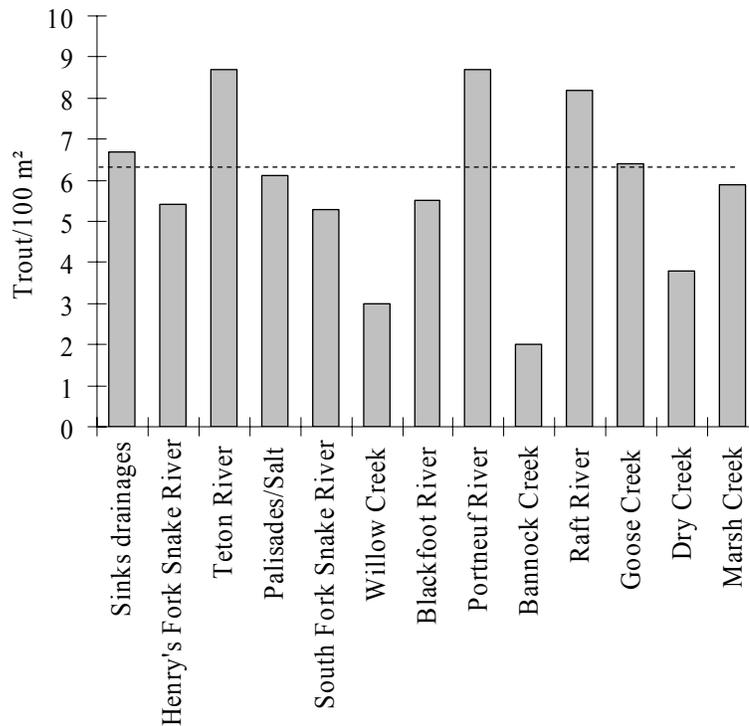




**ASSESSMENT OF NATIVE SALMONIDS ABOVE
HELLS CANYON DAM, IDAHO**

**ANNUAL PROGRESS REPORT
July 1, 2003 — June 30, 2004**



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Assessment of Native Salmonids Above Hells Canyon Dam, Idaho

Project Progress Report

2003 Annual Report

By

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PART #1: STATUS OF YELLOWSTONE CUTTHROAT TROUT IN IDAHO

ABSTRACT

Despite the substantial declines in distribution and abundance that the Yellowstone cutthroat trout *Oncorhynchus clarkii bouvieri* has experienced over the past century, quantitative evaluations of existing population sizes over broad portions of its historical range have not been made. In this study, we estimate trout abundance throughout the Upper Snake River basin in Idaho (and portions of adjacent states), based on stratified sample extrapolations of electrofishing surveys conducted at 961 study sites, the vast majority of which (84%) were selected randomly. Yellowstone cutthroat trout were the most widely distributed species of trout (caught at 457 study sites), followed by brook trout *Salvelinus fontinalis* (242 sites), rainbow trout *O. mykiss* and rainbow x cutthroat hybrids (136 sites), and brown trout *Salmo trutta* (70 sites). Of the sites that contained cutthroat trout, more than half did not contain any other species of trout. Where nonnative trout were sympatric with cutthroat trout, brook trout were most commonly present. In the 11 Geographic Management Units (GMUs) where sample size permitted abundance estimates, there were about 2.2 million trout ≥ 100 mm, and of these, about one-half were cutthroat trout. Similarly, we estimated that about 2.0 million trout < 100 mm were present, of which about 1.2 million were cutthroat trout. The latter estimate is biased low because our inability to estimate abundance of trout < 100 mm in larger-order rivers negated our ability to account for them at all. Cutthroat trout were divided into approximately 70 subpopulations but estimates could be made for only 55 subpopulations; of these, 44 subpopulations contained more than 1,000 cutthroat trout and 28 contained more than 2,500 cutthroat trout. Using a logistic regression model to predict the number of spawning cutthroat trout at a given study site, we estimate that an average of about 30% of the cutthroat trout ≥ 100 mm are spawners. We compared visually-based phenotypic assessments of hybridization with subsequent genetic analyses from 55 of the study sites and found that: 1) genetic analysis corroborated our visual determination that hybridization was absent at 37 of 55 sites; 2) at the seven sites where we visually failed to discern genetically-detected hybridization, the percent of rainbow trout alleles in the population was low (< 1 %) at all but two locations; and 3) where we detected hybridization both visually and genetically (11 sites), levels of introgression were positively correlated between methods ($r^2 = 0.65$). Based on this strong agreement, we phenotypically classified cutthroat trout as “pure” and “ $\geq 90\%$ pure” at 81% and 90%, respectively, of the study sites within these GMUs. Our results suggest that, despite the presence of nonnative threats (genetic and competitive) in much of their current range in Idaho, Yellowstone cutthroat trout populations remain widely distributed and appear healthy in several river drainages in the Upper Snake River basin. Nevertheless, ongoing efforts to secure core cutthroat trout populations, protect areas from further nonnative invasions, and restore disturbed habitat are recommended for further protection of Yellowstone cutthroat trout in Idaho.

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INTRODUCTION

Like most other native salmonids in the western United States, the Yellowstone cutthroat trout *Oncorhynchus clarkii bouvieri* has over the past century or more experienced substantial declines in abundance and distribution in large portions of its historical range (Gresswell 1995; May 1996; Kruse et al. 2000; May et al. 2003;). Declines have been ascribed to a number of factors, but most notably to 1) hybridization with or displacement by nonnative trout, 2) over-exploitation by anglers, and 3) habitat alterations due to water storage and diversion, grazing, mineral extraction, and timber harvest (Thurow et al. 1988; Varley and Gresswell 1988; Gresswell 1995). Such widely described declines have, in part, resulted in a somewhat fragmented distribution of isolated populations and ultimately led to a petition in August 1998 to list Yellowstone cutthroat trout under the Endangered Species Act (ESA), a petition that was denied (USFWS 2001).

Within the last 20 years, a number of status assessments have been conducted for Yellowstone cutthroat trout (e.g., Thurow et al. 1988; Varley and Gresswell, 1988; Gresswell 1995; May 1996; Thurow et al. 1997; Kruse et al. 2000; May et al. 2003; Meyer et al. 2003a). Most of these assessments have been qualitative in nature or have focused on the proportion of assumed historical range that is no longer occupied. None has had the capability of quantitatively estimating (with associated confidence bounds) the abundance of cutthroat trout within individual populations or river drainages in the Upper Snake River basin. Thus, in much of its historical range, true population size, distribution, and extinction risk due to demographic or genetic concerns remain unclear for Yellowstone cutthroat trout. In this study, we attempt to fill this information gap by conducting broad-scale random sampling of fish distribution and abundance throughout the Upper Snake River basin where Yellowstone cutthroat trout are native. A primary study objective was to estimate overall abundance of Yellowstone cutthroat trout (and nonnative trout) in Idaho (and portions of adjacent states; see below), and to estimate abundance within major river drainages. We also sought to identify metapopulations or subpopulations within major river drainages and estimate abundance within them.

While estimation of census population size for major river drainages or subpopulations has obvious utility in evaluating risk to population persistence, assessment of genetic risks stemming from small population size is also desirable. Genetic risks to small populations are related to declines in heterozygosity, which is a function of observed or census population size (N_{census}). However, it is not the absolute number of individuals in a population that is relevant to the amount of genetic variation in the population, but rather the effective population size (N_e ; Wright 1931). The importance of N_e has led to the development and general acceptance of the "50/500" rule (Franklin 1980; Soule 1980), which states that an N_e of at least 50 is needed to avoid inbreeding depression in the short term, while at least 500 is needed to avoid serious genetic drift and maintain genetic variation in the long term.

Unfortunately, N_e is difficult to estimate, especially when relying on demographic data. However, precise estimates of this parameter for management purposes are not always crucial. Rough approximations can provide managers with useful information regarding the relative degree of genetic loss likely to take place, and seem especially helpful in prioritizing conservation efforts across multiple populations (Harris and Allendorf 1989). Frankham (1995) reviewed 192 estimates of N_e/N_{census} and found that the ratio was about 0.10. Rieman and Allendorf (2001) approximated N_e by using a generalized age-structure simulation model to relate N_e to adult spawning numbers under a variety of bull trout life history characteristics (some of which closely match Yellowstone cutthroat trout), and suggested the most realistic

estimates of N_e were between 0.5–1.0 times the mean number of adults spawning annually. Previously we developed a method of estimating the number of spawners in a population by developing models that predict the size at which Yellowstone cutthroat trout mature at any given location (Meyer et al. 2003b). Our second study objective was to use this information and the data we gathered to approximate N_e within as many subpopulations as possible.

OBJECTIVE

1. Determine the distribution and abundance of Yellowstone cutthroat trout and other trout in the Upper Snake River basin;
2. Determine the genetic status of Yellowstone cutthroat trout in the Upper Snake River basin;
3. Estimate the number of Yellowstone cutthroat trout spawners and approximate N_e in the Upper Snake River basin.

STUDY AREA

The Snake River flows through southern Idaho from east to west, flowing 1,674 km from the headwaters in Yellowstone National Park to its confluence with the Columbia River at Pasco, Washington, USA. The Upper Snake River basin is defined herein as that portion of the Snake River drainage from Shoshone Falls (a 65 m natural waterfall that isolated Yellowstone cutthroat trout from other native trout in the Columbia River basin) upstream to the headwaters of all tributaries, except the South Fork of the Snake River drainage above its confluence with the Salt River at the Idaho-Wyoming border (Figure 1). Thus, our surveys included streams within the state boundaries of Nevada, Utah, and Wyoming where small portions of the headwaters of river drainages lay outside the state of Idaho. Discharge in most of the 27,682 km of stream in this portion the Upper Snake River basin is heavily influenced by snowmelt and peaks between April and June. However, streamflow in the Snake River and in a number of major tributaries is highly regulated for agricultural and hydroelectric uses by dams and diversions. Elevation within the basin ranges from over 4,000 m at mountain peaks to 760 m at Shoshone Falls. The climate is semiarid with an average precipitation of about 25 cm.

The historical range of Yellowstone cutthroat trout in Idaho included the entire Upper Snake River basin, excluding the Big Lost and Little Lost rivers (Behnke 1992). Although the finespotted cutthroat trout has sometimes been listed within the study area as a separate subspecies, distinct from the Yellowstone form (Behnke 1992, 2002), they have not been genetically differentiated (Loudenslager and Kitchin 1979). The original distribution relative to one another is not known other than that there apparently was some degree of overlap. Consequently, we made no distinction between the two forms. Nonnative trout, including rainbow trout *O. mykiss*, brook trout *Salvelinus fontinalis*, and brown trout *Salmo trutta* have been introduced throughout the basin and have widely established self-sustaining populations. Other native fish in the basin include mountain whitefish *Prosopium williamsoni*, three species of Cottidae, three species of Catostomidae, and five species of Cyprinidae (Simpson and Wallace 1982).

To facilitate summary of available information and to provide geographic focus for conservation efforts, we subdivided the Upper Snake River basin into 15 Geographic Management Units (GMUs; Lentsch et al. 2000) based largely on major river drainages, which in general also characterized presumed historical distribution, present population status, and suspected or known movement patterns of Yellowstone cutthroat trout, as well as other management considerations (Figure 1). The Shoshone-Bannock Indian Reservation overlaps several river drainages; all streams within the reservation were excluded as a separate but unsampled GMU. Henrys Lake (in the Henrys Fork Snake River GMU), Palisades Reservoir (in the Palisades/Salt GMU), Lower and Upper Palisades lakes (in the South Fork Snake River GMU), and the mainstem of the Snake River (below the confluence of the South and Henrys forks of the Snake River) contained Yellowstone cutthroat trout but were not included in our analyses because we could not obtain recent reliable abundance estimates for these bodies of water.

METHODS

Study site selection

Our data collection occurred between 1999 and 2003. We selected study sites separately for each GMU. We used a standard 1:100,000 hydrography layer throughout the study. We randomly selected study streams, then randomly distributed study sites throughout each selected study stream. The density of sites (i.e., the sample size) within a study stream, and ultimately within a GMU, was based on: 1) time constraints, considering the vastness of the study area; 2) other recent (i.e., within the last eight years) existing data which we used to the extent possible (16% of the sites, not necessarily distributed at random); and 3) the limited distribution of Yellowstone cutthroat trout in some GMUs, where we avoided extensive random sampling (see below).

When sites randomly fell on private property, access was routinely obtained from landowners. Access was denied less than 1% of the time. First-order streams (see Strahler 1964) make up a large (64% at 1:100,000 scale) portion of the stream network in the Upper Snake River basin, but often these headwater streams in the Rocky Mountains are either intermittent or so small that they cannot support salmonid populations (Platts 1979; Kruse et al. 1997; Dunham and Rieman 1999; Harig and Fausch 2002). In an effort to minimize confidence bounds around population estimates, sampling was proportionally reduced in first-order streams and proportionally increased in streams second-order and higher by not sampling streams that were only first-order. That is, streams that did not themselves become second-order or higher (they instead joined other streams which were or became second-order and higher) were excluded from sampling consideration and subsequently from further interpretation. This eliminated from consideration 12,850 of the 17,795 km of first-order stream, a 72% reduction. We assumed the streams that were removed contributed little to the overall abundance of trout in the Upper Snake River basin and checked this assumption by arbitrarily surveying 40 locations in these first-order streams. For our purposes, we felt the above methodology would adequately characterize the distribution and abundance of trout within GMUs while providing conservative abundance estimates, an appropriate approach when evaluating status and risk.

We followed this methodology except in three GMUs where Yellowstone cutthroat trout distribution was too limited to accurately rely on entirely random site selection to estimate cutthroat trout, and where our goal was also to find known or verify suspected subpopulations to

assess their distribution and abundance. Within this more restricted sampling framework, we distributed sites randomly so that abundance estimates could be made at the subpopulation level (see below). Using the above two sample site selection approaches across the entire study area, an average of about one study site for every 18 km of stream (range between GMUs of one site for every 9 to 37 km of stream) was thus established.

Fish sampling/abundance

At each study site, fish were captured using electrofishing gear. Sampling occurred during low to moderate flow conditions (i.e., after spring runoff and before the onset of winter) to facilitate effective fish capture and standardize sampling conditions. Fish were identified, enumerated, measured to the nearest millimeter (total length, TL) and gram, and eventually released. Fish of the genus *Oncorhynchus* were classified as Yellowstone cutthroat trout, rainbow trout, or cutthroat trout x rainbow trout hybrids (hereafter hybrids) by visual examination of morphological characteristics. Yellowstone cutthroat trout were considered pure when the fish 1) had red throat slashes, 2) lacked white margins on the pelvic fins, 3) lacked a red band of color along the lateral line, and 4) contained fewer, larger spots concentrated posteriorly (Meyer et al. 2003a). Any fish in the genus *Oncorhynchus* that had white fin margins, numerous spots toward the anterior of the body (especially the head area), and/or had no or a faint red slash on the throat were pooled into a category of "rainbow trout and hybrids."

Fish abundance in small streams (i.e., less than about 8 m wide) was determined with depletion electrofishing, using one or more backpack electrofishers with pulsed DC. Block nets were installed at the upper and lower ends of the sites to meet the population estimate modeling assumption that the fish populations were closed. Depletion sites were typically (69% of the time) between 80–120 m in length (depending on habitat types and ability to place block nets) and averaged 116 m (range 28–2,554 m). Maximum-likelihood abundance and variance estimates were calculated with the MicroFish software package (Van Deventer and Platts 1989). When all trout were captured on the first pass, we estimated abundance to be the total catch.

To increase the number of sites that could be sampled in a given amount of time, we did not make multi-pass depletions at all backpack electrofishing sites. Instead, using data from the multi-pass depletion sites, we developed within each GMU a linear relationship between the numbers of trout captured in first passes and maximum-likelihood abundance estimates. From this relationship, we then predicted trout abundance at sites where only a single removal pass was made (cf. Lobón-Cerviá et al. 1994; Jones and Stockwell 1995; Kruse et al. 1998). Separate regression models were built for trout <100 and ≥100 mm TL, and standardized residuals were investigated to remove outliers from the regression models (Montgomery 1991) before population estimates were made. Such relationships were consistently strong across all GMUs (mean $r^2 = 0.95$; range 0.77–0.99).

At sites too large to perform depletions (n = 29), mark-recapture electrofishing passes were made using a canoe- or boat-mounted unit and DC (if possible) or pulsed DC. Recapture runs were made two to seven days after marking fish, and we assumed there was no movement of marked or unmarked fish into or out of the study site. Site length was much longer than for depletion sites, averaging 4,951 m (range 332–12,000 m) and thus reducing the likelihood of fish movement. Log-likelihood estimates of trout abundance were made using the Mark Recapture for Windows software package (Montana Fish, Wildlife and Parks 1997). Estimates were made for each 100 mm size class and summed to produce an estimate of total number of trout present. However, we could not estimate trout <100 mm at the mark-recapture sites due to

low capture efficiencies of small fish. Abundance data at four study sites on the mainstem of the Salt River in Wyoming were obtained from Gelwicks et al. (2002), for which abundance estimates were made only for trout ≥ 150 mm; we used their data uncorrected and thus underestimated abundance of trout ≥ 100 mm at those four sites.

For both depletion- and mark/recapture-based techniques, we first estimated overall abundance of trout, then partitioned abundance for each species by multiplying trout abundance by the proportion of the catch that each species comprised. Because electrofishing is known to be size selective (Reynolds 1996), trout were separated into two length categories, < 100 mm TL and ≥ 100 mm TL; abundance estimates were made separately for these two size groups. After a review of the data, we concluded that the variation in emergence time and in catchability precluded inclusion of abundance estimates of trout < 100 mm at 33 study sites where depletions were made.

Estimation of trout abundance

We estimated total trout abundance separately for each GMU using the stratified random sampling formulas from Scheaffer et al. (1996). We first summed the total length of stream for each stream order (or strata, except those first-order streams that were excluded above) using the ArcView® geographic information system (GIS), and divided this total by 100 meters of stream (our typical study site length) to calculate the number of sampling units (N_i) in each strata (L). Abundance was standardized to density per 100 linear meters of stream. We calculated a mean abundance (\bar{y}_i) within each stream order (strata) and an associated variance. For total population size (N_{census}), we used the formula:

$$N_{census} = \sum_{i=1}^L N_i \bar{y}_i$$

and for variance of N_{census} we used the formula:

$$\widehat{V}(N_{census}) = \sum_{i=1}^L N_i^2 \left(\frac{N_i - n_i}{N_i} \right) \left(\frac{s_i^2}{n_i} \right)$$

where s_i^2 is the variance of the observations in strata i , and n_i is the sample size within strata i . All sample sites, including dry and fishless sites, were included in these estimates. We assumed the addition of other sources of data from nonrandomly selected study sites (17% of total sample size) did not bias our results.

Within each GMU, we determined the number of presumably unconnected Yellowstone cutthroat trout subpopulations based on 1) our sampling and that of others, 2) personal observations and local biologists' knowledge, 3) information from a parallel study on Yellowstone cutthroat trout genetic population structure in the Upper Snake River basin (Cegelski et al. in review), and 4) workshops from a separate study that were held to qualitatively assess current Yellowstone cutthroat trout status (May et al. 2003). At these workshops, current distribution (present or absent) of Yellowstone cutthroat trout was classified on a 1:100,000 stream layer by fisheries biologists using existing data, professional judgment, and local expertise (see May et al. 2003 for details). Subpopulations for this study are defined as those that were physically disconnected from and/or not exchanging gene flow with other

populations within the GMU. We assumed there was no connectivity between GMUs based on genetic results cited above and on local biologists' knowledge of irrigation structures/activities and other obvious migration barriers.

We estimated individual subpopulation abundance by the same methods and formulas as above but only included stream kilometers labeled in the workshops as containing cutthroat trout, because we believed it would more accurately represent subpopulation size and distribution. Because of small sample sizes within stream orders, variance often could not be calculated or was unreliable; thus, we did not calculate confidence intervals around subpopulation estimates. We added abundance from all size categories into one estimate for each species. For these reasons the estimates are less reliable, but we present the results for managers to use as a qualitative assessment of the risk individual GMUs and subpopulations within GMUs are facing relative to one another.

For the three GMUs where we had foregone completely random sampling for more focused random sampling within limited cutthroat trout distributions (i.e., Henrys Fork Snake River, Rock Creek, and Bannock Creek), we could not estimate trout abundance for the entire GMUs. However, we did estimate trout abundance within individual subpopulations following the methods described above.

Estimation of mature cutthroat trout and approximation of N_e

Using the above estimates of trout abundance, we also estimated the number of mature Yellowstone cutthroat trout by employing the established maturity modeling approach and demographic data from Meyer et al. (2003b). Logistic regression analysis was used to develop models to predict, at any given stream location, the length at which the probability of a cutthroat trout being mature was 0.5 (termed the maturity transition point, or *MTP*). Following the methods of Meyer et al. (2003b), we collected at each fish survey location four independent variables that were easy to measure and correlated to *MTP*: elevation (*E*), width (*W*), gradient (*G*), and stream order (*SO*). For each study site, we predicted *MTP* using the following logistic regression equations:

$$\text{Males : } MTP_M = \frac{(-1.2948 + 0.004 * E + 0.1115 * W - 0.795 * G + 1.0137 * SO)}{0.0383}$$

$$\text{Females : } MTP_F = \frac{(1.4368 + 0.0064 * E + 0.0873 * W - 0.9294 * G + 0.9145 * SO)}{0.0581}$$

These models explained 56 and 68% of the variation (using the adjusted R^2 for discrete models from Nagelkerke 1991), respectively, in the probability of maturity for 261 male and 208 female cutthroat trout captured across the Upper Snake River basin in Idaho. These models were applied to all study sites except those on the mainstem of the South Fork Snake River ($n = 3$), where instead we used the *MTP* values published in Meyer et al. (2003b) for the South Fork Snake River.

For all study sites, we assumed the sex ratio was 50:50 (see Meyer et al. 2003b) and divided cutthroat trout abundance by two to account for both sexes. At each study site, the actual length frequency for cutthroat trout was compared to the estimates of *MTP* at the site for

both males and females to determine how many of the cutthroat trout present were estimated to be of mature size. Total estimates of the number of mature cutthroat trout were then extrapolated for each GMU using the same methods as above.

N_e was approximated by assuming that values were 0.5–1.0 times the mean number of adults spawning annually (Rieman and Allendorf 2001). Because the application of the maturity model to cutthroat trout abundance estimates introduced an unknown increase in error bounds, we did not attempt to calculate confidence limits on estimates of the number of spawning adults in GMUs or individual populations. For comparison, we also approximated N_e by multiplying total abundance of Yellowstone cutthroat trout (all sizes) by 0.1 (Frankham 1995).

First, Frankham (1995) reviewed 192 estimates of N_e/N_{census} and found that the ratio was about 0.10; we applied this proportion to our estimates of N_{census} . Second, Rieman and Allendorf (2001) approximated N_e by using a generalized age-structure simulation model to relate N_e to adult spawning numbers under a variety of bull trout life history characteristics (some of which closely match Yellowstone cutthroat trout), and suggested the most realistic estimates of N_e were between 0.5–1.0 times the mean number of adults spawning annually. Previously we developed a method of estimating the number of spawners in a population by developing models that predict the size at which Yellowstone cutthroat trout mature at any given location (Meyer et al. 2003b).

Population estimate assumptions

In using the above methodology, we made the following additional assumptions, which may have biased our estimates. First, we assumed that our electrofishing removals accurately estimated trout abundance, but recent work by Peterson et al. (2004a) suggests that we probably drastically underestimated true fish abundance by overestimating capture efficiency with electrofishing gear, especially for trout <100 mm. Moreover, our inability to estimate density of trout <100 mm at our mark-recapture sites completely negated our ability to include these fish in many fourth- and all fifth- and sixth-order study sites, resulting in no additional fish being added for these stream orders and further negatively biasing our estimates.

Second, we assumed our 1:100,000 hydrography layer accurately represented true stream length; this assumption was probably reasonable considering that Firman and Jacobs (2002) found field-measured stream length to be on average only 6% longer than map-based measurements. However, a more significant source of stream layer bias was the use of the 1:100,000 stream layer, rather than a 1:24,000 stream layer (unavailable at this time). Although streams existing on both layers are probably of similar length, many first-order streams that appear at the 1:24,000 scale are absent at the 1:100,000 scale, which reduces the number of first-order stream kilometers for extrapolation and results in an underestimation of cutthroat trout in first-order streams.

Finally, we assumed that our one-time fish survey at each study site accurately portrayed trout abundance at the site. Although we recognize that trout abundance changes seasonally (Decker and Erman 1992) and annually (Platts and Nelson 1988; House 1995), we do not believe our study design would have positively or negatively biased our trout abundance estimates. Considering all the sources of bias, we believe that we most likely underestimated trout abundance in the Upper Snake River basin, especially for trout <100 mm.

Genetic status

An assessment of the extent of hybridization occurring throughout the Upper Snake River basin was made visually by calculating at each study site the proportion of rainbow trout and hybrids captured to the total number of *Oncorhynchus* captured based on morphological characteristics identified above. To check the accuracy of our visual assessment of hybridization, we collected at least 30 fin clips randomly from individuals of *Oncorhynchus* spp. at all locations where cutthroat trout were encountered. We selected 55 study sites for genetic analysis, based largely on hypotheses being tested in a parallel study of Yellowstone cutthroat trout genetic population structure and diversity in the Upper Snake River basin (Cegelski et al. in review). The level of rainbow trout introgression occurring at these study sites was assessed genetically using three codominant nuclear DNA markers (RAG3', Occ38, and Occ42) diagnostic between rainbow trout and cutthroat trout (Baker et al. 2002; Ostberg and Rodriguez 2002).

The level of hybridization and introgression at a study site was calculated two ways. To compare with our visual assessment, hybridization was calculated as the proportion of *Oncorhynchus* samples that contained at least one rainbow trout allele. However, for a more accurate look at population-level rates of introgression, we also calculated the percentage of rainbow trout alleles observed out of the total number of alleles examined. Our sample size objective of 30 fish per site gave us 84% confidence in detecting 1% hybridization, or 99% confidence of detecting 5% hybridization. We used simple linear regression to evaluate the relationship between phenotypic and genotypic estimates of introgression at our study sites.

RESULTS

The current assessment of Yellowstone cutthroat trout covered a total of 14,379 km of stream (not including the 12,850 km of first-order stream that was removed from consideration). The assessment included our fish surveys at 806 randomly selected study sites throughout the Upper Snake River basin, plus additional data obtained from the U.S. Forest Service (31 sites; J. Capurso, unpublished data), Wyoming Game and Fish Department (four sites; Gelwicks et al. 2002), Utah Department of Natural Resources (24 sites; Thompson 2002), and the University of Wyoming (96 sites; Isaak 2001) (Figure 1). Roughly 26% and 74% of the sites visited occurred on private and public land, respectively. Two hundred thirty-nine (25%) sites were dry or had too little water to contain fish (Table 1). Study sites occurred in stream reaches that were 23% first-order, 43% second-order, 25% third-order, 6% fourth-order, 2% fifth-order, and 1% sixth-order. Sites ranged from 0.3 to 79 m wide (mean 4.3 m), from 1,378 to 2,667 m in elevation (mean 1890 m), and from 0.01% to 19.2% in gradient (mean 3.1%). The sample length of all study sites totaled 0.9% of the entire stream network (1:100,000 scale) in the Upper Snake River basin.

Forty arbitrarily-selected sites were surveyed in the 12,850 km of first-order streams that had been removed from sampling consideration ahead of time in order to test the assumption that they truly were absent of salmonids. Twenty-four (60%) of the sites were dry. We found trout at five (13%) sites, including four that contained Yellowstone cutthroat trout. Although no formal population estimates were made at these sites, where trout were found their abundance was low (around one or fewer trout per 10 m of stream). These data were not included in any further analyses.

Yellowstone cutthroat trout were the most widely distributed species of trout in the Upper Snake River basin, captured at 457 (48%) of the study sites (Table 1). Two hundred forty-two sites (25%) contained brook trout, 136 sites (14%) contained rainbow trout and hybrids, and 70 sites (7%) contained brown trout. Of the sites that contained cutthroat trout, almost half (224 of 457) contained nonnative trout. Brook trout were the most common nonnative trout found in sites with cutthroat trout, occurring in 27% of those sites. Brown trout had the most restricted distribution; only within the Palisades/Salt GMU did they occur at more than 7% of the sites within a GMU. Of the 806 randomly distributed study sites, cutthroat trout were captured at 328 (41%) of the sites, compared to 129 (83%) of the 155 nonrandomly distributed sites. Thirty-eight percent of the study sites on private property contained cutthroat trout, compared to 51% for sites on public property.

Estimation of trout abundance

For trout ≥ 100 mm TL, average linear and areal density in all GMUs combined in the Upper Snake River basin was 19.6 trout/100 m and 6.3 trout/100 m², respectively (Figure 2). Mean linear density was highest in the South Fork Snake River (28.8 trout/100 m), Palisades/Salt (26.5 trout/100 m), and Teton River (24.4 trout/100 m) GMUs, and lowest in the Bannock Creek (3.7 trout/100 m) and Willow Creek (5.8 trout/100 m) GMUs. Mean areal density was highest in the Portneuf River (8.7 trout/100 m²), Teton River (8.7 trout/100 m²), and Raft River (8.2 trout/100 m²) GMUs, and lowest in the Bannock Creek (2.0 trout/100 m²) and Willow Creek (3.0 trout/100 m²) GMUs.

We estimated there were 4,214,329 ($\pm 2,748,901$) trout present in the 11 GMUs where trout abundance could be estimated (Table 2). Of these, about 2,202,000 were Yellowstone cutthroat trout, 1,234,000 were brook trout, 481,000 were rainbow trout and hybrids, and 297,000 were brown trout. Of the 2.2 million Yellowstone cutthroat trout estimated to be present in the study area, 1,017,965 ($\pm 360,752$) were estimated to be ≥ 100 mm, while 1,184,473 ($\pm 720,339$) were estimated to be < 100 mm. For trout ≥ 100 mm, Yellowstone cutthroat trout made up 47% of the total abundance of trout, followed by brook trout (27%), brown trout (13%), and rainbow trout and hybrids (13%) (Table 2).

Most of the overall abundance occurred in second- and third-order streams for Yellowstone cutthroat trout (55%) and rainbow trout and hybrids (57%) (Figure 3). In contrast, for brook trout, first- and second-order streams comprised 75% of the overall abundance, whereas for brown trout, fifth- and sixth-order streams comprised 85% of the overall abundance. Even after the removal of much of the first-order stream kilometers, first-order streams still comprised 34% of the total stream kilometers, but only 18% of the total trout abundance (Figure 3).

Based on biologists' knowledge of Yellowstone cutthroat trout movement patterns and migration barriers, and on genetic population structure (Cegelski et al. in review), the Palisades/Salt, Willow Creek, Bannock Creek, and Dry Creek GMUs each were comprised of one entire subpopulation. For the remaining seven GMUs where cutthroat trout existed, we estimated there were from two to 14 subpopulations within individual GMUs, ranging in size from an estimated 42 cutthroat trout in the Wildcat Creek subpopulation to 206,000 cutthroat trout in the South Fork Snake River and connected tributaries subpopulation (Tables 2 and 3). We estimated that of the 55 subpopulations (out of 70 total) where abundance estimates could be made, 44 (80%) contained more than 1,000 cutthroat trout, but in only 16 of those 44 (36%) were cutthroat trout allopatric (Tables 2 and 3).

Estimation of mature cutthroat trout and approximation of N_e

On average about 30% (range 8–74%) of cutthroat trout ≥ 100 mm were estimated to be adult spawners. Within the 11 GMUs where cutthroat trout abundance extrapolations could be made, we estimated about 241,000 were spawners (Table 4). Of the 55 subpopulations we identified and for which estimates could be made, 23 had more than 500 mature cutthroat trout, 17 had more than 1,000, and 11 had more than 1,500 (Tables 3 and 4).

In approximating N_e from the number of spawners, we estimated that N_e exceeded 500 in 17 instances, compared to 20 instances when approximating N_e from N_{census} . N_e exceeded 500 for neither estimate in 31 instances, for both in 13 instances, and for one or the other in 24 instances. This general agreement between estimation methods was further evidenced by strong correlation between estimates for each subpopulation ($r^2 = 0.70$), but estimates for N_e tended to be about two times higher for the N_{census} method than the number of spawners method.

Genetic status

Our results indicated high concordance between phenotypic (i.e., visual) and genetic identification of hybridization. Phenotypic identification correctly classified the presence or absence of hybrids in 48 of the 55 sites genetically tested (Table 5). At the seven sites where hybrids were detected genetically but not phenotypically, the percent of rainbow trout and hybrid alleles was 1% or less at all but two sites, one of which was Midnight Creek where over 90% of the fish captured were < 100 mm TL. Of the 11 sites where hybridization was detected both phenotypically and genotypically, phenotypic and genotypic rates of introgression were positively correlated ($r^2 = 0.65$; $P = 0.003$; $n = 11$).

We assumed that the strong agreement we found between our phenotypic characterization of hybridization and the subsequent results obtained from genetic analysis would be applicable to the remaining sites where no genetic information was available. Subsequently, within the 10 GMUs where Yellowstone cutthroat trout were present and abundance estimates were made, cutthroat trout were classified phenotypically as “pure” and “ $\geq 90\%$ pure” at 341 (81%) and 379 (90%) sites, respectively, out of the 420 study sites where they were found (Table 6). Among these 10 GMUs, hybridization was proportionally most common in the Portneuf River (21 of 47 sites) and Blackfoot River (19 of 45 sites) drainages, least common in the Palisades/Salt (7 of 148 sites), Raft River (6 of 35 sites), and Teton River (8 of 45 sites) drainages, and completely absent in the Willow Creek (0 of 21 sites) and Dry Creek (0 of 3 sites) drainages. Average phenotypic hybridization of cutthroat trout at study sites within these GMUs was 5% (Table 6).

DISCUSSION

Our results indicate that the Yellowstone cutthroat trout is the most abundant and widely distributed species of trout in the Upper Snake River basin. We estimated that about 2,000,000 Yellowstone cutthroat trout overall, about 1,000,000 cutthroat trout ≥ 100 mm TL, and about 240,000 mature cutthroat trout were scattered across 12 of the 14 GMUs we surveyed in Idaho. Such findings indicate that, despite undoubtedly substantial declines from historical levels, Yellowstone cutthroat trout in Idaho remain relatively widespread and appear to contain

numerous strong populations, at least in terms of distribution and abundance. Combined with our recent study that suggested the distribution and abundance of Yellowstone cutthroat trout at a large number ($n = 77$) of fixed stream segments in the Upper Snake River basin had not changed appreciably in the last 10-20 years (Meyer et al. 2003a), it appears that Yellowstone cutthroat trout in Idaho remain relatively widespread and abundant. Similarly, May et al. (2003) recently estimated that YCT currently occupy about 43% of historical habitats range-wide (61% in Idaho), a much higher occupation level than most previous assessments (e.g., Varley and Gresswell 1988; Gresswell 1995; May 1996) that were primarily based on qualitative data.

A number of sources may have biased our estimates of trout abundance. First, the use of nonrandomly selected study sites, which were over twice as likely (84% compared to 40%) to have Yellowstone cutthroat trout than randomly selected sites, may have positively biased our abundance estimates, although this affect was probably small since the vast majority of sites were randomly distributed. Second, the removal of 72% of the total kilometers of first-order stream from our abundance estimates and acceptance of the assumption that these first-order streams contained minimal numbers of trout may have led us to drastically underestimate abundance, considering that trout were found in 13% of the sites we spot-checked for fish within these streams. Indeed, average abundance of trout was around 10 fish/100 m of stream at these study sites, and most of these fish were cutthroat trout. Considering that we removed over 12,000 km of streams from our estimates, it is possible that this eliminated an additional one million cutthroat trout from our consideration. Moreover, our use of depletion estimates probably vastly underestimated true trout abundance (Peterson et al. 2004a), including cutthroat trout. Finally, no estimates could be made for trout <100 mm at all mark-recapture sites, so that for more than 1,200 km of stream, no trout <100 mm were added to the total abundance. Considering all potential sources of bias, we believe that estimates for trout ≥ 100 mm were biased low. Estimates for trout <100 mm were almost certainly biased low and subsequently should be used as minimal estimates only.

Based on our results, it appears that Yellowstone cutthroat trout hybridization (with rainbow trout) in the Upper Snake River basin, although relatively widespread, is far from ubiquitous. Indeed, at the level of individual study sites, only 19% of the sites containing Yellowstone cutthroat trout also contained rainbow trout or hybrids. However, at the subpopulation level, of the 70 presumed cutthroat trout subpopulations in the Upper Snake River basin, at least 28 (40%) contained rainbow trout or hybrids. Such a discrepancy suggests that even within presumed subpopulations, hybridization is not always uniform when hybridization rates are low (Woodruff 1973) or it has not yet spread throughout some subpopulations. Alternatively, we may have inadvertently joined two or more unconnected subpopulations as one.

Our findings that hybridization is not uniform across the Upper Snake River basin concurs with the range-wide findings of May et al. (2003) for Yellowstone cutthroat trout, but they contrast those of earlier assessments (Varley and Gresswell 1988; Gresswell 1995; May 1996), which concluded that genetically unaltered populations of Yellowstone cutthroat trout remained in as little as 10% of their historical habitat, nearly all of which existed in Yellowstone National Park. Our genetic sample size, however, gave us only 84% confidence in detecting 1% hybridization, or 99% confidence of detecting 5% hybridization. Thus, some of the populations we considered “pure” may in fact have been slightly hybridized.

Despite an apparent wide distribution, abundance estimates easily in excess of 2 million fish, and numerous pure or lightly introgressed populations, we do not deem Yellowstone cutthroat trout in Idaho to be safe from possible further reductions in any or all of these indices.

The fact that nonnative trout occurred in all but two of the smallest GMUs, and that they apparently outnumbered cutthroat trout in seven GMUs, clearly demonstrates the risk nonnative trout pose to the long-term persistence of Yellowstone cutthroat trout. In fact, nonnative trout—most notably brook trout for their apparent competitive displacement abilities and rainbow trout for their hybridization capabilities—most likely pose the largest threat to long-term persistence of healthy, viable populations of Yellowstone cutthroat trout in Idaho. Cutthroat trout could probably occupy most or all stream habitat currently occupied by other trout in the Upper Snake River basin if nonnative trout had not displaced them through hybridization or competition.

Brook trout were the second most common trout in the Upper Snake River basin. Although brook trout have often been implicated with displacement of native cutthroat trout in streams in western North America (Griffith 1988; Fausch 1989; Dunham et al. 2002), the mechanisms of displacement have rarely been isolated. Recent work by Peterson et al. (2004b) suggests that the presence of brook trout may reduce survival of age-0 and age-1 cutthroat trout, but more studies are needed to assess the extent that this finding holds true. Most stream studies of brook trout/cutthroat trout interaction or competition have been made in small streams where brook trout were already well established, potentially because the streams were especially conducive to brook trout colonization. Results from such study designs are difficult to broadly extrapolate as a steadfast generalization, and there is much evidence that the success of brook trout invasion or expansion in streams in western North America is variable (Dunham et al. 2002). Nevertheless, the fact that brook trout are in various stages of sympatry in at least 25 subpopulations of cutthroat trout in the Upper Snake River basin is cause for concern. Projects to eradicate brook trout, using chemical treatment (Gresswell 1991) or electrofishing removals (Thompson and Rahel 1996; Shepard et al. 2002; Peterson et al. 2004b), have met with mixed results. In the Upper Snake River basin, more information may be needed on current trends for each species or for better resolution of current distribution and overlap between species before relative risks can be evaluated and management actions can be prioritized.

In addition to potential displacement, rainbow trout also have the ability to hybridize with native cutthroat trout populations, reducing or eliminating populations through admixture of genetic material. That a large number of subpopulations appear to be pure, and that fertile rainbow trout are no longer stocked in Idaho waters containing native cutthroat trout, suggests that the threat of expanding hybridization is relatively low except 1) in the Teton River, South Fork Snake River, and Blackfoot River GMUs where hybridization is already widely established and the persistence of fluvial life history traits may serve to further spread hybridization within the GMU, and 2) within subpopulations where hybridization has been documented but complete dispersal of introgression throughout the population has apparently not yet occurred. There arises a common dilemma in the management of inland cutthroat trout, in that most small “pure” subpopulations are less vulnerable to future hybridization but more prone to risks associated with demographic or environmental stochasticity, whereas the larger subpopulations are demographically more secure but genetically at risk to continued or expanding hybridization. Repeated genetic screening to monitor Yellowstone cutthroat trout hybridization throughout the Upper Snake River basin is needed to 1) prioritize further genetic analysis of as-yet unscreened subpopulations, 2) assess whether introgression is increasing or likely to increase (in terms of individual numbers, or numbers of subpopulations) over time, and 3) prioritize conservation, restoration, and translocation activities.

This survey, although conducted over a four-year period (and longer for data obtained from other entities), in reality constitutes status only for the time period in which the study took place. Had our study sites been surveyed at different time periods, our conclusions may have been different. For example, data collected in 2003 has shown marked reductions in large

adfluvial populations of Yellowstone cutthroat trout in the South Fork Snake River, Teton River, Willow Creek, and Blackfoot River relative to previous years (D. Teuscher and B. Schrader, IDFG, unpublished data). Reasons for the declines vary and remain uncertain in some instances. Nevertheless, since our data includes all study sites that have been recently sampled, and only some of the study sites were surveyed in 2003, the average densities of cutthroat trout within these large adfluvial populations were only moderately lowered by this recent decline in abundance.

Such recent declines reinforce our suggestion that, although nonnative trout may be the most important long-term threat to the health of most Yellowstone cutthroat trout subpopulations in Idaho, that is not to suggest that habitat conditions have not been altered from historical conditions or that such alterations have not contributed to declines in Yellowstone cutthroat trout distribution and abundance. Preliminary analysis of fish and habitat data collected during this study suggested that, in general, cutthroat trout presence at a particular study site within a GMU was associated with a higher percentage of public property, higher elevation, more gravel and less fine substrate, and more upright riparian vegetation (K. Meyer, unpublished data), all indications that cutthroat trout are more likely to persist where alterations are less frequent and less intensive. However, there was much variation between GMUs in the direction and magnitude of the relationships between stream characteristics and Yellowstone cutthroat trout distribution and abundance, as is typical of most models attempting to relate broad ecological patterns to the factors that produce them (see reviews in Fausch et al. 1988; Huston 2002).

Theoretically, in the absence of nonnative trout, existing or additional habitat alterations may lead to continued or even further fragmentation of subpopulations of Yellowstone cutthroat trout, but it is unlikely that either current or future fragmentation would soon threaten the actual existence of the subspecies in Idaho. However, that most GMUs can be divided into several (as many as 14) reproductively isolated populations does suggest that many subpopulations of cutthroat trout are facing a variety of risks inherent to their low abundance, both directional (compensation and depensation) and random (catastrophes, and demographic, genetic, and environmental stochasticity) in effect. Small populations have been shown to lose adaptive genetic variation and gain maladaptive genetic variation at higher rates than larger populations (Lande 1995). However, most literature addressing small population sizes do not refer to species (or subspecies) of vertebrates that contain over one million individuals scattered across a large geographic area and broken into numerous populations, some of which are extremely large (over 200,000 individuals).

At a smaller scale, it is difficult to resolve how many cutthroat trout are needed in a given subpopulation for long-term persistence and the maintenance of genetic diversity within that particular population, and there is no definitive standard. Applying the 50/500 rule to our results, we found that of the 55 subpopulations where an estimate of cutthroat trout abundance could be made, 31 (56%) did not meet the 500 rule and 6 (11%) did not meet the 50 rule. Thus, some of the smallest populations may already be experiencing reduced fitness through inbreeding depression, and many appear to be subject to loss of genetic diversity over the long term. However, there is empirical evidence that suggests cutthroat trout may not exhibit such extinction risk patterns. Indeed, Rieman and Dunham (2000), working at scales similar to our subpopulations, found that small isolated populations of cutthroat trout produced no localized extinctions despite extreme isolation and very low densities of fish. Regardless of how many individuals are needed to maintain genetic diversity, Lande (1988) argued that demography is likely to be more important in determining population viability. Thus, while our genetic results suggest that smaller populations have experienced some reduction in genetic diversity (Cegelski et al. in review), we believe that such reductions are currently less important than the

small size of some subpopulations. In general, maintaining demographically viable subpopulations of Yellowstone cutthroat trout would seem the foremost need, while monitoring genetic viability and maintaining it through reconnection of fragmented habitats where feasible or through introduction of genetic material via translocations from nearby pure populations if necessary.

We chose not to quantify the amount of Yellowstone cutthroat trout historical range currently occupied because of the difficulty in delineating actual historical distribution. Our results suggest that, at least for some streams in the Upper Snake River basin, historical distribution was probably extremely limited or nonexistent. For example, in the Rock Creek GMU, of the 15 study sites surveyed (on 15 different streams), 14 were dry. Moreover, nearly all of the dry sites in this GMU contained no indication of a stream channel whatsoever, not even a remnant ephemeral channel, suggesting that even ephemeral flow in recent history has been lacking. Nevertheless, these streams appeared on the 1:100,000 stream hydrography layer as actual streams, and would be erroneously included in any assessment that included a summation of historically occupied stream kilometers. Such “streams” occurred throughout the Upper Snake River basin.

CONCLUSION

Despite substantial declines in distribution and abundance from historical levels, we found that Yellowstone cutthroat trout were the most widespread and numerous species of trout in the Upper Snake River basin and that the majority of subpopulations appeared to be absent of hybridization. We also found, however, that cutthroat trout were often divided into numerous small (i.e., less than 1,000 individuals), presumably unconnected subpopulations. Dual and seemingly conflicting conservation strategies of isolating subpopulations at risk of competition and introgression with nonnative salmonids, yet connecting subpopulations where feasible, must be balanced in their implementation for sound adaptive management of pure or nearly pure populations of Yellowstone cutthroat trout. The distribution of nonnative salmonids must be controlled and reduced through use of chemicals where feasible. The use of electrofishing techniques for selective removal of nonnatives has had a dubious past (Moore et al. 1983; Thompson and Rahel 1996; Buktenica et al. 2000), and it is almost inconceivable that such methods can be successful over meaningful stream lengths (Finlayson et al. 2005).

Establishing and regularly monitoring cutthroat trout presence and abundance at study sites in small tributaries (in addition to several already-established large river trend sites) would more completely address current trends and factors that influence those trends. Preserving metapopulation function and multiple life-history strategies by connecting occupied habitats would help preserve more subpopulations. Where Yellowstone cutthroat trout populations are depressed (<500 adults) but genetically pure, a temporary program of fish translocations may need to be initiated to avoid inbreeding depression problems. The possibility of reconnecting isolated populations should be considered, keeping in mind the hybridization, competition, and diseased risks such actions might pose. Such management objectives and activities will help ensure that Yellowstone cutthroat trout are a sustained part of the fish fauna of the State of Idaho.

RECOMMENDATIONS

1. Develop and implement a protocol to monitor future demographic status and trends of Yellowstone cutthroat trout in the Upper Snake River basin.
2. Exert effort to collect fish population data from subpopulations of YCT where data is currently sparse or lacking and thus status is less known. Such work should focus on the Sinks, Henrys Fork, Teton, and Portneuf drainages.
3. Develop a strategy to monitor future genetic status and trends (i.e., unacceptable loss of genetic diversity, expansion of hybridization, etc.) and a protocol for fish management intervention when data indicates it is necessary.
4. Continue to implement management actions designed to remove or curtail the expansion of nonnative trout in the Upper Snake River basin.
5. Encourage data collection standardization between IDFG and other federal, state, private, and tribal agencies to facilitate easier data sharing and similarity.

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Table 1. Stream network and distributional extent of trout in the Upper Snake River basin (USRB) by Geographic Management Units. HFSR is Henrys Fork Snake River; SFSR is South Fork Snake River; YCT is Yellowstone cutthroat trout; RT/HY in rainbow trout and hybrids; BKT is brook trout; and BNT is brown trout.

Stream network and study sites	Sinks	HFSR ^a	Teton	Palisades/Salt	SFSR	Willow	Blackfoot	Portneuf	Bannock ^a	Rock ^a	Raft	Goose	Dry	Marsh
Total kilometers in USRB	2,604	3,546	2,383	2,938	1,822	1,699	2,178	2,225	641	650	3,769	2,446	135	437
Kilometers included in trout estimates ^b	1,437	2,184	1,278	1,531	897	865	1,155	1,094	257	315	1,826	1,273	75	194
Total number of sites sampled	69	119	95	163	78	58	82	83	7	15	95	80	7	10
Sites containing trout	35	87	59	150	47	23	49	51	3	0	53	37	3	8
Sites containing YCT	10	34	45	148	46	21	45	47	3	0	35	20	3	0
Sites containing RT/HY	13	20	12	7	13	0	19	21	0	0	17	14	0	0
Sites containing BKT	25	72	53	22	0	4	13	8	0	0	24	13	0	8
Sites containing BNT	2	7	3	37	6	2	0	7	0	0	6	0	0	0
YCT sites containing other trout	8	27	40	56	14	4	25	25	0	0	18	7	0	0
YCT sites containing RT/HY	5	6	8	7	12	0	19	21	0	0	6	4	0	0
YCT sites containing BKT	4	24	38	21	0	2	9	4	0	0	17	3	0	0
YCT sites containing BNT	0	2	3	36	6	2	0	7	0	0	0	0	0	0
Dry or nearly dry sites	19	32	24	6	27	23	14	10	2	14	32	30	4	2

^a GMUs where Yellowstone cutthroat trout distribution was restricted and sites were not selected at random.

^b Excludes the "first-order only" streams not included in our analysis (see methods)

Table 2. Estimates of total trout abundance (N_{census}) and 95% confidence intervals (CIs) for trout in 14 Geographic Management Units (GMUs) in the Upper Snake River basin, Idaho. NA indicates where adequate data from which to make estimates was not available.

GMU	Yellowstone cutthroat trout				Rainbow trout and hybrids				Brook trout				Brown trout			
	≥ 100 mm TL		< 100 mm TL		≥ 100 mm TL		< 100 mm TL		≥ 100 mm TL		< 100 mm TL		≥ 100 mm TL		< 100 mm TL	
	N_{census}	± 95% CI	N_{census}	± 95% CI	N_{census}	± 95% CI	N_{census}	± 95% CI	N_{census}	± 95% CI	N_{census}	± 95% CI	N_{census}	± 95% CI	N_{census}	± 95% CI
Sinks drainages	15,943	14,773	7,868	8,668	43,219	35,782	16,996	23,470	99,537	45,758	52,834	30,716	377	522	0	
Henry's Fork Snake River ^a	-----NA-----				-----NA-----				-----NA-----				-----NA-----			
Teton River	85,272	26,473	120,120	80,683	22,902	24,134	1,518	908	193,186	56,881	304,146	107,861	1,135	1,399	502	979
Palisades/Salt	282,141	76,979	212,503	139,461	802	539	0		11,906	11,161	898	1,026	70,155	27,790	11,778	16,528
South Fork Snake River	205,917	79,774	136,783	53,601	58,925	104,410	1,622	2,722	0		0		160,719	176,169	6,737	9,802
Willow Creek	53,509	18,632	27,526	24,820	0		0		9,162	14,937	27,223	50,540	2,398	NA	640	NA
Blackfoot River	117,021	36,406	427,034	264,446	11,748	5,980	423	652	4,614	4,824	4,545	5,397	0		0	
Portneuf River	97,961	39,312	62,460	35,420	13,577	11,773	1,639	1,402	60,816	67,368	53,424	55,107	29,476	39,028	2,969	4,166
Bannock Creek ^a	-----NA-----				-----NA-----				-----NA-----				-----NA-----			
Rock Creek ^a	0 ^b		0 ^b		-----NA-----				0 ^b		0 ^b		0 ^b		0 ^b	
Raft River	101,222	35,812	100,201	55,258	91,858	55,565	163,808	177,273	117,293	64,829	99,864	66,212	9,811	10,661	446	870
Goose Creek	50,209	30,201	86,554	57,981	47,053	37,493	4,723	5,646	57,440	53,556	75,352	86,342	0		0	
Dry Creek	8,770	2,390	3,425	NA	0		0		0		0		0		0	
Marsh Creek	0		0		0		0		30,412	24,581	31,284	35,880	0		0	
Total	1,017,965	360,752	1,184,473	720,339	290,085	275,676	190,729	212,074	584,366	343,894	649,568	439,080	274,071	255,569	23,071	32,345

^a GMUs where Yellowstone cutthroat trout distribution was restricted and sites were not selected at random.

^b Although no trout abundance estimates were possible, this species was absent from the GMU.

Table 3. Estimates of stream kilometers, numbers of trout, and N_e within individual subpopulations of Yellowstone cutthroat trout in the Upper Snake River basin. GMUs with one entire connected population are not listed. YCT is Yellowstone cutthroat trout; RT/HY is rainbow trout and hybrids; BKT is brook trout; BNT is brown trout. NA indicates where adequate data from which to make estimates was not available.

Sub-Population	Total stream km	Estimate of total abundance within each YCT sub-population				Mature YCT	N_e from:	
		YCT	RT/HY	BKT	BNT		Total abundance	Maturity estimate
Sinks drainages								
1 Crooked Creek	23.8	-----NA-----						
2 Fritz Creek	24.6	70	165	0	0	0	7	0
3 Webber Creek	17.2	79	158	79	0	0	8	0
4 Irving Creek	17.7	158	487	1,002	0	158	16	79
5 Middle Creek	NA	-----NA-----						
6 Indian Creek	45.9	5,012	11,240	0	0	944	501	472
7 WF Rattlesnake Creek	10.8	-----NA-----						
8 EF Rattlesnake Creek	15.6	1,237	0	2,960	0	296	124	148
9 Moose Creek	2.6	56	0	1,311	0	0	6	0
10 Dry Creek	17.8	3,035	0	0	0	1,230	303	615
11 Corral Creek	8.9	-----NA-----						
Henry's Fork Snake River								
1 Henry's Lake tributaries	21.6	-----NA-----						
2 Tygee Creek	9.8	2,388	0	0	0	53	239	27
3 Conant Creek	26.1	1,483	69	3,183	0	155	148	77
4 Squirrel Creek	13.8	1,925	27	2,152	0	39	192	19
5 Boone Creek	15.5	814	0	12,982	0	46	81	23
6 Calf Creek	7.2	2,347	0	0	0	0	235	0
7 Wyoming Creek	13.6	421	269	0	0	316	42	158
8 Robinson Creek	14.0	-----NA-----						
9 Bechler River	NA	-----NA-----						
10 Twin Creek	8.7	185	123	740	0	0	18	0
Teton River								
1 Moody Creek	34.3	3,184	0	22,041	112	255	318	128
2 Packsaddle Creek	13.0	8,273	60	8,092	0	60	827	30
3 Horseshoe Creek	19.6	4,991	37	4,806	0	141	499	70
4 Mahogany Creek	13.3	2,931	0	6,250	0	188	293	94
5 Badger Creek	21.5	11,128	0	0	0	813	1,113	407
6 Teton Creek	31.3	-----NA-----						
7 North Leigh Creek	33.0	2,265	47	19,281	0	236	227	118
8 South Leigh Creek	NA	-----NA-----						
9 Darby Creek	NA	-----NA-----						
10 Twin Creek	10.2	-----NA-----						
11 Trail Creek and tribs.	77.0	7,048	840	19,253	0	117	705	59
12 Teton River and tribs.	256.2	54,577	16,745	63,479	1,038	11,975	5,458	5,988
South Fork Snake River								
1 Garden Creek	11.3	1,715	0	0	0	318	172	159
2 Fall Creek	51.7	15,202	0	0	0	1,187	1,520	594
3 Upper Palisades Creek	30.8	23,089	19	0	0	3,873	2,309	1,937
4 SF Snake River and tribs.	396.7	205,608	54,080	0	150,946	51,794	20,561	25,897
Blackfoot River								
1 Lower Blackfoot R. and tribs.	214.9	132,314	2,007	1,177	0	4,742	13,231	2,371
2 Upper Blackfoot R. and tribs.	262.7	134,195	6,802	2,874	0	4,290	13,420	2,145
Portneuf River								
1 Rapid Creek	51.3	14,765	1,364	0	532	3,920	1,477	1,960
2 Walker Creek	10.4	232	0	0	0	127	23	63
3 Bell Marsh Creek	10.3	1,652	0	0	0	291	165	146
4 Goodenough Creek	10.9	2,241	0	0	0	1,036	224	518
5 Robbers Roost Creek	8.9	1,061	0	0	0	543	106	272
6 Harkness Creek	9.2	-----NA-----						
7 Mink Creek	16.5	2,113	221	0	38	936	211	468
8 Gibson Jack Creek	14.1	1,270	339	269	0	482	127	241
9 East Bob Smith Creek	8.1	1,592	0	1,065	0	1,309	159	655
10 Dempsey Creek	20.4	-----NA-----						
11 Fish Creek	11.5	-----NA-----						
12 Pebble Creek	29.8	12,749	334	0	0	2,355	1,275	1,178
13 Toponce Creek	31.2	6,130	1,553	0	6,858	1,128	613	564
14 Right Hand Fk Marsh Creek	6.6	104	0	0	0	52	10	26
Raft River								
1 South Junction Creek	21.3	3,923	0	0	0	341	392	171
2 Wildcat Creek	1.8	42	0	0	0	11	4	5
3 Johnson Creek	13.4	3,003	0	4,890	0	194	300	97
4 George Creek	12.6	4,971	6,093	0	0	1,011	497	506
5 Onemile Creek	5.3	2,874	0	0	0	426	287	213
6 Clear Creek	3.3	1,762	0	0	0	368	176	184
7 Eightmile Creek	9.3	5,265	0	0	0	731	526	366
8 Grape Creek	8.7	1,163	0	0	0	317	116	159
9 Cassia Creek	67.8	11,182	1,432	13,051	0	1,501	1,118	751
10 Edwards Creek	6.1	801	0	0	0	133	80	67
11 Almo Creek	12.8	2,038	0	0	0	0	204	0
Goose Creek								
1 Goose Creek	62.3	33,763	2,628	3,353	0	456	3,376	228
2 Big Cottonwood Creek	35.5	20,043	263	0	0	909	2,004	454

Table 4. Estimates of the number of mature cutthroat trout within GMUs in the Upper Snake River basin in Idaho. NA indicates where adequate data from which to make estimates was not available.

GMU	Mature	
	cutthroat trout	± 95% CI
Sinks drainages	6,810	7,700
Henry's Fork Snake River	NA	
Teton River	20,545	4,230
Palisades/Salt	41,289	15,898
South Fork Snake River	70,076	35,806
Willow Creek	8,906	1,161
Blackfoot River	12,700	6,601
Portneuf River	39,770	18,563
Bannock Creek	NA	
Rock Creek	0	
Raft River	29,999	14,494
Goose Creek	4,033	3,173
Dry Creek	6,477	1,547
Marsh Creek	0	

Table 5. Comparison of the estimates of phenotypic (i.e., visual) and genotypic rates of hybridization at 55 study sites in the Upper Snake River basin in Idaho. NA indicates not available.

Study site	Phenotypic		Genotypic hybridization		
	hybridization		N	Percent rainbow trout:	
	N	%		Alleles	Fish
Thirty-seven individual study sites across the Upper Snake River Basin	-	0	1,117	0	0
North Moody Creek	34	0	31	< 1	3
North Fork Rapid Creek	56	0	31	<1	3
Mike Harris Creek	92	0	31	<1	3
South Fork Badger Creek	74	0	31	1	6
Fall Creek	54	0	31	1	6
Middle Dry Creek	66	0	31	3	13
Midnight Creek	94	0	24	23	48
Timothy Creek	104	5	31	14	33
Lower Blackfoot River	249	4	31	3	3
Big Springs Creek	108	7	48	2	6
Pine Creek	NA	8	47	NA	17
Webb Creek	35	9	31	19	42
Burns Creek	NA	11	48	3	6
Rawlins Creek	170	13	31	6	6
Rapid Creek	80	13	28	17	26
Teton River	NA	16	31	6	13
Blackfoot River	204	25	24	10	25
Middle Fork Toponce Creek	29	55	31	42	86

Table 6. Summary of Yellowstone cutthroat trout phenotypic hybridization at study sites in the Upper Snake River basin within GMUs where cutthroat trout were widely distributed.

GMU	Sites with YCT	Sites where YCT are:		Percent hybridization at YCT sites	
		> 90% pure	Pure	Mean	Range
Sinks drainage	10	6	5	32	0-93
Teton River	45	40	37	6	0-98
Palisades/Salt	148	147	142	0	0-1
South Fork Snake River	46	43	36	3	0-57
Willow Creek	21	21	21	0	
Blackfoot River	45	38	26	5	0-59
Portneuf River	47	34	26	12	0-81
Raft River	35	30	29	12	0-94
Goose Creek	20	17	16	9	0-79
Dry Creek	3	3	3	0	

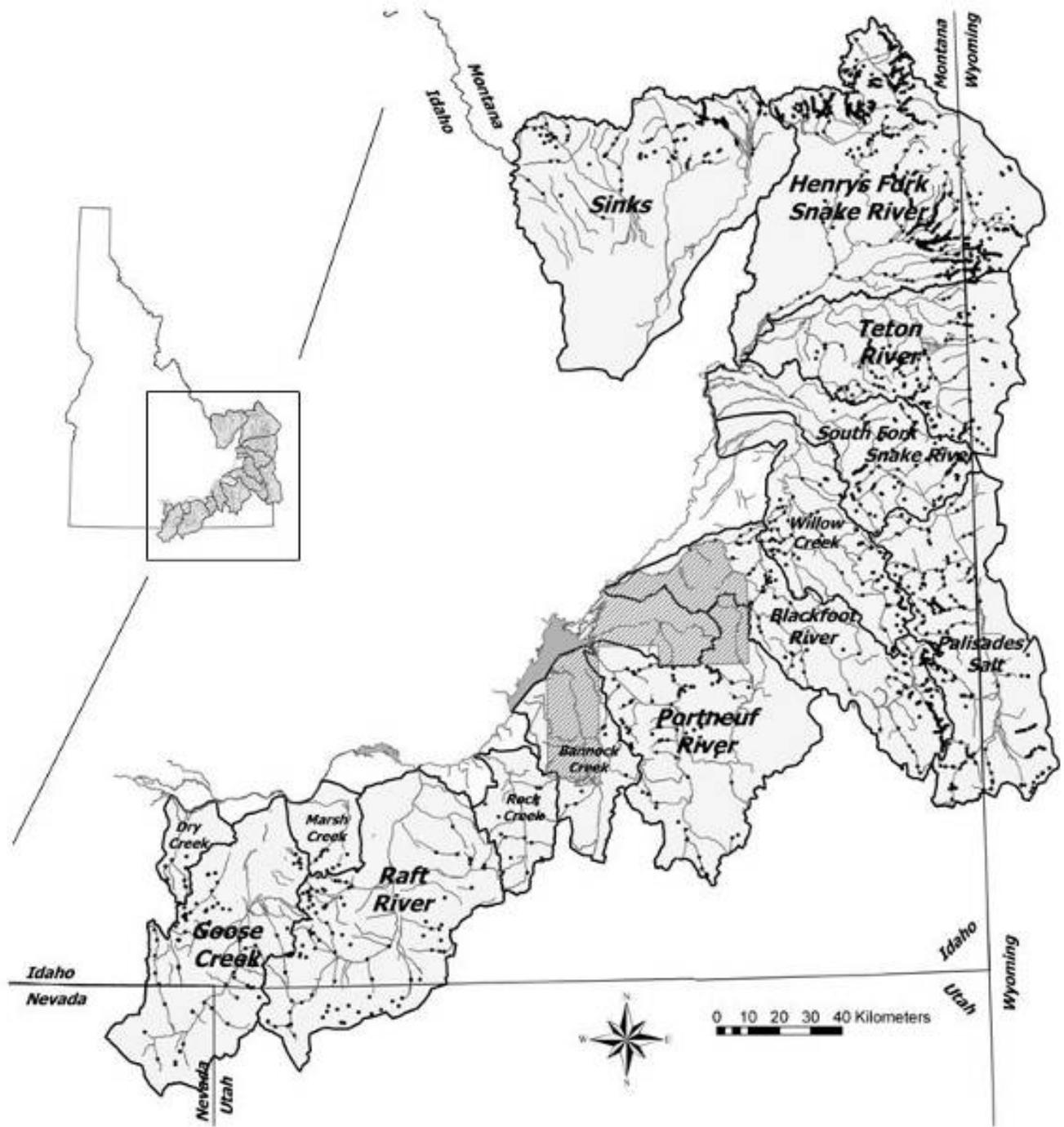


Figure 1. Distribution of geographic management units (GMUs) and study sites (dots) across the Upper Snake River basin in southeastern Idaho.

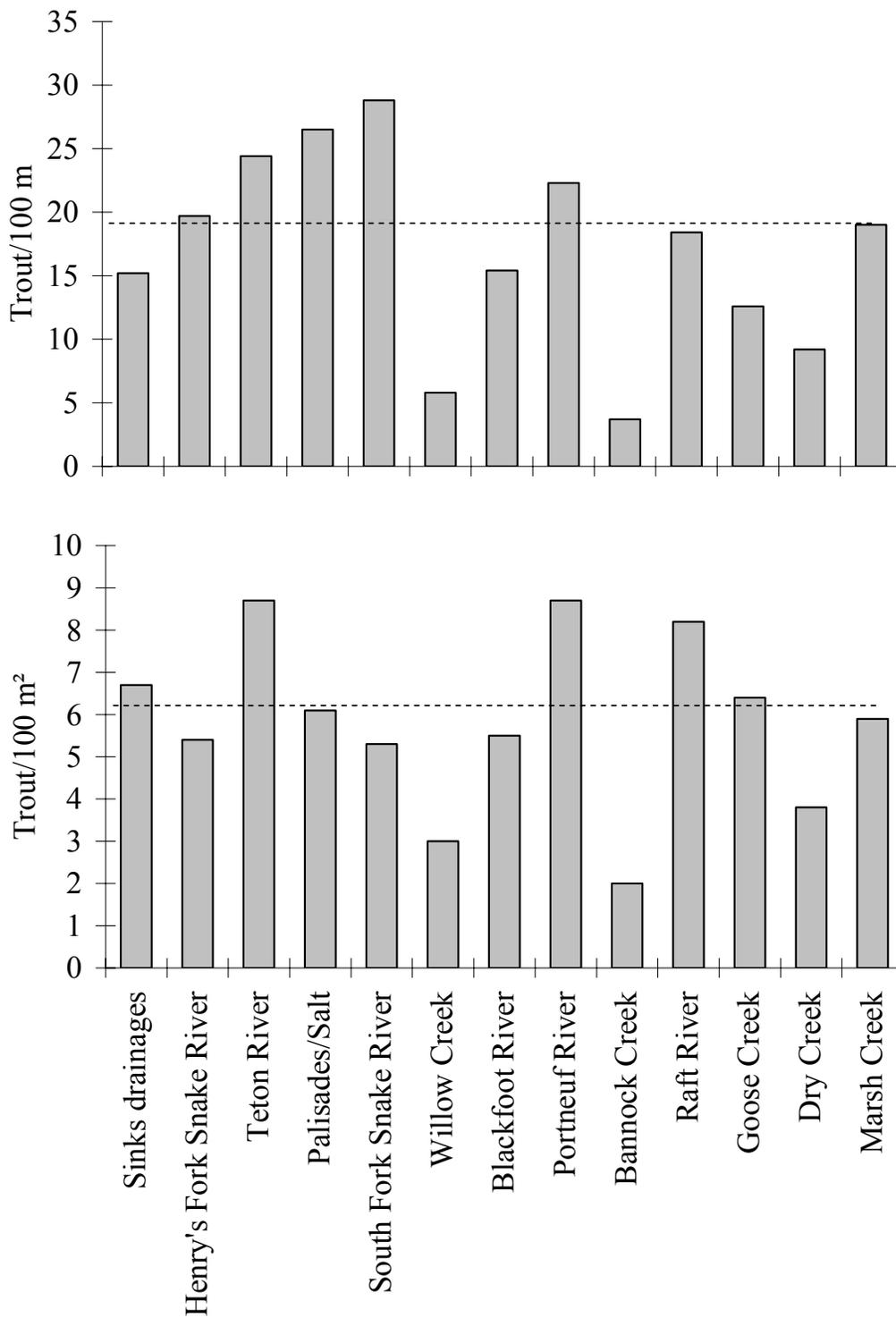


Figure 2. Average linear (fish/m) and areal (fish/m²) trout densities in GMUs in the Upper Snake River basin in Idaho. Dashed line is mean among all study sites.

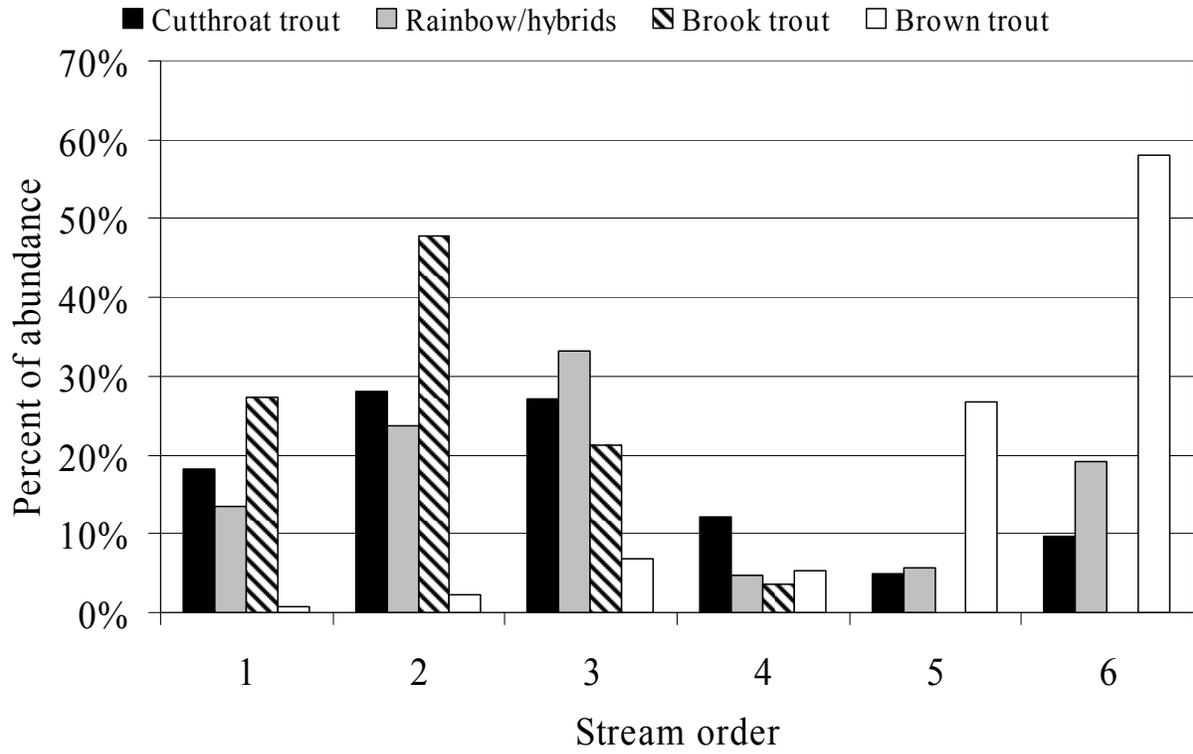


Figure 3. Percent of total trout abundance (≥ 100 mm TL only) by stream order in the Upper Snake River basin.

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