sr3	167	171	208	212	225	249	177	177	117	119	175	191
	90018	A	YCTyr1/sr5	159	163	195	216	219	261	173	173	113	117	258	285
	90019	B	YCTyr2/sr3	155	163	208	208	225	227	177	204	113	117	171	171
	90020	-	-	151	175	-	-	214	214	177	179	117	117	-	-
	90022	A	YCTyr1/sr5	163	167	208	212	219	219	171	204	117	117	171	175
	90023	A	YCTyr1/sr5	163	167	258	261	214	225	160	177	117	117	269	289
	90024	-	-	163	167	229	233	-	-	-	-	-	-	-	-
	90025	B	YCTyr2/sr3	171	171	208	242	214	227	177	204	117	117	187	199
	90026	A	YCTyr1/sr5	163	171	-	-	-	-	-	-	117	117	-	-
	90027	A	YCTyr1/sr5	167	171	212	254	-	-	173	173	117	117	269	277
	90028	A	YCTyr1/sr5	163	171	203	216	201	231	173	195	117	121	187	273
	90030	-	-	159	163	195	229	-	-	-	-	117	117	-	-
Yellowstone River at LeHardy Rapids	90031	B	YCTyr2/sr3	163	163	195	208	214	214	147	175	115	117	171	269

Yellowstone River at LeHardy Rapids	90032	E1	YCTyr20	167	167	195	212	225	225	154	175	117	121	-	-
	90033	B	YCTyr2/sr3	163	171	208	258	214	216	164	164	117	117	-	-
	90034	B	YCTyr2/sr3	167	175	195	195	-	-	181	195	117	117	171	203
	90035	A	YCTyr1/sr5	-	-	-	-	-	-	177	177	117	123	-	-
	90036	B	YCTyr2/sr3	167	167	195	273	216	249	177	181	117	117	-	-
	90037	F1	YCTyr22	167	171	195	208	214	219	179	183	115	117	199	273
	90038	B	YCTyr2/sr3	163	167	195	195	225	225	175	175	117	117	195	195
	90039	B	YCTyr2/sr3	167	167	195	203	225	229	177	179	117	117	167	262
	90040	B	YCTyr2/sr3	163	163	208	246	225	249	177	179	117	117	183	254
	90041	G1	YCTyr24	163	171	199	212	184	203	177	181	115	117	-	-
	90042	D1	YCTyr5	163	167	250	258	223	235	160	195	117	117	175	191
	90073	B	YCTyr2/sr3	163	167	208	258	249	261	-	-	117	117	175	273
	90074	B	YCTyr2/sr3	167	167	208	250	225	229	177	187	117	117	183	203
	90075	H1	YCTyr26	163	171	195	265	225	261	177	181	117	117	175	191
	90076	A	YCTyr1/sr5	-	-	-	-	216	249	177	179	117	117	246	273
	90077	A	YCTyr1/sr5	167	171	195	212	225	261	173	177	117	117	269	269
	90078	-	-	167	167	195	203	249	249	152	179	115	117	179	273
	90079	B	YCTyr2/sr3	167	167	212	212	225	249	162	177	117	117	163	191
	90080	A	YCTyr1/sr5	163	167	212	212	225	225	177	179	117	117	273	273
	90081	B	YCTyr2/sr3	163	167	195	195	225	257	177	183	117	117	-	-
	90082	I1	YCTyr28	163	163	208	250	249	261	171	177	117	119	246	254
	90083	J1	YCTyr30	159	179	208	273	214	249	177	177	117	117	183	191
	90084	B	YCTyr2/sr3	163	171	233	265	214	244	173	183	117	117	-	-
	90085	K1	YCTyr32	159	167	212	212	225	244	-	-	115	117	207	262
	90086	B	YCTyr2/sr3	167	167	195	273	216	249	177	181	117	117	-	-
	188678	A	YCTyr1/sr5	163	171	203	203	214	242	177	183	117	117	175	258
	188679	T	YCTyr50	167	171	199	216	201	214	177	177	117	119	-	-
	188680	A	YCTyr1/sr5	163	167	242	246	225	249	177	177	117	117	183	191
	188681	B	YCTyr2/sr3	163	163	191	250	225	249	177	177	117	117	175	269
	188682	U2	-	167	171	199	199	214	214	177	183	117	117	175	183
	188683	B	YCTyr2/sr3	163	167	208	273	242	261	177	177	117	117	179	179
	188684	B	YCTyr2/sr3	163	167	208	258	229	249	175	177	117	123	262	273

Yellowstone River at LeHardy Rapids	188685	B	YCTyr2/sr3	159	163	195	203	201	244	171	181	117	117	191	199
	188686	A	YCTyr1/sr5	163	167	195	208	225	249	171	177	117	117	167	281
	188687	W2	-	167	167	195	208	225	225	177	181	117	117	191	250
	188688	Y	YCTyr58	167	171	203	208	219	249	162	179	121	121	179	265
	188689	U2	-	163	167	199	208	229	261	175	177	117	117	191	273
	188690	-	-	163	163	208	216	219	242	175	177	117	117	216	277
	188691	L	YCTyr33	163	171	212	212	214	253	177	177	117	117	171	199
	188692	A	YCTyr1/sr5	159	167	195	199	214	225	177	179	117	123	191	199
	188693	A	YCTyr1/sr5	171	175	208	216	225	229	181	197	115	115	187	281
	188694	B	YCTyr2/sr3	163	175	208	242	225	240	191	193	117	117	183	187
	188695	P2	-	159	163	195	208	225	249	-	-	121	123	-	-
	188696	A	YCTyr1/sr5	163	171	195	242	216	225	179	181	117	123	167	269
	188697	T	YCTyr50	159	163	199	258	214	214	177	177	117	117	171	183
	188698	V2	-	167	171	208	208	214	225	175	177	117	117	191	203
	188699	A	YCTyr1/sr5	167	167	203	258	214	225	162	177	117	117	179	254
	188700	V2	-	167	171	195	208	214	225	177	183	117	117	237	269
	188701	B	YCTyr2/sr3	159	171	203	212	184	214	177	177	117	119	191	199
	188702	V1	YCTyr55	167	171	195	216	184	249	177	181	115	117	195	212
	188703	G1	YCTyr24	155	167	208	212	184	201	160	197	117	117	187	195
	188704	-	-	167	171	195	195	225	251	175	175	117	117	163	195
	188705	-	-	163	163	212	246	242	249	171	179	117	117	195	269
	188706	A	YCTyr1/sr5	163	163	195	212	251	253	162	193	117	117	179	203
	188707	X2	-	163	167	195	261	214	225	175	179	115	117	183	273
	188708	B	YCTyr2/sr3	155	167	203	203	227	242	-	-	117	117	171	199
	188709	-	-	159	171	195	195	223	249	177	181	117	117	183	187
	188710	R	YCTyr47	151	167	203	261	201	249	177	177	117	117	171	191
	188711	W1	YCTyr9	167	171	212	246	214	244	162	183	117	117	167	250
	188712	Y2	-	163	167	195	199	249	261	175	177	117	123	163	183
	188713	A	YCTyr1/sr5	171	175	208	246	214	229	171	177	117	117	179	269
	188714	A	YCTyr1/sr5	159	167	212	212	225	249	168	195	117	117	203	225
	188715	C	YCTyr15	163	171	261	261	219	249	171	177	117	117	183	191
	188716	B	YCTyr2/sr3	167	171	208	208	225	225	175	179	117	117	171	187

Yellowstone River at LeHardy Rapids	188717	B	YCTyr2/sr3	167	171	199	261	201	251	181	181	117	123	183	195
Clear Creek	90043	L	YCTyr33	-	-	-	-	-	-	177	181	117	117	-	-
	90044	L	YCTyr33	163	167	195	203	249	249	168	177	117	117	269	269
	90045	A	YCTyr1/sr5	167	171	195	203	214	229	177	181	117	117	262	265
	90046	B	YCTyr2/sr3	155	163	229	250	219	244	187	191	117	117	167	187
	90047	A	YCTyr1/sr5	167	171	195	212	242	251	177	177	117	119	191	281
	90048	B	YCTyr2/sr3	-	-	-	-	-	-	164	179	117	117	191	273
	90049	A	YCTyr1/sr5	155	171	208	261	225	261	-	-	-	-	-	-
	90050	B	YCTyr2/sr3	-	-	-	-	-	-	175	187	117	117	167	183
	90051	A	YCTyr1/sr5	163	167	208	246	240	251	177	179	117	117	265	269
	90052	M	YCTyr37	175	175	195	254	244	244	173	177	117	117	167	281
	90053	B	YCTyr2/sr3	171	175	212	250	229	249	173	177	117	117	265	265
	90054	N	YCTyr39	159	187	199	208	249	263	177	179	117	117	187	258
	90055	L	YCTyr33	167	171	208	258	-	-	177	177	117	117	-	-
	90056	O	YCTyr41	171	171	195	250	249	251	177	179	117	117	167	175
	90057	P	YCTyr43	-	-	-	-	-	-	177	177	115	117	175	289
	90058	A	YCTyr1/sr5	167	171	246	261	249	249	177	177	117	121	187	269
	90059	B	YCTyr2/sr3	151	163	191	261	249	251	168	183	117	117	179	187
	90060	B	YCTyr2/sr3	167	171	208	208	229	253	177	183	117	117	179	265
	90061	A	YCTyr1/sr5	163	167	203	212	225	251	164	179	117	117	171	187
	90062	B	YCTyr2/sr3	159	167	203	254	249	251	177	177	117	117	179	191
	90063	A	YCTyr1/sr5	155	167	212	269	225	231	175	181	117	117	171	183
	90064	A	YCTyr1/sr5	163	167	195	269	214	231	177	177	117	117	167	269
	90065	A	YCTyr1/sr5	163	167	208	208	251	253	-	-	-	-	-	-
	90066	Q	YCTyr45	163	163	250	254	225	244	175	177	115	117	183	273
	90067	L	YCTyr33	163	171	224	261	201	225	177	177	117	117	187	199
	90068	B	YCTyr2/sr3	159	167	250	250	223	227	181	181	117	117	175	273
	90069	A	YCTyr1/sr5	-	-	212	250	201	214	177	191	117	119	183	250
	90070	A	YCTyr1/sr5	163	175	195	261	214	249	177	179	117	119	199	262
	90071	B	YCTyr2/sr3	167	175	195	269	225	249	181	183	117	117	179	273
	90072	R	YCTyr47	167	167	233	258	229	257	191	195	117	117	167	191

Clear Creek	142175	E1	YCTyr20	163	167	208	212	225	229	-	-	117	117	171	269
	142176	B	YCTyr2/sr3	163	167	208	269	249	249	-	-	115	117	265	273
	142177	A	YCTyr1/sr5	163	171	199	208	219	261	177	177	117	117	195	269
	142178	B	YCTyr2/sr3	163	167	208	250	227	249	177	181	117	117	-	-
	142179	B	YCTyr2/sr3	167	171	208	208	249	249	162	164	117	121	179	179
	142180	B	YCTyr2/sr3	171	179	208	258	249	263	177	181	117	117	171	187
	142181	A	YCTyr1/sr5	-	-	195	250	227	244	179	179	117	121	179	269
	142182	Z2	-	163	167	195	258	214	214	179	179	117	117	171	199
	142183	-	-	163	171	203	208	249	249	183	183	117	117	175	281
	142184	A	YCTyr1/sr5	163	171	250	261	244	253	179	179	117	117	171	265
	142185	B	YCTyr2/sr3	167	167	208	220	225	225	179	191	117	117	183	265
	142186	B	YCTyr2/sr3	167	167	212	212	225	251	173	177	117	119	195	269
	142187	B	YCTyr2/sr3	163	163	258	265	225	225	162	171	113	117	171	175
	142188	A3	-	167	171	191	258	201	225	179	181	117	119	207	265
	142189	A	YCTyr1/sr5	159	179	208	208	249	253	179	179	117	117	171	171
	142190	B	YCTyr2/sr3	163	171	229	250	244	244	171	177	117	117	171	175
	142191	A	YCTyr1/sr5	159	167	208	250	223	257	181	195	117	117	187	187
	142192	B	YCTyr2/sr3	163	171	208	261	229	261	177	177	117	117	175	183
	142193	-	-	167	167	208	208	229	249	173	173	-	-	-	-
	142194	B	YCTyr2/sr3	171	171	203	265	225	229	158	179	117	117	203	265
	142195	B	YCTyr2/sr3	163	171	208	258	225	249	177	181	117	117	171	289
	142196	B3	-	159	167	203	212	229	249	177	181	117	117	-	-
	142197	-	-	171	183	199	212	201	227	177	177	117	117	171	183
	142198	A	YCTyr1/sr5	167	167	203	250	223	227	160	177	117	121	246	254
	142199	A	YCTyr1/sr5	167	167	250	250	212	244	181	189	117	117	167	273
	142200	C3	-	-	-	-	-	-	-	177	183	113	123	195	220
	142201	B	YCTyr2/sr3	163	167	216	261	229	251	168	183	117	119	262	269
	142202	B	YCTyr2/sr3	163	163	203	269	214	249	179	181	117	117	167	175
	142203	B	YCTyr2/sr3	163	167	203	212	214	249	164	177	115	117	-	-
	142204	B	YCTyr2/sr3	163	167	208	212	216	251	171	171	117	117	171	187
	142205	A	YCTyr1/sr5	167	171	195	258	225	249	181	181	117	117	191	277
	142206	A	YCTyr1/sr5	167	167	208	212	225	249	179	187	117	117	175	277

Clear Creek	142207	B	YCTyr2/sr3	167	171	258	258	201	216	177	179	117	117	171	191
	142208	A	YCTyr1/sr5	-	-	-	-	-	-	181	189	117	117	195	273
	142209	L	YCTyr33	167	171	229	246	225	249	181	181	117	117	175	265
	142210	B	YCTyr2/sr3	163	167	208	208	249	259	166	177	117	117	258	269
	142211	L	YCTyr33	163	163	208	261	225	253	177	177	115	117	-	-
	142212	A	YCTyr1/sr5	167	167	258	261	249	253	183	193	117	119	265	269
	142213	B	YCTyr2/sr3	167	167	195	208	249	261	166	183	117	117	163	171
	142214	B	YCTyr2/sr3	167	167	246	261	249	249	179	181	117	117	175	183
Pelican Creek	90087	-	-	163	163	195	208	229	238	187	197	117	117	-	-
	90088	A	YCTyr1/sr5	159	163	208	212	-	-	179	181	113	117	-	-
	90089	-	-	167	167	203	212	214	225	179	195	117	117	-	-
	90090	A	YCTyr1/sr5	167	171	195	233	-	-	177	177	117	117	195	195
	90091	-	-	167	167	212	212	-	-	160	173	117	119	-	-
	90092	-	-	163	163	208	208	225	249	173	193	117	117	171	171
	90093	-	-	163	163	195	212	201	225	181	187	117	117	179	187
	90094	A	YCTyr1/sr5	167	171	208	208	-	-	160	177	117	117	191	191
	90095	-	-	163	167	-	-	-	-	185	189	117	117	-	-
	90096	A	YCTyr1/sr5	163	175	-	-	-	-	-	-	117	117	-	-
	90097	A	YCTyr1/sr5	163	167	195	208	-	-	177	177	117	117	-	-
	90098	B	YCTyr2/sr3	163	167	208	208	225	225	160	181	117	117	-	-
	90099	J	YCTyr29	163	163	195	212	225	251	181	181	117	117	-	-
	90100	Z	YCTyr59	167	167	195	208	201	214	181	183	117	117	183	187
	90101	B	YCTyr2/sr3	167	167	208	250	219	225	173	177	117	117	179	179
	90102	B	YCTyr2/sr3	163	171	208	216	214	225	160	177	117	117	-	-
	90103	A	YCTyr1/sr5	163	171	208	208	-	-	181	193	117	117	-	-
	90104	-	-	171	171	212	261	-	-	164	175	117	117	-	-
	90105	A	YCTyr1/sr5	155	171	212	216	-	-	162	177	117	117	187	187
	90106	-	-	167	179	208	216	225	225	173	199	117	123	191	233
	90107	-	-	167	171	203	208	244	249	177	177	117	117	167	179
	90108	A	YCTyr1/sr5	159	167	195	216	225	251	175	179	117	117	187	258
	90109	-	-	159	163	208	212	-	-	-	-	117	117	-	-
	90110	R	YCTyr47	159	167	-	-	-	-	177	181	117	117	-	-

Pelican Creek	90111	B	YCTyr2/sr3	163	167	195	195	214	249	177	179	117	117	-	-
	90112	B	YCTyr2/sr3	163	211	208	233	214	259	181	191	117	117	163	163
	90113	A	YCTyr1/sr5	167	167	208	208	225	249	160	160	117	117	-	-
	90114	-	-	159	163	195	208	-	-	156	187	115	117	-	-
	90115	-	-	159	163	265	265	214	229	164	173	117	117	-	-
	90116	-	-	167	167	195	212	201	249	164	195	117	117	171	183
Flat Mountain Arm Creek	90147	A	YCTyr1/sr5	155	171	208	212	214	249	171	202	117	117	183	273
	90148	M1	YCTyr38	159	163	208	220	249	249	160	164	117	117	167	281
	90149	A	YCTyr1/sr5	167	167	191	265	253	253	173	173	117	119	195	269
	90150	A	YCTyr1/sr5	167	167	229	258	225	261	166	179	117	117	187	262
	90151	B	YCTyr2/sr3	167	171	203	212	225	225	173	181	117	117	171	262
	90152	O	YCTyr41	163	207	208	212	214	229	177	183	-	-	265	281
	90153	A	YCTyr1/sr5	159	167	208	208	225	249	177	177	117	121	175	179
	90154	N1	YCTyr40	155	171	208	250	212	225	160	181	117	117	191	273
	90155	L1	YCTyr34	151	167	208	250	225	225	160	168	115	117	187	273
	90156	O1	YCTyr42	163	167	195	229	214	229	173	177	117	117	187	191
	90157	B	YCTyr2/sr3	167	171	195	203	225	227	168	181	117	117	171	262
	90158	-	-	171	171	212	212	216	225	162	181	117	117	269	269
	90159	B	YCTyr2/sr3	159	171	203	212	225	225	177	179	117	121	191	258
	90160	B	YCTyr2/sr3	159	171	195	208	214	229	177	181	117	117	258	273
	90161	L	YCTyr33	167	171	195	212	249	249	160	164	117	117	273	277
	90162	J	YCTyr29	167	175	203	220	214	231	162	171	117	117	175	277
	90163	A	YCTyr1/sr5	163	163	203	208	249	261	164	175	117	121	171	273
	90164	P1	YCTyr44	155	167	195	233	216	249	175	183	117	117	179	277
	90165	B	YCTyr2/sr3	171	171	208	258	216	249	171	179	117	117	171	171
	90166	A	YCTyr1/sr5	167	171	208	216	249	251	185	202	117	117	175	277
	90167	L1	YCTyr34	163	167	195	208	225	231	175	179	117	117	258	273
	90168	A	YCTyr1/sr5	163	179	208	224	214	225	177	179	115	117	171	187
	90169	A	YCTyr1/sr5	167	171	195	216	251	261	164	187	117	119	163	175
	90170	Q1	YCTyr46	167	171	195	208	203	214	171	177	117	117	171	175
	90171	E1	YCTyr20	159	163	203	208	225	225	175	177	113	117	167	187
	90172	A	YCTyr1/sr5	171	179	208	212	201	229	164	177	117	117	254	273

Flat Mountain Arm Creek	90173	B	YCTyr2/sr3	163	171	212	212	227	263	164	195	117	117	195	195
	90174	B1	YCTyr13	159	171	195	208	225	255	156	179	117	117	-	-
	90175	B	YCTyr2/sr3	167	167	203	212	214	225	158	177	117	117	175	258
	90176	M1	YCTyr38	159	167	208	212	249	261	177	179	117	117	175	258
Grouse Creek	90177	A	YCTyr1/sr5	163	171	195	258	225	229	177	181	117	117	171	183
	90178	J	YCTyr29	159	167	195	216	214	249	158	189	117	117	183	265
	90179	B	YCTyr2/sr3	159	167	195	208	214	225	162	183	117	117	171	199
	90180	-	-	175	175	250	250	214	225	177	183	117	117	179	277
	90181	-	-	167	171	250	261	214	253	160	175	117	117	167	265
	90183	B	YCTyr2/sr3	167	171	203	208	214	251	160	166	117	117	175	273
	90184	B	YCTyr2/sr3	167	171	208	229	212	249	173	175	117	117	183	183
	90185	A	YCTyr1/sr5	167	171	-	-	238	253	177	179	117	117	167	262
	90186	-	-	-	-	-	-	-	-	-	-	117	117	-	-
	90187	-	-	163	171	-	-	214	225	179	183	117	117	171	179
	90188	K	YCTyr31	151	167	208	212	225	263	179	179	117	117	183	187
	90189	B	YCTyr2/sr3	163	167	195	203	214	249	179	179	117	117	191	269
	90190	B	YCTyr2/sr3	155	171	208	212	225	253	171	177	113	117	171	273
	90191	B	YCTyr2/sr3	171	171	208	250	229	249	177	177	117	117	175	273
	90192	G	YCTyr23	159	163	208	265	214	225	177	177	117	117	187	273
	90193	A	YCTyr1/sr5	171	171	212	250	229	249	177	177	117	119	175	199
	90194	A	YCTyr1/sr5	167	175	208	261	249	249	177	177	117	117	277	277
	90195	-	-	-	-	-	-	-	-	-	-	117	117	-	-
	90196	A	YCTyr1/sr5	159	163	195	208	214	225	162	177	117	117	175	277
	90197	G	YCTyr23	-	-	-	-	219	225	177	183	117	121	-	-
	90198	A	YCTyr1/sr5	171	175	195	208	214	251	166	177	117	117	262	269
	90199	A	YCTyr1/sr5	167	171	212	246	236	263	177	179	117	117	191	195
	90200	A	YCTyr1/sr5	163	167	-	-	229	251	177	179	117	117	179	187
	90201	B	YCTyr2/sr3	171	179	195	208	249	261	171	175	117	117	171	175
	90202	A	YCTyr1/sr5	167	183	212	258	201	249	171	177	117	117	183	265
	90203	-	-	159	163	195	208	-	-	162	183	117	117	258	273
	90204	A	YCTyr1/sr5	167	175	191	208	214	225	164	177	117	117	183	262
	90205	-	-	163	163	250	273	-	-	-	-	115	117	-	-

Grouse Creek	90206	-	-	163	167	195	208	-	-	-	-	117	119	-	-
Hatchery Creek	90211	D	YCTyr18	-	-	-	-	-	-	177	189	117	117	262	269
	90212	B	YCTyr2/sr3	167	171	208	208	219	225	177	199	117	121	187	277
	90213	A	YCTyr1/sr5	163	167	212	216	253	261	154	177	117	117	195	269
	90214	E	YCTyr19	151	167	208	250	225	253	173	175	117	117	187	300
	90215	-	-	167	175	195	195	229	261	177	179	117	117	191	273
	90216	B	YCTyr2/sr3	155	163	212	212	216	219	158	177	113	121	187	277
	90217	B	YCTyr2/sr3	167	215	195	212	214	255	175	177	117	117	179	269
	90218	A	YCTyr1/sr5	151	155	212	250	225	229	177	181	117	121	183	273
	90219	C	YCTyr15	167	167	208	208	225	225	177	177	117	119	195	199
	90220	B	YCTyr2/sr3	167	171	195	203	225	261	173	179	117	117	195	220
	90221	F	YCTyr21	159	171	258	261	225	249	175	187	117	117	171	185
	90222	A	YCTyr1/sr5	159	171	195	208	225	249	175	177	117	117	195	273
	90223	B	YCTyr2/sr3	167	167	216	265	225	225	175	175	117	117	171	183
	90224	C	YCTyr15	163	163	208	208	214	253	179	183	117	117	187	187
	90225	G	YCTyr23	163	163	195	233	225	249	156	177	117	117	171	277
	90226	-	-	163	167	208	212	225	227	177	177	117	117	269	281
	90231	A	YCTyr1/sr5	155	171	208	212	229	249	175	177	117	121	179	187
	90232	-	-	163	163	195	250	-	-	-	-	117	117	183	183
	90233	-	-	167	167	203	212	225	229	177	179	117	119	175	273
	90234	A	YCTyr1/sr5	167	167	208	261	214	214	173	187	117	117	171	258
	90235	B	YCTyr2/sr3	159	167	195	212	227	255	175	177	117	117	179	269
	90236	B	YCTyr2/sr3	163	167	208	208	225	225	162	177	117	117	258	277
	90237	A	YCTyr1/sr5	167	167	208	216	216	225	173	193	115	117	167	195
	90240	A	YCTyr1/sr5	167	187	195	265	225	261	171	189	117	117	179	183
Day Bed Creek	90241	B	YCTyr2/sr3	167	179	203	216	225	249	171	177	117	119	179	187
	90242	A	YCTyr1/sr5	159	163	212	261	249	261	173	177	117	117	-	-
	90243	B	YCTyr2/sr3	163	207	212	269	227	249	175	177	117	117	-	-
	90244	A1	YCTyr11	159	167	224	229	242	261	177	189	115	117	-	-
	90245	A	YCTyr1/sr5	163	167	-	-	218	261	177	202	113	117	171	262
	90246	B1	YCTyr13	167	171	250	254	225	249	177	177	117	121	-	-
	90247	B	YCTyr2/sr3	163	163	216	224	-	-	160	166	115	117	171	262

Day Bed Creek	90248	L	YCTyr33	159	167	199	261	225	227	177	189	117	117	262	273
	90249	B	YCTyr2/sr3	163	167	212	246	249	255	175	177	117	117	-	-
	90250	A	YCTyr1/sr5	-	-	-	-	-	-	179	181	117	117	191	195
	90251	B	YCTyr2/sr3	163	171	212	233	227	249	179	181	117	117	187	187
	90252	X	YCTyr57	163	171	-	-	249	249	175	177	117	117	-	-
	90253	B	YCTyr2/sr3	-	-	203	203	-	-	177	177	117	119	171	171
	90254	B	YCTyr2/sr3	167	171	-	-	225	249	173	175	117	117	179	191
	90255	B	YCTyr2/sr3	-	-	229	265	-	-	177	179	113	117	195	273
	90256	A	YCTyr1/sr5	-	-	208	208	-	-	179	181	117	117	-	-
	90257	A	YCTyr1/sr5	167	167	195	212	225	249	160	177	117	117	-	-
	90258	B	YCTyr2/sr3	-	-	203	212	201	229	173	177	117	119	-	-
	90259	C1	YCTyr16	171	171	212	250	229	259	171	171	117	119	187	265
	90260	B	YCTyr2/sr3	159	163	208	242	225	231	179	185	117	117	175	175
	90261	B	YCTyr2/sr3	-	-	199	199	-	-	177	183	119	123	167	258
	90262	A	YCTyr1/sr5	163	167	199	212	201	249	181	189	117	117	187	277
	90263	B	YCTyr2/sr3	163	167	199	220	201	249	179	183	117	117	187	187
	90264	A	YCTyr1/sr5	167	167	208	212	214	261	160	179	117	117	-	-
	90265	D1	YCTyr5	163	171	229	250	201	249	185	195	117	119	199	265
	90266	B	YCTyr2/sr3	167	175	208	242	214	251	177	177	119	119	254	254
	90267	B	YCTyr2/sr3	163	163	242	246	225	231	179	179	117	117	265	269
	90268	B	YCTyr2/sr3	167	175	208	242	214	251	177	177	119	119	254	254
	90269	A	YCTyr1/sr5	171	175	250	250	249	253	173	177	117	121	171	171
	90270	A	YCTyr1/sr5	163	167	-	-	216	225	166	171	117	117	187	277
Little Thumb Campground Creek	90271	B1	YCTyr13	159	159	195	199	253	261	164	183	117	121	273	273
	90272	-	-	151	167	208	265	225	236	177	177	117	119	167	269
	90273	B	YCTyr2/sr3	171	207	195	269	214	249	175	177	117	117	195	273
	90274	A	YCTyr1/sr5	167	171	195	254	219	249	173	175	117	117	195	281
	90275	B	YCTyr2/sr3	163	167	208	258	225	249	173	177	117	119	167	258
	90276	B	YCTyr2/sr3	163	167	212	233	201	201	177	183	117	117	-	-
	90277	A	YCTyr1/sr5	159	171	208	250	223	244	164	175	117	117	171	179
	90278	O	YCTyr41	155	163	208	212	201	225	160	179	117	117	-	-
	90279	B	YCTyr2/sr3	-	-	-	-	-	-	177	187	117	119	167	167

Little Thumb Campground Creek	90280	G	YCTyr23	163	171	195	212	214	214	162	166	117	117	167	187
	90281	B	YCTyr2/sr3	163	167	195	229	225	229	183	193	117	117	167	167
	90282	-	-	159	163	195	261	249	255	173	173	117	119	187	277
	90283	U1	YCTyr53	167	171	208	216	214	261	162	195	117	117	167	171
	90284	-	-	159	167	195	212	201	249	173	177	117	119	171	203
	90285	A	YCTyr1/sr5	163	167	195	208	201	249	177	179	117	117	171	273
	90286	E1	YCTyr20	163	167	203	208	249	251	183	185	117	117	187	265
	90287	A	YCTyr1/sr5	163	167	203	212	214	249	177	177	117	117	167	171
	90288	A	YCTyr1/sr5	163	211	212	216	214	216	171	181	117	121	183	199
	90289	V1	YCTyr55	163	163	265	269	238	253	171	181	113	121	171	183
	90290	B	YCTyr2/sr3	159	163	208	212	249	261	-	-	-	-	-	-
	90291	B	YCTyr2/sr3	163	167	195	229	225	229	185	193	117	117	167	167
	90292	A	YCTyr1/sr5	163	167	208	208	201	225	181	183	117	119	258	262
	90293	N1	YCTyr40	155	167	212	265	225	251	177	183	117	117	175	185
	90294	B	YCTyr2/sr3	155	167	195	212	225	249	177	181	121	121	171	187
	90295	M1	YCTyr38	159	159	203	258	249	261	171	179	117	121	187	225
	90296	B	YCTyr2/sr3	155	163	216	224	225	249	177	199	117	121	171	187
	90297	A	YCTyr1/sr5	163	171	212	250	201	223	177	177	117	117	273	277
	90298	B	YCTyr2/sr3	167	175	203	212	201	225	177	187	117	117	163	265
	90299	B	YCTyr2/sr3	167	167	208	208	249	261	177	187	117	119	167	167
	90300	A	YCTyr1/sr5	159	167	203	208	225	249	177	179	117	117	199	269
Yellowstone River near Fishing Bridge	90301	-	-	163	171	208	212	229	249	168	175	117	117	-	-
	90302	B	YCTyr2/sr3	163	171	208	212	229	249	168	175	117	117	179	269
	90303	A	YCTyr1/sr5	167	175	208	220	216	249	171	189	117	117	-	-
	90304	-	-	167	167	203	208	219	249	173	179	117	117	-	-
	90305	A	YCTyr1/sr5	171	175	199	208	249	249	162	162	117	117	187	265
	90306	S	YCTyr48	163	171	191	258	225	225	181	193	117	121	258	265
	90307	-	-	167	171	195	203	225	225	177	185	117	117	167	242
	90308	A	YCTyr1/sr5	171	175	208	208	214	229	177	177	117	117	171	191
	90309	T	YCTyr50	167	167	195	195	225	251	171	179	117	117	171	273
	90310	A	YCTyr1/sr5	163	163	208	208	249	261	152	164	121	121	175	285
	90311	T	YCTyr50	167	171	203	212	216	249	181	185	117	117	171	175

Yellowstone River near Fishing Bridge	90312	A	YCTyr1/sr5	163	171	195	208	219	249	168	179	117	117	187	246
	90313	B	YCTyr2/sr3	159	167	191	212	249	259	152	185	115	115	265	265
	90314	B	YCTyr2/sr3	-	-	195	208	-	-	173	175	-	-	-	-
	90315	-	-	163	171	195	199	-	-	-	-	117	117	-	-
	90316	B	YCTyr2/sr3	167	171	208	216	214	225	177	177	117	117	175	199
	90317	-	-	163	163	195	208	201	225	175	177	117	121	175	265
	90318	J	YCTyr29	163	163	199	203	219	225	162	162	117	121	179	269
	90319	Y	YCTyr58	163	167	208	261	225	265	160	160	115	121	265	273
	90320	A	YCTyr1/sr5	167	167	208	208	214	225	173	185	117	117	171	175
	90321	A	YCTyr1/sr5	163	167	195	199	249	249	152	173	121	121	183	254
	90322	A	YCTyr1/sr5	163	163	208	212	263	263	177	195	117	117	199	203
	90323	U	YCTyr52	163	171	195	208	214	225	177	177	117	117	195	199
	90324	A	YCTyr1/sr5	159	167	203	208	249	249	152	189	117	121	179	265
	90325	A	YCTyr1/sr5	159	167	208	208	214	225	160	189	117	121	175	229
	90326	-	-	163	163	195	212	219	249	152	177	117	117	273	281
	90327	-	-	-	-	195	199	-	-	-	-	-	-	-	-
	90329	WCT	-	-	-	-	-	-	-	-	-	-	-	-	-
	90330	-	-	163	175	203	250	214	249	189	195	115	121	179	179
Thorofare Creek	135899	U	YCTyr52	167	167	208	261	219	249	160	177	117	117	183	304
	135900	B	YCTyr2/sr3	155	167	195	250	212	216	-	-	117	117	-	-
	135901	A	YCTyr1/sr5	167	175	212	212	225	263	158	177	117	117	199	296
	135902	B	YCTyr2/sr3	163	167	195	212	201	214	160	175	117	117	183	269
	135903	K	YCTyr31	167	171	224	250	223	246	177	181	117	117	175	269
	135904	E3	-	163	167	195	250	244	244	-	-	117	117	195	258
	135905	A	YCTyr1/sr5	163	171	195	208	201	214	173	177	117	117	171	179
	135906	F3	-	163	171	216	216	201	225	-	-	117	119	183	265
	135907	B	YCTyr2/sr3	163	171	208	208	214	229	177	179	117	117	171	258
	135908	-	-	159	167	203	237	249	249	177	185	117	117	175	183
	135909	B	YCTyr2/sr3	163	167	212	224	214	225	177	199	117	117	183	195
	135910	B	YCTyr2/sr3	163	163	254	258	225	251	-	-	117	121	167	191
	135911	-	-	163	163	203	250	249	251	171	179	117	117	183	269
	135912	B	YCTyr2/sr3	163	163	195	254	214	225	173	177	117	117	171	262

Thorofare Creek	135913	A	YCTyr1/sr5	167	171	199	208	229	249	-	-	117	121	179	269
	135914	B	YCTyr2/sr3	159	167	208	250	225	225	177	177	117	121	-	-
	135915	B1	YCTyr13	163	167	212	261	201	249	-	-	117	117	-	-
	135916	A	YCTyr1/sr5	167	175	208	212	229	253	158	177	117	117	175	191
	135917	-	-	159	167	212	254	214	251	177	179	117	117	175	285
	135918	A	YCTyr1/sr5	163	167	195	203	249	251	173	173	117	117	179	191
	135919	A	YCTyr1/sr5	163	167	208	265	246	249	160	173	117	117	187	191
	135920	A	YCTyr1/sr5	151	159	208	261	201	229	168	181	117	117	-	-
	135921	A	YCTyr1/sr5	163	171	237	250	201	251	160	177	117	117	179	187
	135922	A	YCTyr1/sr5	163	163	203	258	214	249	177	177	117	117	199	254
	135923	G3	-	163	167	208	258	201	249	-	-	117	117	216	277
	135924	A	YCTyr1/sr5	163	163	208	216	214	255	-	-	115	117	-	-
	135925	A	YCTyr1/sr5	159	163	195	208	214	246	-	-	117	121	179	269
Yellowstone River inlet	188778	B	YCTyr2/sr3	163	171	216	229	214	227	177	179	117	117	183	281
	188779	A	YCTyr1/sr5	163	163	212	250	225	249	183	197	117	117	191	203
	188780	A	YCTyr1/sr5	163	171	250	254	225	242	156	193	117	117	171	179
	188781	A	YCTyr1/sr5	163	163	195	212	201	249	162	179	117	117	183	265
	188782	D2	-	163	167	195	212	225	229	168	183	117	119	187	281
	188783	K	YCTyr31	163	163	207	265	214	219	173	173	117	117	269	269
	188784	B	YCTyr2/sr3	163	167	250	254	214	261	164	173	117	117	179	258
	188785	A	YCTyr1/sr5	163	171	246	258	249	261	156	179	117	117	175	273
	188786	A	YCTyr1/sr5	159	159	207	216	214	229	175	177	117	117	191	191
	188787	A	YCTyr1/sr5	163	175	203	207	214	225	-	-	-	-	167	183
	188788	A	YCTyr1/sr5	159	163	203	250	225	249	158	185	117	117	199	289
	188789	E2	-	163	167	207	250	225	249	160	175	117	119	269	277
	188790	F2	-	159	171	195	250	214	216	160	185	117	117	179	265
	188791	G2	-	-	-	237	250	214	249	179	197	117	117	187	199
	188792	A	YCTyr1/sr5	167	171	216	265	225	261	171	177	117	117	167	281
	188793	B	YCTyr2/sr3	163	167	207	224	219	225	175	177	115	117	179	195
	188794	B	YCTyr2/sr3	167	167	246	261	225	229	175	177	117	117	179	281
	188795	B	YCTyr2/sr3	167	171	212	258	214	225	164	166	117	117	175	195
	188796	M	YCTyr37	-	-	258	258	201	249	177	181	117	117	183	281

Yellowstone River inlet	188797	H2	-	163	167	199	258	225	265	158	160	117	117	179	183
	188798	B	YCTyr2/sr3	167	171	212	216	225	249	160	179	117	117	195	212
	188799	A	YCTyr1/sr5	159	163	212	233	225	249	173	177	117	117	171	179
	188800	A	YCTyr1/sr5	167	167	250	250	214	249	-	-	-	-	-	-
	188801	Z	YCTyr59	167	167	195	269	225	249	177	177	117	117	171	187
	188802	A	YCTyr1/sr5	167	171	195	207	221	225	162	177	113	117	175	269
	188803	B	YCTyr2/sr3	167	167	250	258	225	249	168	177	117	117	265	296
	188804	M	YCTyr37	179	203	207	212	214	214	175	175	117	117	179	273
	188805	A	YCTyr1/sr5	163	167	195	207	201	267	175	175	117	117	183	277
	188806	I2	-	163	167	195	265	225	249	179	181	117	117	-	-
	188807	A	YCTyr1/sr5	163	163	195	261	214	240	160	187	117	117	175	277
Atlantic Creek	135883	M	YCTyr37	167	203	195	250	225	261	175	175	117	117	269	269
	135884	W1	YCTyr9	163	167	258	269	219	229	168	187	117	117	171	273
	135885	X1	YCTyr10	151	167	208	212	255	257	175	189	117	117	175	191
	135886	A	YCTyr1/sr5	163	167	195	208	201	249	183	183	117	117	-	-
	135887	A	YCTyr1/sr5	167	171	208	216	225	249	160	171	117	117	-	-
	135888	A	YCTyr1/sr5	159	163	212	246	219	229	168	177	117	117	179	191
	135889	A	YCTyr1/sr5	163	167	203	233	214	214	166	173	117	117	179	187
	135890	B	YCTyr2/sr3	167	171	208	261	214	225	160	179	117	117	167	179
	135891	A	YCTyr1/sr5	159	167	212	269	214	214	177	177	117	117	171	269
	135892	-	-	159	167	208	212	225	229	175	177	117	117	175	175
	135893	C1	YCTyr16	163	171	212	233	225	251	175	177	117	117	171	175
	135894	A	YCTyr1/sr5	167	167	203	242	201	225	177	179	117	117	191	265
	135895	A	YCTyr1/sr5	167	171	212	265	227	227	181	183	-	-	-	-
	135896	A	YCTyr1/sr5	167	167	216	250	216	251	177	177	117	117	203	258
	135897	B	YCTyr2/sr3	167	167	195	233	214	249	160	173	117	117	-	-
	135898	B	YCTyr2/sr3	167	171	258	261	214	251	-	-	-	-	-	-
Heart River	141886	-	-	163	175	191	229	255	255	-	-	119	121	-	-
	141887	S1	YCTsr4	167	167	233	237	255	255	181	191	117	119	171	187
	141888	A	YCTyr1/sr5	171	203	233	254	223	255	-	-	117	119	195	195
	141889	B	YCTyr2/sr3	159	175	191	237	223	251	162	187	117	119	195	195
	141890	B	YCTyr2/sr3	179	183	216	229	251	261	-	-	119	119	-	-

Heart River	141891	S1	YCTsr4	163	183	195	233	208	261	171	187	119	119	195	199
	141892	A	YCTyr1/sr5	171	183	203	216	214	255	154	154	117	117	-	-
	141893	B	YCTyr2/sr3	159	175	-	-	255	255	189	189	117	121	-	-
	141894	B	YCTyr2/sr3	167	179	229	246	255	261	168	168	117	119	159	199
	141895	A	YCTyr1/sr5	167	175	265	273	208	208	-	-	117	117	171	199
	141896	M2	-	171	203	191	233	219	221	156	156	117	119	191	216
	141897	S1	YCTsr4	175	183	191	237	223	270	171	187	119	119	171	195
	141898	S1	YCTsr4	171	171	-	-	-	-	181	181	117	117	167	258
	141899	B	YCTyr2/sr3	163	175	191	216	219	255	187	187	119	121	171	258
	141900	B	YCTyr2/sr3	159	167	233	273	208	259	171	185	117	119	212	216
	141901	S1	YCTsr4	159	167	229	246	214	259	177	187	117	117	171	175
	141902	S1	YCTsr4	167	179	195	195	208	219	171	185	117	117	159	258
	141903	L2	-	167	183	195	216	255	255	164	181	119	121	163	171
	141904	S1	YCTsr4	163	167	237	246	255	270	-	-	117	119	171	195
	141905	S1	YCTsr4	171	175	191	195	208	261	177	191	117	117	171	195
	141906	A	YCTyr1/sr5	159	179	237	273	208	223	179	179	117	117	199	207
	141907	B	YCTyr2/sr3	175	179	216	246	219	269	191	191	117	121	195	258
	141908	A	YCTyr1/sr5	171	203	191	277	208	270	168	168	117	117	175	203
	141909	L2	-	167	183	224	229	225	269	166	193	117	117	195	195
	141910	S1	YCTsr4	171	179	191	237	208	227	168	189	117	117	195	195
	141976	B	YCTyr2/sr3	167	199	191	237	219	223	181	181	121	121	220	220
	141977	B	YCTyr2/sr3	167	199	224	233	223	270	181	191	117	121	207	220
	141987	B	YCTyr2/sr3	167	167	224	237	255	261	189	189	119	119	195	199
	142008	B	YCTyr2/sr3	167	167	199	246	208	208	177	187	117	117	187	207
	142009	B	YCTyr2/sr3	167	175	195	237	219	261	164	191	117	119	171	195
	142010	-	-	167	179	195	224	255	261	166	189	117	119	159	159
	142011	B	YCTyr2/sr3	163	175	237	237	219	251	171	181	117	121	195	212
	142012	B	YCTyr2/sr3	167	203	195	258	255	269	187	191	117	117	175	191
	142013	S1	YCTsr4	163	179	216	229	208	270	154	168	117	121	199	261
Heart Lake	91012	S1	YCTsr4	159	175	233	237	255	255	189	191	119	121	171	199
	91013	S1	YCTsr4	167	171	195	199	-	-	166	166	119	121	-	-
	91014	S1	YCTsr4	155	207	191	273	219	225	177	191	117	117	207	212

Heart Lake	91015	S1	YCTsr4	159	171	216	233	259	270	189	191	117	119	171	195
	91016	B	YCTyr2/sr3	163	175	229	233	255	261	189	189	121	121	-	-
	91017	B	YCTyr2/sr3	163	207	191	237	208	214	177	191	119	119	-	-
	91018	A	YCTyr1/sr5	179	207	233	265	208	257	181	181	117	117	-	-
	91019	B	YCTyr2/sr3	183	203	224	242	208	257	191	191	117	117	191	195
	91020	B	YCTyr2/sr3	163	179	237	237	219	255	181	189	117	117	171	199
	91021	B	YCTyr2/sr3	167	171	229	229	208	251	181	181	117	117	-	-
	91022	S1	YCTsr4	183	191	191	233	208	246	189	189	117	119	187	195
	91023	S1	YCTsr4	167	183	246	246	219	255	179	179	117	117	195	195
	91024	B	YCTyr2/sr3	163	187	224	237	251	269	189	189	117	117	195	207
	91025	S1	YCTsr4	167	183	224	269	208	257	191	193	117	119	220	225
	91026	B	YCTyr2/sr3	167	199	195	273	249	255	164	191	119	121	212	258
	91027	S1	YCTsr4	159	167	229	246	208	257	179	189	117	117	171	203
	91028	S1	YCTsr4	171	171	191	277	214	255	179	189	117	119	220	258
	91029	S1	YCTsr4	171	207	191	246	219	255	177	177	117	119	-	-
	91030	S1	YCTsr4	167	199	191	246	208	242	177	177	115	119	171	171
	91031	S1	YCTsr4	167	175	233	265	225	246	181	181	117	117	-	-
	91032	S1	YCTsr4	171	183	191	216	208	259	175	189	119	119	163	195
	91033	RT	RT	-	-	-	-	-	-	-	-	-	-	-	-
Sickle Creek	141911	S1	YCTsr4	175	179	229	258	223	257	162	185	119	121	195	203
	141912	S1	YCTsr4	167	183	195	229	227	255	147	191	117	119	179	195
	141913	S1	YCTsr4	171	175	191	254	208	219	185	191	117	121	191	195
	141914	T2	-	167	175	224	229	225	255	147	191	117	119	175	187
	141915	B	YCTyr2/sr3	163	167	191	242	255	261	187	195	117	117	191	207
	141916	-	-	159	163	195	237	-	-	191	195	117	119	203	207
	141917	S1	YCTsr4	167	175	199	265	221	259	168	191	117	119	195	273
	141918	-	-	163	167	191	229	221	255	177	189	119	119	207	220
	141919	S1	YCTsr4	167	167	191	191	216	261	175	175	117	117	183	187
	141920	B	YCTyr2/sr3	151	179	195	229	255	255	177	195	117	119	191	233
	141921	B	YCTyr2/sr3	175	199	242	277	214	223	164	166	117	119	175	191
	141922	S1	YCTsr4	171	175	191	233	201	255	175	187	117	117	183	183
	141923	S1	YCTsr4	167	175	208	233	214	219	162	187	117	117	179	216

Sickle Creek	141924	A	YCTyr1/sr5	159	167	191	233	249	251	191	197	117	117	183	203
	141925	A	YCTyr1/sr5	167	171	191	229	255	269	154	179	117	117	195	237
	141926	T1	YCTsr1	163	171	203	237	221	227	189	191	117	117	207	216
	141927	S1	YCTsr4	167	167	191	237	249	259	166	168	117	117	187	187
	141928	B	YCTyr2/sr3	171	179	191	224	201	214	189	191	117	117	179	233
	141929	S1	YCTsr4	167	171	224	250	214	255	177	185	115	117	171	237
	141930	S1	YCTsr4	167	175	246	246	201	251	191	191	117	121	191	199
	141931	A	YCTyr1/sr5	159	167	199	258	255	263	187	191	117	119	191	195
	141932	T2	-	159	175	246	265	214	251	191	197	117	117	199	207
	141933	B	YCTyr2/sr3	175	183	229	233	208	249	179	191	117	119	195	199
	141934	B	YCTyr2/sr3	167	171	233	246	208	208	191	191	117	121	183	199
	141935	T2	-	167	203	191	195	208	208	175	191	117	117	191	207
	141936	B	YCTyr2/sr3	167	179	246	273	208	261	162	191	117	119	183	207
	141937	S1	YCTsr4	171	175	246	258	208	221	185	193	117	121	195	216
	141938	A	YCTyr1/sr5	171	175	195	254	214	223	191	197	121	121	203	207
	141939	A	YCTyr1/sr5	163	167	191	254	255	265	147	177	117	119	179	220
	141940	A	YCTyr1/sr5	163	167	191	229	255	265	177	189	117	117	179	220
	141941	A	YCTyr1/sr5	167	171	229	254	221	265	189	189	117	119	179	220
	141942	A	YCTyr1/sr5	163	163	195	254	-	-	177	191	117	121	183	207
	141943	S1	YCTsr4	167	171	191	229	221	265	147	177	115	117	183	207
	141944	-	-	159	167	229	242	223	225	-	-	117	117	171	183
	141945	A	YCTyr1/sr5	167	175	191	229	208	255	147	147	117	117	207	216
	141946	S1	YCTsr4	159	179	191	191	259	265	147	191	117	119	183	183
	142014	B	YCTyr2/sr3	167	171	191	254	255	255	189	195	117	121	179	203
Crooked Creek	141947	S1	YCTsr4	175	207	250	250	216	225	189	189	119	121	195	254
	141948	S1	YCTsr4	167	211	191	195	227	257	-	-	117	117	-	-
	141949	S1	YCTsr4	163	163	250	250	-	-	189	191	117	117	207	233
	141950	S1	YCTsr4	211	211	199	224	257	257	166	191	117	121	233	262
	141951	S1	YCTsr4	211	211	195	250	246	251	164	206	117	121	187	220
	141952	S1	YCTsr4	175	175	195	250	251	251	171	171	117	119	179	254
	141953	S1	YCTsr4	167	179	195	199	257	257	189	191	121	121	179	258
	141954	S1	YCTsr4	175	211	191	199	257	257	179	195	117	117	203	237

Crooked Creek	141955	S1	YCTsr4	175	175	208	233	257	257	166	179	117	117	212	220
	141956	S1	YCTsr4	175	211	250	261	253	257	189	189	117	117	233	262
	141957	S1	YCTsr4	175	175	195	233	214	257	166	171	117	121	179	250
	141958	B	YCTyr2/sr3	167	175	195	208	257	257	189	191	117	117	207	250
	141959	-	-	171	175	208	254	214	255	191	195	117	117	179	207
	141960	S1	YCTsr4	175	211	191	250	253	255	191	191	117	119	262	262
	141961	S1	YCTsr4	163	211	250	254	253	257	191	191	119	119	199	237
	141962	S1	YCTsr4	179	215	229	250	212	212	185	191	119	121	179	237
	141963	S1	YCTsr4	175	179	195	199	257	257	185	195	117	119	179	195
	141964	S1	YCTsr4	163	163	195	199	214	255	191	191	119	119	179	179
	141965	-	-	175	179	191	254	257	257	-	-	117	117	212	262
	142027	S1	YCTsr4	171	215	250	250	212	212	187	187	119	121	179	254
	142028	S1	YCTsr4	171	207	195	224	219	257	191	191	117	119	179	233
	142029	S1	YCTsr4	175	207	250	250	201	255	191	191	117	119	179	258
	142030	S1	YCTsr4	175	207	229	250	253	253	166	189	119	121	179	254
	142031	-	-	175	207	199	254	219	257	171	191	119	121	254	262
	142032	S1	YCTsr4	175	207	250	250	216	253	168	189	117	117	229	233
	142033	S1	YCTsr4	179	207	229	250	253	253	179	191	117	117	212	212
	142034	S1	YCTsr4	163	207	195	199	201	257	191	191	117	117	179	254
	142035	S1	YCTsr4	171	175	191	208	214	259	191	195	117	117	179	254
	142036	S1	YCTsr4	163	171	195	195	-	-	187	191	117	117	191	258
	142037	S1	YCTsr4	167	207	250	254	212	212	168	191	117	119	179	254
	142038	S1	YCTsr4	171	207	191	224	255	255	189	189	117	117	207	233
	142039	S1	YCTsr4	175	175	195	250	253	253	168	189	117	119	179	254
	142040	S1	YCTsr4	171	175	191	250	216	253	189	189	119	121	195	258
	142041	B	YCTyr2/sr3	159	159	229	229	227	261	189	189	117	117	212	233
	142042	S1	YCTsr4	203	211	208	233	214	255	171	189	117	119	233	254
	142043	B	YCTyr2/sr3	163	175	250	250	253	253	189	191	117	121	237	254
	142044	B	YCTyr2/sr3	207	211	199	203	208	255	189	191	119	121	233	262
	142045	S1	YCTsr4	175	175	191	250	212	246	191	195	117	117	179	250
Snake River (upper)	141978	O2	-	163	167	195	250	201	251	154	154	117	119	207	258
	141979	S1	YCTsr4	167	175	208	229	214	219	177	195	117	117	183	195

Snake River (upper)	141980	A	YCTyr1/sr5	167	167	191	250	255	257	181	185	117	119	199	207
	141981	S1	YCTsr4	159	167	195	199	255	255	181	197	117	117	171	175
	141982	-	-	167	167	191	191	255	255	193	197	117	119	220	233
	141983	S1	YCTsr4	179	211	233	237	223	269	154	156	117	121	203	207
	141984	B	YCTyr2/sr3	167	211	199	254	201	208	189	189	117	117	183	195
	141985	A	YCTyr1/sr5	175	175	199	265	216	261	168	191	117	117	183	233
	141986	-	-	183	183	233	233	261	269	171	197	117	121	159	195
	141988	-	-	171	183	191	246	208	259	187	208	117	119	191	195
	141989	B	YCTyr2/sr3	155	163	246	254	214	227	181	185	115	117	187	246
	141990	G	YCTyr23	171	175	191	216	221	227	191	191	117	117	-	-
	141991	G	YCTyr23	171	171	191	216	223	246	156	191	117	119	207	233
	141992	S1	YCTsr4	155	159	233	237	201	225	187	191	119	121	187	258
	141993	S1	YCTsr4	167	183	229	242	214	261	152	189	117	121	171	175
	141994	S1	YCTsr4	179	183	237	265	246	257	154	177	117	121	179	207
	141995	N2	-	163	171	233	250	225	265	154	191	117	117	167	233
	141996	M2	-	163	171	233	246	201	219	185	185	115	117	191	261
	141997	N2	-	171	207	233	237	214	246	179	191	117	121	171	171
	141998	S1	YCTsr4	167	199	191	195	214	223	162	162	119	119	191	207
	141999	S1	YCTsr4	167	183	216	237	223	265	154	171	117	119	159	229
	142000	B	YCTyr2/sr3	163	175	229	233	242	251	181	187	119	119	199	229
	142001	S1	YCTsr4	163	167	216	242	214	225	168	168	115	115	195	199
	142002	G	YCTyr23	163	175	246	277	223	255	175	189	117	121	195	207
	142003	S1	YCTsr4	163	175	191	242	201	221	156	189	117	119	195	233
	142004	B	YCTyr2/sr3	167	175	237	237	255	261	-	-	117	117	171	220
	142005	L2	-	167	167	216	237	251	255	187	189	117	117	171	203
	142006	N2	-	159	171	246	254	201	214	154	189	117	119	229	273
	142007	S1	YCTsr4	163	163	246	254	246	255	168	179	117	117	167	187
	142015	S1	YCTsr4	163	211	195	199	214	216	173	191	117	117	233	246
	142016	S1	YCTsr4	163	175	233	254	219	257	189	191	117	117	237	254
	142017	S1	YCTsr4	163	203	199	208	255	257	166	189	117	119	195	195
	142018	S1	YCTsr4	175	175	208	233	214	216	166	191	117	119	195	233
	142019	S1	YCTsr4	175	211	250	250	251	253	187	189	117	119	233	233

Snake River (upper)	142020	S1	YCTsr4	179	211	199	199	214	255	164	189	117	117	187	258
	142021	S1	YCTsr4	175	175	208	250	212	244	164	195	117	117	179	187
	142022	S1	YCTsr4	163	175	195	233	255	257	166	166	119	121	187	258
	142023	S1	YCTsr4	171	211	191	208	214	249	164	195	117	117	179	250
	142024	S1	YCTsr4	167	171	195	208	225	255	189	189	117	117	261	261
	142025	S1	YCTsr4	203	211	250	250	212	251	166	189	117	117	187	199
	142026	S1	YCTsr4	175	175	199	199	259	259	191	191	117	121	233	258
Forest Creek	141841	A	YCTyr1/sr5	167	171	208	246	214	214	-	-	100	117	175	175
	141842	N2	-	163	175	195	269	214	259	179	189	117	117	203	229
	141843	S1	YCTsr4	163	163	195	203	214	219	168	179	117	117	183	273
	141844	N2	-	163	171	237	254	214	261	164	179	117	121	233	237
	141845	A	YCTyr1/sr5	159	179	246	277	219	255	154	191	117	117	187	212
	141846	S1	YCTsr4	159	171	233	242	255	257	154	154	117	119	171	175
	141847	M2	-	171	175	195	258	259	263	166	168	117	119	171	207
	141848	R2	-	163	171	242	265	214	214	166	173	115	117	179	273
	141849	R2	-	163	163	208	242	214	227	162	162	100	100	175	175
	141850	-	-	163	167	203	242	214	214	173	179	100	100	175	175
	141851	R2	-	163	167	246	246	214	214	166	171	100	100	175	175
	141852	-	-	159	167	208	265	214	214	166	177	100	117	175	273
	141853	R2	-	163	167	208	265	214	214	162	187	100	115	175	269
	141854	A	YCTyr1/sr5	159	163	246	246	214	214	162	171	117	117	167	175
	141855	R2	-	163	167	212	246	201	214	166	173	100	100	175	187
	141856	R2	-	159	171	208	233	214	214	158	173	100	117	175	265
	141857	A	YCTyr1/sr5	163	171	195	212	214	261	177	177	100	117	-	-
	141858	R2	-	159	171	242	246	-	-	162	181	100	100	167	187
	141859	R2	-	163	171	208	237	214	225	162	181	100	100	179	191
	141860	R2	-	159	167	246	246	214	225	166	173	100	117	167	179
	141861	-	-	159	171	195	237	214	225	162	162	100	117	167	179
	141862	R2	-	159	167	195	237	214	225	162	162	100	117	171	175
	141863	R2	-	159	167	208	237	214	225	162	171	117	117	175	179
	141864	R2	-	159	163	195	237	225	225	162	171	100	117	175	175
	141865	R2	-	167	171	246	246	214	225	162	171	117	117	167	179

Forest Creek	141866	R2	-	159	167	208	246	214	225	162	171	100	100	167	175
	141867	R2	-	159	163	195	265	214	214	160	160	100	117	175	265
	141868	R2	-	163	171	208	216	214	225	162	162	100	100	175	179
	141869	R2	-	163	163	216	242	214	214	162	162	100	100	179	179
	141870	R2	-	159	171	242	265	214	225	162	171	100	100	175	179
	141871	R2	-	167	171	208	237	214	214	162	162	100	100	179	191
	141872	R2	-	163	167	208	216	214	214	162	162	100	100	179	179
	141873	R2	-	159	159	195	195	214	214	171	171	-	-	175	175
	141874	R2	-	159	171	208	237	214	225	166	171	-	-	175	191
Pacific Creek	136751	R1	YCTsr7	159	159	250	250	201	238	177	199	115	119	212	258
	136752	B	YCTyr2/sr3	159	163	242	261	221	238	197	210	117	117	179	191
	136753	R1	YCTsr7	163	167	242	258	221	223	-	-	117	121	183	225
	136754	B	YCTyr2/sr3	163	167	195	250	219	246	147	195	117	119	179	229
	136756	S1	YCTsr4	159	175	237	269	223	261	173	177	117	119	207	225
	136757	B	YCTyr2/sr3	167	175	199	224	223	261	185	195	117	117	212	225
	136758	-	-	159	175	195	203	-	-	-	-	-	-	-	-
	136759	R1	YCTsr7	159	179	233	237	-	-	173	185	117	119	191	191
	136760	B	YCTyr2/sr3	159	163	233	258	221	261	173	175	115	117	207	237
	136761	R1	YCTsr7	167	171	250	254	201	219	154	210	117	119	225	229
	136762	B	YCTyr2/sr3	-	-	233	246	-	-	154	185	117	121	191	207
	136763	R1	YCTsr7	163	167	229	250	208	219	183	191	117	121	191	250
	136764	S1	YCTsr4	163	167	246	258	221	261	185	185	117	117	212	237
	136765	T1	YCTsr1	159	167	233	261	246	261	171	183	121	121	199	258
	136766	B	YCTyr2/sr3	167	167	250	258	201	221	142	179	117	121	187	225
	136767	R1	YCTsr7	167	167	242	250	201	212	185	197	117	117	207	237
	136768	B	YCTyr2/sr3	159	167	195	233	201	210	183	185	117	121	199	237
Sedge Creek	90361	I	YCTyr27	159	159	208	208	251	251	183	183	117	117	167	167
	90362	I	YCTyr27	159	159	208	208	251	251	183	183	117	117	167	167
	90363	I	YCTyr27	159	159	208	208	251	251	183	183	117	117	167	167
	90364	I	YCTyr27	159	159	208	208	251	251	183	183	117	117	167	171
	90365	I	YCTyr27	159	159	208	208	251	251	183	183	117	117	167	167
	90366	I	YCTyr27	159	159	208	208	251	251	183	183	117	117	167	167

Sedge Creek	90367	I	YCTyr27	159	159	208	208	251	251	183	183	117	117	167	167
	90368	I	YCTyr27	159	159	208	208	251	251	183	183	117	117	167	167
	90369	I	YCTyr27	159	159	208	208	251	251	183	183	117	117	167	167
	90370	I	YCTyr27	159	159	208	208	251	251	183	183	117	117	167	167
	90371	I	YCTyr27	159	159	208	208	251	251	183	183	117	117	167	167
	90372	I	YCTyr27	159	159	208	208	251	251	183	183	117	117	167	167
	90373	I	YCTyr27	159	159	208	208	251	251	183	183	117	117	167	167
	90374	I	YCTyr27	159	159	208	208	251	251	-	-	-	-	-	-
	90375	I	YCTyr27	159	159	208	208	251	251	183	183	117	117	167	167
	90376	I	YCTyr27	-	-	-	-	-	-	183	183	117	117	167	167
	90377	I	YCTyr27	159	159	208	208	251	251	183	183	117	117	167	167
	90378	I	YCTyr27	159	159	208	208	251	251	183	183	117	117	167	167
	90379	I	YCTyr27	159	159	208	208	251	251	183	183	117	117	167	167
	90380	I	YCTyr27	159	159	208	208	251	251	183	183	117	117	167	167
	90381	I	YCTyr27	159	159	208	208	251	251	183	183	117	117	167	171
	90382	I	YCTyr27	159	159	203	208	251	251	183	183	117	117	167	167
	90383	I	YCTyr27	159	159	208	208	251	251	183	183	117	117	167	167
	90384	I	YCTyr27	159	159	203	208	251	251	183	183	117	117	167	167
	90385	I	YCTyr27	159	159	208	208	251	251	183	183	117	117	167	167
	90386	I	YCTyr27	159	159	208	208	251	251	183	183	117	117	167	167
	90387	I	YCTyr27	159	159	208	208	251	251	183	183	117	117	167	167
	90388	I	YCTyr27	159	159	208	208	251	251	183	183	117	117	167	167
	90389	I	YCTyr27	159	159	208	208	251	251	183	183	117	117	167	167
	90390	I	YCTyr27	159	159	208	208	251	251	-	-	-	-	-	-
Pelican Creek (upper)	142100	A	YCTyr1/sr5	167	167	199	212	227	249	179	179	117	117	183	269
	142102	S2	-	163	171	195	208	214	225	164	177	115	117	-	-
	142103	A	YCTyr1/sr5	167	175	195	195	214	225	166	183	117	117	191	258
	142105	-	-	159	171	212	212	249	249	177	181	117	117	179	199
	142106	A	YCTyr1/sr5	167	171	195	212	214	225	171	173	113	117	171	187
	142107	-	-	-	-	-	-	-	-	-	-	117	117	-	-
	142109	S2	-	163	171	195	216	214	225	175	183	115	117	191	262
	142110	A	YCTyr1/sr5	159	167	195	254	225	238	173	181	117	117	171	175

Pelican Creek (upper)	142111	A	YCTyr1/sr5	167	171	199	199	219	227	166	166	117	117	171	191
	142112	-	-	167	171	195	212	214	249	-	-	117	117	191	258
	142113	A	YCTyr1/sr5	-	-	-	-	-	-	179	179	113	117	179	265
	142114	S2	-	159	163	208	216	225	225	183	183	117	117	171	171
	142115	A	YCTyr1/sr5	167	171	199	199	227	227	158	173	115	117	171	199
	142116	B	YCTyr2/sr3	167	167	195	220	225	225	175	175	117	121	179	183
	142117	A	YCTyr1/sr5	167	171	195	195	214	225	171	173	117	117	191	258
	142118	A	YCTyr1/sr5	163	167	203	208	214	261	-	-	117	117	191	216
	142119	B	YCTyr2/sr3	163	167	195	212	214	225	162	164	117	117	269	277
	142120	B	YCTyr2/sr3	163	171	195	212	249	253	162	171	117	117	199	216
	142122	A	YCTyr1/sr5	163	167	195	212	225	249	-	-	117	119	171	175
	142123	A	YCTyr1/sr5	159	171	212	229	201	249	177	177	117	121	-	-
	142124	B	YCTyr2/sr3	159	163	208	216	214	225	-	-	117	121	183	216
	142125	A	YCTyr1/sr5	167	167	195	208	225	225	-	-	113	117	179	277
	142127	A	YCTyr1/sr5	167	167	195	195	225	225	179	181	113	117	179	277
	142128	A	YCTyr1/sr5	163	167	195	203	214	225	164	173	117	117	179	262
	142130	A	YCTyr1/sr5	163	167	208	265	225	251	175	181	113	117	179	277
	142131	A	YCTyr1/sr5	167	171	195	212	214	249	139	139	117	117	171	191
	142132	A	YCTyr1/sr5	167	167	208	265	223	251	175	177	117	119	179	265
	142134	A	YCTyr1/sr5	167	171	195	212	225	225	158	173	117	119	171	199
	142136	B	YCTyr2/sr3	163	163	195	208	225	229	177	177	117	117	187	187
	142137	B	YCTyr2/sr3	167	171	208	212	225	225	162	179	117	117	216	277
	142139	A	YCTyr1/sr5	163	167	195	216	201	214	164	177	117	117	195	269
Trout Creek	141966	P2	-	163	167	203	208	219	251	154	177	117	121	171	265
	141967	B	YCTyr2/sr3	163	167	208	242	214	225	162	177	117	117	179	258
	141968	-	-	163	167	208	212	219	225	179	189	117	117	175	175
	141969	S	YCTyr48	163	167	208	269	219	249	160	160	117	121	187	225
	141970	-	-	163	163	212	212	225	225	177	177	117	117	-	-
	141971	J	YCTyr29	163	171	203	208	225	225	175	175	121	121	175	265
	141972	A	YCTyr1/sr5	167	171	208	212	225	225	175	175	117	117	175	273
	141973	-	-	163	167	195	199	249	249	162	189	117	121	179	265
	141974	A	YCTyr1/sr5	163	167	199	208	219	225	162	177	117	117	179	220

Trout Creek	141975	-	-	163	163	199	212	219	225	177	179	117	121	-	-
	142046	J	YCTyr29	163	167	-	-	219	219	160	189	115	117	191	265
	142047	A	YCTyr1/sr5	163	167	-	-	219	225	162	179	117	121	171	277
	142048	E2	-	163	171	208	208	225	227	162	177	117	117	191	207
	142049	B	YCTyr2/sr3	171	175	195	208	216	249	177	177	117	117	-	-
	142050	S	YCTyr48	163	171	203	208	261	261	162	162	121	121	183	265
	142051	B	YCTyr2/sr3	167	171	208	208	225	261	179	189	117	121	179	273
	142052	E2	-	163	163	199	265	249	261	162	162	117	121	175	179
	142053	A	YCTyr1/sr5	167	171	195	254	216	249	177	177	115	117	191	191
	142054	J	YCTyr29	171	179	195	203	249	263	177	177	117	117	-	-
	142055	A	YCTyr1/sr5	167	171	-	-	214	219	177	179	117	117	183	254
	142145	A	YCTyr1/sr5	167	167	203	208	219	249	162	177	117	119	187	269
	142146	A	YCTyr1/sr5	163	167	203	208	219	251	135	179	117	121	195	265
	142147	A	YCTyr1/sr5	159	163	203	208	249	251	162	189	117	117	175	175
	142148	A	YCTyr1/sr5	163	167	-	-	201	219	162	162	117	117	179	281
	142149	A	YCTyr1/sr5	167	167	203	208	225	249	179	189	117	121	-	-
	142150	A	YCTyr1/sr5	163	167	199	212	219	225	177	177	115	117	187	269
	142151	A	YCTyr1/sr5	163	163	203	208	219	249	173	193	117	121	-	-
	142152	A	YCTyr1/sr5	163	167	199	212	225	251	162	177	121	121	175	175
	142153	A	YCTyr1/sr5	167	167	203	212	219	249	173	177	121	121	265	281
	142154	B	YCTyr2/sr3	163	163	199	208	219	255	162	173	115	121	183	187
	142155	A	YCTyr1/sr5	163	163	199	208	219	261	160	189	117	121	171	258
	142156	B	YCTyr2/sr3	163	167	208	212	219	219	160	173	117	121	175	273
	142157	A	YCTyr1/sr5	163	167	203	212	219	225	162	177	117	117	187	281
	142158	A	YCTyr1/sr5	163	171	203	208	219	249	177	187	117	117	183	265
	142159	A	YCTyr1/sr5	163	167	203	203	225	261	177	177	117	121	258	273
	142160	A	YCTyr1/sr5	167	167	208	212	219	225	177	189	115	121	-	-
	142161	A	YCTyr1/sr5	163	163	203	208	219	225	168	189	115	121	167	171
	142162	Q2	-	163	167	212	237	184	225	177	197	117	117	183	212
	142163	A	YCTyr1/sr5	163	163	203	208	249	249	162	173	121	121	220	273
	142164	J	YCTyr29	163	167	199	203	249	261	173	185	117	121	175	265
	142165	A	YCTyr1/sr5	163	163	208	212	219	219	162	189	117	117	175	187

Trout Creek	142166	A	YCTyr1/sr5	163	167	199	208	249	249	162	177	117	121	225	225
	142167	S	YCTyr48	163	163	199	199	219	219	160	191	117	121	225	265
	142168	A	YCTyr1/sr5	163	167	208	208	219	221	160	175	117	121	171	191
	142169	A	YCTyr1/sr5	163	163	203	216	219	261	152	177	117	117	171	183
	142170	B	YCTyr2/sr3	163	163	199	208	225	261	162	177	117	117	175	183
	142171	A	YCTyr1/sr5	163	167	203	203	219	251	152	160	121	121	265	273
	142172	A	YCTyr1/sr5	163	163	203	208	225	249	162	179	117	117	175	269
	142173	A	YCTyr1/sr5	163	167	199	203	201	219	175	177	121	121	225	269
	142174	A	YCTyr1/sr5	163	163	203	208	219	261	162	173	115	121	220	273
Antelope Creek (lower)	188619	A	YCTyr1/sr5	167	175	208	208	214	270	-	-	117	117	167	171
	188620	D3	-	167	171	208	208	246	249	-	-	117	117	167	179
	188621	-	-	-	-	-	-	-	-	-	-	117	117	-	-
	188622	A	YCTyr1/sr5	171	175	208	208	201	214	-	-	117	117	171	216
	188623	J2	-	175	175	208	208	214	214	191	193	117	117	171	179
	188625	J2	-	171	171	208	208	201	249	166	177	117	117	171	216
	188626	A	YCTyr1/sr5	167	171	208	220	214	255	-	-	117	117	171	183
	188627	-	-	167	175	208	208	201	249	-	-	-	-	171	179
	188628	D3	-	167	167	208	208	249	272	-	-	117	117	171	171
	188629	A	YCTyr1/sr5	167	171	208	224	201	249	166	166	117	117	171	171
	188630	A	YCTyr1/sr5	167	167	208	224	201	249	166	173	117	117	171	171
	188631	-	-	167	171	208	220	249	255	-	-	117	117	171	171
	188632	J2	-	171	175	208	208	272	272	166	166	117	117	-	-
	188633	-	-	171	171	208	220	201	270	-	-	117	117		
	188634	J2	-	167	167	208	208	201	214	-	-	117	117	-	-
	188635	-	-	171	171	208	224	-	-	-	-	117	117		
	188636	J2	-	171	171	208	208	214	270	166	191	117	117	167	179
	188637	A	YCTyr1/sr5	171	175	208	208	201	214	166	191	117	117	171	216
	188638	J2	-	167	175	208	208	270	270	166	171	117	117	171	179
	188639	A	YCTyr1/sr5	167	171	208	224	249	255	166	166	117	117	171	171
	188640	A	YCTyr1/sr5	167	167	208	220	201	249	166	166	117	117	171	183
	188641	D3	-	171	175	208	208	249	249	166	177	117	117	171	216
	188642	J2	-	171	175	208	208	249	249	166	166	117	117		

Antelope Creek (lower)	188643	A	YCTyr1/sr5	167	171	208	224	201	249	-	-	117	117	171	171
	188644	J2	-	167	175	208	208	201	201	-	-	117	117	171	171
	188645	J2	-	163	167	208	208	201	249	168	173	117	117	171	171
	188646	-	-	-	-	-	-	-	-	-	-	-	-	187	187
	188647	A	YCTyr1/sr5	167	167	208	224	201	214	166	195	117	117		
	188648	A	YCTyr1/sr5	167	171	208	224	255	270	166	166	117	117	171	183
	188649	A	YCTyr1/sr5	167	171	208	220	201	270	166	195	117	117	171	171
	188650	A	YCTyr1/sr5	167	175	208	224	214	214	166	177	115	115	179	179
Antelope Creek (upper)	188651	J2	-	171	175	208	208	249	270	166	166	117	117	171	171
	188652	J2	-	175	175	208	208	270	270	166	191	117	117		
	188653	J2	-	167	175	208	208	214	214	177	191	117	117	167	171
	188654	A	YCTyr1/sr5	163	175	208	208	201	249	166	191	117	117	171	179
	188655	A	YCTyr1/sr5	167	175	208	208	214	272	177	191	117	117	167	171
	188656	J2	-	175	175	208	208	214	214	166	166	117	117	171	216
	188657	A	YCTyr1/sr5	163	175	208	208	249	272	-	-	-	-	-	-
	188658	J2	-	167	171	208	208	270	270	166	177	117	117		
	188659	A	YCTyr1/sr5	171	175	208	208	214	270	166	166	117	117	-	-
	188660	J2	-	175	175	208	208	214	270	177	191	117	117	167	171
	188661	A	YCTyr1/sr5	167	171	208	208	249	249	177	195	117	121		
	188662	J2	-	167	175	208	208	214	214	177	177	117	117	171	179
	188663	J2	-	175	175	208	208	214	214	166	166	117	117		
	188664	A	YCTyr1/sr5	175	175	208	208	249	270	166	191	117	117	167	171
	188665	J2	-	163	175	208	208	201	272	166	166	117	117	179	216
	188666	J2	-	167	167	208	208	201	214	166	173	117	117	171	171
	188667	J2	-	167	171	208	208	249	270	166	166	117	117	171	171
	188668	J2	-	167	175	208	208	270	270	166	166	117	117	171	171
	188669	A	YCTyr1/sr5	167	171	208	208	201	270	166	166	117	117	179	179
	188670	J2	-	167	167	208	208	214	270	166	166	117	117	171	216
	188671	J2	-	163	175	208	208	214	214	166	166	117	117	171	171
	188672	J2	-	167	175	208	208	201	214	166	177	117	117	171	179
	188673	J2	-	167	167	208	208	201	249	-	-	-	-	-	-
	188674	J2	-	167	171	208	208	214	270	166	177	117	117		

Antelope Creek (upper)	188675	A	YCTyr1/sr5	167	175	208	208	270	270	164	166	117	117		
	188676	J2	-	171	175	208	208	208	270	166	177	117	117	171	179
	188677	J2	-	175	175	208	208	201	214	166	166	117	117	171	216
McBride Lake	90117	Z1	-	159	167	261	269	203	214	173	179	117	117	-	-
	90118	B	YCTyr2/sr3	159	159	208	258	214	214	181	181	117	117	163	265
	90119	Y1	YCTyr3	163	171	258	261	214	214	173	173	117	121	163	273
	90120	Y1	YCTyr3	167	171	224	261	214	214	160	195	117	117	163	163
	90121	A	YCTyr1/sr5	167	179	224	261	214	214	173	175	117	119	-	-
	90122	A	YCTyr1/sr5	159	167	250	258	203	214	173	173	117	117	163	163
	90123	Y1	YCTyr3	163	171	254	258	212	212	173	173	117	121	163	273
	90124	Z1	-	163	171	208	250	214	214	179	179	117	117	163	163
	90125	Y1	YCTyr3	159	159	212	261	203	214	173	173	117	119	163	163
	90126	A	YCTyr1/sr5	163	171	212	261	201	214	179	179	117	121	163	203
	90127	-	-	171	179	224	261	214	214	160	179	117	117	265	273
	90128	B2	YCTyr14	163	167	258	265	203	214	171	195	117	117	179	273
	90129	Z1	-	159	167	258	261	201	214	179	179	117	117	163	163
	90130	A2	YCTyr12	167	171	208	250	201	201	179	179	117	117	163	191
	90131	C2	YCTyr17	-	-	261	265	214	214	173	195	119	121	265	273
	90132	A2	YCTyr12	167	171	212	224	201	214	173	179	117	121	187	262
	90133	Y1	YCTyr3	171	179	261	261	214	214	171	179	117	117	163	171
	90134	-	-	159	167	208	261	201	214	171	181	117	117	258	265
	90135	A2	YCTyr12	159	163	250	258	214	214	171	179	117	119	258	273
	90136	Y1	YCTyr3	159	171	216	224	201	203	171	195	117	117	163	163
	90137	A	YCTyr1/sr5	167	171	216	261	203	214	171	181	117	121	163	273
	90138	Y1	YCTyr3	159	171	208	212	201	214	171	177	121	121	262	273
	90139	Y1	YCTyr3	159	171	261	261	201	214	179	179	117	119	163	171
	90140	Y1	YCTyr3	167	179	208	261	203	203	179	179	117	117	163	163
	90141	A	YCTyr1/sr5	159	171	261	261	201	201	171	179	117	117	265	273
	90142	Y1	YCTyr3	159	159	208	208	214	214	179	179	117	117	262	265
	90143	Y1	YCTyr3	159	179	208	250	203	214	179	179	117	117	163	163
	90144	Y1	YCTyr3	159	167	224	261	214	261	177	179	117	117	163	163
	90145	A	YCTyr1/sr5	159	167	261	261	201	214	195	195	117	119	163	273

McBride Lake	90146	Y1	YCTyr3	167	171	250	261	214	214	171	179	117	117	163	163
Slough Creek (sec. 1)	188718	C2	YCTyr17	-	-	-	-	-	-	-	-	-	-	-	-
	188720	Y1	YCTyr3	-	-	-	-	-	-	-	-	-	-	-	-
	188722	Y1	YCTyr3	-	-	-	-	-	-	-	-	-	-	-	-
	188733	C2	YCTyr17	-	-	-	-	-	-	-	-	-	-	-	-
	188736	C2	YCTyr17	-	-	-	-	-	-	-	-	-	-	-	-
	188741	A2	YCTyr12	-	-	-	-	-	-	-	-	-	-	-	-
	188746	A2	YCTyr12	-	-	-	-	-	-	-	-	-	-	-	-
	188747	Y1	YCTyr3	-	-	-	-	-	-	-	-	-	-	-	-
	188748	B2	YCTyr14	-	-	-	-	-	-	-	-	-	-	-	-
	188749	A2	YCTyr12	-	-	-	-	-	-	-	-	-	-	-	-
	188752	Y1	YCTyr3	-	-	-	-	-	-	-	-	-	-	-	-
	188753	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188757	Z1	-	-	-	-	-	-	-	-	-	-	-	-	-
	188758	A2	YCTyr12	-	-	-	-	-	-	-	-	-	-	-	-
	188760	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188761	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188766	B2	YCTyr14	-	-	-	-	-	-	-	-	-	-	-	-
	188767	B2	YCTyr14	-	-	-	-	-	-	-	-	-	-	-	-
	188774	A2	YCTyr12	-	-	-	-	-	-	-	-	-	-	-	-
Slough Creek at confluence with Elk Tongue Creek	188570	-	-	-	-	-	-	-	-	-	-	117	117	-	-
	188571	B2	YCTyr14	167	167	208	258	214	214	173	195	117	117	-	-
	188572	A2	YCTyr12	167	179	208	212	201	214	171	173	117	117	163	171
	188574	B2	YCTyr14	159	159	208	250	201	214	-	-	117	117	-	-
	188578	B2	YCTyr14	171	171	212	261	214	214	171	171	117	117	163	171
	188580	Y1	YCTyr3	167	167	212	258	203	203	-	-	117	117	-	-
	188581	Z1	-	163	167	208	212	214	214	171	171	117	117	195	262
	188582	Y1	YCTyr3	167	167	208	258	203	214	175	181	117	117	163	254
	188584	A2	YCTyr12	159	167	261	261	214	214	179	179	117	119	163	163
	188585	-	-	159	167	212	261	201	214	177	183	117	117	-	-
	188586	B2	YCTyr14	167	167	220	220	203	251	171	179	117	119	-	-
	188587	B2	YCTyr14	167	171	212	216	203	214	-	-	-	-	-	-

Slough Creek at confluence with Elk Tongue Creek	188588	Z1	-	-	-	-	-	-	-	-	-	117	117	-	-
	188589	Y1	YCTyr3	155	167	212	261	214	216	171	173	117	117	163	175
	188590	Y1	YCTyr3	167	167	258	261	201	221	179	179	117	117	171	187
	188591	Y1	YCTyr3	159	167	212	258	201	214	171	179	119	121	163	163
	188592	Y1	YCTyr3	167	179	261	261	214	214	173	179	117	119	195	254
	188593	B2	YCTyr14	159	179	208	250	214	221	173	179	117	117	-	-
	188594	Y1	YCTyr3	159	167	208	261	203	214	173	179	117	117	163	269
	188596	B2	YCTyr14	-	-	258	265	214	249	171	173	117	117	163	179
	188599	B	YCTyr2/sr3	163	163	212	261	214	214	171	179	117	117	163	171
	188600	Z1	-	167	179	250	261	203	214	171	179	117	119	199	258
	188602	C2	YCTyr17	163	167	212	250	214	214	173	173	117	117	183	273
	188604	-	-	-	-	-	-	-	-	-	-	117	117	-	-
	188606	Z1	-	159	167	212	212	214	214	179	179	117	117	163	195
	188607	-	-	-	-	-	-	-	-	-	-	117	117	-	-
	188609	A2	YCTyr12	-	-	224	258	201	214	173	195	117	117	163	163
	188613	-	-	-	-	-	-	-	-	-	-	113	117	-	-
	188615	Y1	YCTyr3	163	167	250	261	203	214	175	195	117	117	163	179
Lamar River	188862	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188863	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188864	Y1	YCTyr3	-	-	-	-	-	-	-	-	-	-	-	-
	188865	Y1	YCTyr3	-	-	-	-	-	-	-	-	-	-	-	-
	188870	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188872	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188873	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188878	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188879	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188882	C2	YCTyr17	-	-	-	-	-	-	-	-	-	-	-	-
	188883	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188884	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188885	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188887	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188888	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-

Lamar River	188889	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188890	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188891	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188892	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188893	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188894	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188895	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188896	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
Lamar River at Geyser Basin	188943	H3	-	-	-	-	-	-	-	-	-	-	-	-	-
	188944	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188946	H3	-	-	-	-	-	-	-	-	-	-	-	-	-
	188947	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188948	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188949	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188950	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188951	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188952	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188953	I3	-	-	-	-	-	-	-	-	-	-	-	-	-
	188954	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188955	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188956	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188957	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188959	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188960	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188961	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188962	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188963	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188964	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188965	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188966	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188967	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188968	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-

Lamar River at Geyser Basin	188969	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188970	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188971	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
	188972	A	YCTyr1/sr5	-	-	-	-	-	-	-	-	-	-	-	-
Pebble Creek	188808	A	YCTyr1/sr5	159	171	212	212	225	265	177	195	117	117	187	199
	188809	C2	YCTyr17	135	163	208	216	201	201	168	173	117	117	-	-
	188810	Y1	YCTyr3	159	159	208	208	201	214	173	177	117	117	163	187
	188811	Y1	YCTyr3	159	167	216	265	201	214	191	191	117	117	-	-
	188812	A	YCTyr1/sr5	159	167	212	265	201	201	168	191	117	117	191	191
	188813	A	YCTyr1/sr5	171	179	212	265	201	201	168	168	117	117	163	191
	188814	C2	YCTyr17	163	179	208	212	201	214	168	168	117	117	191	195
	188815	A	YCTyr1/sr5	159	179	220	261	201	201	168	173	117	117	163	163
	188816	A	YCTyr1/sr5	159	179	208	265	195	203	168	173	117	117	163	269
	188817	Z1	-	175	179	212	216	214	263	168	195	117	117	163	163
	188818	Y1	YCTyr3	167	175	265	269	201	225	168	181	117	117	163	163
	188819	-	-	171	179	208	269	201	263	197	199	117	117	191	191
	188820	-	-	179	179	212	261	201	214	168	177	117	117	187	191
	188821	A	YCTyr1/sr5	179	219	208	265	225	225	197	199	117	117	163	163
	188822	-	-	167	179	212	212	201	263	177	177	117	117	163	171
	188823	-	-	167	171	208	220	201	263	195	195	117	117	-	-
	188824	A	YCTyr1/sr5	171	179	208	208	225	225	177	199	117	117	-	-
	188825	Z1	-	167	175	208	208	214	214	177	199	117	117	163	163
	188826	A	YCTyr1/sr5	167	171	208	212	216	263	177	195	117	117	163	187
	188827	Y1	YCTyr3	171	171	265	265	214	263	177	199	117	117	163	163
	188828	A	YCTyr1/sr5	167	171	220	265	214	216	195	199	117	117	159	163
	188829	Y1	YCTyr3	159	219	208	212	214	214	195	195	117	117	163	195
	188830	A	YCTyr1/sr5	171	179	208	212	201	214	195	195	117	117	163	191
	188831	-	-	171	179	212	212	201	214	-	-	117	117	163	191
	188832	-	-	167	167	208	208	201	214	181	199	117	117	163	179
	188833	-	-	163	175	269	269	201	263	195	199	117	117	163	163
	188834	A	YCTyr1/sr5	175	227	208	212	201	263	199	199	117	117	163	195
	188835	C2	YCTyr17	171	179	208	212	214	225	177	199	117	117	163	191

Pebble Creek	188836	C2	YCTyr17	167	219	212	265	201	214	177	199	117	117	163	163
	188837	A	YCTyr1/sr5	159	223	208	265	214	263	177	199	117	117	163	191
	188838	C2	YCTyr17	167	219	208	208	225	263	177	195	117	117	163	191
	188839	C2	YCTyr17	167	167	212	265	201	263	195	199	117	117	163	191
	188840	C2	YCTyr17	171	175	212	212	214	263	177	195	117	117	163	187
	188841	A	YCTyr1/sr5	167	171	208	269	216	263	195	195	117	117	163	163
	188842	C2	YCTyr17	171	171	-	-	214	214	177	199	117	117	-	-
	188843	-	-	219	219	212	220	201	214	177	199	117	117	163	191
	188844	Z1	-	167	171	208	212	214	263	177	199	117	117	163	195
	188845	Z1	-	171	179	265	269	201	201	195	199	117	117	163	191
	188846	-	-	167	183	208	265	214	214	177	199	117	117	163	163
	188847	A	YCTyr1/sr5	167	171	212	220	214	214	195	199	117	117	163	163
	188848	C2	YCTyr17	175	179	265	265	214	214	197	199	117	117	163	163
	188849	C2	YCTyr17	171	171	212	269	201	201	195	199	117	117	163	163
Cache Creek	142056	-	-	183	183	208	212	214	214	179	181	117	117	163	187
	142057	-	-	167	203	208	265	201	214	168	206	117	117	163	273
	142058	A	YCTyr1/sr5	179	179	208	220	225	225	168	168	117	117	159	163
	142059	A	YCTyr1/sr5	159	207	212	261	214	225	199	199	117	117	-	-
	142060	-	-	159	179	212	212	214	263	-	-	117	117	171	203
	142061	A	YCTyr1/sr5	167	167	208	212	201	214	199	199	117	117	191	195
	142062	A	YCTyr1/sr5	167	167	212	212	201	225	183	199	117	117	199	199
	142063	Z1	-	159	179	208	216	214	214	195	199	117	117	187	191
	142064	A	YCTyr1/sr5	167	179	212	265	214	216	168	195	117	117	187	191
	142065	A	YCTyr1/sr5	159	171	208	261	201	201	168	181	117	117	163	163
	142066	-	-	167	207	212	265	203	214	-	-	117	117	140	199
	142067	A	YCTyr1/sr5	163	171	212	212	201	203	168	199	117	117	199	203
	142068	A	YCTyr1/sr5	167	167	208	212	214	214	168	191	117	117	187	203
	142069	A	YCTyr1/sr5	167	207	212	261	214	219	177	199	117	117	179	187
	142070	A	YCTyr1/sr5	159	159	212	212	208	214	199	204	117	117	191	191
	142071	A	YCTyr1/sr5	167	175	212	212	201	201	199	202	117	117	191	195
	142072	A	YCTyr1/sr5	167	223	208	212	214	214	168	199	117	117	159	199
	142073	A	YCTyr1/sr5	159	167	212	261	201	201	168	191	117	117	163	265

Cache Creek	142074	-	-	159	183	208	212	225	272	181	181	117	117	159	187
	142075	A	YCTyr1/sr5	167	179	212	265	214	214	195	195	117	117	187	187
	188983	A	YCTyr1/sr5	179	179	216	265	-	-	181	199	117	117	-	-
	188984	A	YCTyr1/sr5	167	167	212	212	201	272	181	202	117	117	187	191
	188985	A	YCTyr1/sr5	179	223	212	212	203	203	177	181	117	117	159	199
	188986	-	-	163	179	212	261	201	201	181	195	117	117	187	195
	188987	A	YCTyr1/sr5	-	-	212	212	214	214	181	181	117	117	163	171
	188988	A	YCTyr1/sr5	167	167	212	265	203	214	181	181	117	117	159	187
	188989	A	YCTyr1/sr5	219	223	212	212	214	214	177	199	117	117	183	199
	188990	A	YCTyr1/sr5	179	203	208	212	201	214	177	199	117	117	203	203
	188991	K2	-	159	179	212	212	203	214	177	199	117	117	-	-
	188992	A	YCTyr1/sr5	167	171	212	216	201	225	181	195	117	117	191	195
	188993	Z1	-	167	179	212	216	201	214	177	181	117	117	187	195
	188994	A	YCTyr1/sr5	167	171	212	265	203	216	-	-	117	117	187	195
	188995	A	YCTyr1/sr5	167	207	212	265	214	225	181	195	117	117	187	203
	188996	A	YCTyr1/sr5	167	179	212	212	214	265	177	181	117	117	183	183
	188997	A	YCTyr1/sr5	167	171	208	212	214	214	177	199	117	117	195	203
	188998	A	YCTyr1/sr5	159	207	208	208	201	214	168	191	117	117	159	191
	188999	A	YCTyr1/sr5	167	207	208	208	201	203	177	199	117	117	191	191
	189000	A	YCTyr1/sr5	159	159	212	224	201	214	168	177	117	117	163	273
	189001	A	YCTyr1/sr5	179	179	212	261	201	214	195	199	117	117	187	187
	189002	Z1	-	167	223	212	212	201	201	168	199	117	117	159	191
	189003	A	YCTyr1/sr5	167	179	208	212	214	214	199	202	117	117	159	187
	189004	A	YCTyr1/sr5	167	167	212	212	203	216	181	199	117	117	187	191
	189005	A	YCTyr1/sr5	163	167	208	216	203	214	177	191	117	117	-	-
	189006	A	YCTyr1/sr5	167	179	212	265	214	216	181	199	117	117	163	195
	189007	A	YCTyr1/sr5	183	203	212	250	214	223	179	181	117	117	187	191
	189008	A	YCTyr1/sr5	163	179	208	212	195	201	181	195	117	117	163	163
	189009	A	YCTyr1/sr5	159	179	208	208	201	201	168	193	117	117	175	187
	189010	A	YCTyr1/sr5	159	179	220	261	201	201	168	168	117	117	191	191
	189011	A	YCTyr1/sr5	159	167	212	212	201	216	181	199	117	117	191	203
	189012	A	YCTyr1/sr5	171	179	212	265	214	272	177	177	117	117	187	199