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IDAHO STEELHEAD MONITORING AND EVALUATION STUDIES

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IDAHO STEELHEAD MONITORING AND EVALUATION STUDIES

Project Progress Report

2005 Annual Report

By

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ABSTRACT

This project was originally titled the Idaho Steelhead Supplementation Studies (SSS), and it was designed to assess the effects of supplementation and to gather life history and genetic data from wild steelhead *Oncorhynchus mykiss* populations. This report provides a summary of project activities from January 1, 2005 to December 31, 2005. Idaho Department of Fish and Game (IDFG) personnel have stocked adult steelhead from Sawtooth Fish Hatchery into Beaver Creek from 1993 to 2004 and have estimated the number of age-1 parr produced from each outplant the following year. I estimated that nine age-1 juveniles were produced per female spawner in Beaver Creek from the 2004 adult outplant. The wild adult steelhead escapement in Fish Creek, a tributary to the Lochsa River in the Clearwater basin, was 121. I estimated that 53,722 steelhead juveniles out-migrated from Fish Creek between March 10 and November 14, 2005. The mean age-1 steelhead densities decreased from those observed in 2004 in five of the 12 tributaries of the Lochsa and Selway rivers and four of the five tributaries in the Salmon River drainage that were surveyed each year. Project personnel began operating a screw trap in the Secesh River, about 1 km downstream of Lick Creek in 2005. Additionally, this project collaborated with the Idaho Supplementation Studies to tag juvenile steelhead captured in their screw trap operations. Trap tenders PIT tagged 22,036 steelhead juveniles at 16 screw trap sites in the Clearwater and Salmon drainages. In 2005, 3,100 and 1,384 steelhead smolts were detected at downriver dams from tagging sites in the Clearwater River and Salmon River drainages, respectively. We aged 3,282 steelhead juveniles from scales that were collected from March 2004 to October 2005 and 235 adults from scales collected at Fish Creek, Pahsimeroi River, and Rapid River in 2005. Dr. Jennifer Nielsen at the U.S. Geological Survey Alaska Biological Science Center, Anchorage completed the microsatellite analysis of the juvenile steelhead tissue samples that were collected from Idaho streams in 2000.

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INTRODUCTION

This project was originally titled the Idaho Steelhead Supplementation Studies (SSS), and it was designed to assess the effects of supplementation and to gather life history and genetic data from wild steelhead *Oncorhynchus mykiss* populations. The experimental design was submitted to BPA in December 1992 (Byrne 1994), and fieldwork began in 1993. The supplementation experiments were completed in 2004. The project was renamed Idaho Steelhead Monitoring and Evaluation Studies (ISMES) in 2005 to acknowledge that collection of steelhead population dynamics, life history, and genetics data are now the primary goal of this project. Basic biological data must be available to assess population abundance and population trends and meet the needs of management agencies to measure recovery of Endangered Species Act (ESA) listed steelhead stocks and the effects of basin-scale restoration activities. This study has focused on gathering this information from wild steelhead populations in Idaho. This report documents the work conducted from January 1, 2005 to December 31, 2005. Previous reports have summarized the work performed before January 1, 2005 (Byrne 1996; Byrne 1997; Byrne 1999; Byrne 2001a; Byrne 2001b; Byrne 2002; Byrne 2003; Byrne 2004; Byrne 2005).

OBJECTIVES

1. Assess the performance of hatchery and wild brood sources to reestablish steelhead *Oncorhynchus mykiss* in streams where extirpated.

The original plan was to assess the performance of hatchery stock and a wild stock with a paired watershed study in tributaries of the upper Salmon River (Byrne 1994). However, this approach was abandoned when wild steelhead abundance declined and Idaho Department of Fish and Game (IDFG) decided that “mining” a wild stock for this experiment was no longer appropriate. Wild steelhead were subsequently listed under the ESA in 1997. Idaho Department of Fish and Game personnel stocked adult hatchery steelhead in Beaver and Frenchman creeks from 1993 to 2004 and estimated the yield of age-1 parr from these outplants (Figure 1). In 2004, IDFG personnel made the final hatchery adult steelhead outplant in Beaver Creek. The final adult outplant in Frenchman Creek was made in 2003. An ISMES crew snorkeled both streams in August 2005 to estimate the juvenile production of the brood year 2004 adults in Beaver Creek and to estimate the post-stocking abundance of age-1 steelhead parr in Frenchman Creek.

2. Evaluate the ability of returning adults from hatchery smolt and fingerling releases to produce progeny in streams.

This objective was designed to assess which life stage of release (fish stocked as fingerlings or those stocked as smolts) would be best for supplementation by comparing the number of age-1 parr produced by the two groups of adults when they returned to spawn naturally. This experiment was implemented in the Red River drainage, a tributary of the South Fork (SF) Clearwater River, with the Dworshak hatchery stock. Personnel from IDFG stocked 50,000 Dworshak Hatchery fingerlings in the SF Red River yearly from 1993 to 1996 and about 4,000 to 8,000 Dworshak Hatchery smolts in Red River yearly from 1996 to 1999. Each fingerling stocking had 5,000 fish marked with a passive integrated transponder (PIT) tag and the other 45,000 with a coded-wire tag (CWT). Half of the 1996 smolt release was marked with a PIT tag, and the other half was marked with a CWT. All smolts released from 1997 to 1999 were PIT tagged (Byrne 2001a). The last year a smolt was detected at the Snake River dams from these stockings was 1999. Based on adult PIT tag detections at Lower Granite Dam, the last adults from the smolt stockings returned to Red River and spawned in spring 2002, and the last adults from the fingerling stockings returned to SF Red River and spawned in spring 2003. The Red River weir has not been operated to trap adult steelhead since the spring 2003.

3. Assess the abundance, habitat, genetic, and life-history characteristics of existing wild and natural steelhead populations in the Clearwater and Salmon river drainages.

The Fish Creek adult weir was operated from March 8 until September 16, 2005 to determine the escapement of wild steelhead and Chinook salmon *Oncorhynchus tshawytscha*. Wild steelhead escapement was also obtained from hatchery weirs in Rapid River and Pahsimeroi River. Project personnel conducted snorkel surveys during the summer to estimate juvenile steelhead abundance in tributaries of the South Fork Salmon, Selway, and Lochsa rivers. The project also operated screw traps and tagged juvenile steelhead with PIT tags in Fish Creek, Lick Creek, Rapid River, and the Secesh River in 2005. This project coordinated the PIT tagging of wild steelhead juveniles throughout the Salmon and Clearwater River drainages at screw traps operated by the Idaho Supplementation Study (ISS). The PIT-tagged fish provide data on the length distribution of juvenile steelhead, timing of juvenile migrants past the trap sites, and timing of smolt passage at Lower Granite Dam, and contribute to estimates of juvenile in-river survival and smolt-to-adult survival rates. Dr. Jennifer Nielsen at the Alaska Biological Science Center in Anchorage completed the genetic analysis of the wild and hatchery steelhead samples IDFG collected in 2000. An ISMES technician aged 3,282 steelhead juveniles and 235 adults from scales that were collected in 2004 and 2005.

METHODS

<u>Objective 1</u>

Evaluation of Spawner Success

I used the mean age-1 juvenile steelhead density (fish/100 m^2) in Beaver Creek as an index of the reproductive success of the 30 male and 29 female hatchery adults that were stocked on April 22, 2004. The length of the stream section used to evaluate the reproductive success in Beaver Creek was approximately 3 km. I assumed that all age-1 steelhead in Beaver Creek were the progeny of the previous year’s hatchery adult outplant. I estimated the age-1 population and the number of age-1 parr produced per female. Although Frenchman Creek was not stocked with hatchery adult steelhead in 2004, we estimated the age-1 steelhead parr density and abundance in this stream.

Systematic snorkel survey was conducted to estimate the density of fish by species and size category in each study stream. Each snorkel site consisted of a single distinct habitat type (pool, pocket water, riffle, or run) and was chosen randomly throughout the stream. A minimum of seven sites per kilometer of stream were snorkeled. The number of snorkel sites per habitat type was proportional to the type's abundance in the stream. One to five snorkelers counted fish in each site, depending on the stream size. Each snorkel site was separated by at least one distinct habitat type change from a prior site. Snorkelers estimated the size of all fish to the nearest inch except Chinook salmon *Oncorhynchus tshawytscha* parr, dace *Rhinichthys sp.,* and sculpin *Cottus sp*. After the crew snorkeled each site, they measured its length and three to six widths to calculate the surface area.

Chinook salmon parr were counted and classified as age-0 (<100 mm) or age-1 (≥100 mm). Steelhead parr were classified as age-1, length 3 in to 5 in (76 mm to 127 mm); and age-2+, length >5 in (127 mm). Because steelhead fry (age-0, <75 mm) are indistinguishable from westslope cutthroat trout *O. clarkii* fry, snorkelers classified both as trout fry. I did not partition westslope cutthroat trout, bull trout *Salvelinus confluentus*, brook trout *S. fontinalis*, or mountain whitefish *Prosopium williamsoni* into age classes. Mean densities (fish/100 m^2) by habitat type in each stream stratum were calculated for trout fry, the two age classes of steelhead and Chinook salmon, resident trout, and mountain whitefish.

I calculated the mean stream density (m_t) for each species as:

$$m_t = \sum p_i \overline{d_{it}}$$

where p_i = proportion of habitat i in the stream,
$\overline{d_{it}}$ = mean age t parr density (fish/100 m^2) in habitat i,
t = fish species (and age class, if steelhead or Chinook), and
i = pool, riffle, run, pocket water.

I estimated the age-1 steelhead population (N) and confidence intervals in Beaver Creek using the stratified sampling estimates of Scheaffer et al. (1986):

$$N = \sum A_i \overline{d_{i1}}$$

where N = population total,
A_i = total surface area (m^2) of habitat i,
$\overline{d_{i1}}$ = mean age-1 parr density (fish/m^2) of habitat i, and
i = pool, riffle, run, pocket water.

An approximate 95% confidence interval (CI) on the age-1 steelhead population estimate was calculated as:

$$CI = 2\sqrt{\sum A_i^2 \left(\frac{A_i - a_i}{A_i}\right)\left(\frac{s_i^2}{x_i}\right)}$$

where A_i = total surface area of habitat i,
s_i^2 = the sample variance of the mean age-1 parr density (fish/m^2) in habitat i,
a_i = total surface area that was snorkeled in habitat i,
x_i = number of habitat i sites snorkeled, and
i = pool, run, pocket water, or riffle habitat.

I treated A_i and a_i as constants when calculating the confidence interval and assumed that the variance was due to differences of densities in each snorkel site, not area measurements. This assumption implies that all area measurements were obtained without error. The total surface area (A_i) of each habitat type in the stream was calculated as:

$$A_i = lp_i w_i$$

where l = length of the study section (m) in each stream,
p_i = proportion of habitat i in the study section, and
w_i = mean width of habitat i.

Objective 2

Estimate Juvenile Production from Naturally Spawning Adult Returns

Crews snorkeled the SF Red River from its mouth upstream to the West Fork (WF) SF Red River in 2005 to assess juvenile steelhead densities, using the procedures outlined in the Methods section for Objective 1. Crews snorkeled the same stream sections that were stocked with fingerlings and smolts. Juvenile steelhead densities in Red River upstream of the SF Red River to Shissler Creek were obtained from six stream transects snorkeled yearly by IDFG Clearwater Region crews. Several habitat types may exist within each Red River snorkel transect. The Red River juvenile steelhead densities were calculated as the average density of the snorkel transects.

Objective 3

Estimate Steelhead Escapement in Fish Creek

We began the installation of a temporary weir in Fish Creek on March 3, 2005. Operations to enumerate and sample adult steelhead and pass them upstream of the weir began on March 8, 2005 (Figure 2). Adult steelhead trapped at the weir entered a holding box that was checked throughout the day. When adults were present, the trap tender removed them with a net and placed them in a large plastic water trough. The trap tender determined the sex of each adult fish based on external characteristics, measured fork length to the nearest cm, scanned for the presence of a PIT tag, collected scales, snipped a small portion of the anal fin for future DNA analysis, and used a paper punch to mark the right operculum before releasing the fish upstream of the weir. Steelhead kelts were collected at the weir and checked for a right operculum punch, sexed, scanned for PIT tag, and measured for length. If the kelt was alive, the trap tender punched the left operculum and passed it downstream of the weir. I estimated the adult steelhead escapement using two methods: 1) summing the number of adults trapped in the upstream live box and the number of unmarked kelts recovered, and 2) a maximum likelihood estimate using the number of marked adults passed upstream of the weir, the total number of kelts recovered, and the number of marked kelts recovered (Steinhorst et al. 2004).

PIT-tagged Adult Steelhead Returns

I queried the PTAGIS database (www.psmfc.org) on June 1, 2005 and obtained the date adult steelhead were detected at Bonneville, McNary, and Lower Granite dams. I restricted the query to include only those fish that were PIT tagged in Fish Creek as juveniles and detected as adults at the three dams between July 1, 2004 and May 30, 2005. These fish were expected to return to Fish Creek and spawn during spring 2005. I calculated the proportion of adults detected at Bonneville Dam that were later detected at McNary Dam, Lower Granite Dam, and the Fish Creek weir. I calculated the number of days the spawners spent in Fish Creek for all PIT-tagged adults that were recaptured as kelts.

Estimate Chinook Salmon Escapement in Fish Creek

The weir used to trap adult steelhead was left in the stream until September 16, 2005 to capture adult Chinook salmon that returned to Fish Creek. Hatchery origin Chinook salmon were marked with a caudal fin clip and released downstream of the weir. The Chinook salmon escapement was made by counting the number of naturally produced adults that were trapped and passed upstream of the weir. The trap tender determined the sex of each naturally produced Chinook salmon based on external characteristics, measured fork length to the nearest cm, scanned for the presence of a PIT tag, collected scales, snipped a small portion of the anal fin for future DNA analysis, and used a paper punch to mark the right operculum before releasing the fish upstream of the weir.

Estimate Wild Juvenile Steelhead Densities

Project crews used the same snorkel methods described for Objective 1 to estimate juvenile fish densities and temporal trends in wild production streams. During the summer of 2005, ISMES crews snorkeled Basin Creek in the Salmon River drainage; Gedney, WF Gedney, and O'Hara creeks in the Selway River drainage; Buckhorn Creek, Fitsum Creek, Lick Creek, Secesh River in the SF Salmon River drainage; and Canyon, Crooked Fork, Deadman, Fish, Hungery, Bald Mountain, Boulder, Stanley, Weir, Post Office, and Lake creeks in the Lochsa River drainage (Figure 3). The strata boundaries of the streams ISMES crews snorkeled are provided in Appendices 1 and 2.

PIT Tag Juvenile Steelhead from Wild Populations

This project operated screw traps in Fish Creek, Lick Creek, Secesh River downstream of Lick Creek, and Rapid River and coordinated steelhead tagging at screw traps used in ISS. Steelhead were tagged at eight ISS screw traps operated by IDFG in Crooked Fork Creek, Colt Killed Creek, Red River, SF Salmon River at Knox Bridge, Pahsimeroi River, Lemhi River 0.2 km downstream of Hayden Creek, Marsh Creek, and the Salmon River at Sawtooth Fish Hatchery; three ISS traps operated by the Nez Perce Tribe in the South Fork Salmon River drainage in Lake Creek, upper Secesh River, and Johnson Creek; and one ISS trap operated by the U.S. Fish and Wildlife Service in Clear Creek (Figure 4). The screw trap in Clear Creek was fished from March 3 to June 19, 2005; the Lick Creek trap was fished from June 29 to July 28, 2005; the IDFG Secesh River trap was fished from July 15 to October 26, 2005; and the Rapid River trap was fished from April 20 to May 16, 2005. At most other sites, the screw traps were fished continuously from early March until ice-up in November, river conditions permitting (Appendix 3). The traps were checked daily, and the number of steelhead captured and tagged was recorded. Each fish was scanned before tagging to verify that it had not been tagged previously. All steelhead >80 mm were PIT tagged, measured (fork length) to the nearest mm, and weighed to the nearest 0.1 g.

In addition to the screw traps, project crews PIT tagged wild steelhead that were collected by angling in Fish Creek on June 26, July 10, and July 11; 2005; Gedney Creek on July 25 and July 26, 2005; and WF Gedney Creek on July 26, 2005. I combined all fishing occasions in each stream for the data analysis. Crews from NOAA Fisheries, Pasco, Washington tagged juvenile steelhead >100 mm that were collected during their summer sampling of Chinook salmon parr in Bear Valley Creek, Big Creek, Camas Creek, Capehorn Creek, Elk Creek, Herd Creek, Loon Creek, Secesh River, SF Salmon River, Sulfur Creek, and Valley Creek from July 26 to August 31, 2005 (Figure 4).

I calculated the mean length, weight, and condition factor of steelhead at each screw trap site for the spring (start of trapping to May 31), summer (June 1 to August 31), and fall (September 1 to end of trapping) periods. I plotted the length frequency of steelhead by grouping fish into 5 mm interval length classes (class 70 = fish 70-74 mm, class 75 = fish 75-79 mm, etc.) at each site where ≥ 200 fish were PIT tagged. I also calculated the mean length, weight, and condition factor of steelhead collected in streams by angling and electrofishing.

Estimate the Number of Juvenile Steelhead Out-migrating from Fish Creek

The trap tender released PIT-tagged steelhead about 600 m upstream of the Fish Creek screw trap and recorded the number of recaptures at the trap daily to estimate trap efficiency. All recaptured fish were released downstream of the trap. When more than 50 steelhead were tagged in a day, only 50 fish were released upstream of the trap and the remainder downstream of the trap. All un-tagged fish were released upstream of the trap for efficiency estimation when less than 50 steelhead were trapped in a day.

I stratified the trapping season based on flow and time of year and determined the number of steelhead trapped, fish released upstream (marks), and recaptured fish in each strata. This data was used as input for a maximum likelihood estimator (Steinhorst et al. 2004) to estimate the number of migrants and a 95% CI that left the stream during each period, during the entire year, and from August 15 to November 14. In Fish Creek, most of the juvenile steelhead are trapped after August 15 (>90% of the total in all years since 1996, except 2004 when 67% of the total were trapped).

Estimate Smolt Detection Rates and Travel Times for PIT-tagged Steelhead Smolts

I queried the PTAGIS database on November 15, 2005 and obtained the date and dam of detection, date of tagging, and the length and weight at tagging of all wild steelhead smolts tagged at ISMES release sites and subsequently detected at Lower Granite (LGR), Little Goose (LGO), Lower Monumental (LMN), McNary (MCN), John Day (JDA), and Bonneville (BON) dams during 2005 (Figure 5). For each release site, I calculated the number of smolt detections from steelhead that were tagged from March 1, 2005 to May 31, 2005 (Period 1); August 15, 2004 to December 15, 2004 (Period 2); June 1, 2004 to August 14, 2004 (Period 3); fish tagged March 1, 2004 to May 31, 2004 (Period 4); and fish tagged before March 1, 2004 (Period 5). For each tag period, I determined the number of steelhead juveniles that were tagged and the number of tagged fish that were detected as smolts in 2005. I calculated the percentage of steelhead that were ≥125 mm when tagged that were detected as smolts in migration year 2005 (MY05) from each period.

I used the length of the fish that were PIT tagged between August 15, 2004 and May 31, 2005 to estimate the mean smolt length from each stream. Steelhead tagged and detected during spring 2005 (Period 1) are undergoing smoltification as they migrate to the ocean. Steelhead that were tagged between August 15, 2004 and December 15, 2004 (Period 2) and detected as a smolt in 2005 may grow after being tagged; however, most steelhead growth occurs before August each year (A. Byrne, unpublished data). Steelhead tagged prior to August 15, 2004 (Periods 3, 4, and 5) had additional time to grow before smolting; hence, their length at the time of tagging would likely underestimate smolt length. Steelhead PIT tagged between August 15, 2004 and May 31, 2005 and detected as smolts in MY05 were grouped into 5 mm interval length classes (class 130 = fish 130-134 mm, class 135 = fish 135-139 mm, etc.), and the length frequency was plotted.

I determined the date that 10%, 25%, 50%, 75%, and 90% of the total number of smolt detections at LGR was attained from each stream regardless of the tagging date. I calculated the median travel time (in days) and migration rate (km/day) and the 90% CI from release site to LGR of fish tagged in 2005 and subsequently detected (in MY05) as smolts at LGR

Estimate Age Composition of Adult and Juvenile Steelhead Populations

Trap tenders collected scales from adult steelhead trapped at the Fish Creek, Pahsimeroi River, and Rapid River weirs. Trap tenders collected scales from juvenile steelhead caught in screw traps in Clear Creek, Fish Creek, Lemhi River, Rapid River, Secesh River (IDFG trap only), SF Salmon River at Knox Bridge, and the Salmon River at Sawtooth Fish Hatchery. The collectors measured the fork length of each fish and obtained scales from the preferred area (MacLellan 1987). This area is located just above the lateral line, posterior of a vertical line drawn from the posterior end of the dorsal fin.

Scales that were collected from adult and juvenile steelhead were mounted between two glass microscope slides. The scales were observed on a computer video monitor using a Leica DME microscope and a Leica DC300 digital camera. A technician chose the best scale(s) for aging the fish and saved the scale as a digitized image. Most juvenile scale images were obtained using 100x magnification, and most adult scale images were obtained using 25x magnification. The saltwater age of adults and the freshwater age of juvenile steelhead were determined by counting the number of overwinter annuli. At least three technicians aged each scale independently using the same digitized scale image without knowledge of the length of the fish. If there was no age consensus among the readers, the readers collectively examined the image to resolve their differences before a final age was assigned to the fish. If a consensus was not attained, the scale was excluded from our analysis.

Characterize Genetic Structure and Introgression Rates of Steelhead Populations

This project collected and analyzed tissue samples from steelhead populations that span the range of geographic, temporal, and phenotypic variability observed in the Salmon and Clearwater basins. IDFG collected tissue samples from juvenile steelhead in 2000 from five hatchery stocks and 74 wild populations. The USGS Alaska Biological Lab did the microsatellite analysis. An interim report based on these analyses was completed in December 2003 (Byrne 2004). The analysis of the remaining populations was completed in 2005 and the final report from the USGS is included in Appendix 4.

Chinook Salmon Parr, Resident Trout, and Other Fish Trapped at Project Screw Traps

Trap tenders recorded the number of steelhead parr that were too small to tag (usually <80 mm), cutthroat trout, bull trout, and Chinook salmon parr that were caught in the Fish Creek, Lick Creek, Secesh River, and Rapid River screw traps each day. We recorded the number of longnose dace *Rhinichthys cataractae* and speckled dace *R. osculus* that were caught each day at the Fish Creek trap. The trap tenders PIT tagged bull trout, Chinook salmon parr, and cutthroat trout at each trap. All Chinook salmon parr, cutthroat trout, and bull trout that were PIT tagged were measured to the nearest 1 mm and weighed to the nearest 0.1 g. A daily subsample of the longnose and speckled dace that were trapped at Fish Creek were measured and weighed.

Document Water Temperature in Steelhead Streams

I recorded water temperatures in tributaries throughout the Clearwater and Salmon river drainages with HOBO™ temperature recorders (Onset Computer Corporation, Bourne, Massachusetts) to obtain yearly temperature profiles from streams with wild steelhead populations. The streams span a range of elevation, geomorphic, and vegetative cover found in Idaho's steelhead streams. The water temperatures were recorded every 0.25 h to 1.6 h from early spring until late October. Winter water temperatures were recorded every 0.25 h to 2.5 h, depending on location and access. The daily mean, maximum, and minimum water temperatures were calculated for each stream.

RESULTS

<u>Objective 1</u>

Evaluation of Spawner Success

Project crews snorkeled Beaver and Frenchman creeks on August 23, 2005. The age-1 steelhead densities in Beaver and Frenchman creeks were 2.45 and 0.02 fish/100m^2, respectively (Figure 6). The estimated age-1 steelhead populations and 95% CI in Beaver and Frenchman creeks were 256 (±64) and 22 (±13) fish, respectively. The estimated number of age-1 steelhead parr produced per female spawner in Beaver Creek for Brood Year (BY) 2004 was nine.

<u>Objective 2</u>

Estimate Juvenile Production from Naturally Spawning Adult Returns

We snorkeled the SF Red River from its mouth upstream to the WF SF Red River on June 27 and June 28, 2005. The mean age-1 and age-2+ steelhead densities (fish/100 m^2) were 1.01 and 1.00, respectively. The IDFG Clearwater Region crew snorkeled Red River upstream of the SF Red River to Shissler Creek on July 6 and July 7, 2005. The mean age-1 and age-2+ steelhead densities (fish/100 m^2) were 0.75 and 0.29, respectively (Figure 7).

Objective 3

Estimate Steelhead Escapement in Fish Creek

An IDFG crew began installing the Fish Creek weir on March 3 and trapping commenced during the afternoon of March 8, 2005. The weir remained intact during the steelhead spawning run. Technicians trapped 82 females and 39 males at the weir and passed them upstream to spawn (Table 1). This year's escapement was the fifth highest since monitoring of the Fish Creek escapement began in 1992 (Figure 8). The median date of arrival of the female and male spawners was April 25 and April 22, respectively (Table 2 and Figure 9). The mean length of females and males were 78 cm (±1) and 80 cm (±2), respectively. Most of the adults were between 72 cm and 84 cm (Figure 10).

Trap tenders captured 65 marked female kelts and 15 marked male kelts. They did not recover any unmarked kelts. The first kelt (a female) was captured on April 15, and the last kelt (a female) was captured on June 23. The median date of kelt capture was May 13 for males and May 25 for females (Table 2 and Figure 11). A higher proportion of the female kelts (79%) were alive than male kelts (38%) when they were recovered at the weir. It was not necessary to make a maximum likelihood estimate (ML) of the escapement since all kelts we recovered were marked.

PIT-tagged Adult Steelhead Returns

There were 11 unique adult steelhead detected at dams on the Columbia and Snake rivers that were PIT tagged as juveniles in Fish Creek. Eight of these adults plus two adults PIT tagged at LGR as smolts were trapped at the Fish Creek weir during spring 2005. The first PIT-tagged adult returning to Fish Creek was detected at Bonneville Dam on August 31, 2004 and the last PIT-tagged adult was detected on October 11, 2004. The median date of passage at Bonneville Dam was September 9, 2004 (Figure 12).

All 11 adults PIT tagged in Fish Creek as juveniles were detected at Bonneville Dam. Ten of the 11 adults of Fish Creek origin that were detected at Bonneville were also detected at McNary, nine were detected at Lower Granite Dam, and eight were captured at the Fish Creek weir (Figure 13). The conversion rate from Bonneville Dam to McNary was 91%, from Bonneville to LGR was 82%, from Bonneville to Fish Creek was 73%, and from LGR to Fish Creek was 89%.

The trap tenders recovered one male and one female PIT-tagged kelt at the Fish Creek weir. The male kelt spent 29 days and the female kelt spent 30 days in Fish Creek.

Estimate Chinook Salmon Escapement in Fish Creek

We left the weir used to trap steelhead in the stream until September 16, 2005 to trap adult Chinook salmon returning to Fish Creek. We trapped five wild male and two wild female Chinook salmon at the weir and passed them upstream to spawn. The first wild adult was caught on June 12 and the last on July 26, 2005. The tenders also trapped eight hatchery origin adult Chinook salmon (four males and four females) at the weir. The first hatchery origin adult was caught on June 11 and the last on August 30, 2005 (Figure 14).

Estimate Wild Juvenile Steelhead Densities

Crews began the snorkel surveys in the SF Red River on June 27, 2005 and completed the surveys in Basin Creek on August 24, 2005. Snorkel conditions were excellent in all streams during the summer surveys. The estimated mean densities by tributary, habitat type, and species for the Clearwater River drainage, Salmon River drainage, and the SF Salmon River drainage are in Tables 3, 4, and 5. The mean age-1 steelhead densities decreased from those observed in 2004 in five of the 12 tributaries of the Lochsa and Selway rivers that were surveyed both years (Table 6). The age-1 steelhead density decreased in Bald Mountain, Fish, Boulder, Deadman, and Lake creeks. However, the steelhead density of all parr declined only in Bald Mountain, Deadman, and Lake creeks (Figure 15).

The mean age-1 steelhead densities decreased from those observed in 2004 in four of the five tributaries of the Salmon River drainage rivers that were surveyed both years (Table 6). The age-1 steelhead density and all parr density increased in Secesh River and declined in Basin, Beaver, Frenchman, and Lick creeks (Figure 16).

We did not complete a habitat survey in Fitsum Creek and Buckhorn Creek; hence, a mean stream density was not calculated. The density of all steelhead parr in pocket water and run habitat in Fitsum Creek was 1.81 and 0.27 fish/100m^2, respectively, a decline from the 2004 pocket water and run habitat densities of 7.63 and 6.78 fish/100m^2, respectively. In Buckhorn Creek the density of all steelhead parr in pocket water habitat was 5.38 fish/100m^2 (5.88 fish/100m^2 in 2004) and 8.98 fish/100m^2 in run habitat (3.21 fish/100m^2 in 2004).

PIT Tag Juvenile Steelhead from Wild Populations

Trap tenders tagged 14,240 juvenile steelhead at the five screw trap sites in the Clearwater River drainage. Eighty-five percent (12,115 fish) were tagged in Fish Creek. The mean length of all tagged steelhead ranged from 115 mm (±6 mm) in Red River to 162 mm (±4 mm) in Colt Killed Creek (Table 7 and Figure 17).

Trap tenders tagged 7,796 juvenile steelhead at the 11 screw trap sites in the Salmon River drainage. Trap tenders tagged >1,000 steelhead only at the Pahsimeroi River, Lemhi River, and SF Salmon River traps. The mean length of all tagged fish ranged from 115 mm (±7 mm) in Lick Creek to 181 mm (±2 mm) in Rapid River (Table 8 and Figure 18).

Summer field crews using flyfishing gear collected and PIT tagged 912 juvenile steelhead in Fish, Gedney, Boulder, and Lick creeks. The mean length ranged from 129 mm (±16 mm) in Boulder Creek to 138 mm (±7 mm) in Lick Creek (Table 9).

The NOAA Fisheries crew used electrofishing gear to collect and PIT tag 1,971 juvenile steelhead from 13 streams for this study. They collected and tagged fewer than 100 steelhead in four of these streams (Table 9). The mean length of the steelhead in the streams where >100 were tagged ranged from 98 mm (±4 mm) in Sulfur Creek to 117 mm in Valley Creek (±5 mm).

Estimate the Number of Juvenile Steelhead Out-migrating from Fish Creek

I split the trapping season into 17 periods. The first period, from March 10 to April 22, was the longest duration. During the first period, the river level was usually between 3.0 and 3.5

feet. In this first period, 45 steelhead were released upstream of the trap and two were recaptured. During the second period, from April 23 to May 25, the river level was >3.5 feet. The river level dropped below 3.5 feet on May 26 and dropped steadily thereafter. The trap was fished in the thalweg once the river level was less than 3.0 feet. The river level dropped below 3.0 feet on June 8 and never exceeded 3.0 for the remainder of the trapping season. Beginning May 26, the trap periods were usually 14 days long. The major exceptions to the 14 day duration were Period 13 and Period 16, which were short high flow spikes caused by a heavy rain (Table 10 and Figure 19). I estimated that 53,263 juvenile steelhead (lower CI = 48,410, upper CI = 55,722) left Fish Creek from March 10 to November 14 (Figure 20). The number of steelhead that left Fish Creek from August 15 to November 14 was 34,361 (lower CI = 32,248, upper CI = 36,641).

Estimate Smolt Detection Rates and Travel Times for PIT-tagged Steelhead Smolts

During MY05, 3,100 and 1,384 smolts were detected at downriver dams from project tagging sites in the Clearwater River and Salmon River drainages, respectively. The Clearwater drainage smolt detections were dominated by Fish Creek (77% of the drainage total), followed by Crooked Fork Creek (9%) and Clear Creek (5%) The remaining four tag sites from the Clearwater drainage each contributed less than 5% of the total drainage smolt detections. The most abundant smolt detections from the Salmon drainage were from Rapid River (24% of the drainage total), Johnson Creek (17%), SF Salmon River (17%), and Pahsimeroi River (10%). The remaining nine sites from the Salmon River drainage each contributed less than 10% of the total Salmon drainage detections (Table 11).

The Period 1 smolt detection rate of fish ≥125 mm when tagged from the Clearwater River sites ranged from 63% at Fish Creek to 86.1% at Colt Killed Creek. The detection rates of fish ≥125 mm when tagged from the Clearwater sites for Period 2 ranged from 15.1% at O’Hara Creek to 56.2% from Colt Killed Creek. The Period 1 smolt detection rate of fish ≥125 mm when tagged from the Salmon River sites ranged from 0% from the Lake Creek to 75.6% from Rapid River. The detection rates of fish ≥125 mm when tagged from the Salmon sites for Period 2 ranged from 4.1% from the Lemhi River to 38.7% from Rapid River. The smolt detection rate for Period 1 was higher than Period 2 at all sites except Lake Creek, Marsh Creek, and Secesh River (Table 11 and Figure 21).

The mean smolt length, based on steelhead tagged between August 15, 2004 and May 31, 2005, ranged from 141 mm (±1 mm) in Fish Creek to 181 mm (±3 mm) from Lemhi River. The mean smolt length at most Clearwater River sites ranged between 164 mm and 174 mm. In the Salmon River drainage, the mean smolt length at most sites ranged from 160 mm to 175 mm (Figure 22).

The median arrival date at Lower Granite Dam of smolts from Clearwater River sites was between April 27 and May 2. The duration of the middle 50% quantile of the smolt run (25% date to 75% date), ranged from five days from Colt Killed Creek to 22 days from Clear Creek. The earliest 90% arrival quantile date was attained on May 8 from Crooked Fork Creek and was attained at all other Clearwater drainage sites by May 14 (Figure 23).

The median arrival date at Lower Granite Dam of smolts from Salmon River sites was between May 1 and May 13. The duration of the middle 50% quantile of the smolt run (25% date to 75% date), ranged from four days from Marsh Creek to 18 days from Lemhi River. The 90%

arrival quantile date ranged from May 10 from Lake Creek to June 1 from the Lemhi River (Figure 23).

The median travel time from all tag sites in the Clearwater drainage was seven days. The travel time from tag sites in the Salmon River drainage ranged from five to 14 days (Table 12). The median smolt migration rate from release site to LGR was >40 km/day from four of the seven sites in the Salmon River drainage and two of the four sites from the Clearwater River drainage. The fastest median migration rate was 119 km/day from the upper Lemhi River and the slowest was 25.1 km/day from Clear Creek (Table 12). The relation of median migration rate and distance to LGR was not significant ($r^2 = 0.356$, $p = 0.053$; Figure 24).

Estimate Age Composition of Adult and Juvenile Steelhead Populations

We collected scales from 124 adult steelhead that returned to Fish Creek, 73 adults that returned to Rapid River, and 41 adults that returned to the Pahsimeroi River in 2005. In the Clearwater River drainage, we collected scales from 165 juvenile steelhead in Clear Creek and 1,175 juveniles in Fish Creek. In the Salmon River drainage, we collected scales from 136 juveniles in Lemhi River, 188 juveniles in Secesh River, 295 juveniles in Pahsimeroi River, 116 juveniles in Rapid River, 130 juveniles in the Salmon River, and 161 juveniles in the SF Salmon River (Table 13).

A technician aged 235 adults from scales that were collected in 2005 and 3,282 juvenile from scales that were collected in 2004 and 2005 (Table 14). All of these scales must be aged by one or two additional readers before a final age is assigned to the fish.

Characterize Genetic Structure and Introgression Rates of Steelhead Populations

Personnel at the Alaska Science Center completed the microsatellite analysis of juvenile *O. mykiss* that IDFG collected in 2000. The final report from the Alaska Science Center is included in Appendix 4.

Chinook Salmon Parr, Resident Trout, and Other Fish Trapped at Project Screw Traps

Fish Creek Screw Trap—In addition to the 12,115 juvenile steelhead we PIT tagged, we captured 1,770 steelhead parr that were not PIT tagged, 404 steelhead fry (age-0), 811 Chinook salmon parr of which 153 were recaptures for a trap efficiency estimate, three bull trout, 414 westslope cutthroat trout, 4,226 longnose dace, and 830 speckled dace. Trap tenders PIT tagged 568 Chinook salmon parr, three bull trout, and 382 westslope cutthroat trout (Table 15). Most of the Chinook salmon parr were trapped after October 1, 2005 (Figure 25A). Although cutthroat trout were caught throughout the trapping season (Figure 25B), we captured 77% of them from June 23 to July 10 (132 fish) and from August 24 to October 5, 2005 (185 fish).

Secesh River Screw Trap—This was the first year IDFG ran a screw trap in the Secesh River. The trap is located at river kilometer 7, about 1 km downstream of Lick Creek. The trap was installed on July 15, 2005 after the high spring flow had subsided. In addition to the 978 juvenile steelhead we PIT tagged (Figure 26), we captured 196 steelhead parr and 24 steelhead fry (age-0). Trap tenders caught 46,875 Chinook salmon parr (Figure 27), 10 westslope cutthroat trout, nine bull trout, and 104 dace that were not identified to species (Table 15). The trap tender PIT tagged 4,137 Chinook salmon parr, nine cutthroat trout, and nine bull trout. Trap tenders tagged a maximum of 50 Chinook salmon parr daily. These fish were tagged for use in the Comparative Survival Study (BPA Project 199602000) and to compare and contrast smolt-to-adult survival rates and migration timing with other summer Chinook salmon that were PIT tagged at the Lake Creek, Johnson Creek, SF Salmon River, and upper Secesh River screw traps.

Rapid River Screw Trap—In addition to the 349 juvenile steelhead we PIT tagged, we captured 18 steelhead parr >80 mm, 45 Chinook salmon parr, and 16 bull trout (Table 15). The trap tender PIT tagged 36 Chinook salmon parr and 15 bull trout. The anchor for the main cable pulled out of the boulder it was secured to on May 16, 2005. This trap was located just upstream of a footbridge above the check dam that provides the main water intake for Rapid River Fish Hatchery. Due to safety concerns to hatchery infrastructure, the trap was not redeployed after the cable failed. Project personnel are trying to find a suitable trap site and obtain permission from a private landowner to place the screw trap downstream of the hatchery.

Lick Creek Screw Trap—In addition to the 192 juvenile steelhead we PIT tagged, we captured 52 steelhead parr that were not tagged, 17 westslope cutthroat trout, and 10 longnose dace. The trap was fished from June 29 to July 28, 2005. The flow in Lick Creek was too low to turn the screw trap after July 28.

Document Water Temperature in Steelhead Streams

The water temperature was recorded at 12 locations in the Salmon River drainage and 25 locations in the Clearwater River drainage (Table 16). All data were entered into a stream temperature database maintained at the IDFG Nampa Fisheries Research Office. The daily mean, maximum, and minimum temperature from Fish Creek is shown in Figure 28.

DISCUSSION

The small-scale supplementation experiments to estimate age-1 parr production from hatchery adult outplants were completed in 2005. Idaho Steelhead Monitoring and Evaluation Studies crews did the final snorkel survey in Beaver Creek in August 2005. The estimated number of age-1 parr produced per female spawner in Beaver Creek this year was nine fish. If we assume that all age-1 parr survive and become smolts and the smolt-to-adult survival rate is 2% (the lowest recommended recovery target), then less than one adult would be expected to return. Given the additional natural mortality that would be expected from over-wintering and the need to rear an additional year and another winter before smolting, this estimate is biased high.

Project personnel began operating a screw trap in the Secesh River about 1 km downstream of Lick Creek in 2005. The trap was fished from July 15 to October 26, 2005. We PIT-tagged nearly 1,000 juvenile steelhead and captured over 46,000 Chinook salmon parr. This trap will provide another site to compare and contrast wild Steelhead migration timing, smolt migration timing through the hydrosystem, and smolt-to-adult survival rates with other project and ISS trap sites in the SF Salmon drainage and the Pahsimeroi River.

The Rapid River screw trap was fished from April 20 to May 16, 2005. On May 16, the eyebolt that secured the main cable failed. Due to worker safety issues arising from operating a trap in a deep pool and possible damage to the hatchery water intake, the trap was not re-installed. Rapid River is an excellent stream to make an estimate of steelhead parr production per female spawner, because all adults are trapped at the hatchery weir. This stream could provide an estimate of migrants per female spawner that could be compared with the Fish Creek estimate on a yearly basis. Currently, Fish Creek is the only Idaho stream where an estimate of migrants per female spawner is made. Given the paucity of wild steelhead production data in Idaho, estimating juvenile production in another stream would provide much needed data for steelhead recovery planning. Project and Rapid River Hatchery staff are attempting to gain permission from private landowners located upstream of the hatchery weir and downstream of the fish hatchery to fish the screw trap. In addition, we plan to contact landowners who have water diversions on their property so we can install box traps on the diversion fish bypass system.

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Table 1. The number of adult steelhead that were captured at the Fish Creek weir and passed upstream to spawn and the number of kelts that were recovered in 2005. Length (cm) measured was the fork length. 95% CI = ± cm.

Sex	Adults trapped	Unmarked kelts recovered	Total handled	Mean length (cm)	95% CI	Maximum length	Minimum length	Marked kelts recovered	Percent of adults recovered as kelts
Female	82	0	82	78	1	88	71	65	79%
Male	39	0	39	80	2	92	63	15	38%
All	121	0	121	79	1	92	63	80	66%

Table 2. The date that the first and last steelhead adult was captured at the Fish Creek weir in 2005, and the date that 10%, 25%, 50%, 75%, and 90% of the total number of adults were captured. The spawner rows are adults that were caught in the trap box and passed upstream to spawn. N = number of fish.

Life stage	Sex	N	Date the quantile was attained						
			First	10%	25%	50%	75%	90%	Last
Spawner	Female	82	3/20	4/5	4/17	4/25	5/6	5/13	6/4
Spawner	Male	39	3/20	4/3	4/10	4/22	5/2	5/6	5/13
Spawner	All	121	3/20	4/4	4/11	4/24	5/3	5/11	6/4
Kelt	Female	65	4/15	5/2	5/12	5/25	6/2	6/13	6/23
Kelt	Male	15	4/27	4/29	5/5	5/13	5/18	5/25	6/1
Kelt	All	80	4/15	4/30	5/12	5/22	6/1	6/7	6/23

Table 3. Mean fish densities (fish/100 m^2) by habitat type in streams of the Clearwater River drainage that were snorkeled during summer 2005. Area = total area snorkeled (m^2); N = number of sites snorkeled; Trout fry = all trout (except brook trout) ≤75 mm; Age-1 steelhead = juvenile steelhead 76 mm to 127 mm; Age-2+ steelhead = all juvenile steelhead >127 mm; Brook fry = all brook trout <75 mm; Brook parr = all brook trout ≥75 mm; PW = pocket water.

							Steelhead parr		Chinook parr						
Stream	**Date**	**Habitat type**	**Strata**	**N**	**Area**	**Trout fry**	**Age-1**	**Age-2+**	**Age-0**	**Age-1**	**Cutthroat**	**Bull**	**Brook fry**	**Brook parr**	**Whitefish**
Bald Mountain Creek	8/8	Pocket	1	17	1,807	5.48	9.25	2.99	0.05	0.00	5.05	0.06	0.00	0.00	0.00
Bald Mountain Creek		Pool	1	3	53	12.45	9.97	10.98	0.00	0.00	15.09	0.00	0.00	0.00	0.00
Bald Mountain Creek		Riffle	1	1	39	2.57	7.70	0.00	0.00	0.00	2.57	0.00	0.00	0.00	0.00
Bald Mountain Creek		Run	1	4	142	16.01	11.85	4.29	0.00	0.00	7.78	0.00	0.00	0.00	0.00
Boulder Creek	8/4	Pocket	1	30	6,536	3.53	9.65	7.82	3.36	0.00	0.19	0.01	0.00	0.00	0.00
Boulder Creek		Pool	1	6	561	4.53	16.04	15.76	23.10	0.00	0.13	0.00	0.00	0.21	0.00
Boulder Creek		Riffle	1	2	246	0.49	5.95	4.77	8.27	0.00	0.00	0.00	0.00	0.00	0.00
Boulder Creek		Run	1	7	991	2.43	13.57	12.55	9.70	0.00	0.00	0.11	0.00	0.00	0.00
Canyon Creek	8/7	Pocket	1	17	1,725	7.34	10.01	3.82	0.05	0.00	0.34	0.00	0.00	0.00	0.00
Canyon Creek		Pool	1	5	157	6.10	18.93	18.16	0.00	0.00	3.22	0.00	0.00	0.00	0.00
Canyon Creek		Riffle	1	2	147	8.59	11.19	3.12	0.00	0.00	2.67	0.00	0.00	0.00	0.00
Canyon Creek		Run	1	5	242	5.02	18.15	8.62	0.32	0.00	1.79	0.00	0.00	0.00	0.00
Crooked Fork Creek		Pocket	1	2	1,658	7.35	3.15	2.52	5.45	0.00	0.13	0.00	0.00	0.00	0.07
Crooked Fork Creek		Pool	1	3	1,169	7.93	1.07	1.68	15.84	0.00	0.94	0.25	0.00	0.00	16.97
Crooked Fork Creek		Run	1	3	1,746	3.17	2.95	1.80	10.67	0.00	0.38	0.00	0.00	0.00	2.36
Deadman Creek	8/7	Pocket	1	13	1,674	14.25	4.66	1.68	0.94	0.00	0.00	0.00	0.00	0.00	0.00
Deadman Creek		Pool	1	5	123	29.65	12.56	10.13	12.21	0.00	0.00	0.00	0.00	0.00	0.00
Deadman Creek		Riffle	1	3	261	18.66	0.00	0.00	6.86	0.00	0.32	0.00	0.00	0.00	0.00
Deadman Creek		Run	1	4	273	16.86	4.93	2.40	2.20	0.00	0.43	0.00	0.00	0.00	0.00
Fish Creek	7/6	Pocket	1	26	11,308	2.68	5.89	6.44	0.12	0.00	0.45	0.00	0.00	0.00	0.02
Fish Creek	to	Pool	1	8	1,161	2.70	10.50	14.47	0.31	0.00	2.17	0.00	0.00	0.00	0.00
Fish Creek	7/12	Riffle	1	7	2,402	3.02	4.86	3.52	0.00	0.00	0.30	0.00	0.00	0.00	0.00
Fish Creek		Run	1	20	5,830	2.67	7.11	8.13	0.21	0.03	0.75	0.00	0.00	0.00	0.00
Fish Creek	7/8	Pocket	2	6	1,342	0.00	8.19	1.99	0.00	0.00	0.38	0.00	0.00	0.00	0.00
Fish Creek		Pool	2	3	218	0.00	22.67	8.81	0.00	0.00	1.71	0.00	0.00	0.00	0.00
Fish Creek		Run	2	8	1,194	2.38	9.97	1.93	0.00	0.00	0.83	0.00	0.00	0.00	0.00
Hungery Creek	7/8	Pocket	1	7	1,400	3.64	3.36	7.17	0.09	0.00	0.28	0.00	0.00	0.00	0.00
Hungery Creek		Pool	1	4	407	8.04	8.63	17.15	0.17	0.00	0.85	0.00	0.00	0.00	0.00
Hungery Creek		Run	1	5	834	6.05	6.17	11.16	0.00	0.00	0.97	0.00	0.00	0.00	0.00

Table 3. Continued.

Stream	Date	Habitat type	Strata	N	Area	Trout fry	Steelhead parr		Chinook parr		Cutthroat	Bull	Brook fry	Brook parr	Whitefish
							Age-1	Age-2+	Age-0	Age-1					
Gedney Creek	7/21	Pocket	1	24	7,413	8.53	5.34	4.55	4.39	0.00	0.07	0.07	0.00	0.00	0.29
Gedney Creek	to	Pool	1	6	790	9.88	8.59	8.68	6.97	0.00	1.69	0.41	0.00	0.00	0.77
Gedney Creek	7/27	Riffle	1	5	1,591	9.70	5.50	3.71	6.72	0.00	0.00	0.00	0.00	0.00	0.19
Gedney Creek		Run	1	11	2,448	12.09	9.07	6.63	12.75	0.00	0.61	0.08	0.00	0.00	0.45
Gedney Creek	7/23	Pocket	2	9	1,223	8.92	14.19	5.75	2.00	0.00	0.00	0.00	0.00	0.00	0.00
Gedney Creek		Pool	2	3	191	5.45	20.37	11.77	6.66	0.00	0.00	0.00	0.00	0.00	0.00
Gedney Creek		Riffle	2	3	258	10.86	12.75	3.15	6.89	0.00	0.00	0.00	0.00	0.00	0.00
Gedney Creek		Run	2	3	209	5.61	19.26	7.32	2.54	0.00	0.00	0.00	0.00	0.00	0.00
WF Gedney Creek	7/23	Pocket	1	8	1,721	10.33	6.99	5.59	0.40	0.00	0.00	0.05	0.00	0.00	0.00
WF Gedney Creek		Pool	1	4	402	17.09	13.04	14.77	0.81	0.00	0.16	0.33	0.00	0.00	0.00
WF Gedney Creek		Riffle	1	3	565	24.49	7.29	1.43	1.45	0.00	0.14	0.00	0.00	0.00	0.00
WF Gedney Creek		Run	1	4	608	23.94	15.44	10.84	1.50	0.00	0.69	0.00	0.00	0.00	0.00
Lake Creek	8/8	Pocket	1	12	2,794	3.23	2.14	0.40	0.00	0.00	0.05	0.00	0.00	0.00	0.04
Lake Creek		Pool	1	5	264	4.14	6.42	1.46	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Lake Creek		Riffle	1	3	604	2.12	2.67	0.00	0.00	0.00	0.16	0.00	0.00	0.00	0.00
Lake Creek		Run	1	5	806	3.37	1.63	0.50	0.00	0.00	0.00	0.13	0.00	0.00	0.00
O’Hara Creek	8/5	Pocket	2	26	4,037	9.64	13.23	4.56	48.70	0.00	0.12	0.00	0.00	0.00	0.00
O’Hara Creek		Pool	2	6	255	11.00	16.66	9.38	117.89	0.00	0.00	0.33	0.00	0.00	0.25
O’Hara Creek		Riffle	2	9	1,783	8.08	4.68	2.47	28.56	0.00	0.06	0.00	0.00	0.00	0.00
O’Hara Creek		Run	2	11	1,724	10.00	8.57	3.32	69.28	0.00	0.31	0.00	0.00	0.00	0.00
Hanby Fork	8/5	Pocket	1	2	209	13.49	7.66	0.00	9.89	0.00	0.00	0.00	0.00	0.00	0.00
Hanby Fork		Pool	1	2	45	19.58	17.45	2.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Hanby Fork		Run	1	2	97	19.18	10.57	1.09	1.09	0.00	0.00	0.00	0.00	0.00	0.00
Pete King Creek		Pool	1	4	174	19.84	19.74	7.28	47.48	0.00	1.30	0.00	0.00	0.00	0.00
Pete King Creek		Riffle	1	13	1,758	14.14	8.22	0.97	7.44	0.00	0.08	0.00	0.00	0.00	0.00
Pete King Creek		Run	1	6	595	16.29	6.47	2.48	30.55	0.00	0.00	0.00	0.00	0.00	0.00
Post Office Creek	8/6	Pocket	1	6	654	30.44	11.55	2.33	1.04	0.00	1.17	0.17	0.00	0.00	0.00
Post Office Creek		Pool	1	6	174	31.02	18.07	14.84	12.32	0.00	5.19	0.00	0.00	0.00	0.00
Post Office Creek		Riffle	1	11	912	30.66	8.47	1.57	2.97	0.00	0.18	0.00	0.00	0.00	0.10
Post Office Creek		Run	1	5	415	33.74	13.38	4.10	4.56	0.00	0.49	0.00	0.00	0.00	0.00

Table 3. Continued.

Stream	Date	Habitat type	Strata	N	Area	Trout fry	Steelhead parr		Chinook parr		Cutthroat	Bull	Brook fry	Brook parr	Whitefish
							Age-1	Age-2+	Age-0	Age-1					
SF Red River	6/27	Pocket	1	4	736	0.00	1.52	0.45	0.00	0.00	0.00	0.00	0.00	0.00	0.00
SF Red River		Pool	1	3	129	0.00	0.00	2.07	0.00	0.00	0.00	0.00	0.00	0.00	0.00
SF Red River		Riffle	1	5	959	0.00	0.96	1.70	0.00	0.00	0.80	0.00	0.00	0.00	0.26
SF Red River		Run	1	9	1,458	0.00	1.30	1.83	0.07	0.00	0.43	0.00	0.00	0.00	0.07
SF Red River	6/27	Pocket	2	5	741	0.00	0.29	0.47	0.00	0.00	0.25	0.00	0.00	0.00	0.00
SF Red River	and	Pool	2	6	268	0.00	0.88	1.99	0.00	0.00	0.92	0.00	0.00	0.00	0.00
SF Red River	6/28	Riffle	2	8	1,205	0.00	0.39	0.36	0.00	0.00	0.60	0.09	0.00	0.00	0.00
SF Red River		Run	2	16	2,089	0.00	1.53	0.73	0.00	0.00	0.66	0.18	0.00	0.09	0.00
Stanley Creek	8/9	Pocket	1	16	1,914	12.31	13.33	2.89	0.00	0.00	0.73	0.04	0.00	0.00	0.00
Stanley Creek		Pool	1	4	180	6.00	17.52	4.85	0.00	0.00	8.13	0.00	0.00	0.00	0.00
Stanley Creek		Riffle	1	1	54	22.32	20.46	3.72	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Stanley Creek		Run	1	4	242	19.84	12.33	2.34	0.00	0.00	1.65	0.00	0.00	0.00	0.00
Trapper Creek	6/28	Pocket	1	8	640	0.00	1.59	0.51	0.00	0.00	0.53	0.00	0.00	0.00	0.00
Trapper Creek		Pool	1	1	23	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Trapper Creek		Riffle	1	1	57	0.00	3.53	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Trapper Creek		Run	1	5	220	0.00	1.70	1.57	0.00	0.00	1.66	0.00	0.00	0.00	0.00
Weir Creek	8/6	Pocket	1	6	691	14.77	3.17	1.05	0.00	0.00	0.43	0.12	0.00	0.00	0.00
Weir Creek		Pool	1	3	67	45.09	12.58	0.00	0.00	0.00	3.84	0.00	0.00	0.00	0.00
Weir Creek		Riffle	1	6	563	21.59	5.15	1.10	0.25	0.00	0.99	0.00	0.00	0.00	0.00
Weir Creek		Run	1	6	356	25.81	7.98	2.27	0.44	0.00	1.57	0.00	0.00	0.00	0.00

Table 4. Mean fish densities (fish/100 m^2) by habitat type in streams of the Salmon River drainage that were snorkeled during summer 2005. Area = total area snorkeled (m^2); N = number of sites snorkeled; Trout fry = all trout (except brook trout) ≤75 mm; Age-1 steelhead = juvenile steelhead 76 mm to 127 mm; Age-2+ steelhead = all juvenile steelhead >127 mm; Brook fry = all brook trout <75 mm; Brook parr = all brook trout ≥75 mm; PW = pocket water.

Stream	Date	Habitat type	Strata	N	Area	Trout fry	Steelhead parr		Chinook parr		Cutthroat	Bull	Brook fry	Brook parr	Whitefish
							Age-1	Age-2+	Age-0	Age-1					
Basin Creek	8/24	Pocket	1	3	525	1.77	1.36	0.43	0.00	0.00	0.00	0.00	0.00	0.00	0.76
Basin Creek		Pool	1	1	140	17.15	3.57	4.29	8.57	0.00	0.71	0.00	0.00	0.00	0.71
Basin Creek		Riffle	1	9	1,390	2.09	1.33	1.36	2.57	0.00	0.00	0.00	0.00	0.00	0.00
Basin Creek		Run	1	9	998	2.30	1.45	2.00	8.92	0.00	0.06	0.18	0.00	0.00	0.65
Beaver Creek	8/23	Riffle	1	2	104	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7.67	2.44	0.00
Beaver Creek		Run	1	1	50	0	0	0	0	0	0	0	7.95	0	0
Beaver Creek	8/23	Pocket	2	3	200	0.00	2.57	0.29	0.00	0.00	0.00	0.00	1.16	0.29	0.00
Beaver Creek		Pool	2	5	277	0.00	3.41	0.18	0.00	0.00	0.00	0.00	11.16	14.42	0.00
Beaver Creek		Riffle	2	7	295	0.38	0.37	0.00	0.00	0.00	0.00	0.00	2.45	2.19	0.00
Beaver Creek		Run	2	15	826	0.20	3.39	1.04	0.00	0.00	0.00	0.00	4.22	8.81	0.00
Beaver Creek	8/23	Run	3	4	362	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.21	13.56	0.00
Frenchman Creek	8/23	Pocket	1	3	138	0.82	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Frenchman Creek		Pool	1	6	131	0.00	0.00	0.00	0.00	0.00	0.00	0.00	17.87	7.66	0.00
Frenchman Creek		Riffle	1	7	204	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6.56	0.00	0.00
Frenchman Creek		Run	1	19	877	0.00	0.32	0.19	0.00	0.00	0.00	0.00	14.90	7.11	0.00

Table 5. Mean fish densities (fish/100 m^2) by habitat type in streams of the SF Salmon River drainage that were snorkeled during summer 2005. Area = total area snorkeled (m^2); N = number of sites snorkeled; Trout fry = all trout (except brook trout) ≤75 mm; Age-1 steelhead = juvenile steelhead 76 mm to 127 mm; Age-2+ steelhead = all juvenile steelhead >127 mm; Brook fry = all brook trout <75 mm; Brook parr = all brook trout ≥75 mm; PW = pocket water.

Stream	Date	Habitat type	Strata	N	Area	Trout fry	Steelhead parr		Chinook parr		Cutthroat	Bull	Brook fry	Brook parr	Whitefish
							Age-1	Age-2+	Age-0	Age-1					
Buckhorn Creek	8/21	Pocket	1	8	1,087	3.87	4.55	0.82	10.71	0.00	0.21	0.18	0.00	0.00	0.07
Buckhorn Creek		Pool	1	2	99	4.29	12.14	11.57	52.14	0.00	1.57	0.00	0.00	0.00	0.00
Buckhorn Creek		Run	1	6	721	3.16	6.65	2.34	30.65	0.00	0.15	0.27	0.00	0.00	0.23
WF Buckhorn Creek	8/21	Pocket	1	3	207	0.89	4.55	0.00	12.13	0.00	0.00	0.00	0.00	0.00	0.00
WF Buckhorn Creek		Pool	1	1	32	6.25	6.25	3.13	109.38	0.00	0.00	0.00	0.00	0.00	0.00
WF Buckhorn Creek		Run	1	2	87	2.10	6.94	0.00	19.56	0.00	0.00	0.00	0.00	0.00	0.00
Fitsum Creek	8/21	Pocket	1	13	1,610	2.33	1.39	0.42	0.00	0.00	0.00	0.00	0.17	0.00	0.00
Fitsum Creek		Pool	1	4	145	2.23	2.25	0.00	0.56	0.00	0.00	0.00	0.00	0.00	0.00
Fitsum Creek		Run	1	4	321	1.05	0.27	0.00	0.00	0.00	0.00	0.00	0.28	0.00	0.00
Lick Creek	8/20	Pocket	1	23	4,042	6.66	5.73	1.96	0.47	0.00	0.04	0.00	0.00	0.26	0.00
Lick Creek		Pool	1	3	212	8.68	11.46	3.94	24.61	0.00	1.54	0.00	0.00	0.00	0.00
Lick Creek		Riffle	1	8	7,060	6.67	4.32	0.25	2.04	0.00	0.00	0.00	0.00	0.00	0.00
Lick Creek		Run	1	7	1,016	9.35	7.05	3.06	4.76	0.00	0.00	0.00	0.12	0.68	0.00
Secesh River	8/18	Pocket	1	40	19,378	0.41	2.94	2.02	9.94	0.00	0.04	0.01	0.00	0.00	0.38
Secesh River	and	Pool	1	2	611	0.00	1.21	3.52	34.41	0.00	0.00	0.11	0.00	0.00	1.03
Secesh River	8/19	Riffle	1	5	4,169	1.20	2.56	0.77	10.06	0.00	0.00	0.00	0.00	0.00	0.25
Secesh River		Run	1	8	3,549	0.22	2.26	2.28	34.61	0.00	0.20	0.05	0.00	0.00	1.74

Table 6. The mean stream density (fish/100m^2) of juvenile steelhead, Chinook salmon parr, cutthroat trout, bull trout, brook trout, and mountain whitefish in streams that were snorkeled in 2005. The age-1 change column is the percent change of the age-1 steelhead parr density from the 2004 survey.

			Steelhead parr		Chinook parr							
Stream	**Strata**	**Trout fry**	**Age-1**	**Age-2+**	**Age-0**	**Age-1**	**Cutthroat**	**Bull**	**Brook fry**	**Brook parr**	**Whitefish**	**Age-1 change**
Fish Creek	1	2.72	6.14	6.69	0.13	0.01	0.54	0.00	0.00	0.00	0.01	-22%
Gedney Creek	1	9.48	6.32	5.14	6.53	0.00	0.28	0.09	0.00	0.00	0.34	6%
	2	8.16	15.12	6.26	2.53	0.00	0.00	0.00	0.00	0.00	0.00	37%
WF Gedney Creek	1	15.12	9.86	8.24	0.75	0.00	0.17	0.10	0.00	0.00	0.00	1%
SF Red River	1	0.00	1.18	1.52	0.03	0.00	0.46	0.00	0.00	0.00	0.12	6%
	2	0.00	0.94	0.71	0.00	0.00	0.61	0.11	0.00	0.04	0.00	14%
Bald Mountain Creek	1	5.96	9.32	3.32	0.05	0.00	5.50	0.06	0.00	0.00	0.00	-30%
Boulder Creek	1	3.42	10.66	9.06	5.73	0.00	0.16	0.02	0.00	0.01	0.00	-11%
Canyon Creek	1	6.95	12.03	5.91	0.08	0.00	0.86	0.00	0.00	0.00	0.00	99%
Deadman Creek	1	15.84	4.03	1.68	2.48	0.00	0.13	0.00	0.00	0.00	0.00	-51%
Lake Creek	1	3.19	2.22	0.41	0.00	0.00	0.05	0.02	0.00	0.00	0.03	-38%
O’Hara Creek	2	9.28	10.85	4.02	45.74	0.00	0.12	0.00	0.00	0.00	0.00	2%
Pete King Creek	1	13.76	8.47	1.87	14.10	0.00	0.22	0.00	0.00	0.00	0.00	49%
Post Office Creek	1	31.26	10.60	2.80	3.21	0.00	0.68	0.04	0.00	0.00	0.05	229%
Weir Creek	1	20.45	5.10	1.22	0.17	0.00	0.97	0.05	0.00	0.00	0.00	10%
Basin Creek	1	2.41	1.41	1.57	4.47	0.00	0.03	0.05	0.00	0.00	0.23	-63%
Beaver Creek	2	0.23	2.45	0.61	0.00	0.00	0.00	0.00	4.14	6.88	0.00	-14%
Frenchman Creek	1	0.02	0.24	0.14	0.00	0.00	0.00	0.00	13.51	5.91	0.00	-55%
Lick Creek	1	7.25	6.03	1.95	2.93	0.00	0.11	0.00	0.02	0.27	0.00	-15%
Secesh River	1	0.41	2.80	2.03	14.01	0.00	0.06	0.02	0.00	0.00	0.59	17%

Table 7. The mean length, weight, condition factor (K), and 95% CI of juvenile steelhead that were PIT tagged at screw traps in the Clearwater River drainage in 2005.

	Fork length (mm)				Weight (g)			Condition factor	
Release site	**Number**	**Mean**	**95% CI**	**Median**	**Number**	**Mean**	**95% CI**	**Mean**	**95% CI**
Spring trapping (March 1 to May 31)									
Crooked Fork Creek	190	171	4	176	188	49.8	2.4	0.93775	0.01151
Clear Creek	262	149	4	156	196	36.2	2.8	0.99927	0.01480
Colt Killed Creek	104	180	4	182	104	53.3	2.8	0.89444	0.01177
Fish Creek	225	119	4	106	224	20.0	2.0	1.02667	0.01402
Red River	8	108	19	105	8	13.3	6.8	0.96387	0.09817
Summer trapping (June 1 to August 31)									
Crooked Fork Creek	1,016	130	2	122	1,016	27.5	1.3	1.05502	0.00594
Clear Creek	68	115	3	112	68	16.8	1.6	1.04671	0.02536
Colt Killed Creek	57	118	6	114	55	19.5	3.5	1.07280	0.03163
Fish Creek	2,393	116	1	113	2,370	18.1	0.4	1.05616	0.00315
Red River	33	103	5	100	29	13.0	2.0	1.10938	0.05112
Fall trapping (September 1 to December 15)									
Crooked Fork Creek	283	163	2	162	282	43.8	1.9	0.97715	0.01335
Colt Killed Creek	83	170	4	165	83	48.0	3.6	0.94068	0.01139
Fish Creek	9,497	133	0	135	4,230	24.3	0.4	0.96786	0.00156
Red River	21	138	11	130	5	35.7	29.3	1.06533	0.17566
Year totals									
Crooked Fork Creek	1,489	142	2	142	1,486	33.4	1.1	1.02541	0.00549
Clear Creek	330	142	3	149	264	31.2	2.4	1.01149	0.01295
Colt Killed Creek	244	162	4	169	242	43.8	2.5	0.95083	0.01289
Fish Creek	12,115	129	0	130	6,824	22.0	0.3	1.00046	0.00182
Red River	62	115	6	112	42	15.8	3.7	1.07642	0.04395

Table 8. The mean length, weight, condition factor (K), and 95% CI of juvenile steelhead that were PIT tagged at screw traps in the Salmon River drainage in 2005.

	Fork length (mm)				Weight (g)			Condition factor	
Release site	**Number**	**Mean**	**95% CI**	**Median**	**Number**	**Mean**	**95% CI**	**Mean**	**95% CI**
Spring trapping (March 1 to May 31)									
Johnson Creek	63	156	6	159	63	39.3	5.5	0.95893	0.01898
Lake Creek	26	124	9	116	26	22.6	6.3	1.07651	0.03251
Lemhi River	1,101	126	2	115	1,091	24.8	1.2	1.08917	0.00453
Marsh Creek	80	130	7	130	78	26.1	4.2	0.99905	0.01813
Pahsimeroi River	1,176	128	1	120	1,173	24.1	0.8	1.06689	0.00574
Rapid River	349	181	2	181	349	59.7	1.5	0.99623	0.00871
Salmon River, Sawtooth	138	161	5	164	129	42.4	3.3	0.93597	0.01447
Upper Secesh River	70	123	6	113	70	22.0	3.9	1.02413	0.02138
SF Salmon River	243	121	3	113	231	20.0	1.6	1.04443	0.01516
Summer trapping (June 1 to August 31)									
Johnson Creek	263	141	4	142	261	33.5	2.4	1.06015	0.01221
Lake Creek	168	122	3	116	168	21.1	1.9	1.09526	0.01912
Lemhi River	446	129	2	122	446	27.7	2.0	1.12362	0.00892
Lick Creek	192	115	3	115	192	18.6	1.7	1.08819	0.01328
Marsh Creek	132	109	6	97	128	17.5	3.7	1.05519	0.01573
Pahsimeroi River	170	125	3	121	170	23.7	2.2	1.12701	0.01291
Salmon River, Sawtooth	43	160	7	162	43	45.6	5.4	1.06217	0.02043
Upper Secesh River	152	128	4	124	152	24.9	2.4	1.08239	0.01427
Lower Secesh River	436	128	3	131	433	27.5	1.7	1.11839	0.00982
SF Salmon River	731	121	1	115	730	21.8	0.9	1.12735	0.00856
Fall trapping (September 1 to December 15)									
Johnson Creek	257	158	3	159	257	42.1	2.1	1.00334	0.00733
Lake Creek	17	144	12	150	17	32.4	7.9	1.01825	0.05393
Lemhi River	629	192	2	194	624	82.3	2.6	1.09378	0.00656
Marsh Creek	28	125	8	120	28	19.2	4.5	0.90083	0.03983
Pahsimeroi River	181	133	4	126	181	29.0	2.8	1.08243	0.01512
Salmon River, Sawtooth	22	174	6	174	22	54.1	5.7	1.01628	0.02983
Upper Secesh River	16	147	15	151	16	33.1	10.3	0.95951	0.07264
Lower Secesh River	542	163	2	162	498	46.2	1.5	1.02740	0.00616
SF Salmon River	125	144	4	144	125	34.1	3.1	1.05587	0.02945
Year totals									
Johnson Creek	583	150	2	154	581	37.9	1.6	1.02404	0.00724
Lake Creek	211	124	3	117	211	22.2	1.8	1.08675	0.01635
Lemhi River	2,176	146	2	128	2,161	42.0	1.5	1.09761	0.00353
Lick Creek	192	115	3	115	192	18.6	1.7	1.08819	0.01328
Marsh Creek	240	118	4	110	234	20.6	2.5	1.01800	0.01303
Pahsimeroi River	1,527	128	1	120	1,524	24.7	0.8	1.07544	0.00506
Rapid River	349	181	2	181	349	59.7	1.5	0.99623	0.00871
Salmon River, Sawtooth	203	162	4	165	194	44.4	2.6	0.97305	0.01336
Upper Secesh River	238	128	3	121	238	24.6	2.0	1.05700	0.01268
Lower Secesh River	978	147	2	153	931	37.5	1.3	1.06972	0.00633
SF Salmon River	1,099	124	1	117	1,086	22.8	0.8	1.10149	0.00769

Table 9. The mean length, weight, condition factor (K), and 95% CI of juvenile steelhead that were captured by flyfishing and electroshocking and PIT tagged during the summer 2005.

	Fork length (mm)				Weight (g)			Condition factor	
Release site	**Number**	**Mean**	**95% CI**	**Median**	**Number**	**Mean**	**95% CI**	**Mean**	**95% CI**
Flyfishing									
Boulder Creek	15	129	16	121	15	24	8.6	0.99009	0.03138
Fish Creek	398	136	2	138	354	30.3	1.8	1.10174	0.01240
Gedney Creek	452	133	2	135	141	26.3	2.6	1.01249	0.01439
Lick Creek	47	138	7	142	47	30.0	4.3	1.05534	0.02487
Electroshocking									
Bear Valley Creek	160	100	3	95	69	13.9	2.5	1.22969	0.03707
Big Creek	315	108	2	104	30	12.2	3.6	1.19964	0.05641
Camas Creek	191	101	3	97	116	14.1	1.8	1.16668	0.02311
Capehorn Creek	16	96	9	93	9	10.6	2.6	1.27695	0.08080
Elk Creek	14	104	9	105	14	14.7	3.6	1.23352	0.06695
Herd Creek	249	116	2	112	136	21.0	2.0	1.18048	0.01683
Lake Creek	31	95	5	93	28	10.6	2.3	1.12550	0.04741
Loon Creek	213	102	2	99	98	14.6	1.3	1.27192	0.03136
Marsh Creek	74	113	7	101	16	22.0	14.6	1.25775	0.06474
Secesh River	137	102	3	96	26	10.7	1.5	1.18133	0.03683
SF Salmon River	217	99	3	93	84	11.1	1.8	1.15516	0.02239
Sulfur Creek	124	98	4	90	38	10.4	2.0	1.22315	0.03962
Valley Creek	230	117	3	111	65	20.8	3.8	1.17738	0.02590

Table 10. The number of juvenile steelhead caught, released upstream of the trap (Marks), and recaptured at the Fish Creek screw trap during each trap period in 2005. p = trap efficiency estimate.

Period	Start date	End date	Catch	Marks	Recaps	p	Migrants	95% CI Lower	95% CI Upper
1	3/15	4/22	47	45	2	0.04	721	202	851
2	4/23	5/25	116	98	2	0.02	3,828	1,172	4,406
3	5/26	6/7	243	197	13	0.07	3,437	2,126	5,891
4	6/8	6/21	589	426	79	0.19	3,144	2,553	3,882
5	6/22	7/5	871	574	133	0.23	3,738	3,185	4,390
6	7/6	7/19	425	374	66	0.18	2,379	1,892	3019
7	7/20	8/2	194	169	33	0.2	970	696	1,353
8	8/3	8/14	218	156	49	0.31	685	532	894
9	8/15	8/28	308	248	62	0.25	1,217	968	1,542
10	8/29	9/11	1,159	621	132	0.21	5,420	4,622	6,369
11	9/12	9/25	2,517	650	194	0.3	8,403	7,473	9,501
12	9/26	10/1	2,457	301	113	0.38	6,509	5,630	7,553
13	10/2	10/5	4,590	199	97	0.49	9,367	8,155	10,949
14	10/6	10/19	585	315	155	0.49	1,185	1,048	1347
15	10/20	10/31	174	126	54	0.43	402	324	508
16	11/1	11/4	501	108	35	0.32	1,517	1,151	1,998
17	11/5	11/14	132	128	49	0.38	341	265	441
Full year estimates:							**53,263**	**48,410**	**55,722**
Fall period (8/15 to 11/14):							**34,361**	**32,248**	**36,641**

Table 11. The number of wild steelhead that were detected as smolts in 2005, the number of steelhead PIT tagged, and the percent of all PIT-tagged fish that were ≥125 mm from each period that were detected in 2005. Tagging periods were Period 1 = March 1, 2005 to May 31, 2005; Period 2 = August 15, 2004 to December 15, 2004; Period 3 = June 1, 2004 to August 14, 2004; Period 4 = March 1, 2004 to May 31, 2004; Period 5 = all fish tagged before December 31, 2003. na = not applicable; no fish were tagged during the period.

	Number of detected smolts tagged in Period						Number of fish tagged in Period					Percent of all fish detected from Period					Percent of fish >125 mm detected from Period				
Release site	**All**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**
<u>Clearwater River drainage</u>																					
Boulder Creek	20	0	6	0	0	14	0	14	0	0	219	na	42.9%	na	na	6.4%	na	46.2%	na	na	1.4%
Crooked Fork Creek	292	145	56	80	1	10	192	119	575	208	993	75.5%	47.1%	13.9%	0.5%	1.0%	81.5%	52.4%	37.9%	0.0%	0.5%
Clear Creek	152	151	0	0	0	1	263	0	3	610	1,288	57.4%	na	0.0%	0.0%	0.1%	74.9%	na	0.0%	0.0%	0.1%
Colt Killed Creek	141	87	41	8	0	5	104	78	76	122	436	13.8%	31.0%	15.0%	13.8%	5.3%	86.1%	56.2%	28.0%	0.0%	0.2%
Fish Creek	2,372	46	1,609	313	16	388	326	6,356	3,802	189	13,079	14.1%	25.3%	8.2%	8.5%	3.0%	63.0%	49.9%	29.2%	1.7%	1.1%
Gedney Creek	94	0	0	91	0	3	0	0	647	0	447	na	na	14.1%	na	0.7%	na	na	23.8%	na	0.0%
O'Hara Creek	22	0	22	0	0	0	0	357	0	0	0	na	6.2%	na	na	na	na	15.1%	na	na	na
Red River	7	0	0	4	3	0	8	1	19	56	171	na	na	10.1%	na	4.2%	0.0%	na	na	0.0%	0.0%
All Clearwater sites	**3,100**	**429**	**1,734**	**496**	**20**	**421**	**893**	**6,925**	**5,122**	**1,185**	**###**	**48.0%**	**25.0%**	**9.7%**	**1.7%**	**2.5%**	**77.1%**	**48.7%**	**28.2%**	**0.1%**	**0.9%**
<u>Salmon River drainage</u>																					
Johnson Creek	232	32	112	34	1	53	63	373	513	106	2,621	50.8%	30.0%	6.6%	0.9%	2.0%	59.3%	36.1%	14.0%	1.0%	1.1%
Lemhi River	131	81	13	7	29	1	1,184	290	186	921	1,142	6.8%	4.5%	3.8%	3.1%	0.1%	17.9%	4.9%	4.1%	2.1%	0.1%
Marsh Creek	87	8	4	14	10	51	81	47	208	227	1,380	9.9%	8.5%	6.7%	4.4%	3.7%	18.2%	18.2%	20.3%	5.9%	3.4%
Pahsimeroi River	143	114	15	0	12	2	1,179	370	51	608	3,453	9.7%	4.1%	0.0%	2.0%	0.1%	22.7%	7.6%	0.0%	1.2%	0.0%
Rapid River	332	264	68	0	0	0	351	185	0	0	0	75.2%	36.8%	na	na	na	75.6%	38.7%	na	na	na
Salmon River (Sawtooth)	72	59	6	3	4	0	139	36	31	354	887	10.6%	18.7%	13.7%	15.0%	8.7%	49.2%	18.2%	10.3%	0.3%	0.0%
Secesh River	60	8	15	17	2	18	70	78	81	12	531	11.4%	19.2%	21.0%	16.7%	3.4%	30.8%	31.3%	27.4%	28.6%	3.5%
SF Salmon River	236	24	88	63	25	36	243	360	471	168	1,239	9.9%	24.4%	13.4%	14.9%	2.9%	34.3%	32.1%	20.3%	10.7%	1.0%
Lake Creek	46	0	5	10	2	29	26	77	105	24	545	0.0%	6.5%	9.5%	8.3%	5.3%	0.0%	10.6%	16.4%	10.0%	4.7%
Lick Creek	45	0	23	0	0	22	0	112	0	0	1,187	na	20.5%	na	na	1.9%	na	27.1%	na	na	1.0%
All Salmon sites	**1,384**	**590**	**349**	**148**	**85**	**212**	**3,336**	**1,928**	**1,646**	**2,420**	**###**	**17.7%**	**18.1%**	**9.0%**	**3.5%**	**1.6%**	**36.4%**	**25.4%**	**16.2%**	**2.4%**	**1.0%**

Table 12. The median travel time (days) and migration rate (km/day) and the 90% upper and lower confidence interval from release site to Lower Granite Dam (LGR). All smolts were PIT tagged and detected during the spring 2005.

			Travel time (days)					Migration rate (km/day)				
Stream	**Number detected**	**Distance to LGR**	**Median**	**Lower CI**	**Upper CI**	**Max**	**Min**	**Median**	**Lower CI**	**Upper CI**	**Slowest**	**Fastest**
Crooked Fork Creek	111	324	7	6	7	22	4	46.3	54.0	46.3	14.7	81.0
Clear Creek	120	176	7	6	8	34	2	25.1	29.3	22.0	5.2	88.0
Colt Killed Creek	68	322	7	6	9	38	4	46.0	53.7	35.8	8.5	80.5
Fish Creek	35	249	7	5	8	24	3	35.6	49.8	31.1	10.4	83.0
Johnson Creek	52	407	13.5	10	16	67	7	30.1	40.7	25.4	6.1	58.1
Lemhi River (upper)	12	595	5	4	7	10	4	119.0	148.8	85.0	59.5	148.8
Lemhi River (lower)	20	630	11.5	9	16	54	5	54.8	70.0	39.4	11.7	126.0
Pahsimeroi River	43	621	9	8	10	58	4	69.0	77.6	62.1	10.7	155.3
Rapid River	205	284	9	9	10	22	4	31.6	31.6	28.4	12.9	71.0
Salmon River	88	747	14	12	15	32	5	53.4	62.3	49.8	23.3	149.4
SF Salmon River	10	460	14	11	20	68	6	32.9	41.8	23.0	6.8	76.7

Table 13. The number of scales collected from adult and juvenile steelhead during 2005.

		Juvenile scales collected		
Stream	**Adult scales**	**3/1 to 6/15**	**6/16 to 8/14**	**8/14 to 12/15**
Clearwater drainage				
Clear Creek	0	158	7	0
Fish Creek	124	269	269	637
Clearwater drainage total	**124**	**427**	**276**	**637**
Salmon drainage				
Lemhi River	0	0	0	0
Pahsimeroi River	41	0	0	136
Rapid River	73	0	0	0
Salmon River (Sawtooth)	0	79	20	31
Secesh River	0	0	0	188
SF Salmon River (Knox Bridge)	0	0	13	148
Salmon drainage total	**114**	**79**	**33**	**503**

Table 14. The number of adult and juvenile steelhead aged in 2005.

Stream	Year collected	Number of fish aged	Number of readers
Adults			
Fish Creek	2005	124	1
Pahsimeroi River	2005	38	1
Rapid River	2005	73	1
Adult total		235	
Juveniles			
Colt Killed Creek	2004	171	1
Crooked Fork Creek	2004	196	1
Fish Creek	2004	615	2
Lemhi River	2004	267	1
Marsh Creek	2004	81	1
Rapid River	2004	107	1
SF Salmon River	2004	260	1
Clear Creek	2005	164	1
Fish Creek	2005	748	1
Lemhi River	2005	136	1
Rapid River	2005	115	1
Salmon River	2005	80	1
Secesh River	2005	188	1
SF Salmon River	2005	154	1
Juvenile total		3,282	

Table 15. The number of steelhead trapped and released untagged, and the length (mm) and weight (g) statistics of Chinook salmon parr, cutthroat trout, bull trout, and dace that were caught in the Fish Creek, Rapid River, and IDFG Secesh River screw traps in 2005. nm = not measured. CI = 95% confidence interval.

	Number of fish			Length (mm)			Weight (g)		
Species	**Trapped**	**Tagged**	**Recaps**	**N**	**Mean**	**CI**	**N**	**Mean**	**CI**
Fish Creek									
Steelhead (<80 mm)	404	0	0						
Steelhead (≥80 mm)	1,770	0	0						
Cutthroat trout	414	382	25	382	195	5	321	88.1	10.1
Chinook parr	811	568	153	568	76	1	442	4.8	0.1
Bull trout [a]	3	3	0						
Longnose dace	4,226	0	na	775	104	1	775	15.1	0.5
Speckled dace	830	0	na	407	89	1	407	9.7	0.3
Rapid River									
Steelhead (<80 mm)	0	0	0						
Steelhead (≥80 mm)	18	0	0						
Chinook salmon	45	36	8	36	103	3	35	12.7	1.0
Bull trout	16	15	1	12	170	12	12	48.0	9.1
Secesh River (IDFG)									
Steelhead (<80 mm)	27	0	0						
Steelhead (≥80 mm)	196	0	0						
Chinook parr	46,875	4,137	1,510	4,092	69	<1	3,881	3.8	<0.1
Cutthroat trout [a]	10	9	1						
Bull trout [a]	11	9	2						
Dace spp .[b]	104	0	0		nm		nm		

[a] Length and weight statistics not reported because of small sample size.
[b] Dace were not identified to species.

Table 16. Streams that were sampled for water temperatures in 2005 and the associated winter and summer temperature recording intervals. The water temperature was measured within 1 km of the mouth of each stream unless noted. The winter recording interval in the Salmon River drainage was used from January 1 to April 30. The winter recording interval in the Clearwater River drainage was used from January 1 to March 21. The Fish Creek air temperature, relative humidity, and barometric pressure were measured at the trailhead. NR = not recorded.

	Recording Interval (Hours)	
Stream	**Winter**	**Other**
Salmon River drainage		
Basin Creek, 500 m upstream of hot springs	2.5	0.33
Beaver Creek, 2 km upstream of irrigation diversion	1.0	0.33
East Fork Salmon River, upstream of Bowery Hot Springs	2.5	0.33
East Fork Salmon River	2.5	0.33
Frenchman Creek, first meadow upstream of mouth	1.0	0.33
Germania Creek	2.5	0.33
Marsh Creek, 100 m downstream of screw trap site	2.5	0.33
Pole Creek, 2 km upstream of irrigation diversion	1.0	0.33
Redfish Lake Creek at weir	2.5	0.33
Salmon River at Sawtooth Fish Hatchery	1.0	0.33
Valley Creek, 200 m upstream of Meadow Creek	2.5	0.33
West Pass Creek at irrigation diversion	2.5	0.33
Clearwater River drainage		
Bald Mountain Creek	2.0	0.5
Bimerick Creek	2.0	0.5
Boulder Creek	1.0	0.5
Brushy Fork Creek	1.0	0.5
Canyon Creek	1.0	0.5
Crooked Fork Creek, 50 m upstream of Brushy Fork Creek	1.0	0.5
Deadman Creek	2.0	0.5
Fish Creek #1 at screw trap site	0.5	0.25
Fish Creek #2, 100 m upstream of screw trap site	1.0	0.5
Fish Creek #3, 2 km upstream of Hungery Creek	1.0	0.5
Fish Creek air temperature	2.0	0.25
Fish Creek barometric pressure	NR	1.0
Fish Creek relative humidity	NR	1.0
Gedney Creek #1	1.0	0.5
Gedney Creek #2 upstream of mouth about 2 km	1.0	0.5
Hungery Creek	1.0	0.5
Lost Creek	2.0	0.5
O'Hara Creek, 2 km downstream of Hanby Fork	1.0	0.5
Post Office Creek	1.0	0.5
Red River, 1 km upstream of SF Red River	1.0	0.5
SF Red River, 50 m downstream of Schooner Creek	1.0	0.5
Squaw Creek	2.0	0.5
Trapper Creek	1.0	0.5
Weir Creek	1.0	0.5
Wendover Creek	2.0	0.5
WF Gedney Creek	1.2	0.5
Willow Creek (tributary of Fish Creek)	1.0	0.5

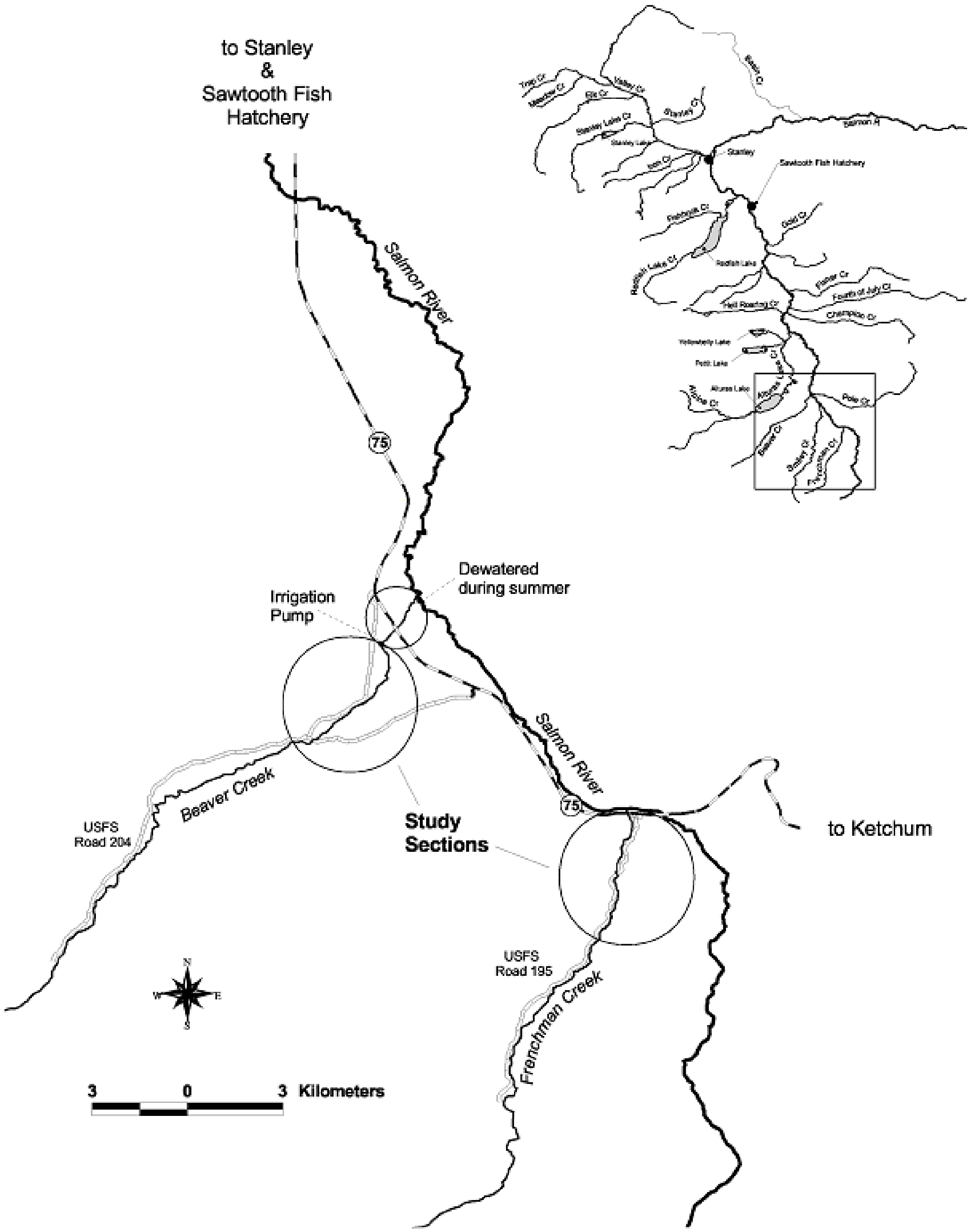

Figure 1. The location of the study sections in Beaver and Frenchman creeks where hatchery adults were stocked and summer snorkel surveys conducted.

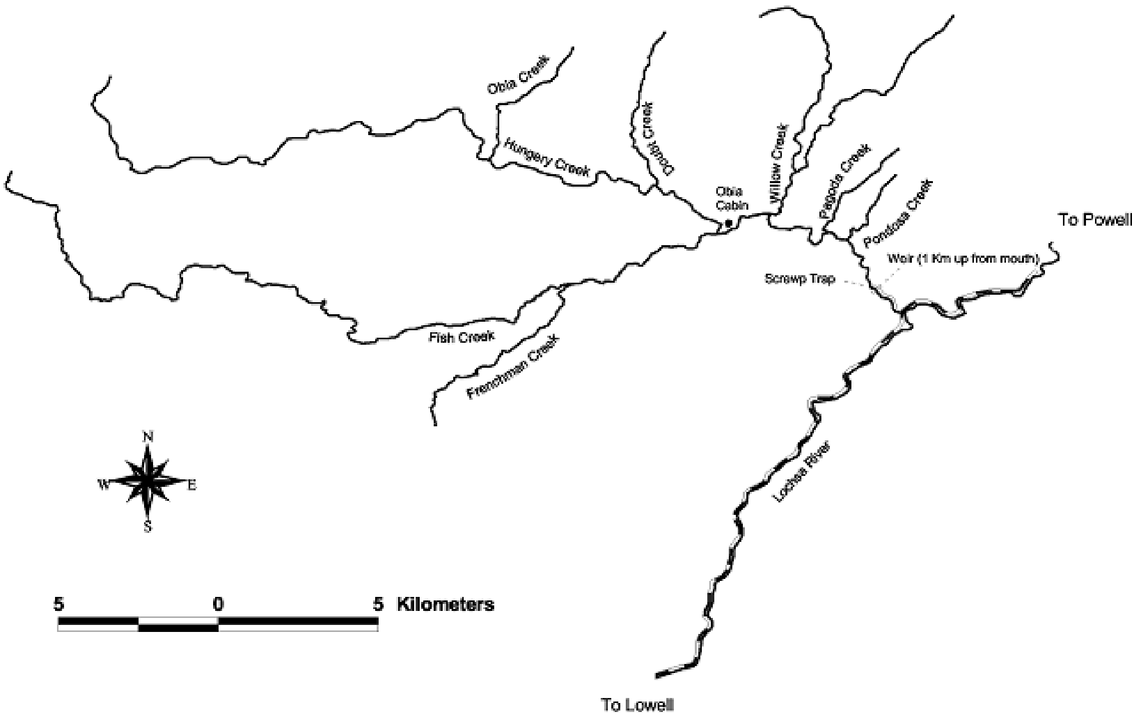

Figure 2. The Fish Creek drainage showing the location of the Fish Creek screw trap and adult weir.

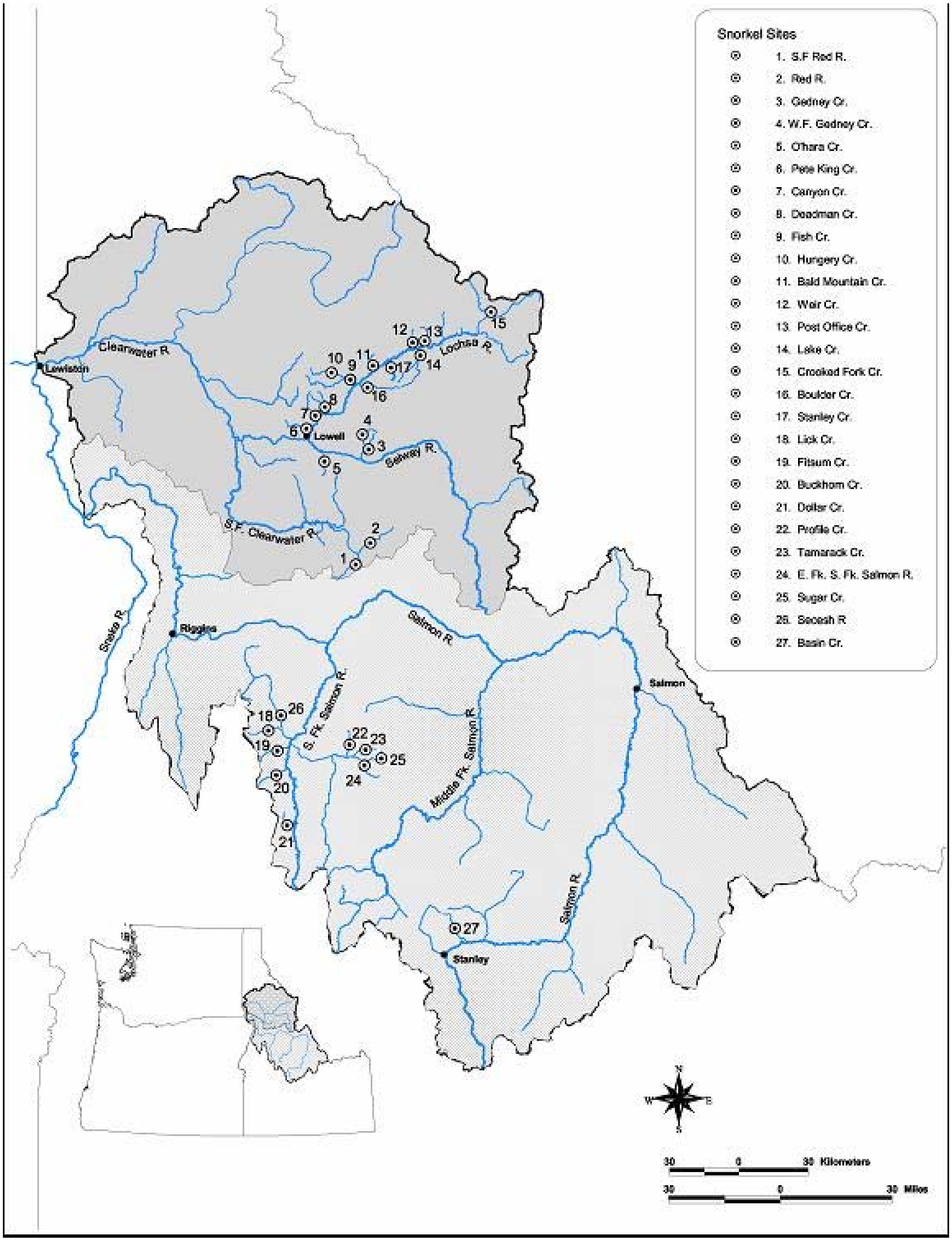

Figure 3. Map of the Clearwater River, Salmon River, and SF Salmon River drainages showing streams that were snorkeled in 2005.

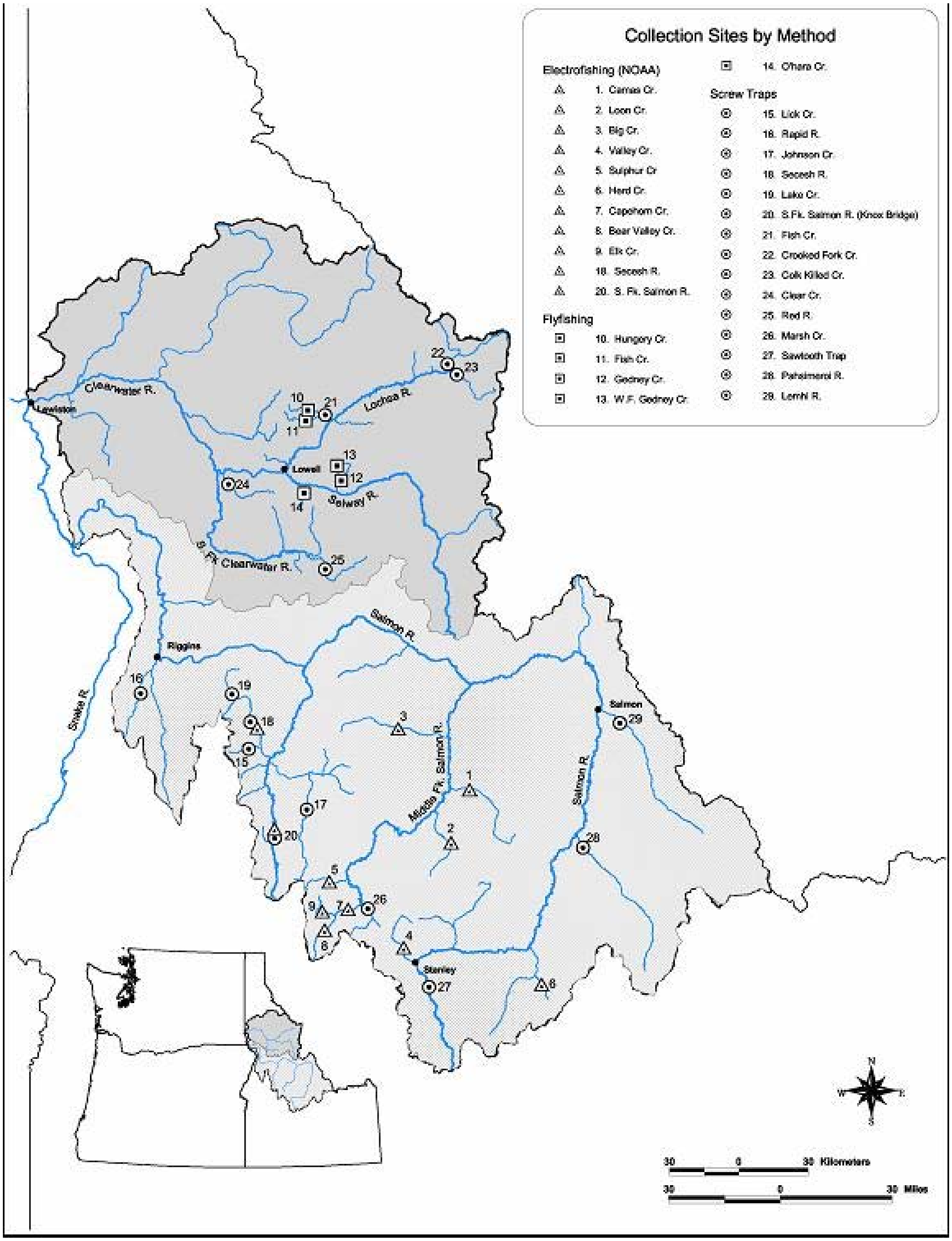

Figure 4. Map of the Salmon and Clearwater drainages showing the locations of the screw traps and the streams where crews captured and PIT tagged juvenile steelhead in 2005.

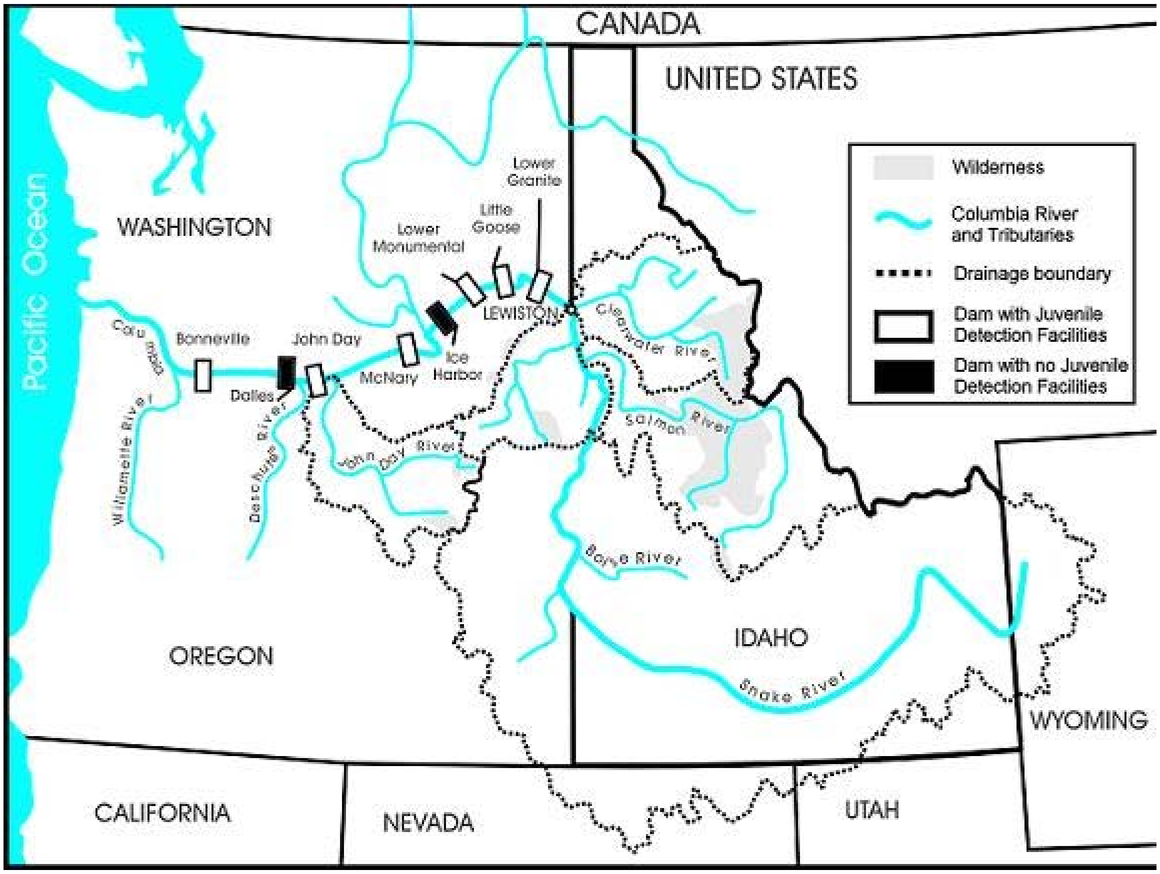

Figure 5. The location of dams on the Snake and Columbia Rivers where PIT tags were detected during the juvenile smolt out-migration in 2005.

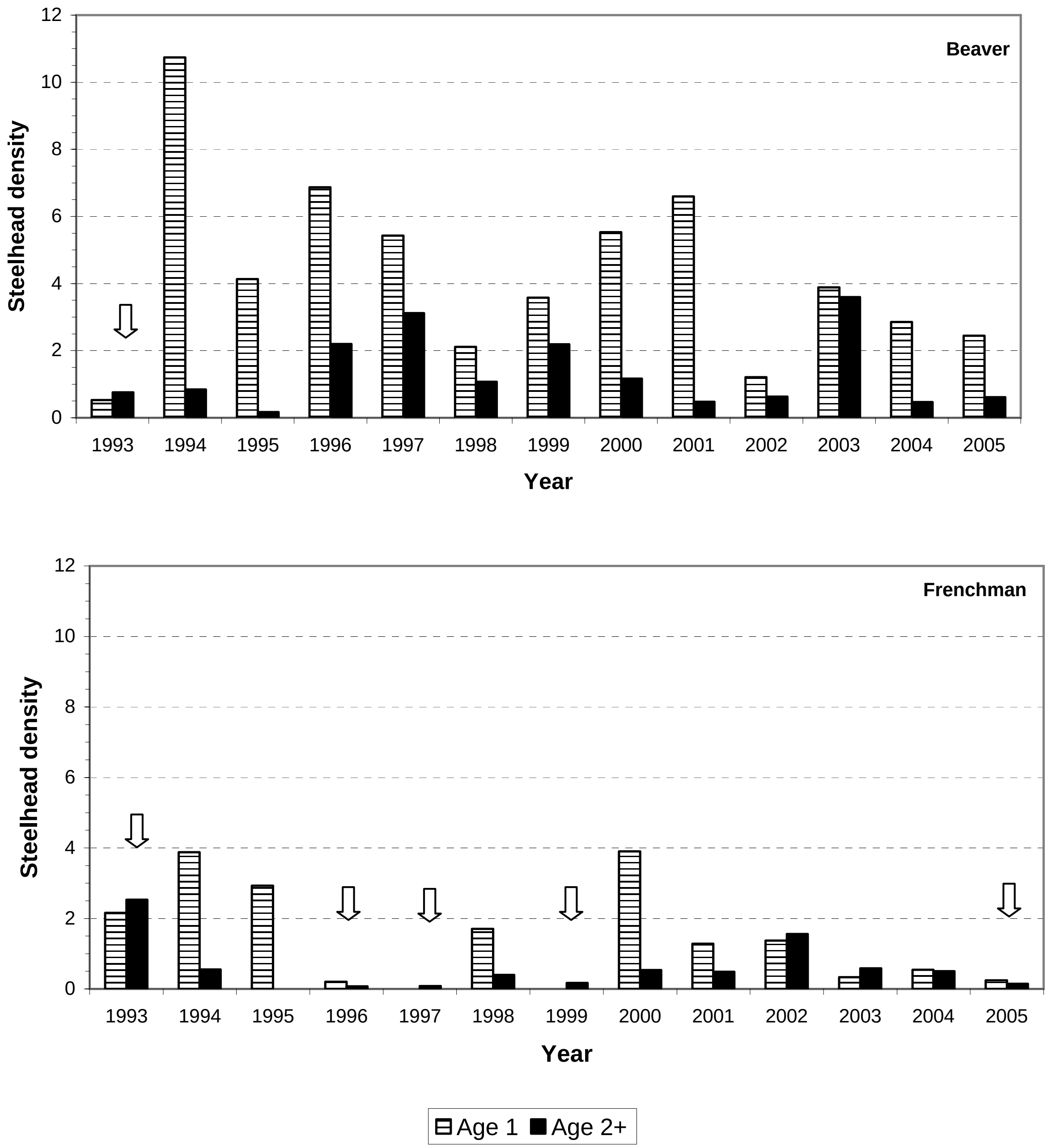

Figure 6. The mean density (fish/100 m^2) of age-1 and age-2+ steelhead in Beaver (top) and Frenchman (bottom) creeks from 1993 to 2005. Adult steelhead were stocked in Beaver Creek annually from 1993 through 2004. The years marked with an arrow in the graphs indicate that adult steelhead were not stocked in the stream the previous year.

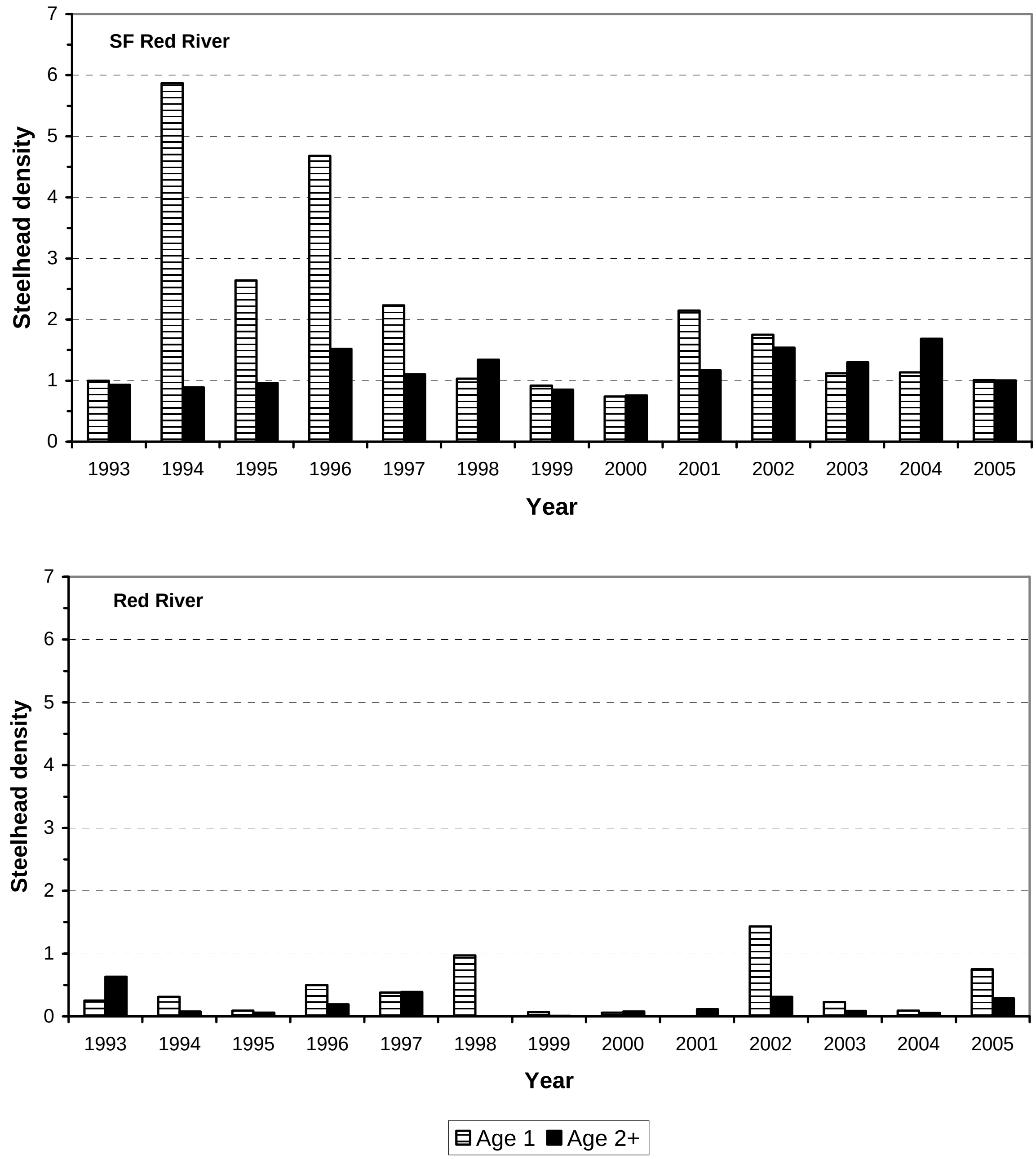

Figure 7. The mean stream density (fish/100 m^2) of age-1 and age-2+ steelhead from 1993 to 2005 in the South Fork (SF) Red River (top) and Red River (bottom) upstream of the SF Red River.

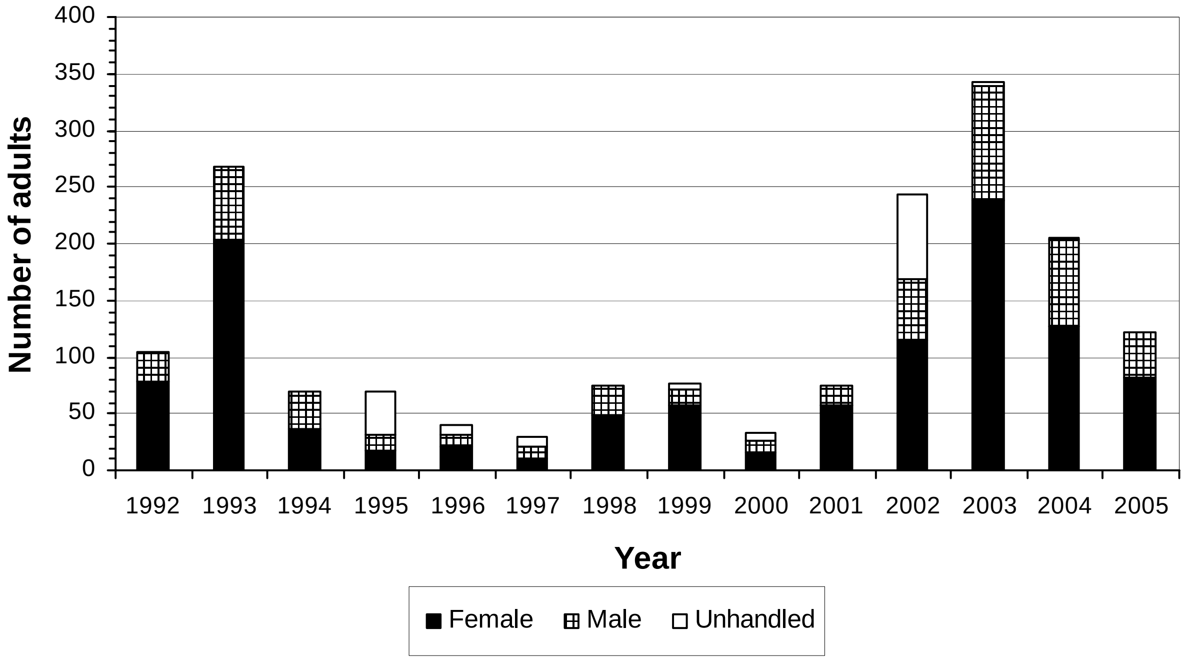

Figure 8. The estimated wild steelhead escapement in Fish Creek from 1992 to 2005. The open bar is an estimate of unhandled adults that entered Fish Creek in the years the weir was breached or damaged. The solid and crosshatched bars are the number of fish that were trapped at the weir and passed upstream plus the number of unmarked kelts that were recovered.

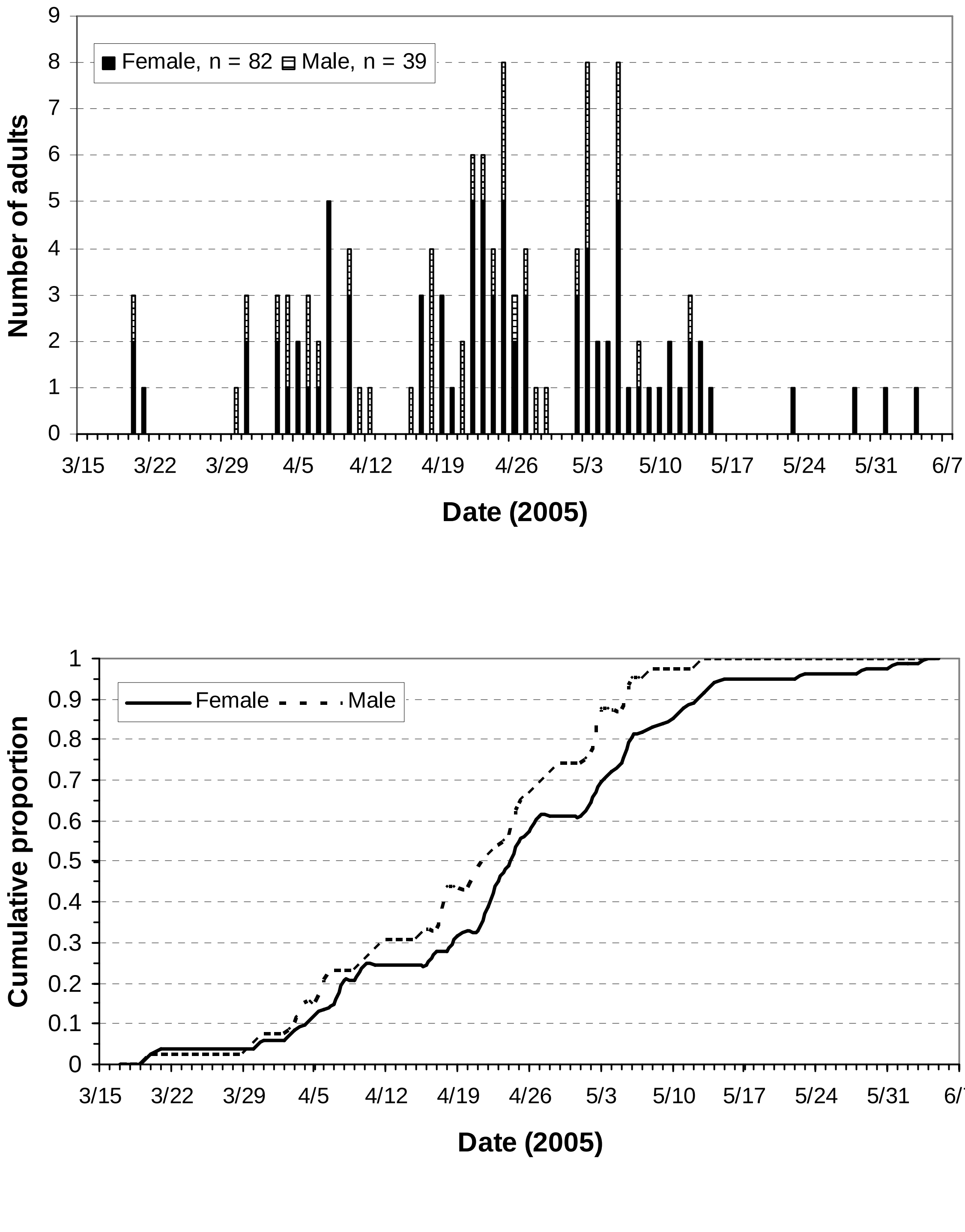

Figure 9. The number of adult female and male steelhead that were trapped at the Fish Creek weir and passed upstream to spawn from March 15 to June 7, 2005 (Upper graph), and the cumulative proportion of the total number of spawners that had been captured on each date (Lower graph).

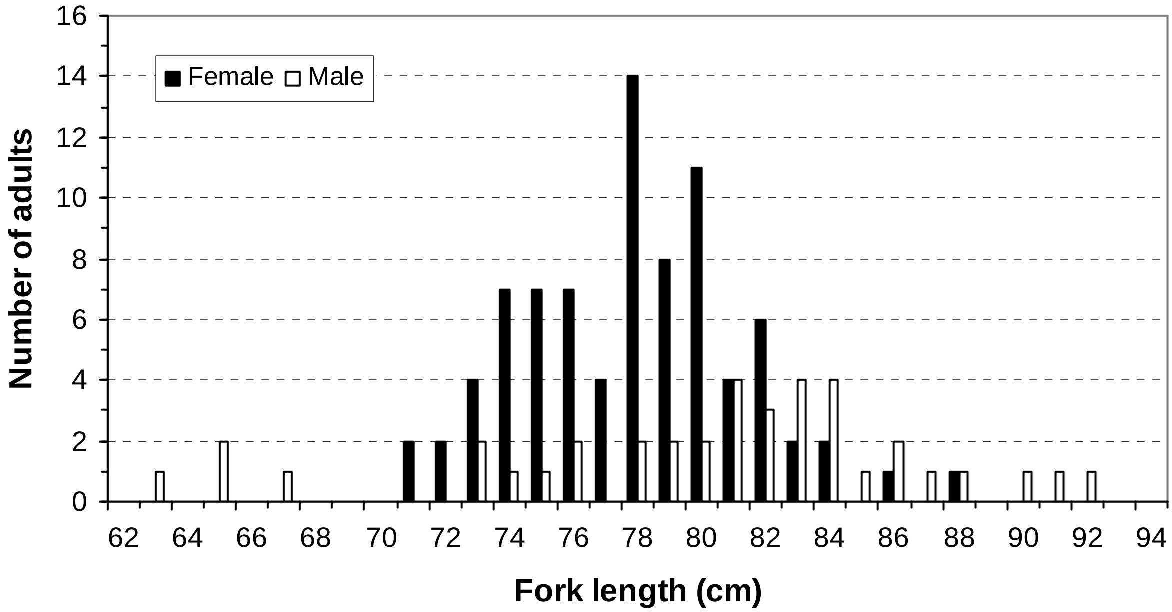

Figure 10. The length frequency of steelhead spawners trapped at the Fish Creek weir during spring 2005.

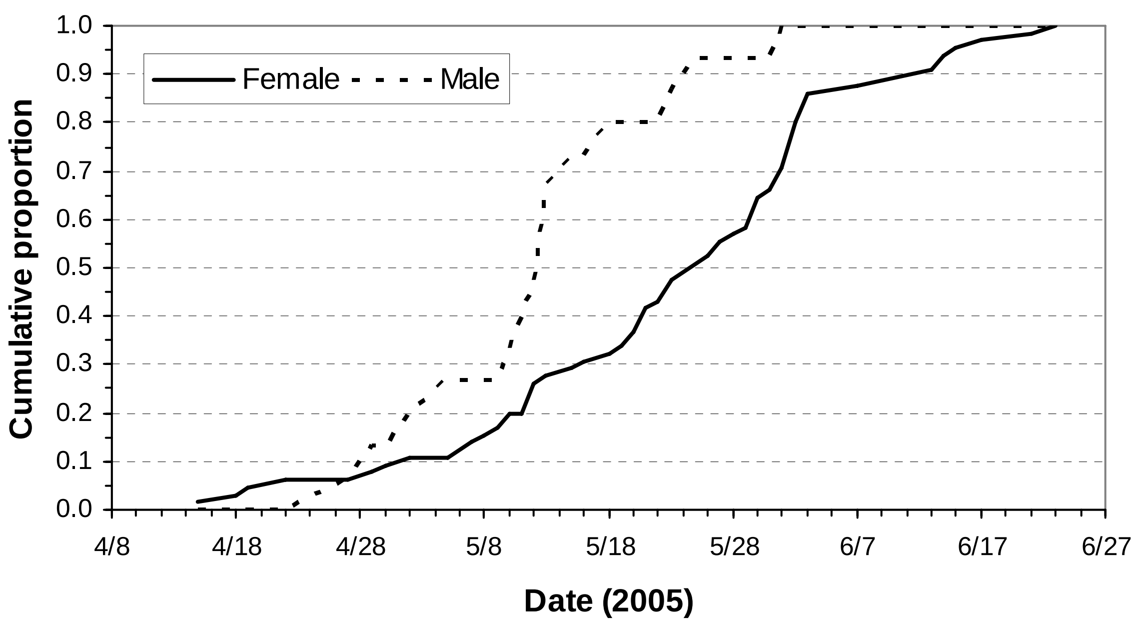

Figure 11. The cumulative proportion of the total number of male and female steelhead kelts recovered at the Fish Creek weir from April 8 to July 27, 2005.

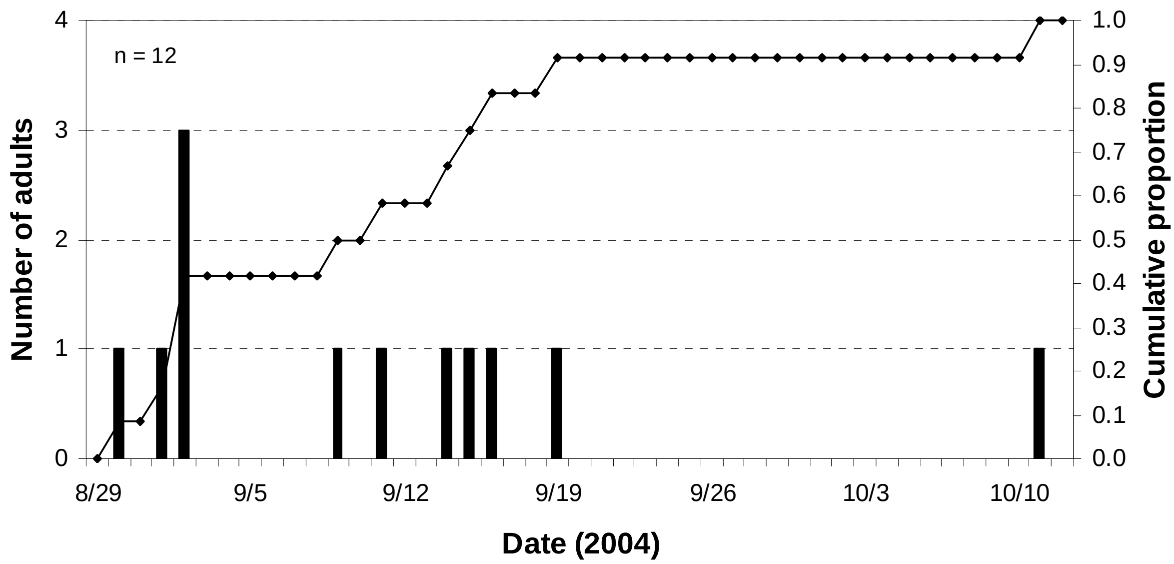

Figure 12. The number of PIT-tagged adult steelhead detected at Bonneville Dam between August 29 and October 12, 2004. These adults were either tagged in Fish Creek as juveniles or were tagged elsewhere and captured at the Fish Creek weir during spring 2005.

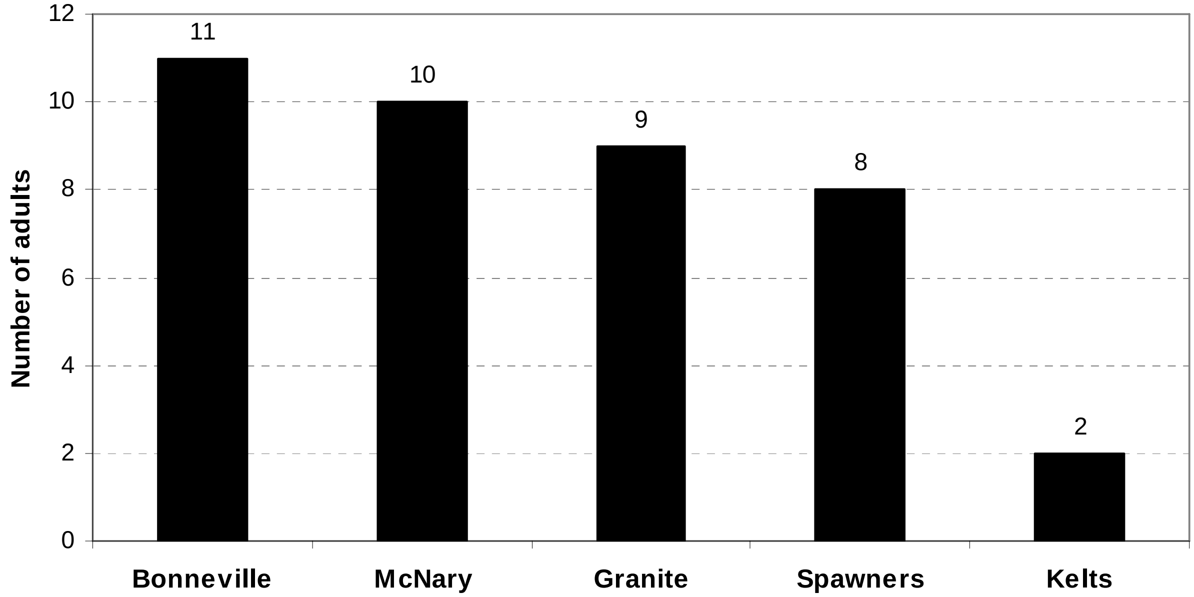

Figure 13. The number of adult steelhead that were PIT tagged in Fish Creek as juveniles and detected at Bonneville, McNary, and Lower Granite dams between August 29, 2004 and October 31, 2004, and subsequently trapped at the Fish Creek weir during spring 2005.

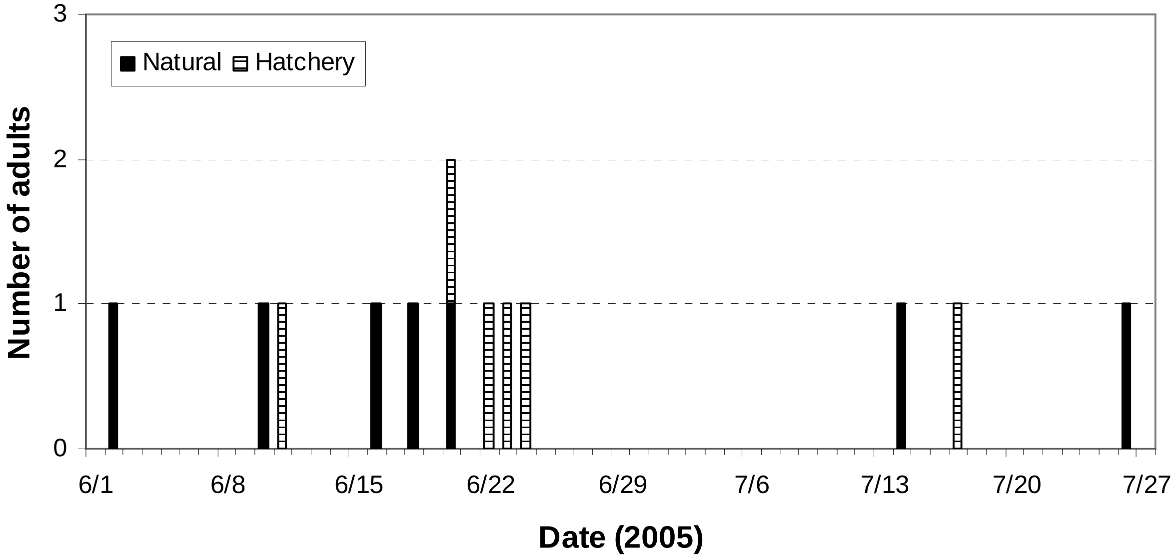

Figure 14. The number of naturally produced adult Chinook salmon (n = 7) and the number of hatchery origin Chinook salmon (n = 6) trapped at the Fish Creek weir between June 9 and July 28, 2004. Two additional hatchery origin Chinook salmon were trapped in August (on August 6, 2005 and August 30, 2005).

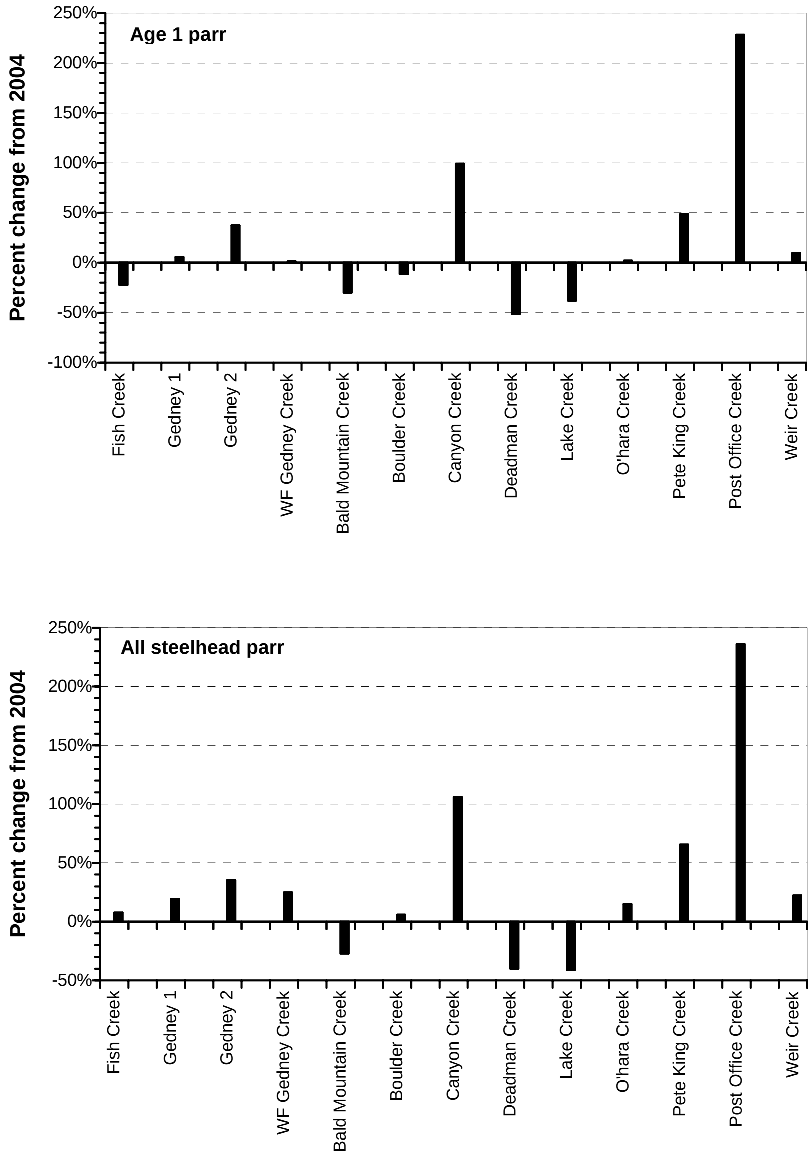

Figure 15. The percent change in the mean density of age-1 steelhead (top graph) and all age-1 and older steelhead parr (bottom graph) from those observed in 2004 in tributaries of the Lochsa and Selway rivers.

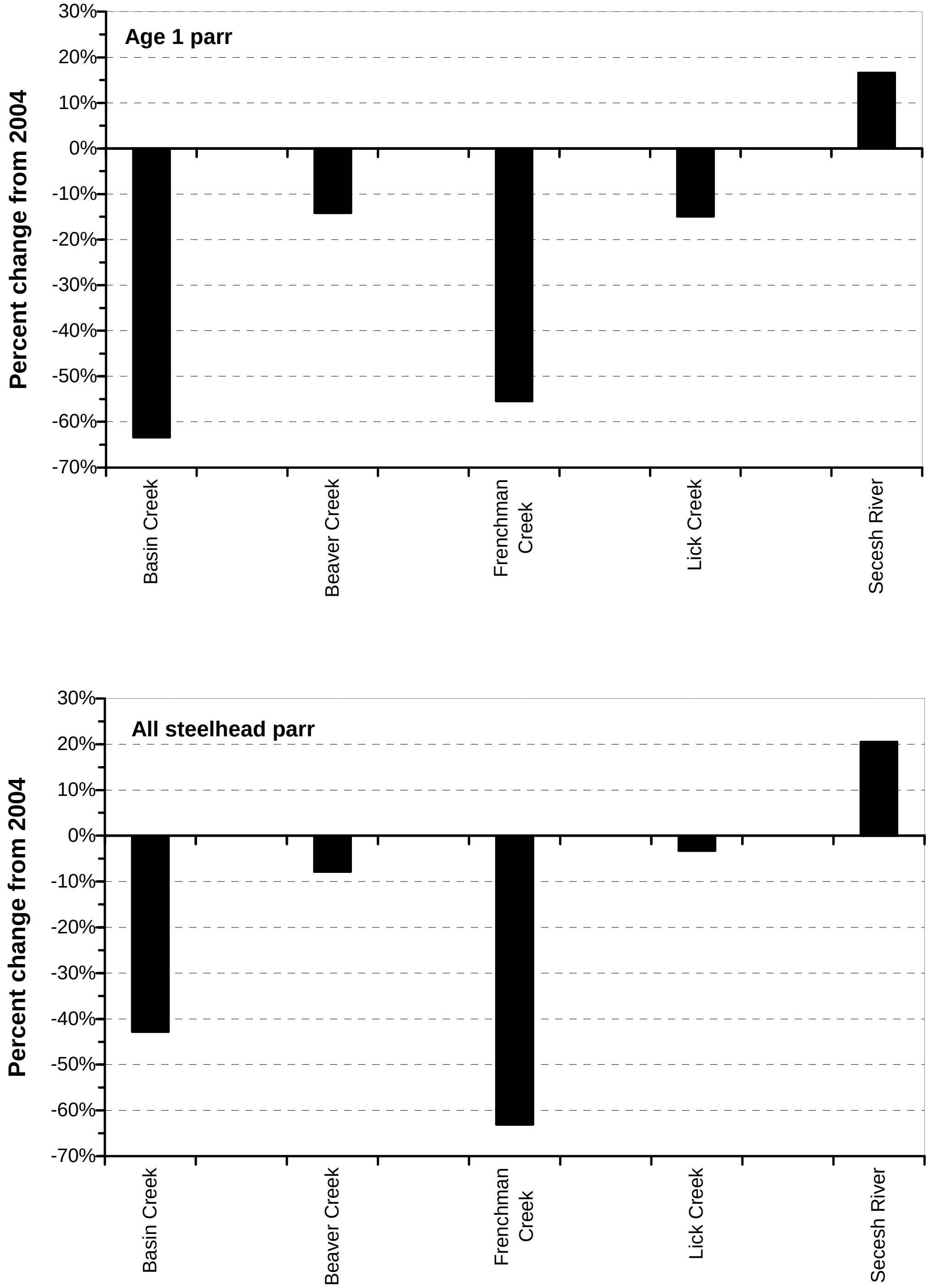

Figure 16. The percent change in the mean density of age-1 steelhead (top graph) and all age-1 and older steelhead parr (bottom graph) from those observed in 2004 in tributaries of the upper Salmon and SF Salmon rivers.

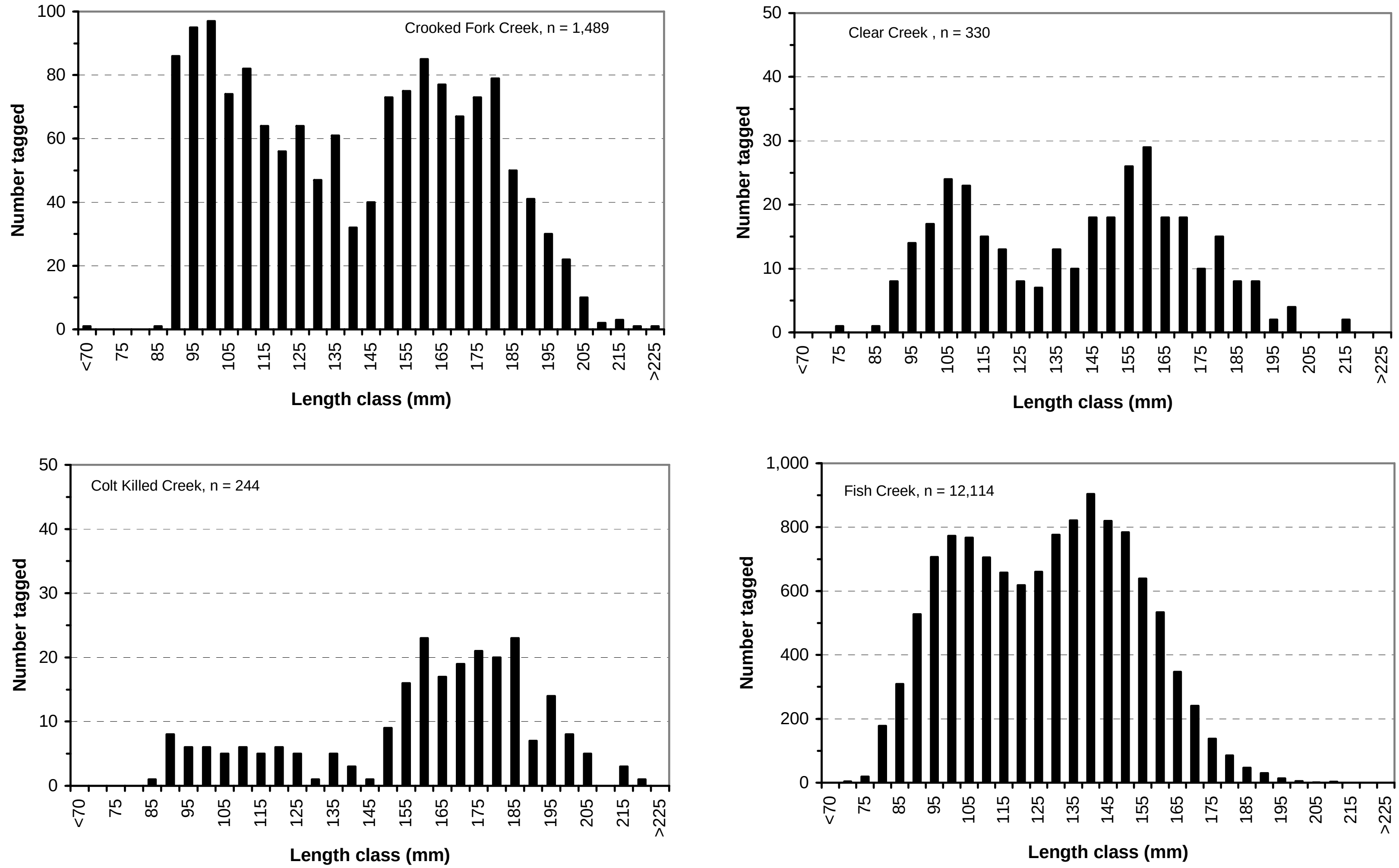

Figure 17. Length frequency of PIT-tagged wild steelhead juveniles captured in screw traps located in tributaries of the Clearwater River drainage during 2005.

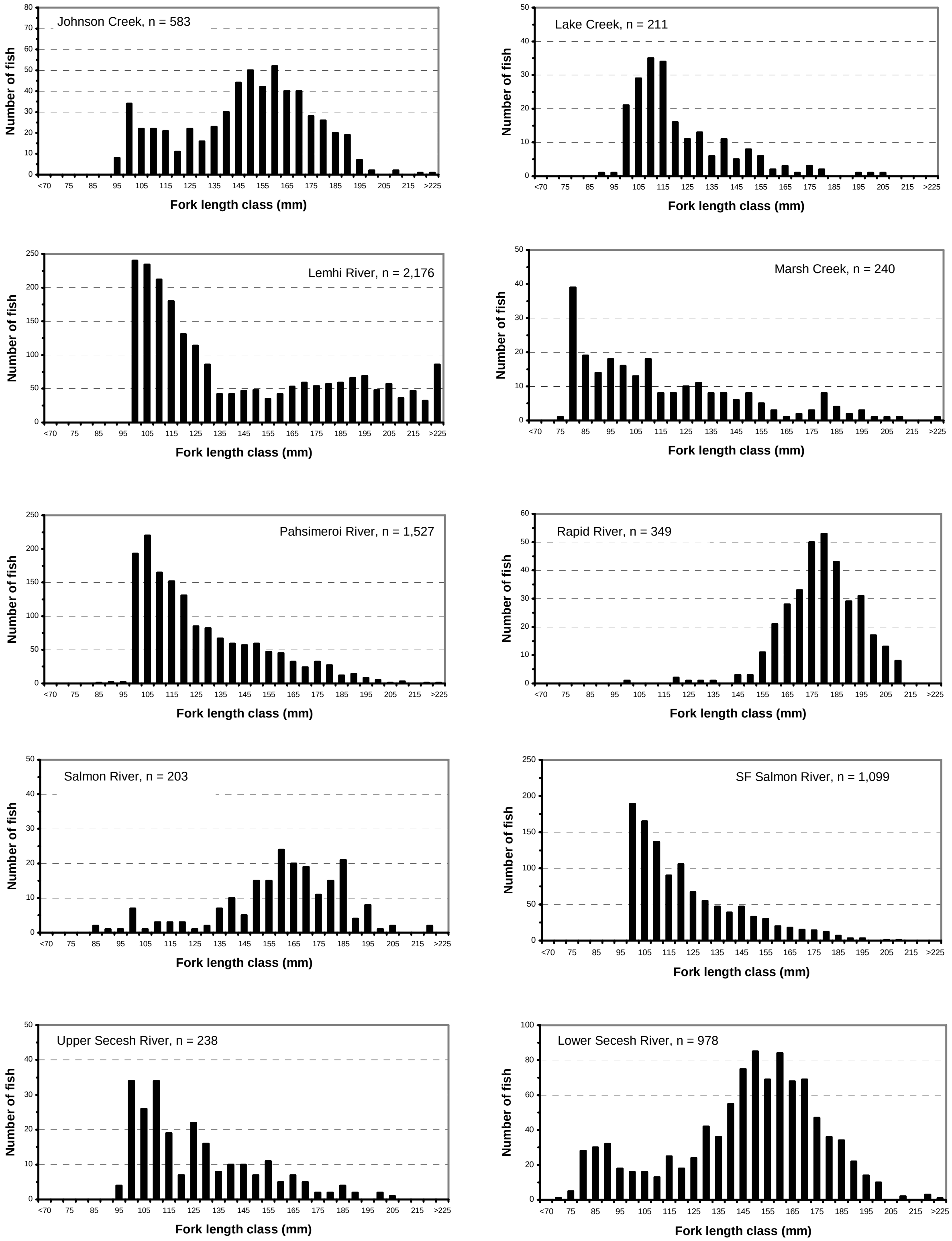

Figure 18. The length frequency of PIT-tagged wild steelhead juveniles captured in screw traps located in tributaries of the Salmon River drainage during 2005.

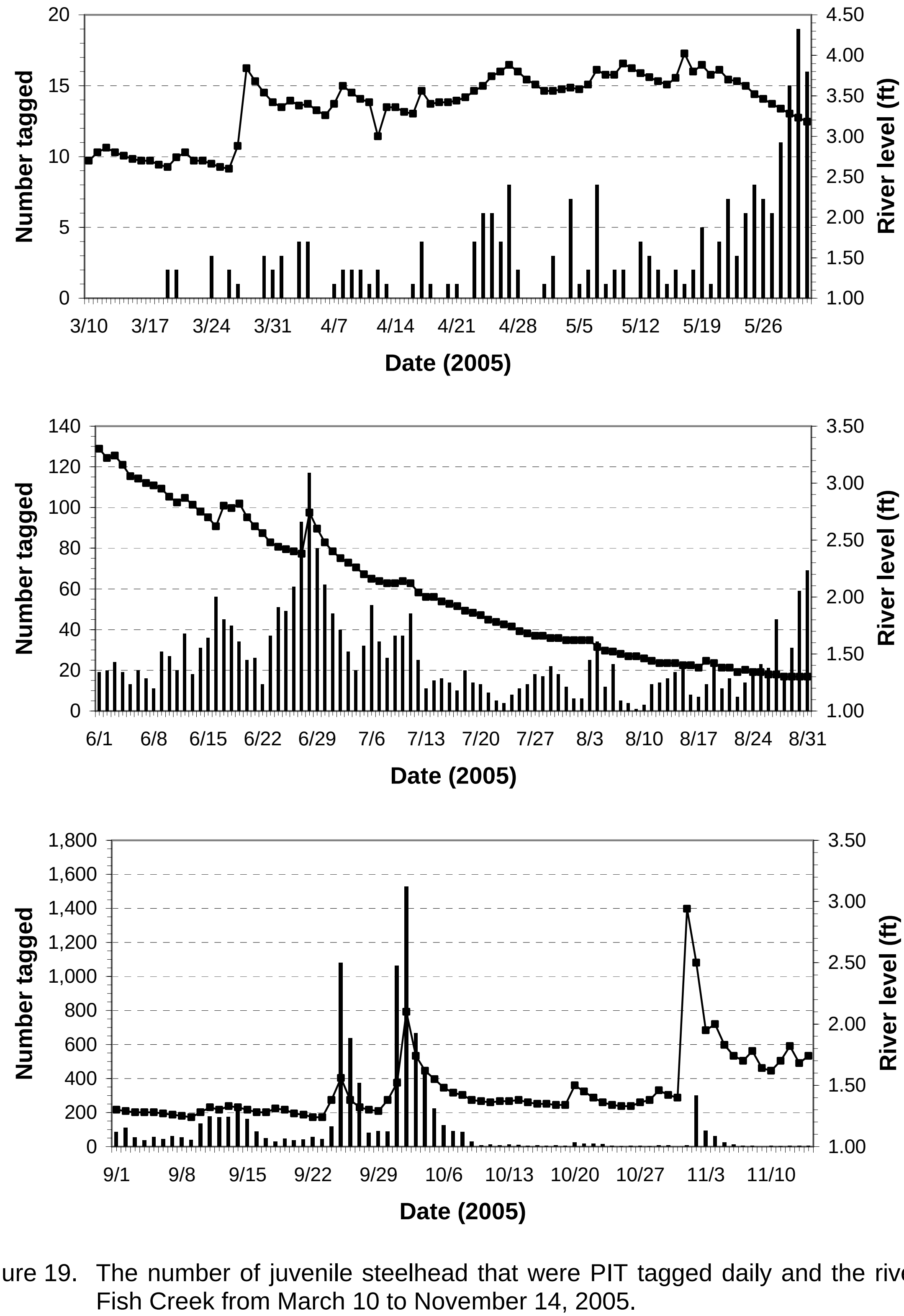

Figure 19. The number of juvenile steelhead that were PIT tagged daily and the river level at Fish Creek from March 10 to November 14, 2005.

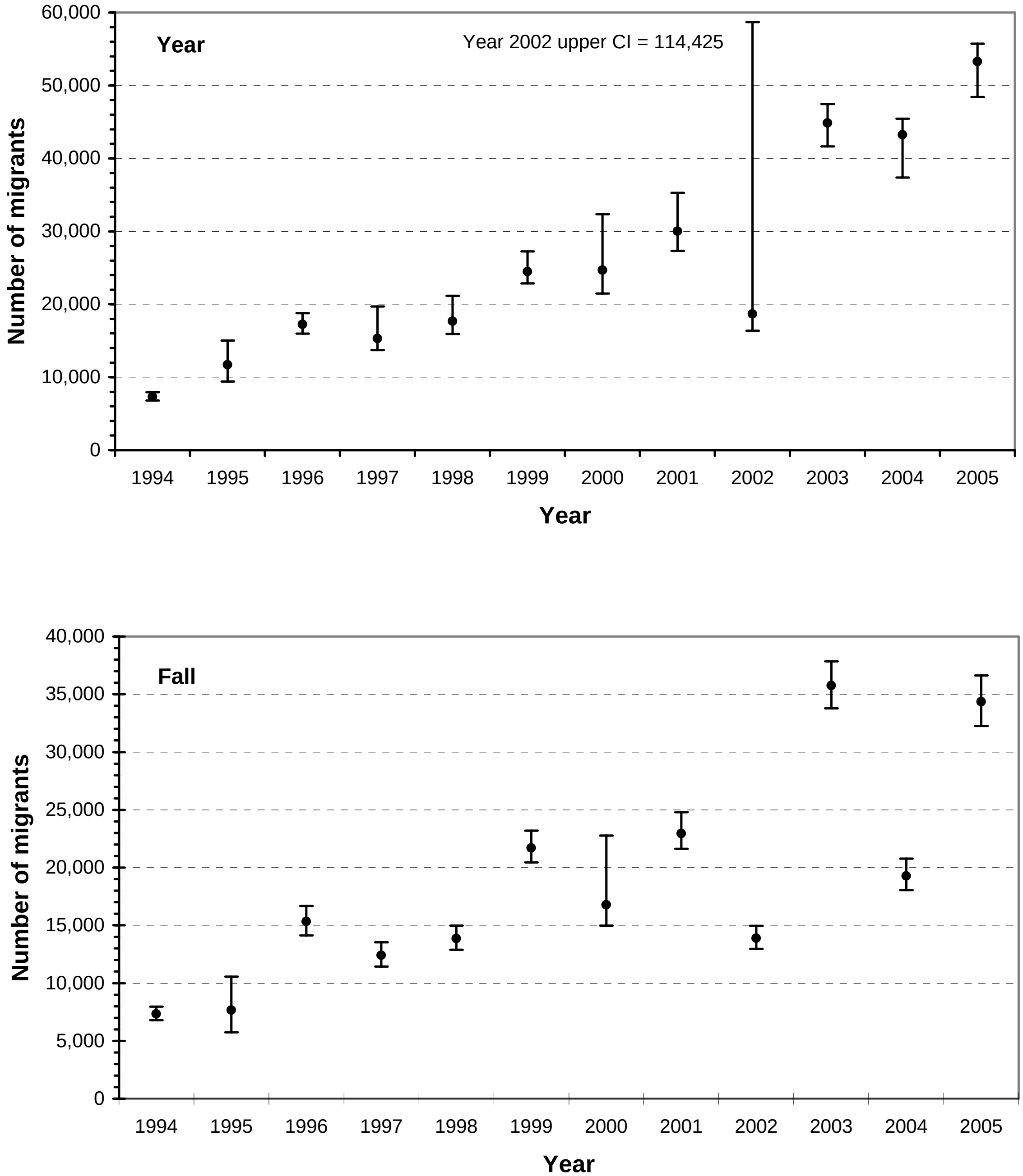

Figure 20. The number of juvenile steelhead (and 95% CI) that migrated past the screw trap in Fish Creek during the entire trapping season (Year, top graph) and from August 15 to the end of trapping in November (Fall, bottom graph) from 1994 to 2005. The large upper CI of yearly migration estimate for 2002 was a result of getting only one recapture during the spring high flow. In 1994, the trap was fished from September 22 to November 2. In 1995, the trap was fished from March 16 to June 14 and from August 18 to November 2. Beginning in 1996, IDFG crews have fished the trap (conditions permitting) continuously from mid-March until the creek freezes in the fall.

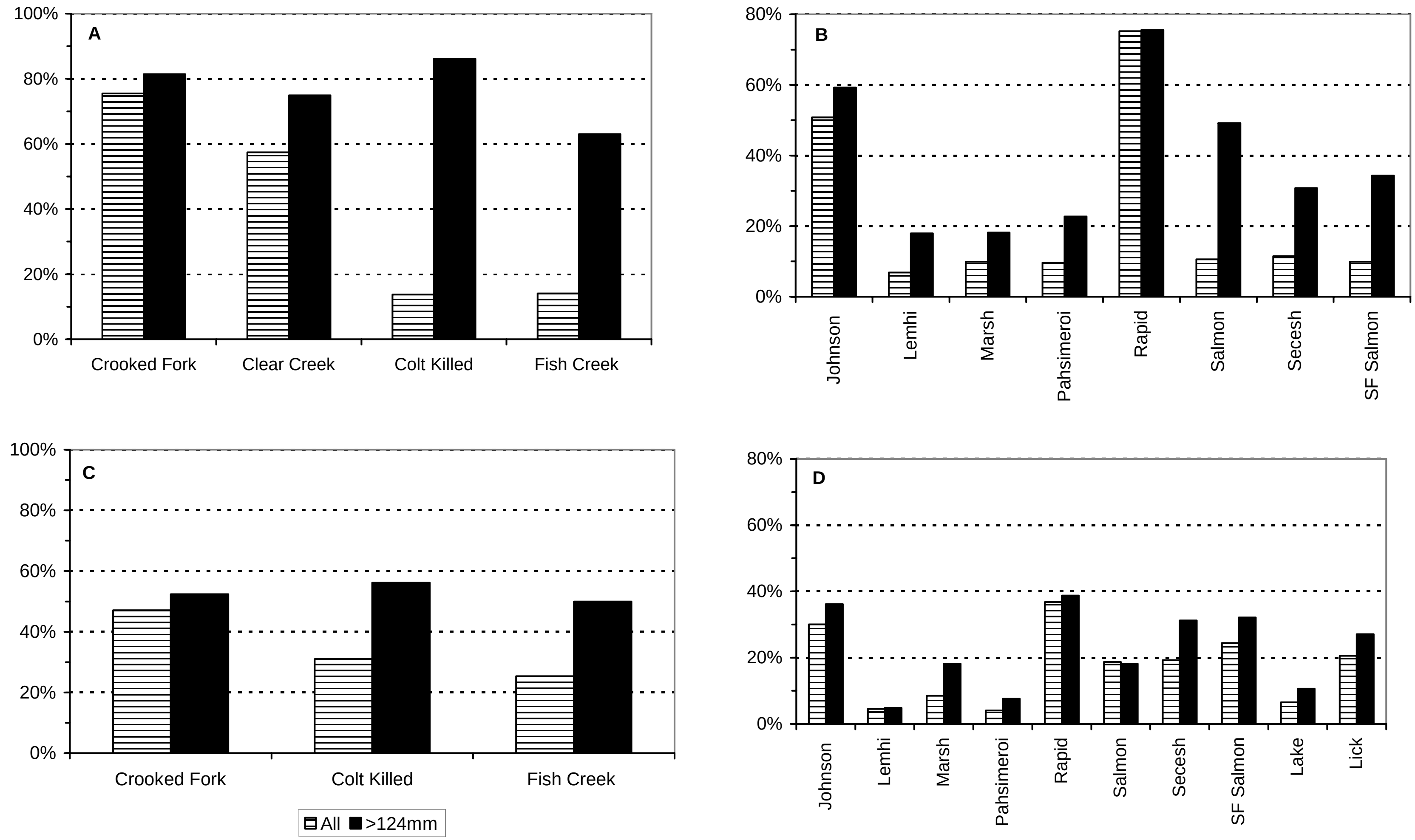

Figure 21. The percentage of all PIT-tagged steelhead and steelhead >124 mm detected as smolts at the downriver dams. Steelhead were tagged in the spring 2005 (Period 1) in the Clearwater drainage (A) and Salmon drainage (B) and during the fall 2004 (Period 2) in the Clearwater drainage (C) and the Salmon drainage (D).

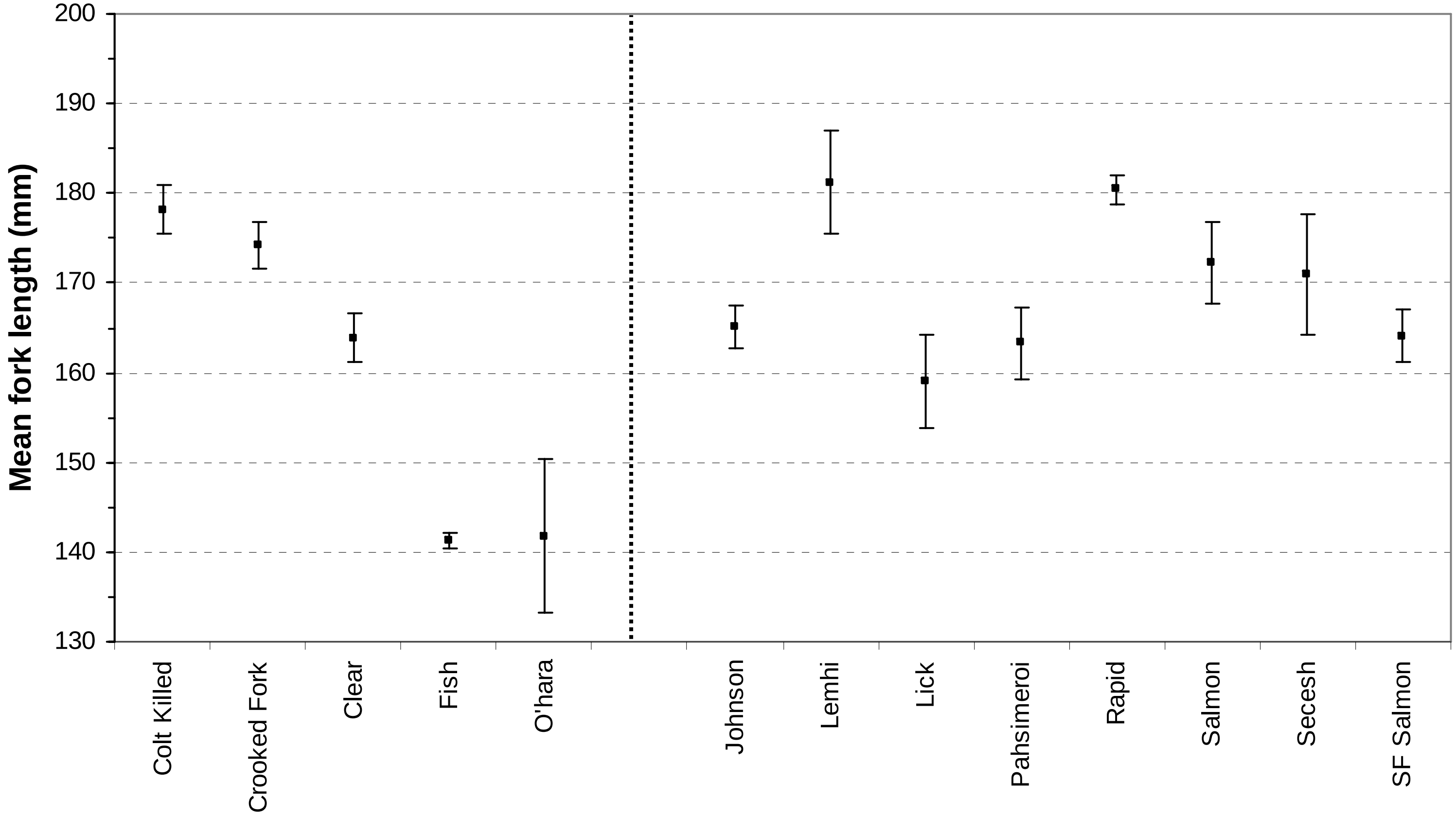

Figure 22. The mean length and 95% CI, at the time of PIT tagging, of smolts that were detected at dams on the Snake and Columbia rivers in 2005. All fish were tagged between August 15, 2004 and May 31, 2005. Streams in the Clearwater drainage are to the left of the dashed line, and streams in the Salmon drainage are to the right of the dashed line.

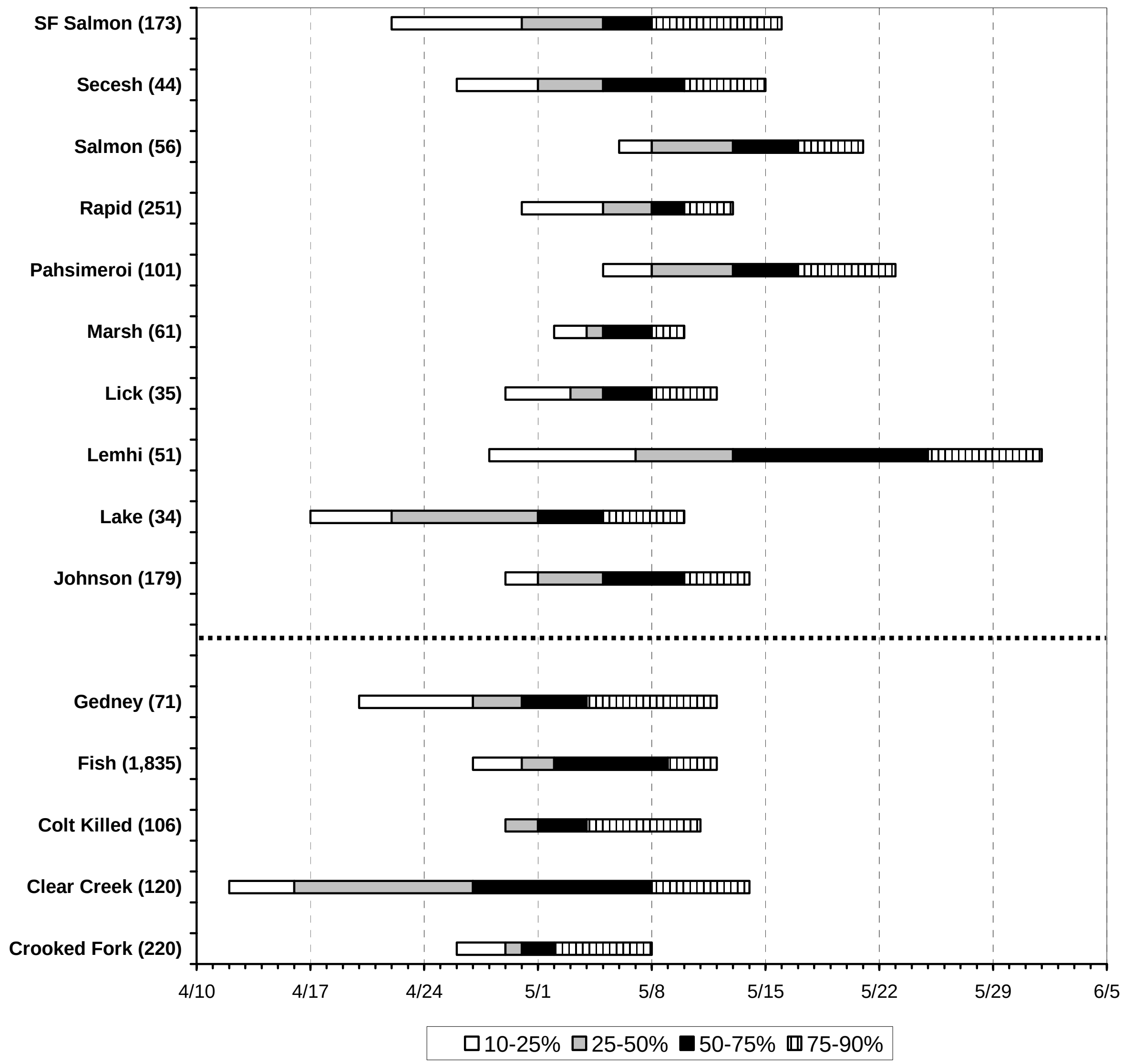

Figure 23. The date that 10%, 25%, 50%, 75%, and 90% of the total number of steelhead smolt detections at Lower Granite Dam in 2005 was attained from tributaries of the Clearwater River (below dashed line) and Salmon River (above dashed line). The left edge of each block is the date that the lower quantile of the block was reached. The number of detections from each site is in parentheses.

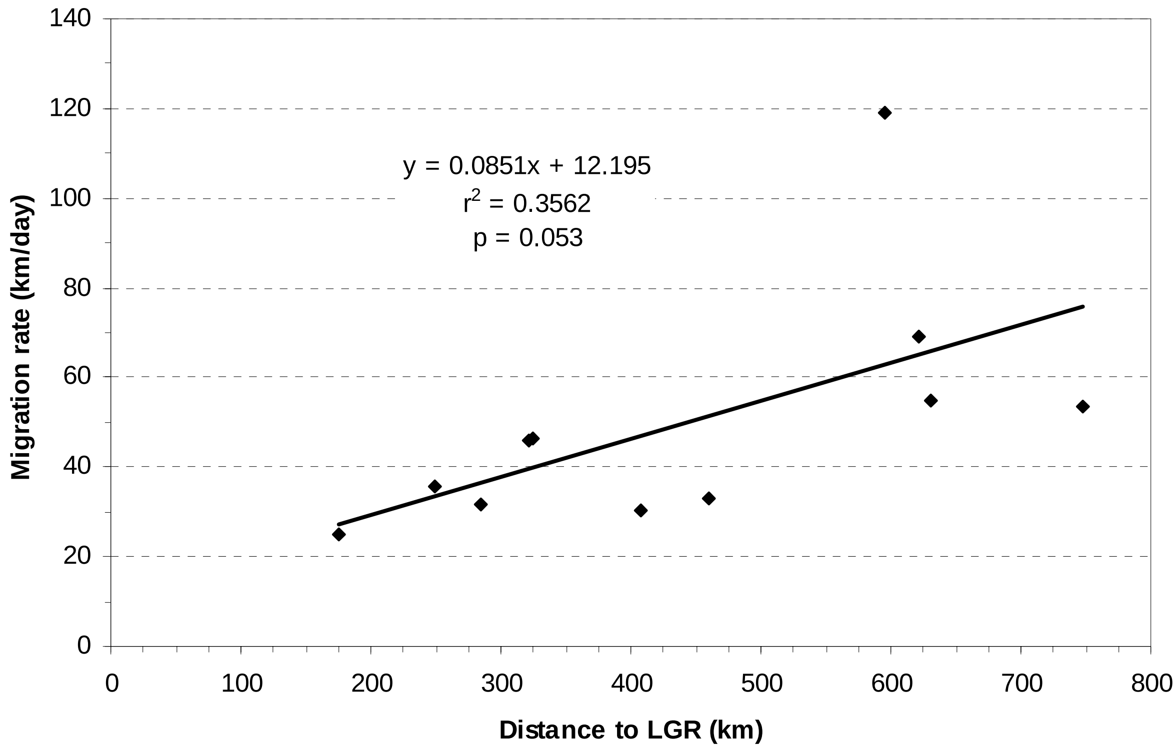

Figure 24. The relationship between median smolt migration rate from the tag site to Lower Granite Dam (LGR) and the distance to LGR in 2005.

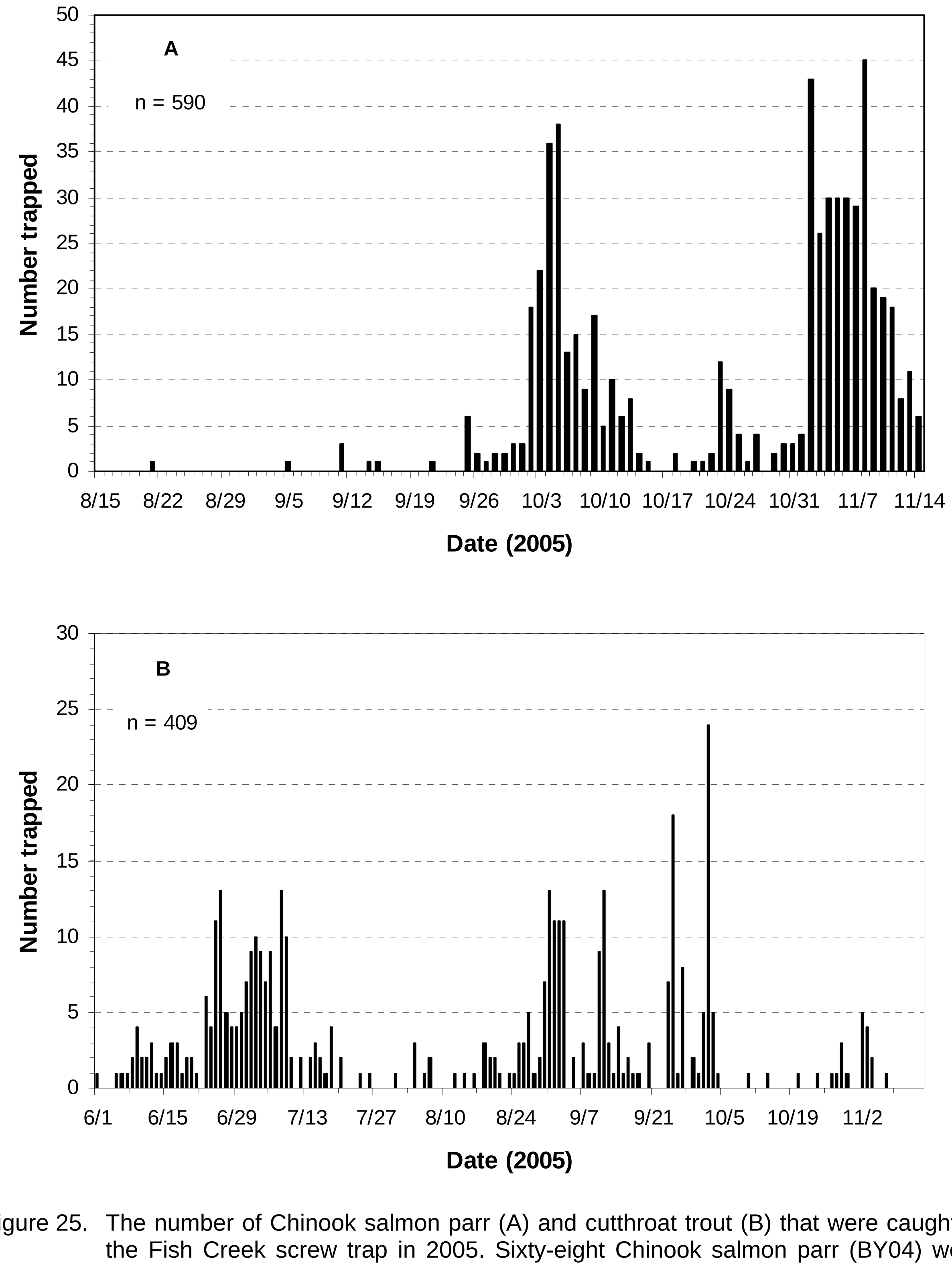

Figure 25. The number of Chinook salmon parr (A) and cutthroat trout (B) that were caught in the Fish Creek screw trap in 2005. Sixty-eight Chinook salmon parr (BY04) were trapped before August 15, 2005. Five cutthroat trout were trapped before June 1, 2005.

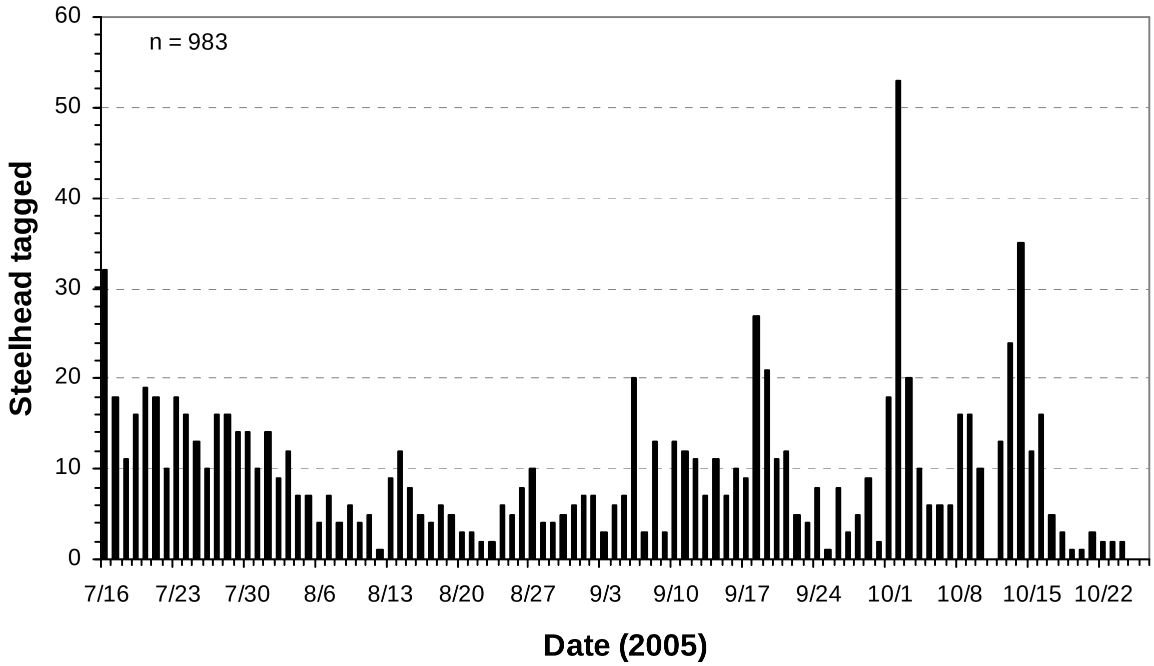

Figure 26. The number of juvenile steelhead that were PIT-tagged each day at the Secesh River screw trap from July 16, 2005 to October 26, 2005

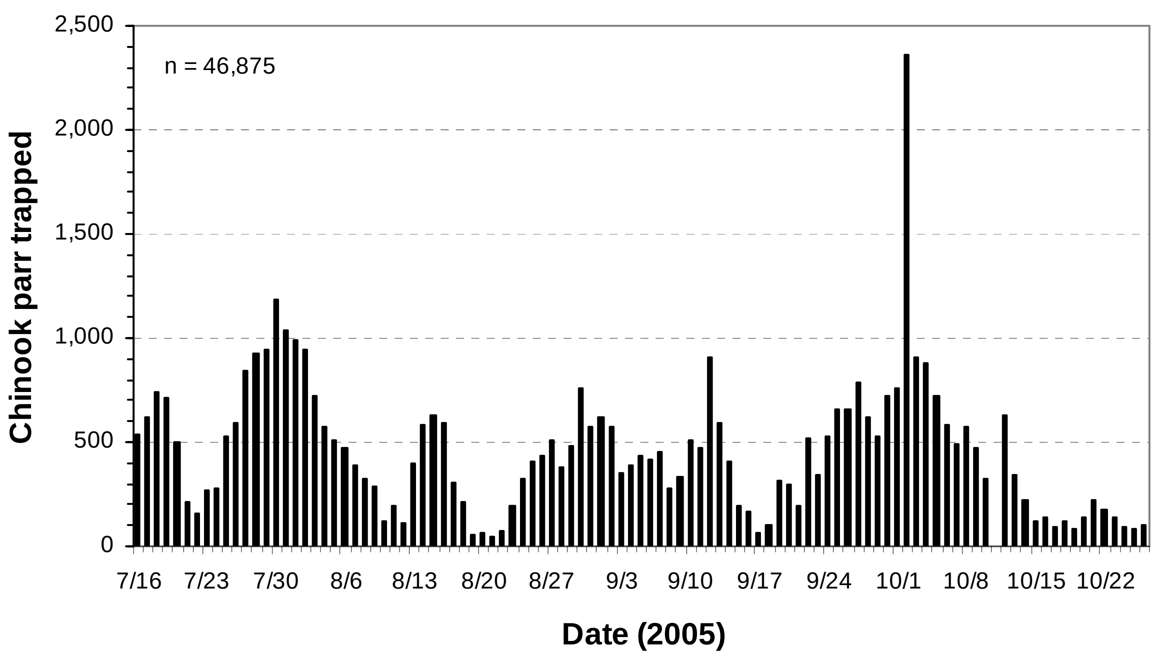

Figure 27. The number of Chinook salmon parr that were caught each day in the Secesh River screw trap from July 16, 2005 to October 26, 2005.

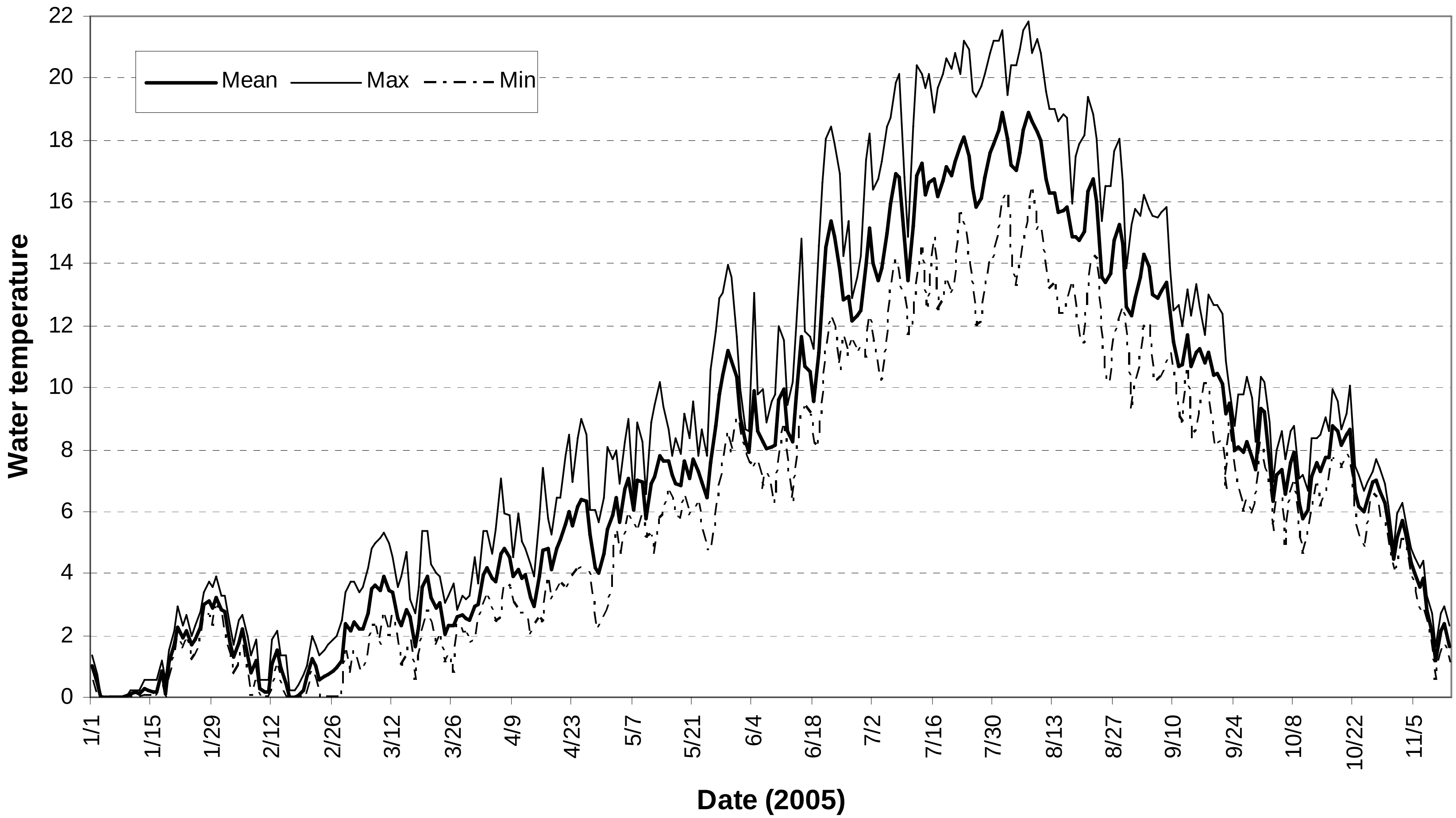

Figure 28. The daily mean, maximum, and minimum stream temperature (°C) recorded in Fish Creek at the screw trap location from January 1, 2005 to November 13, 2005.

APPENDICES

Appendix 1. The boundaries of the streams in the Clearwater River drainage snorkeled in 2005. In streams with more than one stratum, the downstream boundary of stratum 2 begins at the upstream boundary of the previous stratum.

		Stratum boundary	
Stream	**Stratum**	**Downstream**	**Upstream**
Fish Creek	1	mouth	Hungery Creek
	2	—	Frenchman Creek
Hungery Creek	1	mouth	Doubt Creek
Gedney Creek	1	mouth	West Fork Gedney Creek
	2	—	Canteen Creek
West Fork Gedney Creek	1	mouth	Waterfall about 2 km upstream (anadromous barrier)
South Fork Red River	1	mouth	Trapper Creek
	2	—	West Fork South Fork Red River
Canyon Creek	1	mouth	Upstream about 4 km
Crooked Fork Creek	1	mouth	Brushy Fork Creek
Deadman Creek	1	mouth	WF Deadman Creek
Weir Creek	1	mouth	Upstream about 3 km
Post Office Creek	1	mouth	about 2 km upstream of West Fork Post Office Creek
Lake Creek	1	mouth	Upstream about 4 km
Boulder Creek	1	mouth	Huckleberry Creek
Bald Mountain Creek	1	mouth	Upstream about 4 km
Pete King Creek	1	mouth	Placer Creek bridge
O’Hara Creek	1	mouth	Stillman Creek
	2	Stillman Creek	Saddle Creek
Stanley Creek	1	mouth	Gold Meadow Creek
Trapper Creek	1	mouth	upstream about 3 km

Appendix 2. The boundaries of the streams in the Salmon River drainage snorkeled in 2005. In streams with more than one stratum, the downstream boundary of stratum 2 begins at the upstream boundary of the previous stratum.

		Strata boundary	
Stream	Stratum	Downstream	Upstream
Basin Creek	1	mouth	East Fork Basin Creek
	2	—	about 2 km upstream of East Fork Basin Creek
Beaver Creek[a]	1	mouth	Irrigation pump about 0.5 km upstream of Highway 75
	2	—	Jeep trail crossing about 3 km upstream of irrigation pump
	3		Upstream about 5 km
Frenchman Creek	1	mouth	start of the second meadow about 4 km upstream
Buckhorn Creek	1	mouth	Upstream about 4 km at 3rd trail bridge crossing
WF Buckhorn Creek	1	mouth	Upstream about 2 km
Fitsum Creek	1	mouth	About 5 km upstream at first RB tributary upstream of WF Fitsum Creek
Lick Creek	1	mouth	0.5 km downstream of Steep Creek
Secesh River	1	mouth	Butterfly Creek

Appendix 3. Dates the IDFG, U.S. Fish and Wildlife Service (USFWS), and Nez Perce Tribe (NPT) screw traps were installed, removed, and unable to fish during 2005.

Trap site	Date	Comments
Crooked Fork Creek	3/23	Trap installed
	5/8–5/24	not operated due to high flow
	11/1	Trap removed
Colt Killed Creek	3/23	Trap installed
	5/7–5/25	not operated due to high flow
	11/1	Trap removed
Fish Creek	3/9	Trap installed
	11/14	trap removed
Lick Creek	6/29	Trap installed
	7/28	flow too low to fish the trap after 7/28
Marsh Creek	3/22	Trap installed
	11/9	trap removed
Pahsimeroi River	2/28	Trap installed
	3/23–4/6; 4/7; 4/8; 4/11	Not operated—hatchery release
	11/27	Trap removed
Rapid River	4/20	Trap installed
	5/7–5/10	not operated due to high flow
	5/16	Trap removed
Salmon River at Sawtooth	2/24	Trap installed
	11/9	Trap removed
SF Salmon River	3/3	Trap installed
at Knox Bridge	5/16–6/6	not operated due to high flow
	11/3	Trap removed
Lemhi River	3/4	Trap installed
	12/5	Trap removed
Red River	3/15–10/31	Dates of operation
Clear Creek (USFWS)	3/3–6/19	Dates of operation
Johnson Creek (NPT)	3/1–11/22	Dates of operation
Lake Creek (NPT)	4/4	Trap installed
	5/7 and 5/16	not operated due to high flow
	11/6	Trap removed
Secesh River (NPT)	4/13	Trap installed
	5/16 and 5/19	not operated due to high flow
	11/5	Trap removed
Secesh River (IDFG)	7/15	Trap installed
	10/26	Trap removed

Appendix 4. Genetic Population Structure of Snake River Basin Steelhead in Idaho, by Dr. Jennifer L. Nielsen, et al.

Genetic Population Structure of Snake River Basin Steelhead in Idaho

by

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ABSTRACT

Idaho Department of Fish and Game collected tissue samples from 74 wild juvenile steelhead (*Oncorhynchus mykiss*) populations and five hatchery stocks throughout Idaho's Snake River basin in 2000. Samples were sent to the Molecular Ecology Laboratory at the USGS Alaska Science Center to examine the genetic population structure of steelhead in the Clearwater, Salmon and Snake river systems using results from the analysis of 79 Idaho *O. mykiss* populations and 3982 fish samples. Allelic variation found at 11 microsatellite loci was used to describe the population genetic structure and genetic variation found between and among populations and drainages. Mitochondrial DNA (mtDNA) sequence information was used to evaluate three Salmon River drainage populations. Regional spatial structuring of populations was apparent among river drainages. With few exceptions, *O. mykiss* populations were genetically related to other *O. mykiss* from streams within the same drainage. Significant allelic frequency differences were found in 97.9% (6036 out of 6162) of all population pairwise comparisons. AMOVA analysis showed that only 2.66% of the allelic variability could be attributed to differences among the 10 anadromous river drainages (Clearwater, Middle Fork Clearwater, South Fork Clearwater, Salmon, Middle Fork Salmon, South Fork Salmon, Little Salmon, Lochsa, Selway, and Snake). All pairwise comparisons among Oxbow, Pahsimeroi and Sawtooth hatchery populations were not significantly different. Dworshak Hatchery and the Collins Creek population in the North Fork Clearwater River drainage formed a group in the consensus Neighbor-Joining (NJ) tree (80% bootstrap support), but had significantly different allelic frequency structure (pairwise F_{st} = 0.015, $p < 0.000$). The East Fork Salmon "B-run" Hatchery was significantly different from all other populations in pairwise comparisons, but was weakly associated (44% bootstrap support) with Ten Mile Creek (South Fork Clearwater River drainage) in the NJ tree. Two Salmon River populations, Lemhi River and Pahsimeroi River, separated from the rest of the populations in the Snake River basin with 97% bootstrap support in the NJ tree. However, analysis of mtDNA haplotype variation demonstrated no unique lineages within these two populations suggesting that phylogeographic refugia associations do not account for the distinction of these populations detected in microsatellite NJ analysis. Three formerly anadromous *O. mykiss* populations found upstream of the Hells Canyon Dam complex (Little Weiser River, Middle Fork Payette River and Big Smoky Creek) were genetically similar forming a cluster in the NJ tree (53% bootstraps). Average estimated effective population size (*Ne)* for all Snake River steelhead populations ranged from 2010 to 3722 based on the Infinite Allele (IAM) and Stepwise Mutation (SMM) models, respectively. Average observed heterozygosity (*Hz)* for 11 microsatellite loci across all Snake River populations was *Hz* = 0.61. These data suggest that significant genetic population structure remains for steelhead populations within the Snake River basin in Idaho, and careful consideration of this genetic diversity should be part of future conservation and restoration efforts.

INTRODUCTION

Historically, anadromous steelhead (*Oncorhynchus mykiss*) were broadly distributed throughout most Columbia River drainages (Busby et al. 1996). Two phylogeographic lineages of *O. mykis*s have been recognized in North America – coastal (*O. m. irideus*) and inland (*O. m. gairdneri*; Behnke 1992). This subspecific division is thought to result from two *O. mykiss* refugia populations, the upper Fraser River and Puget Sound, during the last glaciation (Brown et al. 2004). However, very little is known about Pleistocene glacial cycles, trout distributions and the temporal scale of *O. mykiss* speciation. This division of *O. mykiss* into two sublineages remains controversial. Genetic analyses using chromosome counts, allozymes, mtDNA, and microsatellite loci have been used to describe the *O. mykiss* subspecific separation across many scales (Utter et al 1980; Currens et al. 1990; Beacham et al. 1999; Ostberg and Thorgaard 1999; McCusker et al. 2000; Docker and Heath 2003; Brown et al. 2004). The Cascade crest is thought to separate the two *O. mykiss* lineages within the Columbia River drainage, making all up-river steelhead found in Idaho part of the putative inland group. Due to a lack of fossil evidence, linkages between genetic variation and the timing of speciation events are scarce in the salmonid literature (see Guinand et al. 2002). Recent estimates of avian diversification rates suggest that most North American speciation events may have happened much earlier than the Pleistocene as current genetic evidence suggests (Zink et al. 2004; Lovette 2005). Similar analyses of present-day taxonomic species splits, including coastal and inland populations, using broader cladistic evidence are needed for *O. mykiss*.

The construction of dams throughout the Columbia River system has markedly changed the temperature and flow regime available to anadromous steelhead compared to historical patterns (Robards and Quinn 2002). There have been substantial declines in these populations over the last 150 years, due primarily to lost spawning and rearing habitats, changes in water quality, and within-basin dams and diversions (Busby et al. 1996). Steelhead that spawn in Idaho are primarily summer-run fish. Idaho steelhead migrate further from the ocean (up to 1,500 km) than all other Columbia River populations and spawn at high elevations (up to 2,000 m). Anadromous steelhead in the Snake River basin found in streams of southeast Washington, northeast Oregon and Idaho, were listed under the Federal Endangered Species Act (ESA) as a threatened Evolutionarily Significant Unit (ESU) in 1997 (Federal Register Vol. 62 No. 159: 43937 - 43954).

Wild steelhead abundance in the Clearwater and Salmon River systems declined relative to their historical abundance after the construction of four lower Snake River dams (Ice Harbor, Lower Monumental, Little Goose and Lower Granite Dams). The construction of the Hells Canyon Dam complex (Hells Canyon, Oxbow and Brownlee Dams) exacerbated steelhead declines in the upper Snake River basin. Declines of wild B-run steelhead[1] have generated particular concern over the potential loss of life history diversity for this species. *O. mykiss* expresses a range of life history strategies, from strongly migratory to non-migratory, throughout the species' range and recent studies have demonstrated that non-anadromous rainbow trout can give rise to anadromous fish in a few generations (Pascual et al. 2001). Individual runs or stocks of *O. mykiss* found within the same drainage cannot be separated

[1] Snake River steelhead runs are commonly referred to as "A-run" or "B-run" stocks based on designations developed from the bimodal migration of adult steelhead at Bonneville Dam. Adult A-run fish migrate upstream earlier (June to August) than B-run fish (August to October); B-run fish are primarily defined as 2-ocean adults having spent two years at sea (as opposed to 1-ocean A-run fish) and are on average 75-100 mm larger than A-run fish of the same age.

taxonomically based on migration timing or the distribution of different life histories (Allendorf and Utter 1979; Behnke 1992). Highly flexible life history strategies in *O. mykiss* have been well documented (Shapovalov and Taft 1954; Rybock et al. 1975; Zimmerman and Reeves 2000). Genetic studies (Gall et al. 1990; Nielsen et al. 1997a) suggest that resident fish in freshwater habitats may contain relic components of the *O. mykiss* gene pool found in geographically proximate anadromous populations.

In recent years, over 80% of the adult steelhead passing Lower Granite Dam derived from hatchery origins (Busby et al. 1996). In the Clearwater River drainage, large-scale hatchery releases began in the 1970's after the Dworshak National Fish Hatchery was built. The Dworshak summer steelhead stock was developed from native B-run North Fork (NF) Clearwater River steelhead in 1969 (Howell et al. 1985). Dworshak National Fish Hatchery released between 1.9 and 2.4 million smolts each year since 1997 into the Clearwater River system (Fish Passage Center 2004). Large-scale artificial propagation of steelhead in the Snake and Salmon rivers began in the 1960's with the construction of Oxbow Hatchery, Niagara Springs Hatchery, and Pahsimeroi Hatchery. Oxbow, Niagara Springs, and Pahsimeroi hatcheries were all part of Idaho Power Company's (IPC) program to relocate steelhead stocks from the upper Snake River to the Salmon River after the construction of Hells Canyon dams (Busby et al. 1996). The goal of Lower Snake River Compensation Plan (LSRCP) hatcheries (Sawtooth, Hagerman and Magic Valley) was also to mitigate anadromous fish losses in the Salmon, Little Salmon and upper Snake rivers. Hatchery steelhead releases in the Salmon and Snake river drainages has ranged from 4 to 6 million yearly since 1997 (IDFG hatchery release database).

The impact of hatchery *O. mykiss* on wild stocks in streams and reservoirs throughout North America has been the subject of many studies (Reisenbichler and McIntyre 1977; Waples and Do 1994; Campton 1995; Nielsen 1999). Straying and introgression by hatchery fish presents a high risk to the genetic integrity of some wild steelhead populations according to some authorities (Busby et al. 1997; Levin and Williams 2002). Genetic integrity of locally adapted stocks of *O. mykiss* is of critical importance to issues of restoration and recovery. Local adaptation includes genotypic and phenotypic traits at both individual and population scales (Reeve and Sherman 1993). However, it is not clear what roles selection, mutation and chance play in an individual's response to local conditions, and it is probably a combination of all of these factors that leads to evolutionary success through local adaptation (Rose and Lauder 1996). Therefore, the process of adaptation is difficult to define, but is most commonly regarded as a process that promotes fitness of the organism to specific environments (Gould and Lewontin 1979; Mayr 2002).

This study represents genetic analyses of allelic diversity in samples of *O. mykiss* with different states of local adaptation, i.e. fish collected above and below dams, natural spawning anadromous populations, non-anadromous populations and hatchery propagated stocks. Genetic investigations (Gall et al. 1990; Nielsen et al. 1997a) have suggested that anadromous steelhead have residualized as freshwater fish behind man-made structures and dams throughout their natural range. Four landlocked *O. mykiss* populations found above man-made barriers (Collins Creek, NF Clearwater River; Big Smoky Creek, Boise River; Middle Fork (MF) Payette River, Payette River; Little Weiser River, Weiser River) were compared to geographically proximate anadromous populations in this study.

The Idaho Department of Fish and Game (IDFG) collected juvenile *O. mykiss* samples during the summer of 2000. DNA was extracted, visualized, and analyzed at the USGS Alaska Science Center's Molecular Ecology Laboratory. *O. mykiss* genetic diversity based on 11 microsatellite loci was analyzed within and among samples and groups of samples at several spatial scales: 1) allelic diversity among and between large river drainages; 2) pairwise comparisons of genetic diversity between 79 independent *O. mykiss* populations; 3) within population genetic diversity was used for comparisons across broad spatial scales and among different life histories. We compared genotypes and allelic frequencies for *O. mykiss* populations to data from known steelhead hatchery strains with a history of stocking in Idaho. Genetic relationships among and between all *O. mykiss* populations and between hatchery and wild populations within and among drainages were evaluated.

METHODS

<u>Sample Collections, DNA extraction and Microsatellites</u>

IDFG collected fin tissues from *O. mykiss* throughout the Snake River basin, Idaho (Figure 1). Fin tissue was stored in 100% ethanol and DNA was extracted using the Puregene extraction protocol *(*Minneapolis, Minnesota). DNA was recovered and analyzed for 3982 fish (Table 1). Microsatellite loci taken from the published literature were selected for analysis based on documented variability in *O. mykiss*, ease of amplification in polymerase chain reaction (PCR), and a history of allele scoring rigor within our laboratory.

Multiplex systems using 13 microsatellite loci were developed for amplification. Several primers were redesigned in order to establish the three multiplex systems described in Table 2. *Oneµ10* forward *(F)*, *Ogo4-(F)*, *Ogo4* reverse *(R)* and *Ots3-(R)* were redesigned as follows: *Oneµ10-(F)* was renamed *Oneµ10.2-(F)* (5'-TGTTGGCACCATTGTAACAG-3'); *Ogo4-(F)* was renamed *Ogo4.2-(F)* (5'-CAGAATCAGTAACGAACGC-3'); *Ogo4-(R)* was renamed *Ogo4.2-(R)* (5'-GAGGATAGAAGAGTTTGGC-3'); and *Ots3-(R)* was renamed *Ots3.2-(R)* (5'-CACAATGGAAGACCAT-3'). *Ogo1a*, *Ogo4.2*, *Oneµ10.2* and *Ots3* forward primers were modified by the addition of M13(R) tails (5'-GGATAACAAT-TTCACACAGG-3'), and *Oneµ8* and *Oneµ11* forward primers were modified by the addition of M13(F) tails (5'-CACGACGTTGTAAAACGAC-3'). All M13 tails were added to primers at the 5' end and allowed for allele fragment visualization by annealing to labeled complementary M13 tails added to the PCR mix. The remaining loci were visualized by adding directly labeled forward primers.

In the interim progress report on Idaho's 36 priority *O. mykiss* populations, *Omy77* and *Omy207* were removed from statistical analyses due to lack of conformity to Hardy-Weinberg equilibrium (HWE; Nielsen et al. 2004). Results from these loci were not collected for the rest of this study. Eleven microsatellite loci were used to assess genetic variation in 79 Idaho *O. mykiss* populations: *Ogo1a, Ogo4, Omy27, Omy325, Oneµ8, Oneµ10, Oneµ11, Oneµ14, Ots1, Ots3* and *Ots4* (Table 3).

PCR reactions were conducted in 10-12µl volumes using approximately 50ng of genomic DNA, 0.06-0.1 U of DNA polymerase (Perkin Elmer), 10mM Tris-HCl (pH 8.3), 1.5mM $MgCl_2$, 50mM KCl, 0.01% gelatin, 0.01% NP-40, 0.01% Triton X-100, and 200µM each dNTP. Gel electrophoresis and visualization of microsatellite alleles was performed using a LI-COR Model IR2 automated fluorescent DNA sequencer and allele sizes were determined using V3.00 Gene ImagIR software (LI-COR, Lincoln, NE, USA). Microsatellite allele sizes were quantified in relation to the M13 ladder, *O. mykiss* DNA samples of known size, and/or the GeneScan-350 internal size standard (P-E Biosystems, Foster City, CA, USA). Approximately 10% of all samples were run on a second gel and scored independently to verify allelic sizes across all loci.

Assessing Interspecific Alleles

In our laboratory, four microsatellite loci (*Ogo4, Oneμ8, Oneμ14 and Ots1*) have demonstrated diagnostic capacity to distinguish *O. mykiss* alleles from coastal cutthroat (*O. clarki clarki*) alleles based on allelic size ranges at individual loci (Graziano and Nielsen 2004; Williams 2004). Loci carrying putative *O. clarki* alleles outside of the expected range for *O. mykiss* were removed from individual fish genotypes. Data from individual samples containing putative *O. clarki* alleles at two or more loci (50% of the diagnostic loci) were removed from the database used for statistical analyses.

Statistical Analyses

Genetic data were analyzed using a variety of software from different statistical packages including GENEPOP version 3.3 (Raymond and Rousset 1997), ARLEQUIN version 1.1 (Schneider et al. 1997), BOTTLENECK (Piry et al. 1999), WHICHLOCI (Banks and Eichert 2000), AGARst (Harley 2001) and PHYLIP (Felsenstein 1993).

Hardy-Weinberg equilibrium estimates were generated using GENEPOP. Tests of HWE were performed to look at the performance of different loci among *O. mykiss* sample populations to gain inference on population structure. ARLEQUIN's *Fst* comparisons were used to test for differences in allele frequencies between and among populations and drainages. Statistical significance levels for allelic frequency comparisons were adjusted for multiple tests across 11 loci ($\alpha = 0.0045$) using a Bonferroni correction (Rice 1989). Partitioning of microsatellite allelic variation based on analysis of molecular variance (AMOVA) was generated by ARLEQUIN. WHICHLOCI (Banks and Eichert 2000) was used to rank the relative contribution of each microsatellite locus to the analysis of population genetic structure based on the allelic frequency differential method.

AGARst provided (1) population estimates of Garza and Williamson's (2001) *M,* the mean ratio of the number of alleles to the range of allele size across multiple loci used to detect recent reductions in population size, and (2) estimates of effective population size (*Ne*) under assumptions of two mutation models: Infinite Allele and Stepwise Mutation Model (IAM and SMM, respectively). The published threshold of $M < 0.68$ was used to determine if populations in this study had undergone recent reductions in population size (Garza and Williamson 2001). Appropriate application of Garza and Williamson's *M* as a test for recent population declines requires specific selection criteria for microsatellite loci. Three loci (*Omy27, Ogo1a and Ots1)* were removed from the analysis of *M* due to the presence of single base pair variants that do not conform to the mutational model upon which this test is based (Garza and Williamson 2001). We removed two other loci based on underlying allelic structure that did not conform to test expectations, *Oneμ10* and *Oneμ11*, because of low allelic polymorphism and low observed heterozygosity ($Hz < 0.5$). Although 10 alleles are reported for *Oneμ10*, this locus was essentially monomorphic with one allele (121) dominating the frequency distribution across most populations (91% average occurrence). Only four alleles were identified for *Oneμ11*, two of which were rare. Sheep Creek (Salmon drainage, N = 19) and Boulder Creek (Lochsa drainage, N = 21) were excluded from this analysis because of failure to meet population size criteria ($N \geq 25$) established for the determination of *M* (Garza and Williamson 2001). *M* values by drainage were calculated using all samples collected from within the drainage as a single population.

Variance effective population size (*Ne*) was assessed using the temporal method (Nei and Tajima 1981; Waples 1990; Williamson and Slatkin 1999) and all 11 microsatellite loci with

AGARst. The program BOTTLENECK was used to estimate probabilities of mutation-drift equilibrium under three models (IAM, SMM and the Two-Phase Model, TPM) to infer recent reductions in population size based on heterozygosity excess (HZE). Probabilities of mutation-drift equilibrium were also assessed by drainage using BOTTLENECK.

Genetic distance values reflecting the proportion of shared alleles between individuals and groups of individuals can be used to graphically depict genetic relationships and population structure. Allele frequency data was used to create 2000 genetic distance matrices based on Cavalli-Sforza and Edward's genetic chord distance (1967) using GENEDIST from PHYLIP. Neighbor-Joining (NJ) trees were generated using the NEIGHBOR application of PHYLIP from each distance matrix. A consensus tree was created using CONSENSE from PHYLIP. SEQBOOT from PHYLIP was used to bootstrap allele frequencies creating 2000 datasets for the consensus NJ tree depicting 79 *O. mykiss* populations (Felsenstein 1985). TreeView version 1.6.6 was used to visualize the consensus NJ tree with bootstrap values (Page-1996).

Mitochondrial DNA Analysis

A portion of the mtDNA non-coding D-loop was amplified and sequenced using the S-Phe/P2 primer set (Nielsen et al. 1994b) for three Salmon River drainage populations (Lemhi and Pahsimeroi rivers and Morgan Creek). E-SEQ and ALIGNIR were used to automate the sequencing and alignment of mtDNA haplotypes (LI-COR Inc., Lincoln, Nebraska).

RESULTS

Microsatellite Loci and HWE

Heterozygosity (*Hz*) averaged across all 11 loci is given by population in Table 1. Average heterozygosity, the total number of alleles and size range of alleles are given by locus in Table 3. Four loci, *Omy325* (*Hz* = 0.878), *Oneμ8* (*Hz* = 0.837), *Ots1* (*Hz* = 0.803) and *Ogo4* (*Hz* = 0.788), contributed the greatest numbers of alleles to this study (33, 20, 27 and 12, respectively). The combined contribution (sum of the % relative scores) of *Omy325, Oneμ8, Ots1* and *Ogo4* resulted in greater than 55% assignment power of individuals to their respective populations using the program WHICHLOCI (Table 3).

GENEPOP's analyses of HWE expectations gave mixed results among the microsatellite loci and *O. mykiss* populations in this study (Table 4). Twenty-six populations fell significantly out of HWE for 11 loci combined (Table 5). Deviations from HWE were primarily due to heterozygote excess. Sample size for all populations not conforming to HWE for these loci exceeded N = 41. We judged the allelic diversity found within these populations to be informative despite non-conformity to HWE and retained these populations in our analyses.

Among Drainage Analyses

BOTTLENECK's analysis of drainages in the Snake River basin detected heterozygosity excess ($p < 0.05$) for seven drainages under the IAM, but no drainage exhibited HZE under the SMM or TPM (Table 6). Snake River drainages showed no evidence of recent declines based on *M* values derived from the drainage mean ratio of the total number of alleles and allelic size range (Table 7). The MF Clearwater River drainage was represented by only one sample, Clear Creek, where *M* = 0.668. The Salmon River drainage recorded the highest *M* value (0.907), and was predicted to have the largest average effective population size based on SMM (*Ne* = 5018).

AMOVA analysis of 10 anadromous steelhead drainages, excluding hatchery populations, distributed 2.66% of the molecular variance to differences among drainages, 2.35% among populations within drainages, and 94.99% within populations.

All drainages were significantly different based on pairwise F_{st} values (Table 8). Pairwise comparisons resulting in the greatest allelic differentiation occurred between the MF Salmon and the Lochsa drainages (F_{st} = 0.057, p< 0.000). The lowest allelic differentiation occurred between the Salmon and Snake drainages (F_{st} = 0.005, p < 0.000).

GENETIC ANALYSES WITHIN DRAINAGES

Boise River Drainage

Allelic variation was analyzed for 37 *O. mykiss* from Big Smoky Creek, the only population from the Boise River drainage collected for this study (map location 78, Figure 1). This population represents one of four landlocked, formerly anadromous, *O. mykiss* populations evaluated in this study. The average number of alleles across all 11 loci for Big Smoky Creek was 6.27 and average observed heterozygosity across all loci was *Hz* = 0.63 (Table 1). A reduction in population size was suggested for Big Smoky Creek based on Garza and Williamson's *M* statistic (*M* = 0.67; Table 9). Allelic frequencies in Big Smoky Creek *O. mykiss* were significantly different from all other Snake River populations analyzed based on F_{st} pairwise comparisons. Populations with the greatest allelic differentiation based on F_{st} comparisons using Big Smoky Creek were Brushy Fork Creek (Lochsa drainage, F_{st} = 0.133), Collins Creek (NF Clearwater drainage, F_{st} = 0.117) and Storm Creek (Lochsa drainage, F_{st} = 0.114).

Clearwater River Drainage

We visualized allelic diversity at 11 microsatellite loci for 252 *O. mykiss* sampled from five populations within the Clearwater River drainage (Table 1). The average number of alleles per locus was 7.0 and the average observed heterozygosity (*Hz*) across all populations and all loci was 0.66. ARLEQUIN's population pairwise comparisons found significant differences in allelic frequencies among all Clearwater River drainage *O. mykiss* populations. Allelic frequency differences were not detected in comparisons between Big Canyon Creek and two Salmon River drainage populations (Chamberlain Creek, F_{st} = 0.000, p = 0.327; Horse Creek, F_{st} = 0.004, p = 0.061; Appendix I). Garza and Williamson's *M* detected recent population reductions in Jack's and Little Bear creeks (*M* = 0.585 and 0.643, respectively). Estimated effective population size (*Ne*) based on SMM ranged from *Ne* = 3721 (Mission Creek) to *Ne* = 4493 (Big Canyon Creek) (Table 9). AMOVA distribution of the allelic variation found within the Clearwater River drainage showed that 2.22% of the variation was found among populations and 97.78% was found within populations (Table 7). A branch in the unrooted NJ tree (Figure 2 and 3) grouped Little Bear Creek and EF Potlach River with 50% bootstrap support.

Middle Fork Clearwater River Drainage

Allelic diversity was analyzed for 55 fish from a single population in the Middle Fork Clearwater River drainage (Clear Creek, Table 1). The average number of alleles found for the 11 loci at this location was 6.36 and average observed heterozygosity (*Hz*) across all loci was 0.59. ARLEQUIN's population pairwise comparisons found no significant differences in allelic frequencies between Clear Creek and two other populations: O'hara Creek (Selway drainage, F_{st} = 0.009, p = 0.012) and Sheep Creek (Salmon River drainage, F_{st} = 0.015, p = 0.011).

Garza's *M* value for this sample location was 0.668 indicating a possible recent reduction in population size. Estimated effective population size (*Ne*) for Clear Creek was 2909 based on SMM. Based on genetic distance data represented in the consensus NJ tree, Clear Creek weakly clustered (11% bootstraps) with Red River (SF Clearwater River drainage), Dworshak Hatchery, and Collins Creek (NF Clearwater River drainage).

North Fork Clearwater River Drainage

Allelic diversity was analyzed for 50 fish from Collins Creek in the NF Clearwater River drainage (map location 21, Figure 1). Collins Creek was a formerly anadromous population that is currently blocked from anadromy by the Dworshak Dam. The average number of alleles was 6.45 and observed heterozygosity across all loci was Hz = 0.61. ARLEQUIN's population pairwise comparisons found significant differences in allelic frequencies between Collins Creek and all other populations in this study. Population pairwise F_{st} values for Collins Creek ranged from F_{st} = 0.012 (O'Hara Creek, Selway River drainage) to F_{st} = 0.156 (Pahsimeroi River, Salmon River drainage). Pairwise F_{st} was low (0.015), but significantly different ($p < 0.000$) in comparisons between Collins Creek and the Dworshak Hatchery. Collins Creek and the Dworshak Hatchery shared similar allelic profiles across all loci evaluated in this study. The final consensus NJ tree grouped Collins Creek and the Dworshak Hatchery with 80% bootstrap support validating this branching pattern. Garza's *M* value for Collins Creek was 0.712 indicating no recent reduction in population size, and the estimated effective population size (*Ne*) was 2733 based on SMM.

South Fork Clearwater River Drainage

We visualized the allelic diversity in 151 fish sampled from three populations within the SF Clearwater River drainage. The average number of alleles per locus was 7.12 and average observed heterozygosity across all populations and loci was Hz = 0.60. ARLEQUIN's population pairwise comparisons found significant differences in allelic frequencies among all SF Clearwater River drainage *O. mykiss* populations. John's Creek was the only population in the SF Clearwater drainage with non-significant out-of-drainage pairwise values (Chamberlain Creek in the Salmon River F_{st} = 0.011, p = 0.007 and O'hara Creek, Selway River F_{st} = 0.005, p = 0.053). SF Clearwater River drainage M = 0.816. Ten Mile Creek was the only population in this drainage with an indicated recent population decline, M = 0.634. Effective population size (*Ne*) for the drainage based on the SMM ranged from *Ne* = 3101 (Ten Mile Creek) to *Ne* = 3752 (Red River). South Fork (SF) Clearwater AMOVA analysis partitioned 3.48% of the variation among populations and 96.52% within populations. NJ analysis placed Ten Mile Creek and the East Fork (EF) Salmon River "B-run" hatchery on the same branch, but this relationship was not highly supported (44% bootstraps).

Salmon River Drainage

Six hundred ninety *O. mykiss* representing 14 populations from the Salmon River were analyzed. The average number of alleles per locus found throughout the Salmon drainage was 7.58. Salmon drainage average observed heterozygosity across all populations and loci was Hz = 0.64. Fifty-six percent (70 out of 126) of all insignificant pairwise comparisons reported in this study involved Salmon drainage populations. The majority (49 out of 70) of the Salmon River non-significant comparisons involved three populations: Chamberlain Creek, Horse Creek and Owl Creek. AMOVA distribution of allelic variation assigned 3.45% of the genetic variation among populations and 96.55% within populations in this drainage. Three populations were predicted to have undergone recent reductions in population size based on *M* (Horse Creek, *M* = 0.665; Valley Creek, *M* = 0.678; WF Yankee Creek, *M* = 0.660). Salmon River drainage average effective population size (*Ne*) based on SMM was *Ne* = 5018. The highest *Ne* was estimated for the Basin Creek population under SMM (*Ne* = 6141). Lemhi River, Pahsimeroi River and Basin Creek were significantly different in all pairwise comparisons. A strong association between Lemhi and Pahsimeroi rivers is depicted in the unrooted NJ consensus tree with 97% bootstrap support. Allele profiles and pairwise F_{st} comparisons separate the Lemhi and Pahsimeroi rivers from all other populations evaluated in this study. Three loci contributed significantly to this association. Both Lemhi and Pahsimeroi *O. mykiss* populations carried lower frequencies of allele 121 in *Oneμ10* than any other sample population (51% and 29%, respectively); this allele occurs at an average frequency of over 91% in all other Snake River basin populations. *Oneμ8* carried an allele (158) at 48% (Lemhi) and 46% (Pahsimeroi); this allele was significantly lower in all other populations (< 29%). Allele 157 at *Oneμ14* occurred at 26% and 34% in Lemhi and Pahsimeroi rivers respectively; this allele was relatively rare (< 10%) in all other Snake River *O. mykiss* populations.

Mitochondrial DNA (mtDNA) sequence analyses of Lemhi and Pahsimeroi *O. mykiss* populations did not reveal unique mtDNA haplotypes for these populations (Table 10). Lemhi and Pahsimeroi river fish did carry two previously reported mtDNA haplotypes, MYS3 and MYS10 (see Nielsen et al. 1994a), that were not found in Snake River hatchery fish sequenced in Brown et al. (2004). Four Lemhi River fish carried haplotype MYS24 that has only been reported in the Oxbow Hatchery stock. Haplotype MYS28 was found in the Pahsimeroi Hatchery (Brown et al. 2004). MYS1, MYS9 and MYS28 were the most common haplotypes represented in 60%, 19% and 8% of individuals, respectively.

Middle Fork Salmon River Drainage

Genetic analysis of the MF Salmon River drainage included nine populations totaling 446 samples. The average number of alleles across all loci for the MF Salmon drainage was 6.02 and the average observed heterozygosity across all populations and loci was *Hz* = 0.58. Recent reductions in population size were predicted for all populations in the MF Salmon drainage based on Garza and Williamson's *M*. Sulphur Creek recorded the highest value for *M* (0.644) and Pistol Creek had the highest estimate for *Ne* (3284) in this drainage. Average *Ne* across all populations based on SMM was *Ne* = 2862 and drainage *M* = 0.737. Rapid River was the only population in this drainage to differ significantly from all other populations in this study based on *Fst* pairwise comparisons. Excluding Rapid River and Bear Valley Creek, all MF Salmon populations were insignificantly different from Pistol Creek (Appendix I). Bear Valley Creek shared allelic similarity with Sulphur Creek within the MF Salmon drainage (F_{st} = 0.006, p = 0.030). Camas Creek was undifferentiated from Chamberlain Creek in the Salmon drainage (F_{st} = 0.004, p = 0.114). AMOVA analysis distributed allelic variation as 2.12% among populations and 97.88% within populations in this drainage. NJ analysis separated MF Salmon River drainage *O. mykiss* populations from all other populations in this study with 92% bootstrap support. Substantial sub-structuring was apparent within this drainage based on NJ and bootstrap analyses.

South Fork Salmon River Drainage

Allelic diversity was analyzed for 368 *O. mykiss* sampled from seven locations in the SF Salmon River drainage. The average number of alleles across all loci for this drainage was 6.66 and average observed heterozygosity across all populations and loci was *Hz* = 0.58. All SF Salmon River populations were estimated to have undergone recent declines in population size based on Garza and Williamson's *M*. The range of estimated effective population sizes based on SMM was *Ne* = 2473 (Lick Creek upper) to 3819 (Johnson Creek). AMOVA analysis distributed 2.56% of the allelic variation among populations and 97.44% within populations. Two pairwise comparisons between SF Salmon drainage populations were not significant: (1) Poverty Flat area - Lick Creek (lower) F_{st} = 0.009, p = 0.010; (2) Stolle Meadow - EF SF Salmon River F_{st} = 0.009, p = 0.014. The Poverty Flat and Johnson Creek populations were not significantly different compared to Chamberlain Creek (Salmon River drainage; Appendix I), and Johnson Creek was not significantly different from Sheep Creek (Salmon River drainage). All SF Salmon drainage populations grouped together in the unrooted NJ tree, but low bootstrap values support within drainage branching patterns (range 23% - 45%).

One location in the SF Salmon drainage provided *O. mykiss* samples found upstream and downstream of a barrier: Lick Creek (lower) and Lick Creek (upstream of barrier). Pairwise F_{st} comparison of allelic frequencies showed significant genetic differences between these two sample locations. Lick Creek (lower) had the highest *M* value (0.68) in the SF Salmon drainage, and *Ne* for this population was estimated to be 3397 based on SMM. Lick Creek (upstream of barrier) fell below the threshold *M* value (*M* =0.672) and carried the lowest estimated effective population size in this drainage (*Ne* = 2473).

Little Salmon River Drainage

Genetic analyses of five populations in the Little Salmon drainage included 246 samples. The average number of alleles across 11 loci for the Little Salmon River drainage was 7.91. Samples collected from Hazard Creek recorded the highest average number of alleles per locus (9.36) found in this study. Average observed heterozygosity across all populations and loci for this drainage was *Hz* = 0.63. Little Salmon (upstream of falls) and Rapid River were the only populations predicted to have undergone a recent reduction in population size in this drainage (*M* = 0.640 and 0.658, respectively). Average effective population size estimated for Little Salmon drainage populations ranged from 3833 (Rapid River) to 4810 (Hazard Creek). Drainage AMOVA analysis placed 2.35% of the allelic variation among populations and 97.65% within populations in this drainage.

Two populations sampled from adjacent tributaries in the headwaters of the Little Salmon River, Hazard and Boulder creeks, were found to contain allelic frequencies similar to four populations in tributaries of the mainstem Salmon River upstream of the confluence with the Little Salmon River (Sheep, Bargamin, Horse and Owl creeks; Appendix I). Boulder Creek and Rapid River were the only Little Salmon drainage populations grouped together in the consensus NJ tree, however bootstrap support was low (26%).

Two populations in the Little Salmon drainage were comprised of samples taken upstream and downstream of a barrier: Little Salmon (Pinehurst area) and Little Salmon (upstream of falls). Garza and Williamson's *M* for Little Salmon (Pinehurst area) was *M* = 0.791, and *Ne* = 4774. Little Salmon (upstream of falls) estimated effective population size was *Ne* = 4236 (SMM), *M* = 0.64.

Lochsa River Drainage

Fourteen populations (715 fish) from the Lochsa River drainage were evaluated for allelic diversity at 11 microsatellite loci. The average number of alleles per locus was 6.17, and average observed heterozygosity (*Hz*) across all populations and loci for Lochsa River *O.*

mykiss was *Hz* = 0.58. ARLEQUIN's within drainage population pairwise comparisons found no significant differences in allelic frequencies between Brushy Fork and Lake creeks. Effective population size (*Ne*) for drainage populations ranged from *Ne* = 2322 (Brushy Fork Creek) to *Ne* = 3374 (Fish Creek - summer). AMOVA allocated 1.66% of the allelic variation among populations and 98.34% within populations. Lochsa River drainage populations formed a cohesive grouping in the NJ tree with the exclusion of Deadman Creek.

Two populations in the Lochsa drainage warranted investigation of genetic differences associated with migration timing for populations within the same creek: Fish Creek (summer) and Fish Creek (fall migrants). Allele frequency data indicated no significant differentiation between fall and summer migrants (F_{st} = 0.001, p = 0.325). Garza and Williamson's *M* for Fish Creek (summer) 0.713, whereas, Fish Creek (fall migrants) may have experienced a recent population reduction (*M* = 0.669). Effective population sizes for Fish Creek (summer) and Fish Creek (fall migrants) were *Ne* = 3374 and Ne = 2815, respectively. Hardy-Weinberg equilibrium expectations for Fish Creek (fall migrants) indicated that all loci were within HWE, while Fish Creek (summer) was out of HWE at four loci (Table 4).

Payette River Drainage

We analyzed microsatellite allelic variation found in 53 *O. mykiss* from one sample location in the Payette River drainage, Middle Fork Payette River (map location 77, Figure 1). This population previously had access to the ocean, but is currently blocked by the Hells Canyon Dam complex. The average number of alleles across all loci was 6.64 and average observed heterozygosity across all loci was *Hz* = 0.58. Estimated effective population size for MF Payette River was *Ne* = 3112 based on the SMM and *M* = 0.679. MF Payette differed in allelic frequency from all other study populations based on F_{st} pairwise comparisons. The greatest allelic differentiation based on significant F_{st} pairwise comparisons with MF Payette River occurred between Pahsimeroi River (Salmon drainage, F_{st} = 0.147), Lick Creek (upstream of barrier, SF Salmon drainage, F_{st} = 0.114) and Brushy Fork Creek (Lochsa drainage, F_{st} = 0.11).

Selway River Drainage

We evaluated allelic diversity at 11 microsatellite loci for 448 *O. mykiss* sampled from nine populations in the Selway River drainage. The average number of alleles per locus found throughout the drainage was 6.43. Average observed heterozygosity for Selway River drainage *O. mykiss* populations across all loci was *Hz* = 0.6. Within-drainage pairwise comparisons showed that Bear Creek was not significantly different in allelic frequency from three streams (East Fork Moose, Gedney, and Three Links creeks). Pairwise comparisons also indicated that allele frequencies within Gedney Creek were not significantly different from East Fork Moose and Three Links creeks. All populations in this drainage were predicted to have undergone a recent population decline, except Gedney and O'Hara creeks (*M* = 0.691 and 0.690, respectively). Estimated effective population size (*Ne*) for the Selway River based on the SMM ranged from *Ne* = 2652 (Mink Creek) to *Ne* = 3603 (O'Hara Creek). AMOVA analysis of the allelic variation placed 2.33% of the variation among populations and 97.67% within populations in this drainage. Selway drainage populations formed a contiguous group in the NJ tree with weak bootstrap support (22%).

Snake River Drainage

We visualized allelic diversity at 11 microsatellite loci for 152 *O. mykiss* sampled from three populations within the Snake River drainage. The average number of alleles per locus was 7.33 and the average observed heterozygosity (*Hz*) across all populations and loci was 0.63. ARLEQUIN's within drainage population pairwise comparisons found no significant differences in allelic frequencies for Granite and Sheep creeks (F_{st} = 0.007, p = 0.026). All Snake River drainage populations (Granite, Sheep and Captain John creeks) shared allelic similarity with Horse Creek (Salmon River drainage) and Pahsimeroi Hatchery. Sheep Creek (Snake River) was not significantly different from six other Salmon River populations (Chamberlain, Hazard, Owl, Sheep, Slate and Valley creeks), one Little Salmon River population (Boulder Creek), and two other hatchery stocks (Oxbow and Sawtooth). No population sampled in the Snake River drainage fell below the threshold predicted for recent population declines based on *M*. Estimated effective population size (*Ne*) within this drainage ranged from *Ne* = 4546 (Captain John Creek) to *Ne* = 5098 (Granite Creek). AMOVA results for the Snake River drainage partitioned 0.96% of the variance among populations and 99.04% within populations.

Weiser River Drainage

The allelic variation of 51 *O. mykiss* from Little Weiser River was analyzed using 11 microsatellite loci. Little Weiser River was the only population sampled from the Weiser River drainage and represents one of four formerly anadromous steelhead populations evaluated in this study (map location 79, Figure 1). The average number of alleles across all loci for Little Weiser River was 7.27, and the average observed heterozygosity for all loci was *Hz* = 0.66. A recent reduction in population size was not detected for Little Weiser River (*M* = 0.693) and estimated effective population size based on the SMM was *Ne* = 4392. All F_{st} pairwise comparisons involving Little Weiser River were significantly different. Largest pairwise F_{st} values for Little Weiser resulted from the comparison with Pahsimeroi (F_{st} = 0.133).

Genetic Structure in Hatchery Populations

Eleven microsatellite loci were analyzed to assess the genetic structure of five *O. mykiss* hatchery populations from the Snake River basin. The average number of alleles across all loci for all hatchery populations combined was 7.04. Average observed heterozygosity for all hatcheries across all loci was *Hz* = 0.63. AMOVA distribution of allelic variation partitioned 3.54% among hatcheries and 96.46% within hatcheries. AMOVA analysis of Oxbow, Pahsimeroi and Sawtooth hatcheries attributed 0.05% of the molecular variance among hatcheries. Hatchery populations were not predicted to have undergone recent declines in population size based on *M*, excluding EF Salmon B-run Hatchery. Average effective population size based on the SMM for all hatchery populations was *Ne* = 4347. No significant differences in allelic structure were discovered between Oxbow, Sawtooth, and Pahsimeroi hatcheries based on *Fst* pairwise comparisons. Oxbow, Sawtooth and Pahsimeroi hatcheries shared similar allelic frequencies with four populations in the Salmon drainage (Horse, Morgan, Owl and Valley creeks) and one in the Snake drainage (Sheep Creek) based on pairwise F_{st} values.

Dworshak Hatchery

The Dworshak Hatchery (N = 52) had the lowest estimated *Ne* based on SMM (2790) of all hatchery populations despite a relatively high *M* value (0.705) and an average annual production of over 1.9 – 2.4 million smolts (Fish Passage Center 2004). Average observed heterozygosity across all loci was 0.6 and average number of alleles per locus was 6.6. This hatchery population was significantly different from all populations in this study based on F_{st} pairwise comparisons. However, NJ analysis depicted a close relationship between Dworshak Hatchery and Collins Creek in the NF Clearwater drainage (80% bootstrap value).

East Fork Salmon B-run Hatchery

The EF Salmon B-run Hatchery was the only hatchery population to fall below the *M* threshold (*M* = 0.632; N = 55). Average observed heterozygosity across all loci was 0.58 and average number of alleles per locus was 6. Six of the eleven loci were out of HWE for this population. The EF Salmon B-run Hatchery was significantly different in F_{st} pairwise comparisons from all other populations in this study. The consensus NJ tree weakly grouped EF Salmon B-run Hatchery with Ten Mile Creek (44% bootstrap support). Estimated effective population size for the EF B-Run hatchery stock was Ne = 3048.

Pahsimeroi Hatchery

Pahsimeroi Hatchery (N = 53) had the highest estimates of *Ne* (5518) and *M* (0.718) relative to other hatcheries. Average observed heterozygosity across all loci was 0.65 and average number of alleles per locus was 7.7. Ten *O. mykiss* populations were not significantly different from Pahsimeroi Hatchery in pairwise F_{st} comparisons. Pahsimeroi Hatchery shared similar allelic frequencies with Captain John and Granite creeks on the Snake River, Warm Springs, and Chamberlain creeks (Salmon River) and Hazard Creek on the Little Salmon River. Pahsimeroi and Sawtooth hatcheries were weakly grouped in the NJ tree (32% bootstraps).

Oxbow Hatchery

Average observed heterozygosity across all loci for the Oxbow Hatchery stock (N = 53) was 0.63 and average number of alleles per locus was 7.3. Oxbow Hatchery *M* = 0.703 and estimated effective population size was *Ne* = 4956. Oxbow Hatchery *O. mykiss* shared allelic frequencies with five Salmon River populations (Chamberlain, Horse, Morgan, Owl and Valley creeks) and one Snake River population (Sheep Creek).

Sawtooth Hatchery

Sawtooth Hatchery (N = 56) average observed heterozygosity across all loci was the highest reported for a hatchery stock (*Hz* = 0.67), and average number of alleles per locus was 7.6. A recent reduction in population size was not detected for this hatchery (*M* = 0.684) and estimated effective population size based on the SMM was *Ne* = 5425. Sawtooth Hatchery *O. mykiss* shared allelic frequencies with four Salmon River populations (Horse, Morgan, Owl and Valley creeks) and one Snake River population (Sheep Creek).

Evidence of Interspecific Genotypes

A total of 74 fish samples collected from 28 populations were found to contain alleles outside the expected range for *O. mykiss* (Table 11). Interspecific genotypes (*O. mykiss* X *O. clarkii*) were recovered from all 10 anadromous river drainages evaluated in this study. A high proportion of interspecific genotypes (81%) found in this study occurred in four drainages (SF Clearwater, Lochsa, Salmon and Selway). Six *O. mykiss* populations in the Salmon River drainage were found to contain interspecific fish representing < 6% of each population. A relatively high proportion of fish found to carry interspecific genotypes occurred in John's Creek (N = 10; 20.4%), Sheep Creek in the Salmon River (N = 4;18.2%), Weir Creek (N = 8; 14.5%), and Papoose Creek (N = 4; 9.8%). The occurrence of putative *O. clarkii* alleles at four diagnostic microsatellite loci (*Ogo4, Oneμ8, Oneμ14* and *Ots1*) is reported on a per sample basis in Appendix II.

DISCUSSION

Microsatellite analyses

This study reports genetic population structure found in 79 Snake River *O. mykiss* populations representing the largest genetic study ever completed for Idaho steelhead. Preliminary analyses of Snake River steelhead populations were reported in Nielsen et al. 2003 and 2004. Eleven published microsatellite loci were used to explore allelic structure among and between Snake River samples at multiple spatial scales. Significant genetic variation was found among these 79 *O. mykiss* populations from the Snake River, Idaho. HWE analyses by individual locus demonstrated 70% (*Ots1*) - 98% (*Oneμ11*) of the sample populations fell within HWE. Deviation from HWE at individual loci may have resulted from the wide distribution of alleles found in some of the loci and/or individual sample locations suffering recent population declines, but there was no significant trend in this relationship in our data. The EF Salmon B-run Hatchery stock was out of HWE at six of the 11 loci analyzed. This supports the inference that differential reproductive success by a few individuals from multiple stocks (Dworshak, Sawtooth, Pahsimeroi, and naturally spawning fish) could have contributed differentially to egg production in this hatchery and the Wahlund effect may have added to the lack of HWE in this population. GENEPOP analyses showed that 26 populations fell out of HWE for all 11 loci due to an excess of heterozygotes bringing into question outbreeding or recent admixtures of stocks i.e., multiple hatchery stocks in broodstock development or interbreeding of hatchery and wild stocks. There were no obvious geographic trends in the location of populations falling out of HWE for all loci combined (Table 5). However, the six populations with low sample sizes in this study (N < 40) were in HWE for all loci combined.

Population level statistics varied widely across Idaho's Snake River basin. Jack's Creek (N = 37), a lower Clearwater River population found downstream of the Dworshak Hatchery, carried the highest observed heterozygosity (*Hz* = 0.69), a relatively high estimated effective population size 4,305 (SMM). However, *M* = 0.585 for Jack's Creek suggests a probable recent population decline. Alternatively, the Dworshak Hatchery population developed from fish from the North Fork Clearwater had a relatively low estimated effective population size (*Ne* = 2,790) and *M* = 0.705, suggesting very different allelic factors contributed to the genetic structure in these two populations. Brushy Fork Creek (Lochsa drainage) carried the lowest observed *Hz* (0.55) and fell just below the published threshold for *M* (0.678). Brushy Fork and Bear Valley creeks (MF Salmon), both with N = 55, had the two lowest estimated SMM effective population sizes (*Ne* = 2322 and 2366, respectively).

The Lemhi and Pahsimeroi river populations separated from the rest of the Idaho Snake River collection with a significant bootstrap value (97%) in the NJ analyses. These populations had relatively high estimates of SMM effective population size (*Ne* = 7116 Lemhi River; *Ne* = 5,903 Pahsimeroi River) and high allelic diversity (7.8 and 8.2 alleles per locus, respectively). They also were significantly different in all pairwise comparisons with all other sample locations throughout the study area suggesting unique *O. mykiss* genetic structure. These *O. mykiss* populations are thought to be highly productive and occur within streams with unique biogeomorphology and habitat conditions.

Population Structure Among and Within Drainages

Significant genetic differentiation among 10 anadromous steelhead drainages in the Snake River basin was evident from pairwise F_{st} comparisons. With few exceptions, populations from any given drainage were more similar to each other than to populations from other drainages based on genetic distance data and relationships presented in the NJ tree. Clusters of populations from individual drainages were weakly supported in our NJ analysis (< 50% bootstraps; Figure 2), with the exception of the branch containing MF Salmon populations (92% bootstraps). The sole MF Clearwater population sampled in this study, Clear Creek, clustered with Red River (SF Clearwater River) in NJ analysis. Populations within the Clearwater, Salmon, Little Salmon and Snake River drainages did not form discrete groups in the NJ tree and distinct structure within and among these drainages was less clear in this analysis.

AMOVA analysis of 10 drainages with anadromous steelhead indicated the greatest proportion of genetic molecular variance occurred within populations (94.99%), suggesting that among drainage genetic structure was limited to a small proportion of the overall genetic variance. Pairwise F_{st} comparisons between drainages based on ARLEQUIN analyses were all significant ($p < 0.000$ in all comparisons). These results suggest that fine-scale population structure exists within drainages.

The MF Salmon River was the most genetically distinct drainage in these analyses. MF Salmon separated from all other drainages in the NJ tree with 92% bootstrap support. Drainage Fst pairwise analyses resulted in high levels of allelic differentiation in MF Salmon comparisons: Lochsa (F_{st} = 0.057); Selway (F_{st} = 0.051); SF Clearwater (F_{st} = 0.049); Clearwater (F_{st} = 0.045); and Salmon River (F_{st} = 0.035).

The Selway, Lochsa, MF Salmon, and the SF Salmon rivers are known to be areas producing wild steelhead with little hatchery supplementation (Brannon et al. 2004). High allelic differentiation inferred from F_{st} pairwise comparisons may reflect relic genetic structure found in these drainages. These putatively wild drainages were characterized by lower average observed *Hz* (< 0.60) and lower estimated effective population sizes (*Ne*) relative to the Little Salmon, Salmon, and Snake river drainages. Hatchery supplementations since the 1960's have been extensive in the Little Salmon, Salmon, and Snake river drainages (Busby et al. 1996; Brannon 2004) and may have contributed to inter-drainage differences.

Genetic substructure within the MF Salmon River was apparent in the NJ tree for the branch containing Marsh Creek and Bear Valley Creek (66% bootstraps). A cluster containing three MF Salmon populations, Big Creek (lower), Big Creek (upper) and Pistol Creek, was supported in 57% of the trees leading to our consensus NJ tree. Within this cluster, Big Creek (upper) and Pistol Creek also formed a separate branch with 57% bootstrap support. A high proportion (75%) of all non-significant F_{st} pairwise comparisons found within MF Salmon involved Pistol Creek. Small sample size for Pistol Creek (N = 28) may have contributed to these relationships due to inadequate sampling of total allelic diversity. Bargamin Creek located on the Salmon River was associated with the MF Salmon cluster in the NJ tree (60% bootstrap support). Bargamin Creek contained significantly different allelic structure relative to MF Salmon populations in all pairwise comparisons, but shared allelic frequency distributions of dominant alleles for most loci.

All sample populations collected from the Lochsa River drainage grouped together in the NJ tree with the notable exception of Deadman Creek. All of the Selway River populations group together, excluding O'Hara Creek. Deadman and O'Hara creeks both occur near the confluence of the Lochsa and Selway rivers and their pairwise F_{st} value (0.008, p = 0.01) suggests the likelihood that gene flow between these creeks may contribute to this relationship. The only significant substructure found within the Lochsa River evident in NJ analyses was the branch containing Brushy Fork Creek and Lake Creek (55% bootstrap support). These two populations were also insignificantly different in F_{st} pairwise comparisons (Fst = 0.003, p = 0.097). SF Salmon River populations formed a weakly supported cohesive group in our NJ tree (45% bootstrap support). Within-drainage bootstrap values in the SF Salmon ranged from 23 – 44%.

In the Clearwater River, EF Potlach River and Little Bear Creek grouped together in 50% of all NJ trees. The geographic separation of the EF Potlatch River and Little Bear Creek populations on a northern tributary of the Clearwater River may contribute to their relationship within this drainage. The F_{st} relationships showing genetic frequency associations between Big Canyon Creek and two Salmon River populations (Chamberlain Creek F_{st} = 0.000, p = 0.327; Horse Creek F_{st} = 0.004, p = 0.061) are not intuitive considering a lack of geographic proximity.

Lemhi and Pahsimeroi rivers

The Lemhi and Pahsimeroi River populations were genetically differentiated from all populations analyzed in this report based on allelic pairwise comparisons, including each other. These populations grouped with high bootstrap support in the NJ tree (97%). Unique allele frequencies at three microsatellite loci (*Oneµ8, Oneµ10* and *Oneµ14*) account for the distinction of Lemhi and Pahsimeroi rivers in pairwise comparisons. These *O. mykiss* populations were collected from high mountain valley, spring-fed streams containing highly productive populations. These streams, unlike other systems in the Snake River basin contain a relatively steady flow regime with groundwater-mitigated stream temperatures that are warmer than average in the winter and cooler than average in the summer. These environmental conditions may have led to unique life history structure in these populations where large components of the population remain in fresh water throughout their life, not migrating to the Pacific Ocean.

Phylogenetic lineages for Lemhi or Pahsimeroi rivers were not supported by unique mtDNA haplotypes. Four haplotypes (MYS1, MYS2, MYS9, MYS28) found in these rivers were also found in Dworshak, Oxbow or Pahsimeroi steelhead hatcheries. Two haplotypes (MYS3, MYS10) found in these rivers were not found in hatchery steelhead, but were common in other studies of coastal *O. mykiss* populations (Nielsen et al. 1997b and 1998). MYS3 was the second most common haplotype found in southern coastal *O. mykiss* populations (Nielsen et al. 1997b). MYS10 has been found in many non-anadromous coastal rainbow trout populations, four California rainbow trout hatchery stocks (Nielsen et al. 1997b) and in one anadromous fish from the Santa Ynez River, California. The presence of common mtDNA haplotypes in wild and hatchery stocks supports the fact these hatchery stocks originated from natural Snake and Salmon River *O. mykiss*.

Effects of Barriers

Formerly Anadromous Populations Blocked by Dams

Three formerly anadromous steelhead populations residing above Hells Canyon Dams (Big Smoky Creek, Little Weiser River and MF Payette River) were significantly different from all populations in this study using F_{st} pairwise comparisons. These populations clustered together in the NJ tree with 53% bootstrap support. Genetic inference drawn from these analyses suggested unique genetic population structure found in landlocked samples that may reflect relic genetic structure previously found in the upper Snake River drainage.

Collins Creek (NF Clearwater) *O. mykiss* have been blocked from anadromous contributions since the early 1970's following the construction of the Dworshak Dam. The Dworshak Hatchery broodstock was developed from locally adapted steelhead from the NF Clearwater River. NJ analyses support a genetic relationship between these two populations by grouping them with 80% bootstrap support. In microsatellite allelic pairwise comparisons in this study, Dworshak Hatchery was significantly different from all other populations, including Collins Creek (F_{st} = 0.015, p < 0.000).

Populations Separated by Barriers

Two sample populations from Lick Creek, a tributary of the Secesh River in the SF Salmon River drainage, were separated by a putative barrier. Lick Creek (lower) and Lick Creek (upstream of barrier) were significantly different in pairwise comparisons (F_{st} = 0.051, p < 0.000). Lick Creek (lower) weakly grouped with the EF SF Salmon River and Stolle Meadow populations in the NJ tree (45% bootstraps). This population was not significantly different from the Poverty Flat population (F_{st} = 0.009, p = 0.01). Lick Creek (upstream) was suggested to have undergone a recent reduction in population size (*M* = 0.672). A putative recent decline was less certain for Lick Creek (lower) because *M* = 0.68. So it is difficult to use this metric to consider differences in changes in population size upstream or downstream of this barrier. Observed heterozygosity for Lick Creek (upstream), *Hz* = 0.495, was lower than Lick Creek (lower), *Hz* = 0.578. Lick Creek (upper) also had a lower average number of alleles per locus (6.2) than Lick Creek (lower; 6.8). These measures of allelic diversity suggest a less diverse community above the barrier.

Genetic diversity found in two Little Salmon River populations was examined to assess potential effects of isolation due to a waterfall. Little Salmon (Pinehurst area) and Little Salmon (upstream of falls) had relatively similar estimates of effective population size (*Ne* = 4774 and 4236, respectively). Garza and Williamson's *M* predicted population declines for Little Salmon (upstream, *M* = 0.64), but not for Little Salmon (Pinehurst, *M* = 0.791), suggesting less diverse allelic structure in the upstream area. This conclusion is supported in the average number of alleles per locus (Pinehurst = 8.8; upstream = 6.5). These populations are significantly different from each other in pairwise comparisons (F_{st} = 0.035, p < 0.000), and are significantly different from all other populations evaluated in this study.

Hatchery and Mitigation Efforts

The broodstock of the Dworshak Hatchery was formed from native NF Clearwater steelhead with the goal of sustaining B-run steelhead life history (August to October spawning returns) in the Clearwater River. Steelhead from the Dworshak Hatchery were most divergent from all other inland populations in earlier allozyme analyses (Busby et al. 1996). In our microsatellite analysis, Dworshak Hatchery (N = 52) was significantly different from all other populations using F_{st} pairwise comparisons. No evidence was found for recent population declines in the Dworshak Hatchery stock (*M* = 0.705), however, this stock carried the lowest estimated *Ne* (2790) of all hatchery populations in this study. BOTTLENECK analyses under the IAM model detected heterozygosity excess and a bottleneck condition at this hatchery (p = 0.01).

Dworshak Hatchery's B-run steelhead were expected to cluster with the East Fork Salmon River B-run Hatchery fish, however, this was not the case. Our NJ analyses show close genetic distance associations among Dworshak Hatchery, Collins Creek (putative source stock discussed above), Red River (SF Clearwater), and Clear Creek (MF Clearwater). Both Red River and Clear Creek have documented hatchery supplementation with Dworshak B-run fish (Fish Passage Center 2005).

The East Fork Salmon River B-run Hatchery (EFRB) is a satellite rearing facility for Dworshak Hatchery. One possible explanation for EFRB not clustering with Dworshak Hatchery is that the egg take for the EFRB stock has included (inadvertently or not) adults from Sawtooth and Pahsimeroi hatcheries as well as natural adults. Incorporating different broodstocks may have contributed to the lack of compliance to Hardy-Weinberg equilibrium noted for this hatchery population (6 of 11 loci out of HWE). EFRB is the only hatchery population in this study to have a predicted recent decline in population size (M = 0.632). The EF Salmon B-run Hatchery population grouped weakly with Ten Mile Creek in the NJ tree (44% bootstrap support). Ten Mile Creek is located on the SF Clearwater River, an area known to be stocked with Dworshak B-run fish (Fish Passage Center 2005).

In F_{st} pairwise analyses, fish collected from three hatcheries, Oxbow, Pahsimeroi and Sawtooth, were virtually indistinguishable. AMOVA analysis of Oxbow, Pahsimeroi and Sawtooth hatchery populations allocated only 0.05% of the molecular variation to differences among these hatchery stocks. Close genetic associations among these hatcheries were expected considering the fact that the Pahsimeroi stock was derived primarily from the Oxbow stock, and the Sawtooth Hatchery stock was derived primarily from the Pahsimeroi hatchery stock.

Natural populations found in geographic proximity to all three hatcheries shared allelic frequencies based on F_{st} analyses. Sawtooth hatchery fish were indistinguishable from fish collected in Valley Creek. Morgan Creek was indistinguishable from the Pahsimeroi Hatchery. Sheep Creek found just downstream from the Oxbow Hatchery, was not significantly different from three hatchery stocks (Oxbow, Pahsimeroi and Sawtooth).

Hazard Creek (Little Salmon River) *O. mykiss* were indistinguishable from the geographically distant Pahsimeroi Hatchery (F_{st} = 0.005), but not the other two hatcheries (Sawtooth F_{st} = 0.009, Oxbow F_{st} = 0.011). Hazard Creek is a known steelhead enhancement location using fish from the Pahsimeroi Hatchery (Fish Passage Center 2005). Three populations (Chamberlain, Horse, and Owl creeks) from tributaries on the middle Salmon River, at some distance from Pahsimeroi and Oxbow hatcheries, shared allelic frequencies with these two hatcheries based on F_{st} analyses.

Interspecific Alleles in Populations of Snake River Steelhead

Interspecific spawning is common among salmonids (Baxter et al. 1997; Bernatchez et al. 1995; Hawkins 1997; McGowan and Davison 1992, Rosenfield et al. 2000; Young et al. 2001; Baker and Bentzen 2002). Introduced rainbow trout have been shown to readily hybridize with various native cutthroat trout subspecies (Bartley 1991; Leary et al. 1995). In addition, the occurrence of natural hybridization (interspecific spawning) between individuals from different natural populations has gained greater acceptance as an evolutionary force (Hubbs 1955; Arnold 1997). Natural hybridization has been documented between rainbow and coastal cutthroat trout in Washington state and Alaska (Campton and Utter 1985; Williams 2004; Graziano and Nielsen 2004).

Various microsatellite markers have been used to demonstrate species specific allele ranges to identify individuals of mixed taxonomic ancestry. Wenburg (1998) reported *Ots1* as a useful species designator between rainbow trout and coastal cutthroat trout (*O. clarkii clarkii*) in Washington State. Subsequent hybrid studies utilized this locus to investigate hybridization between rainbow trout and various subspecies of cutthroat trout (Peackock and Kirkoff 2004, Lahontan cutthroat trout in Nevada (*O. clarkii henshawi)*; Williams 2004, coastal cutthroat trout in Alaska). Brown et al. (2004) reported introgression between westslope cutthroat (*O. clarki lewisi*) and steelhead in the Tucannon River, Washington using *Oneμ2* and mtDNA. Williams (2004) used *Oneμ8* and *Ogo4* as part of a diagnostic protocol to identify individuals of mixed taxonomic ancestry (rainbow/coastal cutthroat) in the Copper River, Alaska. Four markers (*Ots1*, *Oneμ8*, *Oneμ14* and *Ogo4*) used in this study had previously demonstrated diagnostic utility (Graziano and Nielsen 2004; Williams 2004).

O. mykiss specific microsatellite allele size ranges for fish from a broad geographic range have been analyzed in our lab. Snake River *O. mykiss* samples in this study contained alleles outside documented *O. mykiss* size ranges at four markers (*Ots1*, *Oneμ8*, *Oneμ14* and *Ogo4*). Novel alleles were found within ranges previously observed in coastal cutthroat trout. Hybridization with one or more cutthroat trout sub-species is therefore suspected. All alleles falling outside of the expected size range for *O. mykiss* were removed from subsequent statistical analyses. Individuals exhibiting putative cutthroat allelic signatures at two or more diagnostic loci were removed from the study database.

Behnke (1992) stated that the distribution of coastal cutthroat trout does not occur far inland. The distribution of coastal cutthroat trout native to tributaries of the Columbia River ends approximately 225 km from the coast in Oregon (Behnke 2002). Behnke also reports that native cutthroat trout in the upper Snake River basin are thought to belong to the Yellowstone subspecies (*O. clarkii bouvieri*), but many of these populations have been replaced by rainbow trout and/or westslope cutthroat trout in the Salmon and Clearwater river systems. All but one sample location containing fish with putative cutthroat alleles were found in the Salmon and Clearwater river systems. The sample from Sheep Creek (Snake River) had one individual fish showing cutthroat introgression. This fish carried cutthroat alleles at three out of the four diagnostic loci.

Our analyses clearly demonstrated allelic sizes for four loci in Snake River fish falling outside of the expected range for *O. mykiss* based on the broad geographic distribution examined in our lab. However, we were only able to test for putative cutthroat introgression based on allelic signatures drawn from coastal cutthroat and cannot distinguish differences among cutthroat subspecies. Further studies of cutthroat intraspecific allelic size distributions at these loci would add rigor to these analyses, but our lab lacked samples to perform these analyses.

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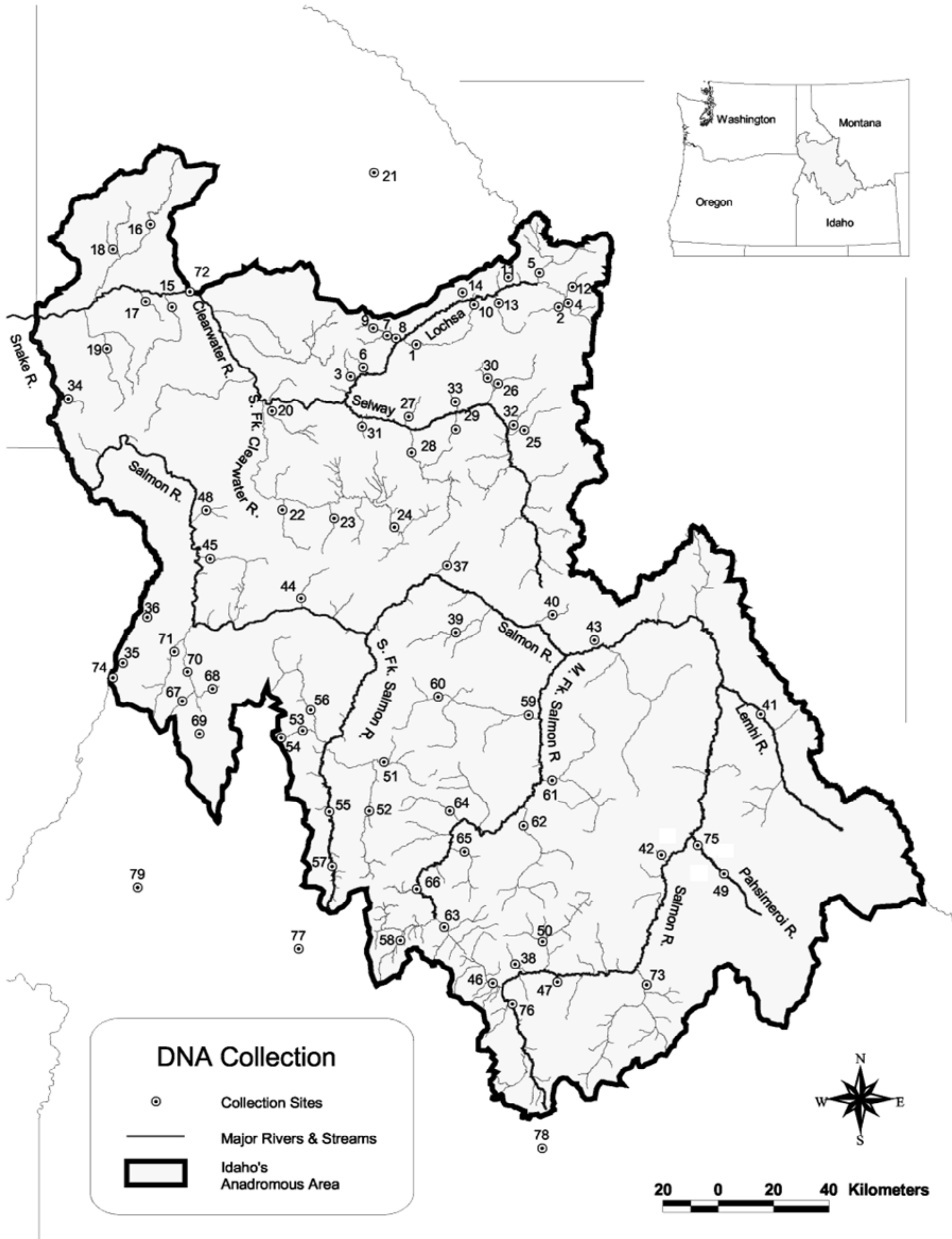

Figure 1. Collection site locations for *O. mykiss* populations sampled in 2000 for Idaho's baseline genetic study. Collection site location numbers are co-listed with their population names in Table 1.

Figure 2. Unrooted consensus Neighbor-Joining radial tree of genetic relationships determined for 79 Idaho *O. mykiss* populations. Bootstrap values (% of 2000 replicate trees) are given for branch points with ≥ 50% bootstrap support. Population codes are listed in Table 1.

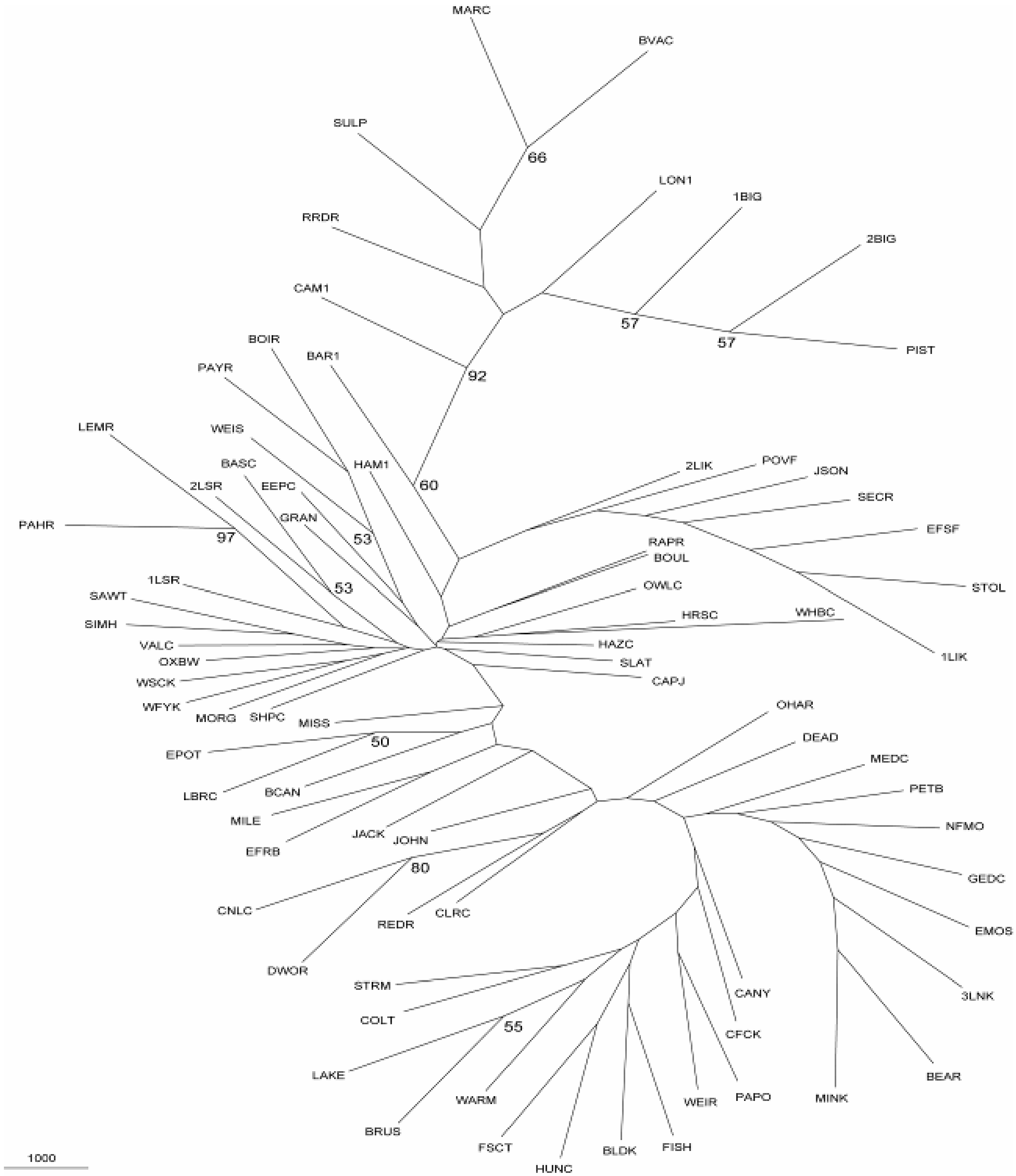

Figure 3. Unrooted consensus Neighbor-Joining cladogram-type tree of genetic relationships determined for 79 Idaho *O. mykiss* populations. Bootstrap values (% of 2000 replicate trees) are given for branch points with ≥ 50% bootstrap support.

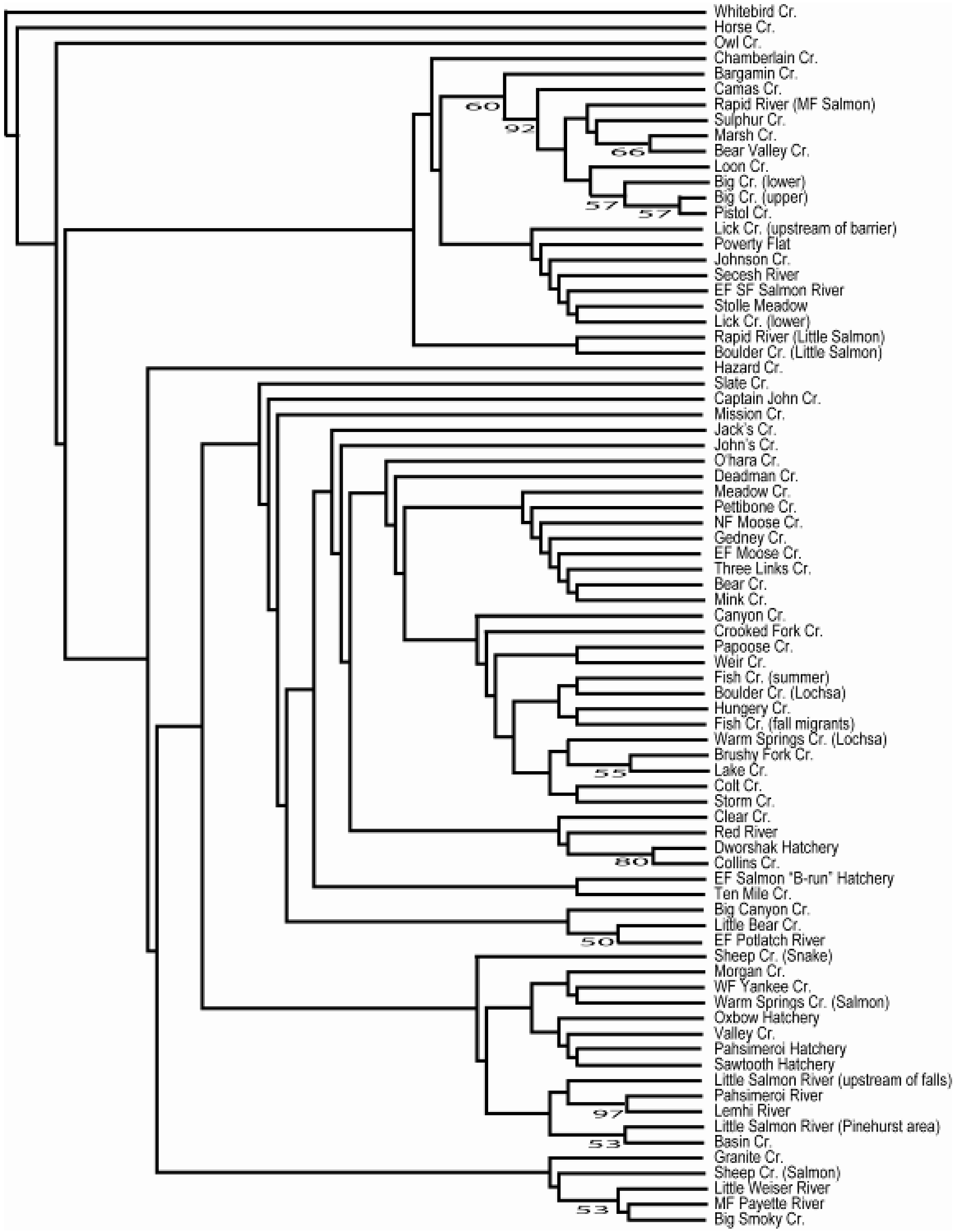

Table 1. Drainage affiliation, population names, number of samples per population (N), population codes, map location (Figure 1), unbiased and observed heterozygosity (*Hz*) estimates for *O. mykiss* populations in this study.

Drainage	Population	N	Population Code	Map Location	Unbiased *Hz* *	Observed *Hz*
Boise	Big Smoky Creek	37	BOIR	78	0.6295	0.6277
Clearwater	Big Canyon Creek	60	BCAN	15	0.6599	0.6773
	EF Potlatch River	51	EPOT	16	0.6407	0.6645
	Jack's Creek	37	JACK	17	0.6570	0.6888
	Little Bear Creek	55	LBRC	18	0.6517	0.6619
	Mission Creek	49	MISS	19	0.6317	0.6218
Little Salmon	Boulder Creek	51	BOUL	67	0.6511	0.6059
	Hazard Creek	51	HAZC	68	0.6715	0.6630
	Little Salmon (upstream of falls)	42	1LSR	69	0.6538	0.6377
	Little Salmon (Pinehurst area)	51	2LSR	70	0.6705	0.6285
	Rapid River	51	RAPR	71	0.6363	0.6260
Lochsa	Boulder Creek	21	BLDK	1	0.6049	0.6387
	Brushy Fork Creek	55	BRUS	2	0.5492	0.5457
	Canyon Creek	53	CANY	3	0.5941	0.5879
	Colt Creek	54	COLT	4	0.5862	0.5541
	Crooked Fork Creek	56	CFCK	5	0.5718	0.5764
	Deadman Creek	56	DEAD	6	0.5964	0.5783
	Fish Creek (summer collection)	56	FISH	7	0.6144	0.5940
	Fish Creek (fall migrants)	56	FSCT	8	0.5834	0.5646
	Hungery Creek	55	HUNC	9	0.5897	0.5575
	Lake Creek	56	LAKE	10	0.5707	0.5924
	Papoose Creek	41	PAPO	11	0.5664	0.5481
	Storm Creek	54	STRM	12	0.5685	0.5981
	Warm Springs Creek	52	WARM	13	0.5900	0.6067
	Weir Creek	49	WEIR	14	0.6077	0.6342
MF Clearwater	Clear Creek	55	CLRC	20	0.5893	0.5931
MF Salmon	Bear Valley Creek	55	BVAC	58	0.5525	0.5524
	Big Creek (lower)	49	1BIG	59	0.6082	0.5983
	Big Creek (upper)	46	2BIG	60	0.5638	0.5529
	Camas Creek	50	CAM1	61	0.6076	0.5691
	Loon Creek	54	LON1	62	0.5617	0.5595
	Marsh Creek	59	MARC	63	0.5836	0.5881
	Pistol Creek	28	PIST	64	0.6159	0.6064
	Rapid River	52	RRDR	65	0.5971	0.5787
	Sulphur Creek	53	SULP	66	0.5838	0.5835
NF Clearwater	Collins Creek	50	CNLC	21	0.5789	0.6106
Payette	MF Payette River	53	PAYR	77	0.6012	0.5785
Salmon	Bargamin Creek	50	BAR1	37	0.6518	0.6353
	Basin Creek	53	BASC	38	0.7061	0.6632
	Chamberlain Creek	46	HAM1	39	0.6441	0.6148

(Table 1 continued)

Drainage	Population	N	Population Code	Map Location	Unbiased *Hz* *	Observed *Hz*
Salmon	Horse Creek	58	HRSC	40	0.6748	0.6166
	Lemhi River	49	LEMR	41	0.7274	0.6682
	Morgan Creek	48	MORG	42	0.6881	0.6602
	Owl Creek	58	OWLC	43	0.6758	0.6309
	Pahsimeroi River	49	PAHR	49	0.7019	0.6689
	Sheep Creek	19	EEPC	44	0.5961	0.6288
	Slate Creek	55	SLAT	45	0.6616	0.6116
	Valley Creek	49	VALC	46	0.6957	0.6566
	Warm Springs Creek	45	WSCK	47	0.6892	0.6559
	Whitebird Creek	56	WHBC	48	0.6527	0.6485
	WF Yankee Creek	55	WFYK	50	0.6753	0.6563
Selway	Bear Creek	41	BEAR	25	0.6034	0.6137
	EF Moose Creek	54	EMOS	26	0.6211	0.6263
	Gedney Creek	56	GEDC	27	0.6063	0.6025
	Meadow Creek	50	MEDC	28	0.6103	0.5983
	Mink Creek	52	MINK	29	0.5733	0.5746
	NF Moose Creek	52	NFMO	30	0.6085	0.5828
	O'hara Creek	51	OHAR	31	0.6258	0.6040
	Pettibone Creek	39	PETB	32	0.5963	0.5928
	Three Links Creek	54	3LNK	33	0.5987	0.5987
SF Clearwater	John's Creek	45	JOHN	22	0.6040	0.5665
	Red River	57	REDR	24	0.6323	0.6237
	Ten Mile Creek	49	MILE	23	0.6014	0.6168
SF Salmon	EF SF Salmon River	52	EFSF	51	0.6273	0.6146
	Johnson Creek	56	JSON	52	0.6350	0.6379
	Lick Creek (lower)	52	1LIK	53	0.6162	0.5779
	Lick Creek (upstream of barrier)	50	2LIK	54	0.5613	0.4950
	Poverty Flat Area	55	POVF	55	0.6142	0.6038
	Secesh River	56	SECR	56	0.6285	0.5559
	Stolle Meadow	47	STOL	57	0.6138	0.5759
Snake	Captain John Creek	55	CAPJ	34	0.6628	0.6725
	Granite Creek	49	GRAN	35	0.6806	0.6771
	Sheep Creek	47	SHPC	36	0.6803	0.6162
Weiser	Little Weiser River	51	WEIS	79	0.6577	0.6571
Hatchery	Dworshak Hatchery	52	DWOR	72	0.5823	0.6006
	EF Salmon "B-run" Hatchery	55	EFRB	73	0.5974	0.5783
	Oxbow Hatchery	53	OXBW	74	0.6758	0.6295
	Pahsimeroi Hatchery	53	SIMH	75	0.6916	0.6535
	Sawtooth Hatchery	56	SAWT	76	0.6886	0.6733
	Total =	3982		Average =	0.6244	0.6112

* Based on Nei's unbiased gene diversity (1987)

Table 2. Multiplex systems used to amplify microsatellite loci for population structure analysis of Snake River basin *O. mykiss*. "Loci 700" and "Loci 800" represent different channels on the LI-COR platform used to visualize alleles.

Multiplex	Anneal Temp (ºC)/ # of cycles	30 minute extension	Loci 700	Loci 800
A	52/40	NO	*Omy325*	*Oneμ14*
			Ots1	*Ots4*
B	52/40	YES	*Omy77*	*Ogo1a*
			Oneμ8	*Ogo4*
				Ots3
C	52/40	YES	*Omy207*	*Omy27*
			Oneμ10	*Oneμ11*

Table 3. Number of alleles, allelic size range and average heterozygosity (*Hz*) for microsatellite loci used in this study. Average *Hz* is the observed heterozygosity per locus averaged across all 79 Idaho populations. Percent (%) relative score indicates the contribution of a single locus in correctly assigning an individual to its population based on the allele frequency differential method of WHICHLOCI (Banks and Eichert 2000).

Locus	Source	Number of alleles	Allelic size range (bp)	Average *Hz*	% Relative score
Omy325	O'Connell et al. 1997	33	87-153	0.878	16.27
Oneμ8	Scribner et al. 1996	20	144-188	0.837	15.27
Ots1	Banks et al. 1999	27	157-247	0.803	12.78
Ogo4	Olsen et al. 1998	12	118-142	0.788	10.98
Ots3	Banks et al. 1999	9	77-93	0.639	8.67
Oneμ14	Scribner et al. 1996	11	143-163	0.521	8.21
Ots4	Banks et al. 1999	9	108-130	0.683	8.06
Ogo1a	Olsen et al. 1998	10	124-168	0.580	6.02
Omy27	Heath et al. 2001	11	99-117	0.520	5.41
Oneμ11	Scribner et al. 1996	4	143-149	0.436	4.30
Oneμ10	Scribner et al. 1996	10	113-131	0.182	4.02

Table 4. Hardy-Weinberg equilibrium (HWE) results for 11 loci showing populations within HWE "-" and out of HWE "+" based on exact tests performed by GENEPOP. "N/A" indicates tests for HWE were not done because the population was monomorphic at this locus.

							Loci					
Population	N	*Ogo1a*	*Ogo4*	*Omy27*	*Omy325*	*Oneμ8*	*Oneμ10*	*Oneμ11*	*Oneμ14*	*Ots1*	*Ots3*	*Ots4*
Big Smoky Creek	37	-	-	-	-	-	-	-	-	-	-	-
Big Canyon Creek	60	-	-	-	-	-	-	-	-	-	-	-
EF Potlach River	51	-	-	-	-	-	-	-	-	-	-	-
Jack's Creek	37	-	-	-	+	+	-	-	-	+	-	-
Little Bear Creek	55	-	-	-	+	+	-	-	+	+	+	-
Mission Creek	49	-	-	-	-	-	-	-	-	-	+	-
Boulder Creek (Little Salmon)	51	-	-	-	-	+	-	-	-	-	-	-
Hazard Creek	51	-	-	-	-	-	-	-	-	+	+	-
Little Salmon (upstream of falls)	42	-	-	-	-	-	-	-	+	-	-	-
Little Salmon (Pinehurst area)	51	-	-	-	-	-	-	-	+	-	-	-
Rapid River (Little Salmon)	51	-	-	-	-	-	-	-	-	-	+	-
Boulder Creek (Lochsa)	21	-	-	-	-	+	-	-	-	-	-	-
Brushy Fork Creek	55	-	-	-	-	-	+	-	-	-	-	-
Canyon Creek	53	-	-	-	-	-	-	-	+	-	-	-
Colt Creek	54	-	+	-	+	-	-	-	-	-	-	-
Crooked Fork Creek	56	-	-	-	-	-	N/A	-	-	-	-	-
Deadman Creek	56	-	-	-	-	-	-	-	-	-	-	-
Fish Creek (fall migrants)	56	-	-	-	-	-	-	-	-	-	-	-
Fish Creek (summer)	56	-	-	+	-	+	+	-	+	-	-	-
Hungery Creek	55	-	-	+	-	-	-	-	-	+	-	-
Lake Creek	56	-	-	-	-	-	-	-	-	-	+	+
Papoose Creek	41	-	-	+	+	+	-	-	-	-	-	-
Storm Creek	54	-	-	+	-	-	-	-	-	-	-	-
Warm Springs Creek (Lochsa)	52	+	-	-	-	-	-	-	+	-	-	-
Weir Creek	49	-	-	-	-	-	-	-	-	-	-	-
Clear Creek	55	-	-	-	-	-	-	-	-	-	-	-
Bear Valley Creek	55	-	-	-	-	-	+	-	-	-	-	-
Big Creek (lower)	49	-	-	-	-	-	-	-	-	+	+	-
Big Creek (upper)	46	-	-	-	+	+	N/A	-	-	-	-	-
Camas Creek	50	-	-	-	-	-	+	-	-	-	-	-
Loon Creek	54	-	-	-	-	+	-	-	-	+	-	-
Marsh Creek	59	-	-	-	-	+	-	-	-	-	-	-
Pistol Creek	28	-	-	-	-	-	-	-	-	+	-	-
Rapid River (MF Salmon)	52	-	-	-	-	-	-	-	-	-	-	+
Sulphur Creek	53	-	-	+	-	-	-	-	-	-	-	+
Collins Creek	50	+	-	+	-	-	-	-	-	-	-	-
MF Payette River	53	-	-	-	-	-	-	-	-	-	-	-
Bargamin Creek	50	-	-	-	-	-	-	-	-	+	+	-
Basin Creek	53	-	-	+	-	-	+	-	+	+	-	-

(Table 4 continued)

Chamberlain Creek	46	+	-	-	-	-	-	-	-	+	-	-
Horse Creek	58	-	-	-	-	-	+	-	-	+	-	-
Lemhi River	49	-	-	-	+	-	-	-	+	+	-	+
Morgan Creek	48	-	-	-	-	-	-	-	-	-	-	-
Owl Creek	58	+	-	-	-	-	-	-	-	+	-	-
Pahsimeroi River	49	-	-	-	-	-	-	-	+	-	-	-
Sheep Creek (Salmon)	19	-	-	-	-	+	-	-	-	-	-	-
Slate Creek	55	-	-	-	-	-	-	-	-	-	+	-
Valley Creek	49	-	-	-	-	-	-	-	-	-	-	-
Warm Springs Creek (Salmon)	45	-	-	-	-	-	-	-	+	+	+	-
Whitebird Creek	56	-	-	-	+	-	-	-	-	-	+	-
WF Yankee Creek	55	-	-	-	+	-	-	-	-	-	-	-
Bear Creek	41	-	+	+	+	-	+	-	+	-	-	-
EF Moose Creek	54	-	-	-	-	-	-	-	-	-	-	-
Gedney Creek	56	-	-	-	-	-	-	-	+	-	-	-
Meadow Creek	50	-	-	-	-	-	-	-	-	-	-	-
Mink Creek	52	+	-	-	+	-	-	-	+	+	-	-
NF Moose Creek	52	-	-	+	+	-	-	-	-	-	-	-
O'hara Creek	51	-	+	-	-	-	-	-	-	-	-	-
Pettibone Creek	39	-	-	-	+	-	-	-	-	-	-	-
Three Links Creek	54	+	-	+	-	-	-	-	-	-	-	+
John's Creek	45	+	-	-	-	-	+	-	-	-	-	-
Red River	57	-	-	+	-	+	-	-	+	-	-	-
Ten Mile Creek	49	-	-	-	-	+	-	-	-	+	-	-
EF SF Salmon River	52	-	+	-	-	-	-	-	-	-	-	-
Johnson Creek	56	-	-	-	-	-	-	-	+	-	+	-
Lick Creek (lower)	52	-	-	-	-	+	N/A	-	-	-	-	-
Lick Creek (upstream of barrier)	50	-	+	-	-	-	-	-	-	+	-	-
Poverty Flat area	55	-	+	-	-	-	-	-	+	+	-	-
Secesh River	56	-	+	-	-	-	+	+	-	+	-	-
Stolle Meadow	47	-	-	-	+	-	N/A	-	+	+	-	-
Captain John Creek	55	-	-	-	+	+	-	+	-	+	-	+
Granite Creek	49	-	-	-	-	-	-	-	-	-	-	-
Sheep Creek (Snake)	47	-	-	+	+	-	-	-	-	+	-	-
Little Weiser River	51	-	-	-	-	-	-	-	-	-	-	-
Dworshak Hatchery	52	-	-	-	-	-	-	-	+	-	-	-
EF Salmon "B-run" Hatchery	55	-	+	-	+	+	-	-	+	-	+	+
Pahsimeroi Hatchery	53	-	-	-	-	+	-	-	-	+	-	-
Sawtooth Hatchery	53	-	-	-	-	-	-	-	-	+	-	-
Oxbow Hatchery	56	-	-	-	-	-	-	-	-	-	-	-
Total # of populations within HWE		72	71	67	63	63	66	77	60	55	67	72

Table 5. Populations out of Hardy-Weinburg equilibrium for all loci combined using Fisher's exact tests ($p < 0.01$).

Population	Chi^2	Df	P value
Bargamin Creek	Infinity	22	< 0.0000
Basin Creek	Infinity	22	< 0.0000
Bear Creek	49.2	22	0.0007
Big Creek (lower)	40.5	22	0.0094
Big Creek (upper)	37.6	22	0.0098
Captain John Creek	58.9	22	< 0.0000
EF Salmon “B-run” Hatchery	89.9	22	< 0.0000
Fish Creek	54.1	22	0.0002
Hazard Creek	41.0	22	0.0083
John's Creek	41.0	22	0.0082
Lemhi River	61.4	22	< 0.0000
Lick Creek (upstream of barrier)	Infinity	22	< 0.0000
Little Bear Creek	69.4	22	< 0.0000
Mink Creek	58.3	22	< 0.0000
NF Moose Creek	41.6	22	0.007
Owl Creek	44.2	22	0.0034
Pahsimeroi Hatchery	Infinity	22	< 0.0000
Pahsimeroi River	Infinity	22	< 0.0000
Papoose Creek	49.2	22	0.0007
Red River	55.0	22	0.0001
Secesh River	61.1	22	< 0.0000
Sheep Creek (Snake)	44.2	22	0.0034
Sulphur Creek	38.2	22	0.0083
Three Links Creek	42.1	22	0.0061
Warm Springs Creek (Salmon)	50.6	22	0.0005
Whitebird Creek	47.3	22	0.0014

Table 6. BOTTLENECK's mutation-drift equilibrium results for *O. mykiss* in 10 anadromous drainages in Idaho's Snake River basin. Probabilities for heterozygote deficiency (HZD), heterozygote excess (HZE), and two-tailed excess and deficiency (TTM) were determined under the assumptions of the Two Phase Model (TPM), Stepwise Mutation Model (SMM) and the Infinite Allele Model (IAM) using Wilcoxon sign-rank tests.

Drainage	TPM Model HZD	TPM Model HZE	TPM Model TTM	SMM Model HZD	SMM Model HZE	SMM Model TTM	IAM Model HZD	IAM Model HZE	IAM Model TTM
Clearwater	0.58	0.45	0.90	0.01	0.99	0.02	0.99	0.03	0.05
MF Clearwater*	0.79	0.23	0.46	0.06	0.95	0.12	0.97	0.03	0.07
SF Clearwater	0.45	0.58	0.90	0.04	0.97	0.08	0.94	0.07	0.15
Little Salmon	0.74	0.29	0.58	0.01	0.99	0.02	0.99	0.03	0.05
Salmon	0.55	0.48	0.97	0.00	1.00	0.00	1.00	0.00	0.00
MF Salmon	0.26	0.77	0.52	0.00	1.00	0.01	0.94	0.07	0.15
SF Salmon	0.14	0.88	0.28	0.00	1.00	0.00	0.97	0.04	0.08
Lochsa	0.65	0.38	0.76	0.00	1.00	0.00	0.91	0.10	0.21
Selway	0.45	0.58	0.90	0.00	1.00	0.00	0.97	0.04	0.08
Snake	0.77	0.26	0.52	0.00	1.00	0.00	1.00	0.00	0.01

* - Drainage with a single population

Table 7. Observed heterozygosity (*Hz*) and average effective population size (*Ne*) using the Stepwise Mutation Model (SMM) and the Infinite Alllele Model (IAM) for Idaho's 10 anadromous drainages. Recent declines in *O. mykiss* by drainage were determined with Garza and Williamson's *M*. AMOVA results describe the proportion of molecular variance allocated among and within populations for each drainage. "N/A" indicates AMOVA analysis was not conducted for a drainge with a single population.

		Ne			AMOVA	
Drainage	Observed *Hz*	SMM	IAM	*M*	% among populations	% within populations
Clearwater	0.6627	4154	2188	0.815	2.22%	97.78%
MF Clearwater*	0.5931	2909	1710	0.668	N/A	N/A
SF Clearwater	0.6038	3333	1879	0.816	3.48%	96.52%
Little Salmon	0.6309	4372	2264	0.836	2.35%	97.65%
Salmon	0.6440	5018	2470	0.907	3.45%	96.55%
MF Salmon	0.5760	2862	1687	0.737	2.12%	97.88%
SF Salmon	0.5823	3385	1898	0.821	2.56%	97.44%
Lochsa	0.5818	2845	1681	0.781	1.66%	98.34%
Selway	0.5997	3183	1820	0.778	2.33%	97.67%
Snake	0.6569	4911	2449	0.805	0.96%	99.04%

* - Drainage with a single population

Table 8. Pairwise *Fst* values among 10 anadromous river drainages in Idaho's Snake River basin are given in the upper diagonal. All pariwise comparisons between drainages were signifcantly different (α = 0.0045).

Drainage	1	2	3	4	5	6	7	8	9
1 Clearwater									
2 MF Clearwater*	0.021								
3 SF Clearwater	0.018	0.011							
4 Little Salmon	0.017	0.023	0.023						
5 Salmon	0.014	0.027	0.022	0.009					
6 MF Salmon	0.045	0.033	0.049	0.030	0.035				
7 SF Salmon	0.024	0.031	0.039	0.022	0.021	0.024			
8 Lochsa	0.031	0.018	0.020	0.049	0.037	0.057	0.044		
9 Selway	0.018	0.018	0.020	0.037	0.027	0.051	0.031	0.010	
10 Snake	0.010	0.027	0.023	0.011	0.005	0.034	0.020	0.039	0.025

* - Drainage with a single population

Table 9. Estimations of recent reductions in population size (Garza and Williamson's *M*) and effective population size (*Ne*) based on the Stepwise Mutation (SMM) and Infinite Allele (IAM) models. "N/A" indicates *M* was not calculated because of low population size.

		Garza & Williamson's		*Ne*	
Drainages	Population	*M*		SMM	IAM
Boise	Big Smoky Creek	0.670		3628	1996
Clearwater	Big Canyon Creek	0.700		4493	2308
	EF Potlatch River	0.709		4013	2138
	Jack's Creek	0.585		4305	2243
	Little Bear Creek	0.643		4238	2219
	Mission Creek	0.730		3721	2030
Little Salmon	Boulder Creek	0.715		4209	2209
	Hazard Creek	0.791		4810	2416
	Little Salmon (Pinehurst area)	0.791		4774	2404
	Little Salmon (upstream of falls)	0.640		4236	2218
	Rapid River	0.658		3833	2072
Lochsa	Boulder Creek	N/A		3023	1757
	Brushy Fork Creek	0.678		2322	1454
	Canyon Creek	0.680		2986	1742
	Colt Creek	0.632		2856	1688
	Crooked Fork Creek	0.664		2635	1593
	Deadman Creek	0.709		3033	1761
	Fish Creek (fall migrants)	0.669		2815	1671
	Fish Creek (summer)	0.713		3374	1898
	Hungery Creek	0.608		2917	1713
	Lake Creek	0.596		2619	1587
	Papoose Creek	0.628		2525	1545
	Storm Creek	0.646		2585	1572
	Warm Springs Creek	0.670		2915	1712
	Weir Creek	0.631		3225	1839
MF Clearwater	Clear Creek	0.668		2909	1710
MF Salmon	Bear Valley Creek	0.626		2366	1475
	Big Creek (lower)	0.599		3234	1842
	Big Creek (upper)	0.557		2500	1535
	Camas Creek	0.630		3226	1839
	Loon Creek	0.600		2487	1529
	Marsh Creek	0.589		2821	1673
	Pistol Creek	0.603		3284	1862
	Rapid River	0.615		3032	1761
	Sulphur Creek	0.644		2812	1669
NF Clearwater	Collins Creek	0.712		2733	1636
Payette	MF Payette River	0.679		3112	1794
Salmon	Bargamin Creek	0.683		4222	2213
	Basin Creek	0.717		6141	2838
	Chamberlain Creek	0.706		3988	2129
	Horse Creek	0.665		4931	2457
	Lemhi River	0.707		7116	3121
	Morgan Creek	0.734		5371	2600

(Table 9 continued)					
		Garza & Williamson's		*Ne*	
Drainages	Population	*M*		SMM	IAM
Salmon	Owl Creek	0.751		4986	2475
	Pahsimeroi River	0.703		5903	2766
	Sheep Creek	N/A		2795	1662
	Slate Creek	0.779		4522	2318
	Valley Creek	0.678		5659	2691
	Warm Springs Creek	0.682		5390	2606
	Whitebird Creek	0.699		4274	2232
	WF Yankee Creek	0.660		4957	2465
Selway	Bear Creek	0.603		3110	1792
	EF Moose Creek	0.656		3499	1946
	Gedney Creek	0.691		3214	1834
	Meadow Creek	0.623		3276	1859
	Mink Creek	0.601		2652	1601
	NF Moose Creek	0.669		3235	1843
	O'hara Creek	0.690		3603	1986
	Pettibone Creek	0.604		2990	1743
	Three Links Creek	0.567		3072	1777
SF Clearwater	John's Creek	0.713		3145	1807
	Red River	0.757		3752	2042
	Ten Mile Creek	0.634		3101	1789
SF Salmon	EF SF Salmon River	0.613		3637	1999
	Johnson Creek	0.667		3819	2067
	Lick Creek (lower)	0.680		3397	1907
	Lick Creek (upstream of barrier)	0.672		2473	1523
	Poverty Flat area	0.678		3364	1894
	Secesh River	0.670		3672	2012
	Stolle Meadow	0.602		3331	1881
Snake	Captain John Creek	0.697		4546	2327
	Granite Creek	0.749		5098	2512
	Sheep Creek	0.691		5088	2508
Weiser	Little Weiser River	0.693		4392	2273
Hatchery	Dworshack Hatchery	0.705		2790	1660
	EF Salmon "B-run" Hatchery	0.632		3048	1767
	Oxbow Hatchery	0.703		4956	2465
	Pahsimeroi Hatchery	0.718		5518	2646
	Sawtooth Hatchery	0.684		5425	2617
			Average	3722	2010

Table 10. Distribution of mitochondrial DNA haplotypes observed in three Salmon River drainage populations (Lemhi River, Pahsimeroi River and Morgan Creek). *O. mykiss* haplotypes identified in this study were compared to a Snake River basin population (Johnson Creek, SF Salmon River drainage) and three hatcheries (Dworshak, Pahsimeroi, Oxbow) evaluated by Brown et al. 2004. "N" indicates the number of samples sequenced per population.

Population	Source	N	MYS1	MYS2	MYS3	MYS9	MYS10	MYS23	MYS24	MYS26	MYS
Lemhi River	this study	20	12	0	1	1	1	0	4	0	1
Pahsimeroi River	this study	26	15	0	4	1	5	0	0	0	1
Morgan Creek	this study	10	6	2	0	0	0	0	0	0	2
Johnson Creek	Brown et al. 2004	10	4	2	0	4	0	0	0	0	0
Dworshak Hatchery	Brown et al. 2004	41	19	0	0	21	0	0	0	1	0
Oxbow Hatchery	Brown et al. 2004	44	30	0	0	4	0	1	2	0	7
Pahsimeroi Hatchery	Brown et al. 2004	42	29	4	0	5	0	0	0	0	4
	TOTAL	193	115	8	5	36	6	1	6	1	15

*MYS28 was previously identified as MYS19 in Brown et al. 2004 (Graziano et al. 2005)

Table 11. Sample locations containing fish with alleles outside the expected range for *O. mykiss*.

Drainage	Population	Interspecific samples	Number analyzed
Clearwater	Jack's Creek	1	38
MF Clearwater	Clear Creek	2	56
SF Clearwater	John's Creek	10	49
	Red River	3	58
Lochsa	Fish Creek (summer)	1	56
	Fish Creek (fall migrants)	2	56
	Colt Creek	1	54
	Deadman Creek	3	56
	Weir Creek	8	55
	Papoose Creek	4	41
Little Salmon	Hazard Creek	1	51
MF Salmon	Camas Creek	4	53
	Rapid River	2	53
SF Salmon	Lick Creek (lower)	3	53
Salmon	Chamberlain Creek	1	46
	Basin Creek	3	53
	Horse Creek	3	58
	Morgan Creek	2	48
	Sheep Creek	4	22
	Bargamin Creek	1	51
	Warm Springs Creek	1	46
Selway	Three Links Creek	1	55
	EF Moose Creek	2	55
	Pettibone Creek	3	41
	NF Moose Creek	3	54
	Mink Creek	3	52
	Bear Creek	1	41
Snake	Sheep Creek	1	48
	Total	74	1399

Appendix I. *Fst* pairwise comparisons indicating no significant genetic differentiation (α = 0.0045) between 79 steelhead populations in Idaho's Snake River basin.

Population	Population	Pairwise *Fst*	*Fst* p
Bear Creek	Three Links Creek	0.006	0.02618
Bear Creek	EF Moose Creek	-0.005	0.91541
Bear Creek	Gedney Creek	0.006	0.02920
Bear Creek	O'hara Creek	0.004	0.10473
Boulder Creek (Little Salmon)	Bargamin Creek	0.008	0.00604
Chamberlain Creek	Bargamin Creek	-0.001	0.47331
Chamberlain Creek	Big Canyon Creek	0.000	0.32729
Chamberlain Creek	Boulder Creek (Little Salmon)	-0.003	0.78651
Chamberlian Creek	Camas Creek	0.004	0.11380
Chamberlian Creek	Hazard Creek	-0.002	0.69486
Chamberlian Creek	Horse Creek	-0.012	0.99799
Chamberlian Creek	John's Creek	0.011	0.00705
Chamberlian Creek	Johnson Creek	-0.004	0.90433
Chamberlian Creek	Morgan Creek	-0.004	0.87210
Chamberlian Creek	Owl Creek	-0.007	0.99396
Chamberlian Creek	Pistol Creek	0.007	0.04834
Chamberlian Creek	Poverty Flat	0.009	0.01208
Chamberlian Creek	Sheep Creek (Snake)	0.000	0.53676
Chamberlian Creek	Pahsimeroi Hatchery	0.001	0.28701
Chamberlian Creek	Slate Creek	0.001	0.33535
Chamberlian Creek	Valley Creek	0.009	0.01813
Chamberlian Creek	WF Yankee Creek	0.004	0.09063
Chamberlian Creek	Whitebird Creek	-0.002	0.63243
Chamberlian Creek	Oxbow Hatchery	0.010	0.00504
Colt Creek	Boulder Creek (Lochsa)	0.002	0.30816
EF Moose Creek	Boulder Creek (Lochsa)	0.013	0.01108
Fish Creek (fall migrants)	Fish Creek (summer)	0.001	0.32470
Fish Creek (fall migrants)	Lake Creek	0.004	0.03424
Fish Creek (fall migrants)	Hungery Creek	-0.002	0.73212
Fish Creek (fall migrants)	Weir Creek	0.007	0.00806
Fish Creek (summer)	Boulder Creek (Lochsa)	0.008	0.04330
Fish Creek (summer)	EF Moose Creek	0.017	0.02216
Gedney Creek	Three Links Creek	0.007	0.00860
Gedney Creek	EF Moose Creek	-0.001	0.53172
Granite Creek	Horse Creek	0.006	0.02920
Granite Creek	Morgan Creek	0.008	0.01108
Granite Creek	Owl Creek	0.008	0.00705
Granite Creek	Sheep Creek (Snake)	0.007	0.02618
Granite Creek	Pahsimeroi Hatchery	0.005	0.04028
Hazard Creek	Bargamin Creek	0.007	0.01007
Hazard Creek	Boulder Creek (Little Salmon)	0.005	0.04230
Hazard Creek	Sheep Creek (Salmon)	0.003	0.16616
Hazard Creek	Horse Creek	-0.001	0.62739
Hazard Creek	Morgan Creek	0.008	0.00604
Hazard Creek	Owl Creek	0.006	0.01208

(Appendix I continued)			
Population	Population	Pairwise *Fst*	*Fst* p
Hazard Creek	Sheep Creek (Snake)	0.007	0.01108
Hazard Creek	Pahsimeroi Hatchery	0.005	0.02719
Horse Creek	Captain John Creek	0.007	0.00705
Horse Creek	EF Moose Creek	0.008	0.01108
Horse Creek	Johnson Creek	0.007	0.01410
Horse Creek	Morgan Creek	0.002	0.25277
Horse Creek	O'hara Creek	0.007	0.01511
Horse Creek	Owl Creek	-0.006	0.99799
Horse Creek	Oxbow Hatchery	0.009	0.00705
Horse Creek	Sawtooth Hatchery	0.004	0.08761
Horse Creek	Sheep Creek (Snake)	-0.004	0.92145
Horse Creek	Pahsimeroi Hatchery	0.004	0.09567
Horse Creek	Slate Creek	-0.001	0.65359
Horse Creek	Valley Creek	0.010	0.00504
Horse Creek	Whitebird Creek	0.002	0.18530
Horse Creek	Bargamin Creek	-0.005	0.95972
Horse Creek	Big Canyon Creek	0.004	0.06143
Horse Creek	Boulder Creek (Little Salmon)	0.004	0.06949
Horse Creek	Sheep Creek (Salmon)	0.016	0.01309
Hungery Creek	Lake Creek	0.004	0.06143
Hungery Creek	Pettibone Creek	0.010	0.00604
Hungery Creek	Weir Creek	0.005	0.04834
Hungery Creek	EF Moose Creek	0.005	0.04431
Hungery Creek	Fish Creek (summer)	0.000	0.57301
John's Creek	O'hara Creek	0.005	0.05337
Johnson Creek	Sheep Creek (Salmon)	0.018	0.00504
Lake Creek	Brushy Fork Creek	0.003	0.09668
Lake Creek	Fish Creek (summer)	0.004	0.05035
Lake Creek	Weir Creek	-0.001	0.39275
Loon Creek	Camas Creek	0.009	0.01208
Loon Creek	Pistol Creek	0.011	0.01208
Marsh Creek	Pistol Creek	0.014	0.00604
Morgan Creek	Owl Creek	0.005	0.06244
Morgan Creek	Oxbow Hatchery	0.008	0.00705
Morgan Creek	Sawtooth Hatchery	0.009	0.00705
Morgan Creek	Pahsimeroi Hatchery	0.006	0.03323
Morgan Creek	Valley Creek	0.006	0.04532
NF Moose Creek	Three Links Creek	0.008	0.00640
O'hara Creek	Clear Creek	0.009	0.01208
O'hara Creek	Deadman Creek	0.008	0.01007
O'hara Creek	EF Moose Creek	0.007	0.01511
O'hara Creek	Weir Creek	0.007	0.01309
Owl Creek	Bargamin Creek	0.006	0.02316
Owl Creek	Boulder Creek (Little Salmon)	0.008	0.00504
Owl Creek	Sheep Creek (Salmon)	0.009	0.03726
Owl Creek	Oxbow Hatchery	0.008	0.00504
Owl Creek	Sawtooth Hatchery	0.007	0.01410

(Appendix I continued)			
Population	Population	Pairwise *Fst*	*Fst* p
Owl Creek	Sheep Creek (Snake)	0.008	0.01007
Owl Creek	Pahsimeroi Hatchery	0.000	0.57402
Owl Creek	Valley Creek	0.007	0.01411
Oxbow Hatchery	Sawtooth Hatchery	0.002	0.20200
Oxbow Hatchery	Sheep Creek (Snake)	0.009	0.00806
Oxbow Hatchery	Pahsimeroi Hatchery	0.002	0.16516
Oxbow Hatchery	Valley Creek	0.000	0.44914
Pahsimeroi Hatchery	Captain John Creek	0.005	0.02216
Pahsimeroi Hatchery	Valley Creek	-0.001	0.55589
Pahsimeroi Hatchery	Warm Springs Creek (Salmon)	0.007	0.02115
Pettibone Creek	EF Moose Creek	0.005	0.07855
Pettibone Creek	Fish Creek (summer)	0.010	0.00604
Pistol Creek	Big Creek (lower)	0.008	0.02115
Pistol Creek	Big Creek (upper)	0.007	0.02115
Pistol Creek	Camas Creek	-0.002	0.62437
Pistol Creek	Sulphur Creek	0.013	0.00705
Poverty Flat Area	Lick Creek (lower)	0.009	0.01007
Sawtooth Hatchery	Sheep Creek (Snake)	0.007	0.02618
Sawtooth Hatchery	Pahsimeroi Hatchery	-0.003	0.83384
Sawtooth Hatchery	Valley Creek	0.002	0.27694
Sheep Creek (Salmon)	Boulder Creek (Little salmon)	0.007	0.10070
Sheep Creek (Salmon)	Clear Creek	0.015	0.01108
Sheep Creek (Snake)	Boulder Creek (Little Salmon)	0.008	0.02115
Sheep Creek (Snake)	Sheep Creek (Salmon)	0.015	0.00906
Sheep Creek (Snake)	Pahsimeroi Hatchery	0.001	0.31017
Sheep Creek (Snake)	Slate Creek	0.008	0.01712
Sheep Creek (Snake)	Valley Creek	0.005	0.08056
Slate Creek	Boulder Creek (Little Salmon)	0.007	0.01410
Stolle Meadow	EF SF Salmon River	0.009	0.01410
Sulphur Creek	Bear Valley Creek	0.006	0.03021
Valley Creek	Warm Springs Creek (Salmon)	0.006	0.04532
Warm Springs Creek (Lochsa)	Weir Creek	0.008	0.00504
Weir Creek	Boulder Creek (Lochsa)	0.009	0.02417
Weir Creek	Fish Creek (summer)	0.001	0.23666

Appendix II. Samples containing alleles outside of the expected range for *O. mykiss* at *Ogo4 (alleles > 142), Oneµ8 (alleles > 188), Oneµ14* (alleles >163) and *Ots1 (allels >247)*. Numbers following population code designations indicate the individual identification number for the interspecific sample.

					Loci		
Drainage	Population	N	Sample	Ogo4	Oneµ8	Oneµ14	Ots1
Clearwater	Jack's Creek	1	JACK09	X	X	X	X
MF Clearwater	Clear Creek	2	CLRC163	X	X	X	X
			CLRC222	X			
SF Clearwater	John's Creek	10	JOHN4347	X	X	X	X
			JOHN4349		X		
			JOHN4353	X			
			JOHN4356		X		
			JOHN4357	X	X		
			JOHN4361	X			
			JOHN4362		X		
			JOHN4363	X	X		
			JOHN4364	X	X		X
			JOHN4368		X		X
	Red River	3	REDR14				X
			REDR24	X	X		X
			REDR30	X			X
Lochsa	Fish Creek (summer)	1	FISH1127	X			
	Fish Creek (fall migrants)	2	FSCT6427	X			
			FSCT6437	X			
	Colt Creek	1	COLT914				X
	Deadman Creek	3	DEAD1041				X
			DEAD1062				X
			DEAD1096				X
	Weir Creek	8	WEIR8080		X		
			WEIR8084	X	X	X	X
			WEIR8103	X	X		
			WEIR8110	X	X	X	
			WEIR8111	X	X	X	X
			WEIR8117	X			
			WEIR8142	X	X	X	X
			WEIR8145	X	X		X
	Papoose Creek	4	PAPO8004				X
			PAPO8014				X
			PAPO8018				X
			PAPO8029				X
Little Salmon	Hazard Creek	1	HAZC503	X			
MF Salmon	Camas Creek	4	CAM11772	X			X
			CAM11781		X		X
			CAM11803	X			X
			CAM11807		X		
	Rapid River	2	RRDR2125		X		
			RRDR2091		X		X
SF Salmon	Lick Creek (lower)	3	LIK14643				X
			LIK14650	X			

(Appendix II continued)

Drainage	Population	N	Sample	Ogo4	Loci Oneμ8	Oneμ14	Ots1
SF Salmon			LIK14656	X			X
Salmon	Chamberlain Creek	1	HAM12699				X
	Basin Creek	3	BASC8564				X
			BASC8598				X
			BASC8611	X			
	Horse Creek	3	HRSC2807	X			
			HRSC2818	X			
			HRSC2823			X	
	Morgan Creek	2	MORG5960		X		
			MORG5961		X		
	Sheep Creek	4	EEPC6164	X	X	X	
			EEPC6171				X
			EEPC6176	X	X	X	
			EEPC6180	X	X		
	Bargamin Creek	1	BAR12527			X	X
	Warm Springs Creek	1	WSCK3254		X		X
Selway	Three Links Creek	1	3LNK4187	X			X
	EF Moose Creek	2	EMOS3685	X			X
			EMOS3740				X
	Pettibone Creek	3	PETB8429				X
			PETB8449			X	X
			PETB8453			X	X
	NF Moose Creek	3	NFMO3922	X		X	
			NFMO3935			X	
			NFMO3943	X		X	
	Mink Creek	3	MINK8487				X
			MINK8494				X
			MINK8540				X
	Bear Creek	1	BEAR3616				X
Snake	Sheep Creek	1	SHPC5209	X	X	X	

Appendix III. BOTTLENECK's mutation-drift equilibrium results for 79 Idaho *O. mykiss* populations under the Two-Phase, Stepwise Mutation and Infinite Allele Models (TPM, SMM and IAM, respectively). Probabilities under heterozygote deficiency (HZD), heterozygote excess (HZE), and two-tailed excess and deficiency (TTM) were determined using Wilcoxon sign-rank tests.

Population	TPM Model HZD	TPM Model HZE	TPM Model TTM	SMM Model HZD	SMM Model HZE	SMM Model TTM	IAM Model HZD	IAM Model HZE	IAM Model TTM
Big Canyon Creek	0.71	0.32	0.64	0.01	0.99	0.02	0.97	0.03	0.07
Clear Creek	0.82	0.21	0.41	0.06	0.95	0.12	0.97	0.03	0.07
EF Potlach River	0.91	0.10	0.21	0.14	0.88	0.28	0.99	0.01	0.02
John's Creek	0.65	0.38	0.76	0.01	0.99	0.02	0.96	0.05	0.10
Fish Creek (summer)	0.77	0.26	0.52	0.01	0.99	0.02	0.91	0.10	0.21
EF SF Salmon River	0.91	0.10	0.21	0.12	0.90	0.24	0.99	0.01	0.02
Rapid River (Little Salmon)	0.93	0.09	0.17	0.26	0.77	0.52	1.00	0.00	0.01
Whitebird Creek	0.65	0.38	0.76	0.03	0.99	0.05	0.99	0.01	0.02
Johnson Creek	0.88	0.14	0.28	0.12	0.90	0.24	1.00	0.00	0.01
Brushy Fork Creek	0.68	0.35	0.70	0.10	0.91	0.21	0.97	0.04	0.08
Colt Creek	0.82	0.21	0.41	0.16	0.86	0.32	0.99	0.01	0.02
Poverty Flat area	0.84	0.18	0.37	0.01	0.99	0.02	1.00	0.00	0.01
Secesh River	0.71	0.32	0.64	0.01	0.99	0.02	0.99	0.03	0.05
Canyon Creek	0.88	0.14	0.28	0.26	0.77	0.52	0.99	0.01	0.02
Camas Creek	0.38	0.65	0.76	0.04	0.97	0.08	0.90	0.12	0.24
Big Creek (lower)	0.65	0.38	0.76	0.12	0.90	0.24	0.97	0.04	0.08
Basin Creek	0.82	0.21	0.41	0.04	0.97	0.08	1.00	0.00	0.00
Chamberlain Creek	0.65	0.38	0.76	0.03	0.97	0.07	0.97	0.03	0.07
Bear Creek	0.91	0.10	0.21	0.38	0.65	0.76	0.99	0.03	0.05
EF Moose Creek	0.77	0.26	0.52	0.09	0.93	0.17	0.99	0.01	0.02
Loon Creek	0.38	0.65	0.76	0.03	0.97	0.07	0.97	0.03	0.07
Gedney Creek	0.82	0.21	0.41	0.14	0.88	0.28	0.97	0.04	0.08
Marsh Creek	0.77	0.26	0.52	0.42	0.62	0.83	0.94	0.07	0.15
Three Links Creek	0.97	0.04	0.08	0.62	0.42	0.83	0.99	0.01	0.02
Lemhi River	0.62	0.42	0.83	0.45	0.58	0.90	1.00	0.00	0.01
Granite Creek	0.86	0.16	0.32	0.03	0.97	0.07	0.99	0.01	0.02
Ten Mile Creek	0.79	0.23	0.46	0.26	0.77	0.52	0.99	0.01	0.02
Red River	0.38	0.65	0.76	0.01	0.99	0.02	0.91	0.10	0.21
Mission Creek	0.62	0.42	0.83	0.03	0.97	0.07	0.99	0.01	0.02
Pahsimeroi River	0.29	0.74	0.58	0.01	0.99	0.02	0.99	0.01	0.02
Little Salmon River (Pinehurst area)	0.52	0.52	1.00	0.03	0.97	0.07	0.99	0.03	0.05
Slate Creek	0.88	0.14	0.28	0.14	0.88	0.28	1.00	0.00	0.01
Lick Creek (lower)	0.86	0.16	0.32	0.04	0.98	0.08	1.00	0.00	0.00
Crooked Fork Creek	1.00	0.00	0.01	0.54	0.50	1.00	1.00	0.00	0.00
Storm Creek	0.86	0.16	0.32	0.14	0.88	0.28	1.00	0.00	0.01
Stolle Meadow	0.90	0.12	0.23	0.22	0.81	0.43	1.00	0.00	0.00
Boulder Creek (Lochsa)	0.68	0.35	0.70	0.16	0.86	0.32	0.97	0.04	0.08
Bear Valley Creek	0.55	0.48	0.97	0.14	0.88	0.28	0.91	0.10	0.21
Sulphur Creek	0.35	0.68	0.70	0.09	0.93	0.17	0.82	0.21	0.41
Bargamin Creek	0.91	0.10	0.21	0.14	0.88	0.28	0.99	0.03	0.05
Fish Creek (fall migrants)	0.82	0.21	0.41	0.32	0.71	0.64	0.88	0.14	0.28

(Appendix III continued)										
	TPM	TPM	TPM		SMM	SMM	SMM		IAM	IAM	IAM
	Model	Model	Model		Model	Model	Model		Model	Model	Model
Population	HZD	HZE	TTM		HZD	HZE	TTM		HZD	HZE	TTM
Big Creek (upper)	0.72	0.31	0.63		0.14	0.88	0.28		0.99	0.01	0.02
Horse Creek	0.91	0.10	0.21		0.07	0.94	0.15		1.00	0.00	0.00
Deadman Creek	0.38	0.65	0.76		0.00	1.00	0.01		0.99	0.03	0.05
Hungery Creek	0.84	0.18	0.37		0.38	0.65	0.76		0.97	0.04	0.08
Meadow Creek	0.77	0.26	0.52		0.09	0.93	0.17		0.97	0.04	0.08
Lake Creek	0.91	0.10	0.21		0.29	0.74	0.58		1.00	0.00	0.00
Pistol Creek	0.42	0.62	0.83		0.05	0.96	0.10		0.96	0.05	0.10
Mink Creek	0.86	0.16	0.32		0.12	0.90	0.24		1.00	0.00	0.01
Papoose Creek	0.14	0.88	0.28		0.00	1.00	0.01		0.82	0.21	0.41
Rapid River (MF Salmon)	0.21	0.82	0.41		0.01	0.99	0.02		0.86	0.16	0.32
NF Moose Creek	0.90	0.12	0.24		0.14	0.88	0.28		1.00	0.01	0.01
Warm Springs Creek (Lochsa)	0.84	0.18	0.37		0.01	0.99	0.02		1.00	0.00	0.00
O'hara Creek	0.84	0.18	0.37		0.18	0.84	0.37		0.96	0.05	0.10
Weir Creek	0.71	0.32	0.64		0.23	0.79	0.46		0.99	0.01	0.02
Pettibone Creek	0.65	0.38	0.76		0.03	0.97	0.07		0.97	0.04	0.08
Captain John Creek	0.97	0.04	0.08		0.01	0.99	0.02		0.99	0.01	0.02
Owl Creek	0.77	0.26	0.52		0.06	0.95	0.12		1.00	0.00	0.00
Sheep Creek (Snake)	0.90	0.12	0.24		0.05	0.96	0.10		1.00	0.00	0.00
WF Yankee Creek	0.99	0.03	0.05		0.16	0.86	0.32		1.00	0.00	0.00
Jack's Creek	1.00	0.00	0.00		0.94	0.07	0.15		1.00	0.00	0.00
Little Bear Creek	0.88	0.14	0.28		0.26	0.77	0.52		0.99	0.03	0.05
Morgan Creek	0.77	0.26	0.52		0.00	1.00	0.01		0.99	0.03	0.05
Boulder Creek (Little Salmon)	0.71	0.32	0.64		0.16	0.86	0.32		0.99	0.03	0.05
Hazard Creek	0.18	0.84	0.37		0.00	1.00	0.00		0.94	0.07	0.15
Valley Creek	0.86	0.16	0.32		0.32	0.71	0.64		1.00	0.00	0.00
Warm Springs Creek (Salmon)	0.93	0.09	0.17		0.14	0.88	0.28		1.00	0.00	0.01
Little Salmon River (upstream of falls)	0.97	0.03	0.07		0.38	0.65	0.76		0.99	0.01	0.02
Collins Creek	0.84	0.18	0.37		0.14	0.88	0.28		0.94	0.07	0.15
MF Payette River	0.35	0.68	0.70		0.01	0.99	0.02		0.99	0.03	0.05
Sheep Creek (Salmon)	0.42	0.62	0.83		0.07	0.94	0.15		0.88	0.14	0.28
Lick Creek (upstream of barrier)	0.18	0.84	0.37		0.01	0.99	0.02		0.82	0.21	0.41
Little Weiser River	0.48	0.55	0.97		0.03	0.99	0.05		0.99	0.01	0.02
Big Smoky Creek	0.55	0.48	0.97		0.04	0.97	0.08		0.96	0.05	0.10
Dworshak Hatchery	0.77	0.26	0.52		0.07	0.94	0.15		0.99	0.01	0.02
EF Salmon "B-run" Hatchery	0.77	0.26	0.52		0.32	0.71	0.64		0.96	0.05	0.10
Oxbow Hatchery	0.94	0.07	0.15		0.38	0.65	0.76		1.00	0.00	0.00
Pahsimeroi Hatchery	0.94	0.07	0.15		0.32	0.71	0.64		1.00	0.01	0.01
Sawtooth Hatchery	0.95	0.06	0.12		0.12	0.90	0.24		1.00	0.00	0.00

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