Independent Populations
of Chinook, Steelhead, and Sockeye
for Listed Evolutionarily Significant Units
Within the Interior Columbia River Domain

Working Draft

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Interior Columbia Basin Technical Recovery Team

Dedication

for

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1932-2001

Scientist, colleague, friend

Member of the Interior Columbia Technical Recovery Team, 2001.

His presence is sorely missed.

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ABBREVIATIONS AND ACRONYMS

EPA	U.S. Environmental Protection Agency
ESU	evolutionarily significant unit
GCFMP	Grand Coulee Fish Maintenance Project
IDFG	Idaho Department of Fish and Game
NMFS	National Marine Fisheries Service
NWFSC	Northwest Fisheries Science Center
ODFW	Oregon Department of Fish and Wildlife
QAR	Quantitative Analytical Report
SASSI	Salmon and Steelhead Stock Inventory
TRT	Technical Review Team
WDFW	Washington Department of Fish and Wildlife

EXECUTIVE SUMMARY

In this document, the Interior Columbia River Basin Technical Recovery Team provides the background, analysis, and recommendations on the identification of independent populations of the seven Evolutionarily Significant Units (ESUs) of anadromous salmonids listed under the Endangered Species Act in this recovery domain. We examined an array of indicators to assess the independence of populations, including: (1) genetic information, (2) geography; (3) life-history traits, (4) morphological traits, and (5) population dynamics. As putative demographically independent units, these main populations become the focus of recovery planning and conservation efforts in the interior Columbia River basin. These delineations will necessarily play an important role in establishing viability goals at both the population and ESU level. Our delineations of extant populations include the following:

- Snake River spring/summer chinook ESU: 31 populations
- Upper Columbia spring chinook ESU: 3 populations
- Snake River Fall chinook ESU: 1 population
- Snake River steelhead ESU: 25 populations
- Upper Columbia steelhead ESU: 3 populations, and 1 of ambiguous status
- Mid-Columbia steelhead ESU: 17 populations
- Snake River sockeye: 1 population

We also identified historic populations within current ESU boundaries, and discussed large areas currently blocked to anadromous passage. Finally, we describe data needs that would improve population delineation efforts.

INTRODUCTION

Purpose and Scope

The interior Columbia River basin is currently home to 12 different anadromous salmonid Evolutionarily Significant Units (ESUs), belonging to three different species: chinook salmon (*Oncorhynchus tshawytscha*), sockeye salmon (*O. nerka*), and steelhead trout (*O. mykiss*). Since 1991, 7 of these 12 ESUs have been listed as threatened or endangered under the Endangered Species Act (ESA), due to dramatic declines in abundance and loss of habitat (Table 1).

The Interior Columbia River Basin Technical Recovery Team (TRT) was formed to synthesize and interpret data related to the recovery of these seven ESUs. The TRT's first task is to delineate independent populations within listed ESUs of anadromous salmonids. Understanding population boundaries is critical for effective conservation planning, since incorrectly lumping or splitting population (or portions of populations) can provide an inaccurate picture of population status. Over- or underestimating the true status (population productivity or demographic risks, for example), can lead to inefficient (or insufficient) recovery efforts. Similarly, if two "true" populations are treated as a single unit, the status of one may mask the other, potentially leading to the loss of one of the populations. Harvest management, which manipulates population abundance and productivity to maintain a sustainable yield, can be similarly confounded by poor understanding of population boundaries. Finally, populations are the units that will be combined to form alternative scenarios for ESU viability (and will ultimately be the object of recovery efforts). Thus, knowledge of population structure within an ESU is critical for effective population and species management (Allendorf et al. 1987).

In this report, we describe current population structure in the seven listed salmonid ESUs in the interior Columbia Basin. In addition, we review historical documentation and describe likely differences in population structure prior to major anthropogenic manipulation of the region. The populations identified in this document are the independent groups of fish for which we will assess status and establish viability goals in future reports.

Table 1**.** Brief descriptions of interior Columbia River basin Evolutionarily Significant Units (ESUs) as defined by NMFS (Myers et al. 1998, Busby et al. 1996, Gustafson et al. 1997).

Interior Basin Columbia ESU	**Status**	**Description**
Snake River spring/summer-run chinook salmon (*O. tshawytscha*)	Threatened	All natural populations of spring/summer-run chinook salmon using tributaries to the mainstem Snake River. Major subbasins are the Tucannon River, Grande Ronde River, Imnaha River, and Salmon River. Spring/summer chinook introduced into the Clearwater River subbasin were excluded from the ESU.
Upper Columbia River spring-run chinook salmon (*O. tshawytscha*)	Endangered	All naturally spawned populations of spring-run chinook salmon in all Columbia River tributaries upstream of the Rock Island Dam and downstream of Chief Joseph Dam in Washington State. Major tributary subbasins with existing runs are the Wenatchee, Entiat, and Methow Rivers.
Middle Columbia River spring-run chinook salmon (*O. tshawytscha*)	Not warranted	Naturally spawned populations of spring-run chinook salmon in the Columbia River basin upstream of the Wind River, Washington, and the Hood River, Oregon, to and including the Yakima River, except for chinook from the Snake River subbasins. Major tributaries in the ESU are the Yakima, Klickitat, Deschutes, John Day, Umatilla, and Walla Walla Rivers.
Snake River fall-run chinook salmon (*O. tshawytscha*)	Threatened	All natural populations of fall-run chinook salmon in the mainstem Snake River and the Tucannon River, Grande Ronde River, Imnaha River, Salmon River, and Clearwater River subbasins.
Upper Columbia River summer/fall-run chinook salmon (*O. tshawytscha*)	Not warranted	Naturally spawned populations of summer and fall-run chinook in streams in the Columbia River basin upstream of and including the Yakima River to the U.S.–Canada border. Major tributary subbasins in this ESU are the Yakima, Wenatchee, Entiat, Methow, and Okanogan Rivers.
Deschutes River summer/fall-run chinook salmon *(O.*	Not warranted	Naturally spawned populations of summer and fall-run chinook in the Deschutes River basin.

Interior Basin Columbia ESU	**Status**	**Description**
tshawytscha)		
Snake River basin steelhead *(O. mykiss*)	Threatened	All naturally spawned populations of steelhead in the Snake River basin. Major tributary subbasins in this ESU are the Tucannon, Clearwater, Grande Ronde, Imnaha, and Salmon Rivers.
Upper Columbia River steelhead *(O. mykiss)*	Endangered	Naturally spawned populations of steelhead in streams in the Columbia River basin upstream of the Yakima River to the U.S.–Canada border. Major tributary subbasins in this ESU are the Wenatchee, Entiat, Methow, and Okanogan Rivers.
Middle Columbia River steelhead *(O. mykiss*	Threatened	Naturally spawned populations of steelhead in the Columbia River basin upstream of the Wind River, Washington, and the Hood River, Oregon, to and including the Yakima River, except for steelhead from the Snake River subbasins Major tributaries in the ESU are the Yakima, Klickitat, Deschutes, John Day, Umatilla, and Walla Walla Rivers.
Snake River sockeye salmon *(O. nerka)*	Endangered	The only extant population of the anadromous form is the Redfish Lake population. Historically, sockeye runs were found in the Stanley River basin, Payette Lake, Warm Lake and Wallowa Lake.
Okanogan River sockeye salmon *(O. nerka)*	Not warranted	Naturally spawned populations of sockeye salmon in Osoyoos Lake and its U.S. tributaries, and the U.S. portion of the Similkameen River.
Lake Wenatchee sockeye salmon *(O. nerka)*	Not warranted	Naturally spawned populations of sockeye salmon in Lake Wenatchee and its tributaries, including the White and Little Wenatchee Rivers.

Population Definition and Concepts

In establishing population structure, we follow the definition of population in McElhany et al. (2000):

> **...**an independent population is a group of fish of the same species that spawns in a particular lake or stream (or portion thereof) at a particular season and which, to a substantial degree, does not interbreed with fish from any other group spawning in a different place or in the same place at a different season. For our purposes, not interbreeding to a "substantial degree" means that two groups are considered to be independent populations if they are isolated to such an extent that exchanges of individuals among the populations do not substantially affect the population dynamics or extinction risk of the independent populations over a 100-year time frame.

This definition is equivalent to Ricker's (1972) characterization of a stock, and similar to the Washington State stock definition (SASSI, WDFW 1993). McElhany et al. (2000) acknowledge that the exact level of reproductive isolation that is required for a population to have substantially independent dynamics has not been well established, but some theoretical work suggests that substantial independence will occur when the proportion of a population that consists of migrants is less than about 10% (Hastings 1993).

Reproductive isolation between groups of fish is likely hierarchical, with structure both above and below the level of the population. Within a population, stream structure or gradations in reproductive timing may result in groups of fish that are more isolated from each other than others, but that are not so isolated as to be a separate population. Similarly, some structuring commonly exists above the level of a population, particularly in the larger ESUs. We use "major grouping" for groups of populations that are isolated from one another over a longer time scale than that defining the individual populations but which retain some degree of connectivity greater than that between ESUs. Thus, we describe a biologically based hierarchy that spans ESUs, major groupings, populations and substructure within populations and reflects the apparent degree of connection between the fish in each of these hierarchical levels.

Approach to Identifying Populations

We initially classified "major groups" of potential populations within ESUs, then identified independent populations within those major groups. We used a variety of data types to define groups at both levels of population hierarchy (Table 2). However, in no case was the entire array of potential information available to inform our decision process. We relied most heavily on genetic information and distances between spawning areas related to dispersal (straying distance) as evidence of reproductive isolation. We also considered drainage structure, particularly at the major grouping level. Phenotypic (life-history and morphological) characteristics can also be indicative of reproductive isolation and therefore population structure; we found this phenotypic information most useful at the population level. In cases where other, more informative data were lacking, such as most steelhead ESUs, we also relied upon environmental characteristics. Finally, we considered two demographic factors. First, because our goal was to identify demographically independent populations, we examined the correlation in abundance time series between areas. Second, we considered historical population size in our determination of population boundaries. Because data collection techniques, hatchery releases, small sample sizes and a variety of other factors have the potential to introduce confounding variation into a data set, we carefully considered the quality of the data available.

Below we briefly describe each data type and associated analyses:

- **Genetic attributes**. Neutral genetic markers can indicate the degree of genetic exchange or isolation between two samples. We used available genetic information, which included both allozyme and microsatellite data, to assess reproductive isolation between samples in the interior Columbia River basin. This information was a primary factor in defining "major groups" and independent populations, particularly where samples had been collected at a relatively fine spatial scale. We report general results for each ESU. More detailed information about our genetic analyses can be found in Appendix A.
- **Dispersal distance and rates, drainage structure.** Adult movement and spawning between sites determines the degree of reproductive isolation and demographic independence between sites. This movement is likely influenced both by distance between spawning areas (Pascual and Quinn 1994, Bentzen et al. 2002) and by the structure of the river system, since migrating fish faced with a choice of streams or rivers are more likely to turn into their stream of origin (Quinn et al. 1983). Thus, drainage structure (i.e., the location and distribution of large tributaries) played a substantial role in our determination of major groupings. In addition, we used species-specific straying rate and distance data from wild fish and primarily locally derived hatchery stock to estimate the distance beyond which less than 5–10 percent of the fish from a spawning aggregate or hatchery were likely to stray. We considered this information in tandem with distances between spawning aggregates to assess the likelihood that these aggregates were demographically coupled. In general, we considered that areas separated by 10–30 km or more were likely to be uncoupled (see Appendix B for further details). Confidence in the dispersal distance metric and lower limit of the spawning aggregates was varied depending on the quality of the spawning distribution data and straying estimates (See Appendix B). For example, spawning distributions of spring/summer chinook salmon have been much more extensively and routinely surveyed than steelhead distributions. There is also a high degree of uncertainty in steelhead spawning areas in higher order, mainstem reaches.

Table 2. Data types supporting population identification efforts. Weight indicates the importance that a particular data type was given at both the major grouping and the population level if all data types were available. In practice, very little information was available for many ESUs. In these cases, lower weight information increased in importance. In addition, the importance of a particular set of data varied depending on the quality of those data.

	Weight		
Data Type	**Major Grouping**	**Population**	**Notes**
Genetic data	High	High	Hatchery influences, small population sizes and resident fish contributions have the potential to affect sample differentiation.
Distance between spawning aggregates and dispersal curve	High	High	Wild fish straying information largely unavailable. See Appendix X for details. In most cases, steelhead spawning locations are poorly known.
Morphological data	Medium	Medium	Morphological data generally not available at a fine-scale.
Age structure	Medium	Medium	
Spawn timing	Low	High	Available spawn-timing data were only qualitative.
Environmental or habitat characteristics	Medium	Low	Environmental and habitat information became very important in cases where other data were lacking as a very weak proxy for likely differentiation.
Run timing	Low	Medium	
Demographic correlation	Medium	Low	Although we sought to identify demographically independent populations, in practice, demographic correlations were generally weighted low due to the confounding effect of out-of-basin factors.
Juvenile migration timing	Low	Medium	
Basin size/habitat capacity	Low	Medium	Capacity sufficient to support 500 spawners (as judged by historic records or professional judgment) was used as a minimum criterion for population identification.

In most cases, genetic and geographic information suggested similar boundaries for major groupings and individual populations. We relied on additional information where these data types did not coincide, particularly at fine-scale levels (within major groupings, for instance) and in situations where other data were lacking:

- **Phenotypic characteristics.** A variety of phenotypic traits, including **life-history characteristics**, have been shown to reflect both environmental influence and underlying genetic variation (Metcalfe 1993). Unlike molecular markers, this genetic basis reflects some degree of selection and can be informative regarding further structure within groupings defined by molecular markers. When available, we examined adult run and spawn timing, juvenile outmigration timing, and age structure for between-stream similarities and differences (Appendix C). In some cases, only a qualitative comparison was possible.
- **Environmental characteristics**. The collective biotic and abiotic characteristics of salmonid habitat form the selective environment in which salmon exist. Because salmon exhibit strong homing behaviors, local adaptation can develop relatively easily (Quinn and Dittman 1990). Thus, environmental or large-scale habitat characteristics might be expected to be a weak proxy for population structure (Whittier et al. 1988). In cases where few additional data were available, we considered ecoregion boundaries (levels 3 and 4) (Omernik and Gallant 1986) as an indicator in population delineation.
- **Demographic factors.**
    - **Population dynamics**. We used abundance data such as run reconstructions or redd counts to explore the degree to which the demographic trajectories of repeatedly sampled sites were correlated. All else being equal, the less correlated time series of abundance are between two groups of fish, the less likely they are to be part of the same population. However, correlations in abundance between groups of fish are often complicated by the potentially confounding influence of correlated environmental characteristics and mortality factors.
    - **Population size.** By definition, independent populations must have the potential to persist over a 100-year time frame. Many authors have addressed the issue of minimum population size necessary to reduce genetic and demographic risks (i.e. to be viable over a reasonable time period. McElhany et al. (2000) reviewed this work. They suggest that to reduce the genetic effects of small population sizes that for salmon and steelhead, a breeding population of approximately 417 (based on the methods of Franklin 1980 and Soule 1980) to 4170 (based on the methods of Lande 1995) is necessary. Waples and Wainwright (1998) note that larger population sizes are likely necessary if demographic factors are considered as well. Because of these considerations, all the populations we defined had estimated historical run sizes and/or habitat potential (determined by historical records or professional judgment) sufficient to support a minimum of 500 spawners, since populations with lower abundance lower would likely be at high risk (Allendorf et al. 1997). In several cases, small, relatively isolated spawning areas clearly did not have sufficient habitat to support populations of this size.

> Consequently, the long-term occupancy of these areas likely depends on straying from other populations. In these cases, we included the smaller spawning area as part of the closest upstream independent population. We recognize that these small, isolated areas probably receive strays from a variety of areas. However, we considered the nearest upstream population likely to be the largest contributor of strays.

Finally, our population boundaries encompass identified spawning reaches and the most closely associated watershed (i.e., a population boundary begins at the mouth of a stream that supports an identified population and extends to the upstream boundary or major blockage). In nearly all cases, there is tributary and mainstem habitat downstream of the area included within the population boundary that is vital for the health of the population as overwintering, rearing, or migratory habitat. In some cases, conditions upstream of the population may affect population viability. **Our population definitions are not intended to indicate that these areas are unimportant for population persistence and recovery, but rather to delineate clearly the groups of spawning adults that appear to be demographically independent from each other. Future TRT efforts aimed at identifying limiting factors will consider these and other areas, such as mainstem migratory corridors, that fall outside the population boundaries but are clearly important for population health.**

Population Characterization

In addition to identifying populations, we provide some preliminary characterization of those populations. In particular, we describe briefly:

- **Primary spawning areas.** We define primary spawning areas as those areas where the highest density of spawning within population boundaries occurs. Because we recognize that our method of grouping small tributaries with the nearest upstream population has the potential to create unusual population boundaries, these designations are intended to distinguish major areas of productivity within a population from less productive and possibly demographically dependent areas. However, we restricted our assessment to those ESUs and populations for which spawning location data were available and complete (i.e., we did not use index area spawning surveys for steelhead, as these surveys did not cover a substantial portion of the available habitat.)
- **Spatial structure**. A population's spatial structure affects not only its susceptibility to catastrophic events, but also the potential for differentiation within a population (McElhany et al. 2000). A variety of management actions have the potential to alter a population's spatial structure and distribution, and thus its viability. We categorized all populations as linear or branched (spawning areas within a population distributed along a single waterway vs. distributed along a dendritic system) and continuous or discontinuous (spawning areas within a population separated by less than 3 km vs. more than 3 km).

- **Diversity.** Many independent populations show within-population diversity that should be recognized in recovery planning. We noted general life-history attributes (e.g., run-time), genetic characteristics, and environmental distinctions within each population.
- **Hatchery influence.** We broadly categorized populations on the basis of their actual or potential influence from hatchery fish. Hatchery programs have been extremely varied across the basin; categorizing them often defied our simple classifications. We have compiled additional details of hatchery releases and source stocks in Appendix D. Although we recognize that there may be ecological interactions between wild and hatchery fish that affect a population's viability, we restricted this categorization to genetic interactions, since these have the greatest impact on population structure.

Our characterizations are necessarily incomplete. Data for many populations were absent altogether, and were limited for the vast majority of populations, precluding a comprehensive descriptive effort. However, we provide this information as an aid to regional planners because these characteristics will play an important role as viability (delisting) goals are generated for both populations and ESUs. Until a final recovery plan is established, we recommend that these attributes be considered in the evaluation of management actions.

A Note about Steelhead

Both resident and anadromous forms of *O. mykiss* are included in steelhead ESUs in the interior Columbia River basin where they have the opportunity to interbreed, since the two forms appear to share a common gene pool over evolutionary time periods (Busby et al. 1996). However, the relationship of resident and anadromous fish in a single population on a shorter time frame has the potential to be more variable. Only a handful of studies examining the interaction between the two life-history types have been conducted; they indicate that a full spectrum of gene flow between the groups likely exists in the Columbia River basin. In the Yakima River, for example, a study using nuclear markers suggests that there is abundant gene flow between resident and anadromous forms. In the Deschutes River, however, maternal data indicates considerable isolation of the two forms (although male contribution was not measured.)

Clearly a case-by-case consideration is necessary to determine how resident fish contribute to demographically independent populations in the interior Columbia ESUs. Unfortunately, data to support such a detailed examination do not exist (available information has been summarized in the draft NWFSC Biological Review Team Report (http://www.nwfsc.noaa.gov/trt/brtrpt.htm). In the absence of better data, we defined populations using data from the anadromous component of the ESU. In addition, we identified situations in which the endemic anadromous component had been extirpated, but in which there may be genetic resources remaining from residualized steelhead.

I. SNAKE RIVER SPRING/SUMMER CHINOOK SALMON

The Snake River Spring/Summer Chinook Salmon Evolutionarily Significant Unit (ESU) includes those fish that spawn in the Snake River drainage and its major tributaries, including the Grande Ronde River and the Salmon River, and that complete their adult, upstream migration (passing Bonneville Dam) between March and July. These stream-type fish rear in freshwater for slightly more than a year before smoltification and seaward migration. Since the late 1800s, the ESU has suffered dramatic declines as a result of heavy harvest pressures, habitat modification and loss, and likely inadvertent negative effects of hatchery practices. More recent declines, since the 1950s, have occurred with the construction of the hydropower system on the Snake and Columbia Rivers. As a result of these declines in abundance, this ESU was listed as threatened under the Endangered Species Act in 1992.

Demographically Independent Populations within the Snake River Spring/Summer Chinook Salmon ESU

Based on genetic (Figures I-1 and I-2) and geographic considerations, we established five major groupings in this ESU:

1. the Lower Snake River Tributaries,
2. the Grande Ronde and Imnaha Rivers,
3. the South Fork Salmon River,
4. the Middle Fork Salmon River, and
5. the Upper Salmon River.

In addition, we identified two unallied areas: the Little Salmon River and Chamberlain Creek. We further subdivided these groupings into a total of 31 extant demographically independent populations (Figure I-3). Because this ESU has been relatively well studied, a wide variety of data types were available to us for this effort (Table II-1). However, no data set provided complete coverage across the ESU; therefore, nearly all population boundaries were determined using a subset of data types. Major groupings and populations, in order moving upstream from the mouth of the Snake River, are described in the subsections that follow.

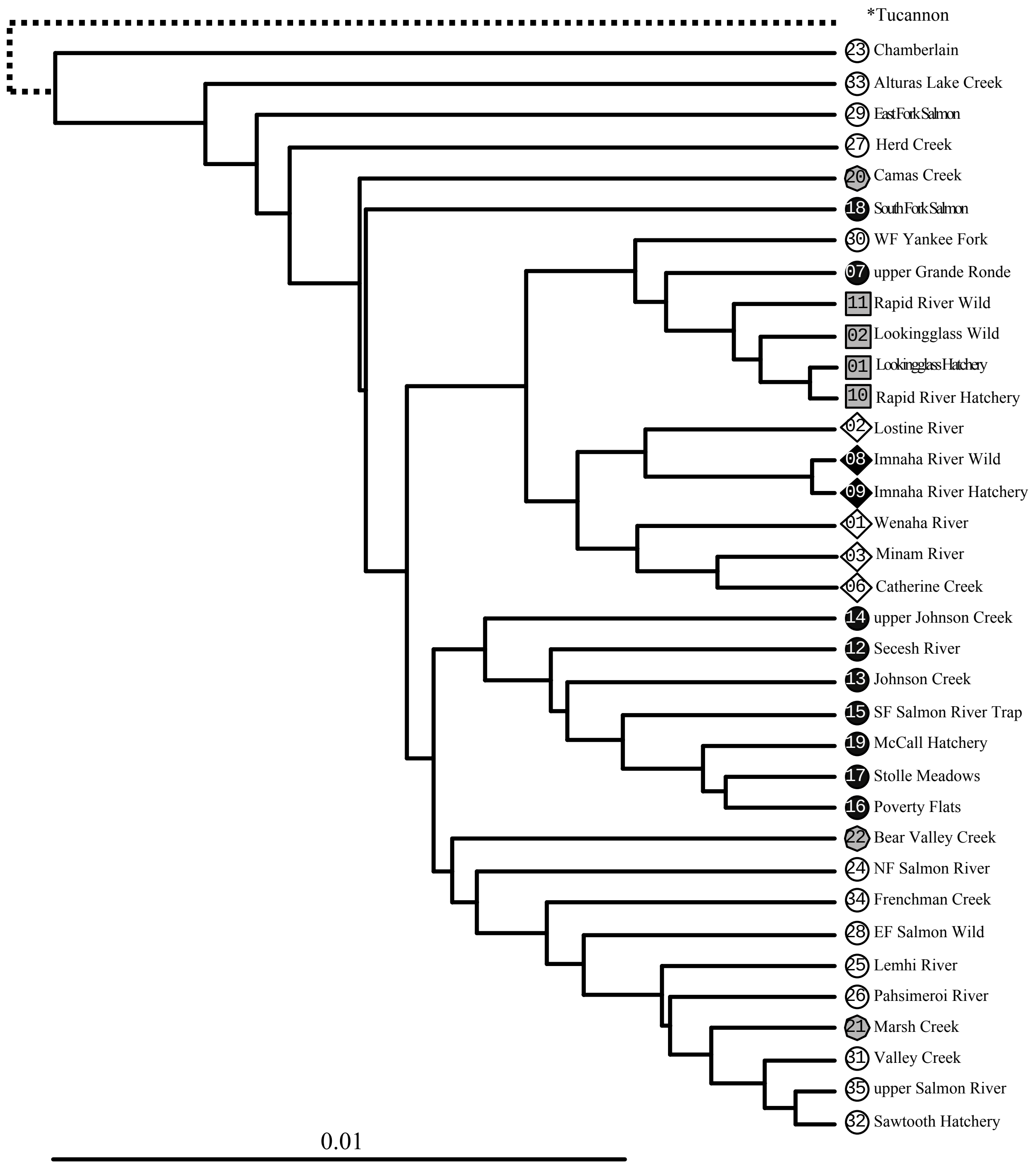


Figure I-1. UPGMA dendrogram based on Cavalli-Sforza and Edwards' chord distance. White diamonds represent samples from the Grande Ronde River basin, black diamonds represent samples from the Imnaha River basin, black circles represent samples from the South Fork Salmon River, white circles represent samples from the Middle Fork and mainstem Salmon River. Sample numbers correspond to locations described in Table CHN1.

*Established from a reduced set of loci (22 out of 26) that included the Tucannon River and indicated largely parallel relationships.

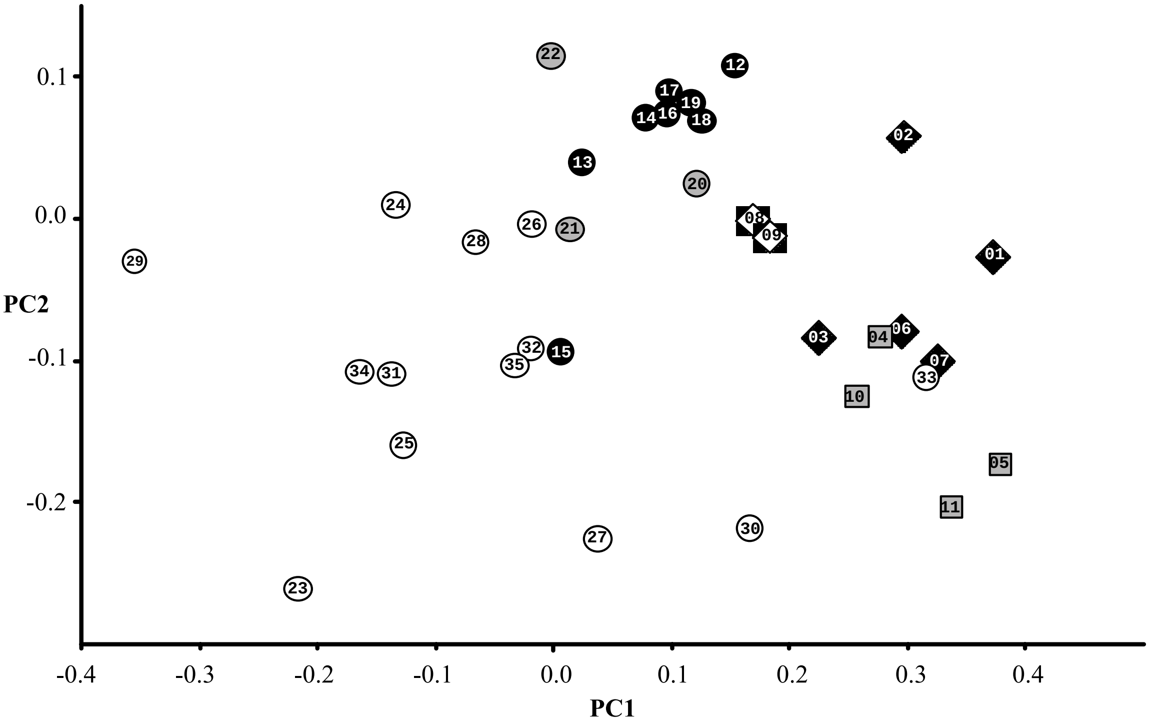


Figure I-2. Principal components analysis of chinook salmon samples based on allele frequencies at 28 allozyme loci. White diamonds represent samples from the Grande Ronde River basin, black diamonds represent samples from the Imnaha River basin, black circles represent samples from the South Fork Salmon River, gray circles represent samples from the Middle Fork Salmon River, white circles represent samples from tributaries to the mainstem Salmon River. Gray squares represent hatchery stocks that may not be representative of a specific geographic region. Sample numbers correspond to locations described in Figure I-1 and Appendix A.

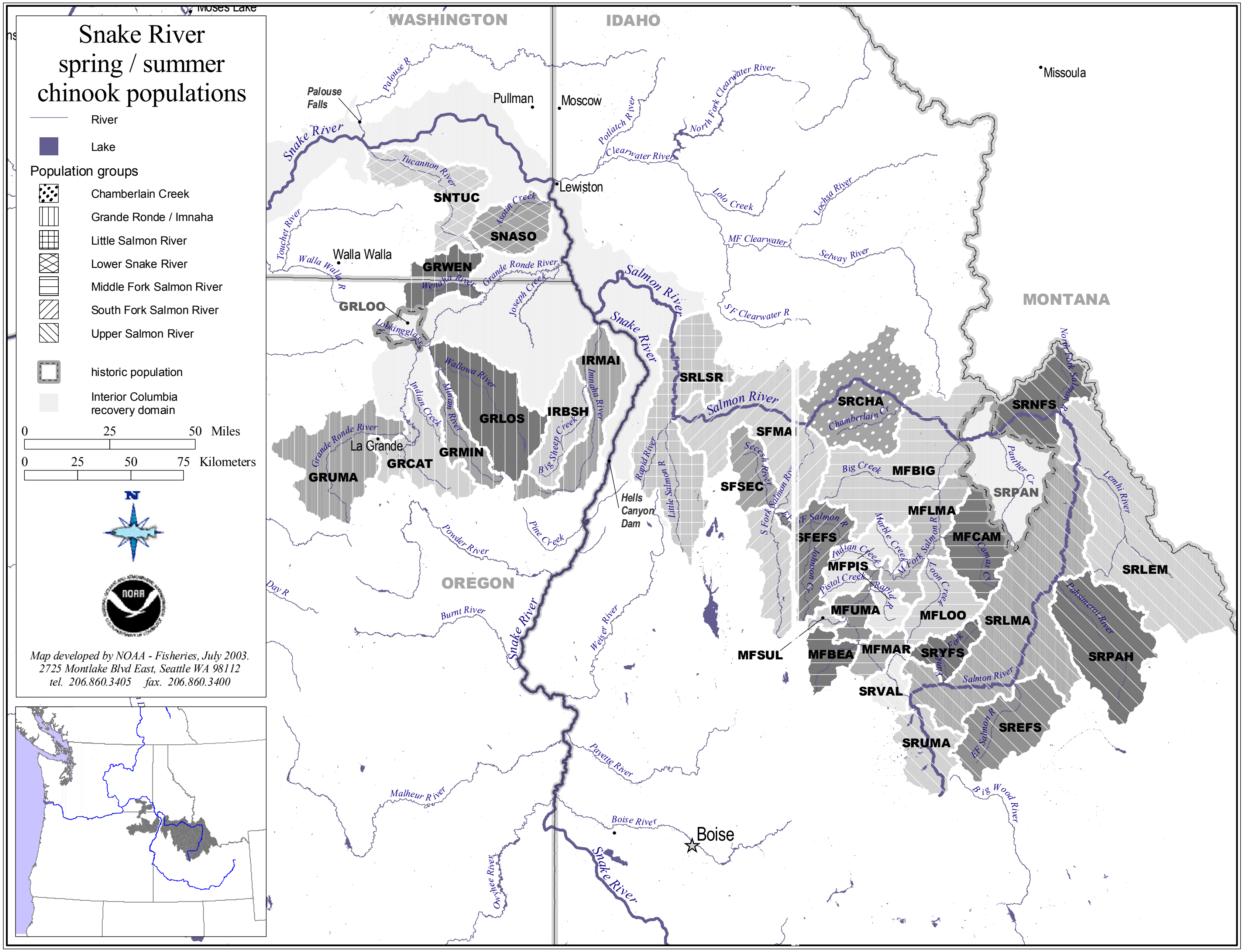


Figure I-3. Snake River spring/summer chinook salmon populations (with major groupings identified).

Table I-1. Available data types and analyses for the Snake River Spring/Summer Chinook ESU.

Data Type	Description
Genetic	Allozyme data (28 loci) for 35 sampling locations collected from 1991 to 1996. Compiled from WDFW and NMFS data sets (unpublished). Samples from multiple years in the same location were combined. We conducted cluster analyses using Cavalli-Sforza and Edwards' chord distance as well as a principal components analysis (PCA) across all locations (Appendix A).
Dispersal/distance	Distance between spawning areas calculated from Streamnet spawning area maps, updated with ODFW and IDFG data. Lacking ESU-specific data on dispersal distances, we used the results from the generalized dispersal distance analysis (Appendix B).
Phenotypic	Length-at-age, age structure, adult run-timing, and juvenile outmigration-timing characteristics compiled from many data sources (see Table 4 for distribution). We conducted ANOVAs to determine whether significant differences existed between sampled areas within major subgroups.
Habitat	EPA-defined ecoregions. Level 4 delineations considered in some population identifications.
Demographic correlation	Index (redds per mile), spawner counts or run reconstructions available for 33 spawning areas. Lengths of data sets vary; many cover the time period from the mid-1960s to the present. We conducted pair-wise correlations on available time series.

Lower Snake River Tributaries

The lower Snake River tributaries, downstream of the Grande Ronde River formed a major group on the basis of shared habitat characteristics (Blue Mountain drainage) and distance from other major groupings.

25. ***Tucannon River (SNTUC).*** Data indicating that chinook from the Tucannon River are genetically distinct from other upriver stocks are compelling (Figure II-1, Myers et al. 1998). Genetic distances between the Tucannon and samples from the Grande Ronde average at least twice the distances between samples within the Grande Ronde (Table I-2). Moreover, samples from the Tucannon have non-overlapping allele frequencies at five loci (Appendix A). In addition to the genetic differentiation, chinook within the Tucannon River are isolated by 197 km from the nearest upstream spawners, a distance well beyond our 10–30-km rule-of-thumb. We found no evidence that the Tucannon was further subdivided into independent units, and thus consider it a single population:

26. ***Asotin Creek (SNASO).*** We consider Asotin Creek as an independent population. Spawning habitat in this tributary to the Snake River appears to be sufficient to

sustain a viable population (similar to that available in the Tucannon River). In addition, it is substantially isolated from other potential spawning areas, both upstream and downstream (Table II-3). However, this population appears to be experiencing a bottleneck. Redd counts from an index area in Asotin Creek have ranged from 0 to 8 since the mid 1980s. [Note that spring chinook smolts were observed during that time period.] (Stovall 2001).

Grande Ronde–Imnaha Rivers

We considered the Grande Ronde and Imnaha Rivers to be a major grouping. Samples from the Grande Ronde and Imnaha Rivers were genetically differentiated from most chinook in the Salmon River basin, with the exception of the Little Salmon–Rapid River group (including Lookingglass Creek and Hatchery), forming one distinct group in both the principle components and cluster analyses (Figures I-1 and I-2). The Rapid River Hatchery stock was derived from fish captured at Hells Canyon Dam (Matthews and Waples 1991), which may account for the clustering of this group and its derivatives (Rapid River wild fish, Lookingglass Hatchery and Creek) with fish from the Grande Ronde and Imnaha Rivers. [The inclusion of the Yankee Fork to the Salmon River within this cluster was interpreted to reflect substantial outplantings of Rapid River fish into the Yankee Fork Salmon River and very limited outplantings in the West Fork Yankee Fork Salmon River (Keifer et al. 1992).]

The Oregon Department of Fish and Wildlife has collected a wide variety of life-history data in this region. On the basis of potential dispersal distances, genetic information, and these life-history traits, we identified seven independent populations within the Grande Ronde–Imnaha major grouping:

27. ***Wenaha River (GRWEN)***. The Wenaha River fish are genetically and geographically distinct from all other Grande Ronde samples, and are also highly differentiated from other potential northeastern Oregon populations based on timing of smolt migrations. This group meets the criteria of an independent population. The environmental characteristics of the Wenaha watershed also differ from other areas of the Grande Ronde and Imnaha subbasins where chinook occur.
28. ***Wallowa–Lostine River (GRLOS)***. This population includes the Wallowa River, the Lostine River, Bear Creek and Hurricane Creek. Of these waterways, only the Lostine River was sampled for genetic analysis. These samples are consistently differentiated from all other analyzed sites in the Grande Ronde drainage (Table II-2; Appendix A). Spawning areas in the Lostine and Wallowa Rivers were less than 30 km apart (Table I-3), and were therefore grouped into the same population. Bear and Hurricane Creeks, which were both judged to have insufficient habitat to support 500 spawners, and are very close to spawning area in the Lostine and Wallowa Rivers were also included in this population.
29. ***Minam River (GRMIN)***. This group is well-separated from most northeastern Oregon tributaries, both genetically and spatially. It is genetically closest to Catherine Creek, but the two areas are isolated by distance (Table I-3). In addition, juvenile migration timing differs significantly between the two areas. Interestingly, although spawning areas in the Minam are closest to the Wallowa–Lostine, the genetic distance

between these two areas is rather high compared to other within-northeastern Oregon comparisons (Table II-2; Appendix A).

30. ***Catherine Creek (GRCAT).*** This population includes Catherine and Indian Creeks. Samples from Catherine Creek are well differentiated genetically from other within-basin populations, except for the Minam River, from which it is distinguished by distance (165 km) and timing of juveniles through the main stem.
31. ***Upper Grande Ronde (GRUMA)***. This population includes the upper Grande Ronde River and Sheep Creek. Genetic analysis indicates that fish spawning in this area were likely influenced by earlier outplantings of Rapid River stock (which have been discontinued). However, this population is spatially segregated from other spawning aggregates in northeastern Oregon is far greater than 30 km (Table I-3). In addition, timing of juvenile migration appears to be different between this area and Catherine Creek, the nearest population.
32. ***Imnaha main stem (IRMAI)***. Hatchery and wild collections from the mainstem Imnaha River were genetically indistinguishable. These samples fell within the cluster containing most of the Grande Ronde collections (Figure I-1), and were distinct from all but the most closely aligned Lostine River samples. The genetic distinction, large distance from other populations (except Big Sheep Creek), and many life-history differences support its status as an independent population.
33. ***Big Sheep Creek (IRBSH)***. This grouping is based on the distance between Big Sheep Creek and Imnaha River primary spawning areas (48 km) and the historically poor demographic correlation between these groups.

The Grande Ronde-Imnaha grouping also includes an historically extirpated population:

Lookingglass Creek. The endemic chinook in Lookingglass Creek are considered extinct as a result of adult collection of natural fish during the early years of Lookingglass Hatchery operations and extensive and continued natural spawning of Rapid River Hatchery stock in Lookingglass Creek. However, this creek is geographically separated from other spawning areas, and likely had the capacity to support an independent population historically.

Table I-2. Grande Ronde–Imnaha genetic distribution. Pairwise Cavalli-Sforza and Edwards Chord distances (km) above the diagonal. Values below the diagonal are standardized to the maximum value (bolded).

	Sample Location									
Sample Location	**1LOOKH**	**2LOOKW**	**3LOSTN**	**4MINM**	**5CATHR**	**6UPRGR**	**7WNAHA**	**8IMNHW**	**9IMNHH**	**36TUCAN**
1LOOKH	--	0.003	0.013	0.009	0.007	0.007	0.011	0.006	0.007	0.033
2LOOKW	0.070	--	0.012	0.010	0.009	0.008	0.012	0.008	0.009	0.040
3LOSTN	0.298	0.275	--	0.012	0.010	0.016	0.011	0.006	0.008	0.043
4MINM	0.210	0.235	0.287	--	0.004	0.008	0.006	0.006	0.007	0.026
5CATHR	0.172	0.217	0.240	0.089	--	0.009	0.006	0.006	0.006	0.031
6UPRGR	0.172	0.189	0.368	0.179	0.214	--	0.013	0.010	0.011	**0.043**
7WNAHA	0.252	0.287	0.252	0.128	0.131	0.301	--	0.010	0.012	0.021
8IMNHW	0.135	0.189	0.149	0.133	0.131	0.224	0.226	--	0.001	0.036
9IMNHH	0.163	0.203	0.175	0.163	0.149	0.245	0.270	0.021	--	0.038
36TUCAN	0.760	0.925	0.998	0.604	0.716	**1.000**	0.485	0.848	0.890	--

Table I-3. Distance matrix for chinook populations within the Snake River spring/summer chinook ESU. Distances were computed using 100k scale hydrography from Streamnet; distance units are in kilometers.

	SNTUC	SNASO	GRWEN	GRLOS	GRMIN	GRCAT	GRUMA	IRMAI	IRBSH	SRLSR	SFMAI	SFSEC	SFEFS	SRCHA	MFBIG	MFLMA	MFCAM	MFLOO	MFPIS	MFSUL	MFBEA	MFMAR	MFUMA	SRNFS	SRLEM	SRPAH	SRLMA	SREFS	SRYFS	SRVAL	SRUMA
SNTUC	0																														
SNASO	194	0																													
GRWEN	291	145	0																												
GRLOS	380	233	110	0																											
GRMIN	384	237	114	55	0																										
GRCAT	375	229	106	79	83	0																									
GRUMA	494	347	224	197	201	129	0																								
IRMAI	303	156	178	266	270	262	380	0																							
IRBSH	317	170	192	280	284	276	394	55	0																						
SRLSR	325	179	200	289	293	284	403	148	163	0																					
SFMAI	383	237	258	347	351	342	461	206	221	58	0																				
SFSEC	510	363	385	473	477	469	587	333	347	184	126	0																			
SFEFS	511	365	386	474	478	470	588	334	348	186	128	1	0																		
SRCHA	458	312	333	421	425	417	536	281	295	133	75	64	66	0																	
MFBIG	537	391	412	500	504	496	614	360	374	211	153	143	144	79	0																
MFLMA	593	446	467	556	560	552	670	416	430	267	209	199	200	134	56	0															
MFCAM	612	466	487	575	579	571	689	435	449	287	229	218	219	154	75	19	0														
MFLOO	628	482	503	592	596	588	706	452	466	303	245	234	236	170	92	36	17	0													
MFPIS	656	510	531	619	623	615	733	479	493	331	273	262	263	198	119	64	44	28	0												
MFSUL	705	558	580	668	672	664	782	528	542	379	321	311	312	247	168	112	93	76	49	0											
MFBEA	724	578	599	687	691	683	801	547	561	399	341	330	331	266	187	131	112	96	68	19	0										
MFMAR	724	578	599	687	691	683	801	547	561	399	341	330	331	266	187	131	112	96	68	19	0	0									
MFUMA	665	519	540	628	632	624	742	488	502	340	282	271	272	207	128	73	53	37	9	40	59	59	0								
SRNFS	600	454	475	563	567	559	678	423	437	275	217	206	208	142	63	82	101	118	145	194	213	213	154	0							
SRLEM	702	556	577	665	670	661	780	525	539	377	319	308	310	244	165	184	203	220	247	296	315	315	256	102	0						
SRPAH	726	580	601	689	693	685	804	549	563	401	343	332	334	268	189	208	227	244	271	320	339	339	280	126	126	0					
SRLMA	696	550	571	659	663	655	773	519	533	371	313	302	303	238	159	178	197	214	241	290	309	309	250	96	96	30	0				
SREFS	794	648	669	757	761	753	871	617	631	469	411	400	401	336	257	276	295	311	339	388	407	407	348	194	194	68	98	0			
SRYFS	843	697	718	806	810	802	921	666	680	518	460	449	451	385	306	325	344	361	388	437	456	456	397	243	243	117	147	49	0		
SRVAL	857	710	732	820	824	816	934	680	694	531	473	463	464	398	320	338	358	374	402	451	470	470	411	256	257	130	161	63	27	0	
SRUMA	865	719	740	829	833	824	943	688	702	540	482	471	473	407	328	347	366	383	411	459	478	478	420	265	265	139	169	71	36	9	0

Table I-4. South Fork Salmon River genetic distribution. Pairwise Cavalli-Sforza and Edwards Chord distances (km) above the diagonal. Values below the diagonal are standardized to the maximum value (bolded).

Sample Location	**Sample Location**									
	12JOHNS	**13UJOHN**	**14SECSH**	**15MCCLL**	**16STLLE**	**17POVRT**	**18SFTRP**	**19SFSAL**	**10RAPDH**	**11RAPDW**
12JOHNS	--	0.013	0.012	0.008	0.009	0.009	0.012	0.023	0.013	0.018
13UJOHN	0.547	--	0.013	0.011	0.013	0.011	0.013	0.017	0.017	**0.025**
14SECSH	0.486	0.531	--	0.006	0.011	0.008	0.013	0.016	0.015	0.020
15MCCLL	0.322	0.433	0.245	--	0.005	0.004	0.007	0.011	0.010	0.015
16STLLE	0.347	0.522	0.461	0.212	--	0.004	0.008	0.016	0.012	0.017
17POVRT	0.367	0.457	0.314	0.167	0.155	--	0.007	0.016	0.012	0.018
18SFTRP	0.494	0.518	0.531	0.286	0.343	0.286	--	0.020	0.011	0.017
19SFSAL	0.935	0.694	0.637	0.429	0.669	0.637	0.800	--	0.016	0.024
10RAPDH	0.522	0.706	0.592	0.420	0.473	0.473	0.457	0.661	--	
11RAPDW	0.714	**1.000**	0.824	0.629	0.686	0.735	0.694	0.996	0.131	0.003

Little Salmon River

The Little Salmon River has been heavily influenced by Rapid River Hatchery stock. Beyond genetic samples taken in the Rapid River (both hatchery and instream), few data were available from this area. Based on the large distance from other spawning aggregations and lack of information supporting any further subdivision, we delineated a single population for the Little Salmon River and Rapid River drainages:

34. ***Little Salmon River (SRLSR).*** This population includes the Little Salmon River and its tributaries as well as Whitebird and Slate Creeks, tributaries to the Salmon River.

South Fork Salmon River

The South Fork Salmon River supports a largely genetically cohesive grouping of summer-run fish, supplemented by the McCall Hatchery, which uses locally derived (South Fork) stock. However, both genetic analyses did identify an outlier (different in each case) that may reflect transitory hatchery influences or sampling error (Figures I-1 and I-2). Based on this genetic similarity, basin topography and the common adult run-timing in the basin, we consider the South Fork to be a major grouping, including three independent populations:

35. ***South Fork Main Stem (SFMAI).*** This population includes the South Fork main stem, Poverty Flat and Stolle Meadows. Extending the full length of the South Fork Salmon River and to contiguous minor downstream tributaries to the Little Salmon River, the grouping includes both the clustering (**18-**South Fork) and PCA (**15**-South Fork Trap) genetic outlier samples (see also Table I-4). The clustering of genetic samples from Poverty Flat and Stolle Meadows with McCall Hatchery samples likely reflects the local origin of McCall stock and its outplanting in the area. Geographic distances among spawning localities within the South Fork were consistent with a potential spawning continuum as were adult and juvenile life-history variables.
36. ***Secesh River (SFSEC).*** The Secesh River, including Lake and Lick Creeks is genetically distinguished within the South Fork Salmon River basin at two loci (Appendix A). In addition, the main spawning areas in this population were farther than 30 km from spawning areas in the adjacent South Fork mainstem population, and timing of juvenile mainstem migration was highly differentiated from other locations sampled in the South Fork Salmon River.
37. ***East Fork South Fork (SFEFS).*** This population includes both Johnson Creek and the extirpated upper East Fork South Fork Salmon River. Johnson Creek collections are distinguished genetically within the basin at the PGK1* locus. In addition, Johnson Creek fish have distinct juvenile mainstem migration timing. On this basis we designated the East Fork South Fork an independent population, in spite of its close proximity to the Secesh (Table I-3) Chinook salmon in the upper East Fork South Fork Salmon River were extirpated by mining operations early in the twentieth century; this historically may have constituted an independent population. The East Fork South Fork has received supplementation from the McCall Hatchery in recent years.

Chamberlain Creek

38. ***Chamberlain Creek (SRCHA).*** Chamberlain Creek was identified as an independent population based on its genetic distinction from other groups upstream from the confluence of the South Fork Salmon River and mainstem Salmon River. With the exception of the Tucannon, it is the most genetically divergent population within the ESU (Table I-5), and the only one with variation at the PGDH* locus ($p = 0.087$). Independence is supported by substantial geographic isolation from adjacent South Fork and Middle Fork Salmon River tributaries. We found no basis to further subdivide the population.

Middle Fork Salmon River

Genetic data for three sampled locations in the Middle Fork Salmon River were scattered throughout the cluster analysis and fell intermediate to South Fork Salmon River and mainstem samples in the PCA plot (Figures I-1 and I-2). This apparent genetic differentiation may be due in part to genetic drift; returns to this region during the sampling period were extremely low. Because of this consideration, and the large distance separating the Middle Fork Salmon River from both the South Fork Salmon River and the upper mainstem spawning locations, we regard the Middle Fork Salmon River as a major grouping. No hatcheries are located within this drainage, which includes fish with both spring and summer adult run-timing. We identified nine independent populations in the Middle Fork Salmon River major group:

39. ***Big Creek (MFBIG)***. Identified as an independent population based on drainage size and historical escapement, the drainage is only moderately isolated from spawning habitat in the lower main stem of the Middle Fork Salmon River (Table I-3), although primary spawning areas are better separated. Data were insufficient to distinguish between upper, spring-run, and lower, summer-run portions of the drainage.

40. ***Lower Middle Fork main stem (MFLMA)***. Summer chinook spawning in the Middle Fork Salmon River between Indian Creek and Big Creek were classified as an independent population based on isolation from spawning areas in tributaries. Independence was supported by qualitative habitat differences (hydrology, temperature, elevation, and substrate).

41. ***Camas Creek (MFCAM).*** Camas Creek and its tributaries are considered an independent population. Genetic data indicated isolation from other Middle Fork Salmon River and Upper Salmon River populations, notably at the sAAT4* locus (Table I-5, Appendix A). Geographic isolation within the grouping was moderate from the Lower Middle Fork mainstem population and high from all others. Historical demographic population data supported independent population designation.

42. ***Loon Creek (MFLOO).*** Loon Creek was identified as an independent population based on high geographic isolation from other potential Middle Fork Salmon River populations. In addition, historical redd counts indicate that the threshold population size was met. Although the Idaho Department of Fish and Game (IDFG) classifies fish returning to upper reaches as spring chinook and those to lower reaches as

summer chinook, data were insufficient to designate more than one independent population.

43. ***Pistol Creek (MFPIS).*** Pistol Creek and adjacent small tributaries (Marble Creek, Indian Creek, and Rapid River) were identified as an aggregate independent population based on low geographic distances within this grouping and large distances to other Middle Fork Salmon River spawning areas. Individual streams in this population are not likely to meet our population size rule-of-thumb.

44. ***Sulphur Creek (MFSUL).*** Little data existed to characterize fish spawning in Sulphur Creek. We considered grouping this creek with the Upper Middle Fork main stem (see population 23). However, the vast majority of spawning in Sulphur Creek occurs in higher elevation meadows, well-separated from other spawning areas. In addition, historical records indicate that spawners were abundant (>500) in this tributary. Due to this isolation and size, we defined Sulphur Creek as an independent population.

45. ***Bear Valley Creek (MFBEA)***. High genetic distances from Middle Fork Salmon River tributaries Marsh Creek and Camas Creek identified Bear Valley Creek (and its tributary Elk Creek) as an independent population. Geographic distances from any spawning area in adjacent groupings were moderate to low (0-19 km), although much spawning happens farther upstream. Historical population estimates were strongly correlated with those of Marsh Creek.

46. ***Marsh Creek (MFMAR)***. As with Bear Valley and Camas Creeks, multiple sample years indicated that spawners in Marsh Creek were genetically differentiated from nearby spawning aggregates. It was therefore defined as an independent population even though it is highly correlated with Bear Valley Creek in life-history and abundance criteria.

47. ***Upper Middle Fork main stem (MFUMA)***. Qualitative habitat differences (hydrology, temperature, elevation, and substrate) from adjacent tributaries led to provisional designation of the Upper Middle Fork main stem as an independent population. Geographic distances from these groups were low (9 km). No historical or genetic data were available.

Upper Mainstem Salmon River

Genetic samples from tributaries of the upper mainstem Salmon River were genetically very divergent from one another and in many cases individual sites were highly differentiated from all others (Table II-5). Populations in this area include both spring and summer adult run-timing. These patterns are interpreted to reflect the enormous geographic area and impressive array of environmental diversity encompassed by the upper mainstem tributaries. Although clearly not representing a genetically homogeneous group, spawning locations are interspersed along the main stem, making any further division based on geographic isolation difficult. We therefore treated the remaining samples as a single major grouping for more detailed investigation during the next level of analysis.

24. ***North Fork Salmon River (SRNFS)***. The North Fork Salmon River was identified as an independent population based on genetic differentiation from other upper mainstem Salmon River samples. In addition, spawning aggregates in the North Fork are separated from other spawning areas by 63 km. Basin size (indicating potential capacity) and historical redd counts further supported this designation.
25. ***Lemhi River (SRLEM)***. An independent population designation for the Lemhi River and Hayden Creek spring chinook was based largely on geographic distance (102 km). Genetic distinction from some groups was high (upper East Fork, Herd Creek, Alturas Lake, Frenchman Creek) and low for others (Valley Creek, upper Salmon River, Sawtooth Hatchery, Pahsimeroi River). However, adult migration time differed significantly from Pahsimeroi River. Historical run size was high.
26. ***Pahsimeroi River (SRPAH)***. Geographic distance and isolation (96 km), coupled with moderate to high genetic differentiation, distinguished Pahsimeroi River summer-run chinook salmon from other populations. This status was supported by a substantial drainage area and high (2,500) historical estimates of adult abundance.
27. ***Upper Salmon lower main stem (SRLMA)***. This population includes fish spawning in the main stem of the upper Salmon River from the mouth of the Lemhi River to Redfish Lake Creek, as well as tributaries including Thompson and Squaw Creeks. These areas include nearly contiguous spawning aggregates of fish with both summer and spring adult run-timing.
28. ***East Fork Salmon River (SREFS)***. The East Fork Salmon River, including Herd Creek, was designated as a single independent population based largely on distance from other spawning aggregates and genetic differentiation from other upper Salmon River samples. Within this population, Herd Creek and the upper East Fork Salmon River are also distinct, but this may be related to sampling error, as escapement to Herd Creek was extremely low the year before juveniles were sampled. However, juvenile migration timing also differed between Herd Creek and the upper East Fork Salmon River, suggesting that there may be subdivision within this population.
29. ***Yankee Fork (SRYFS).*** Yankee Fork and West Fork Yankee Fork Salmon River spring chinook salmon were designated as one independent population based on geographic distance (minimum 49 km) from all other upper Salmon spawning aggregations (except the summer-run lower mainstem spawners) and habitat capacity.

The Yankee Fork Salmon River is also highly differentiated genetically, but this likely reflects the outplanting of Rapid River stock into this tributary.

30. ***Valley Creek (SRVAL)***. Valley Creek and its tributaries support both spring and summer-run fish. Although genetic samples from Valley Creek cluster closely with those from the upper Salmon River (population 31), this is likely due to the influence of extensive outplanting from the Sawtooth Hatchery (which also clusters with these populations. The bulk of spawning in this population occurs upstream, sufficiently separated from upper Salmon River spawning areas to warrant independent population status. Substantial estimated historical run size (2,500) supports this designation.

31. ***Upper Salmon River main stem (SRUMA)***. This designated independent population includes spawners in the mainstem Salmon River above Redfish Lake Creek and all tributaries to the main stem including Alturas Lake Creek. Historical estimated median run size (637) supports the independent designation. However, there are several suggestions that there is some substructure in this population. Alturas Lake Creek historically supported a population spawning in the inlet stream, above Alturas Lake, suggesting that there may have been some ecological segregation. In addition, a single year genetic sample (of parr) from Alturas Lake Creek was distinct from Upper Salmon River samples (notably differing in the frequency of ADA*, sDHP1, and mMDH2 loci). However, we consider this distinction likely to be the result of genetic drift, since only three redds were located in Alturas Lake Creek during surveys the year before genetic samples were collected. We consider Alturas Lake Creek part of the upper Salmon River mainstem population, but suggest that this substructure be considered when evaluating management actions.

The upper Salmon River also includes one extirpated population:

Panther Creek. Beginning in the 1940s, mining operations in Panther Creek seriously impaired water quality in this tributary to the Salmon River. By the 1970s, the endemic fish had been extirpated. Panther Creek has been stocked several times with hatchery fish from a variety of stocks. This creek is sufficiently distant from other spawning aggregates and has sufficient available habitat to be considered a separate, independent population.

Primary spawning areas for each population are presented in Table II-6. Populations are characterized with respect to genetics, life-history and habitat diversity, and hatchery influence in Tables II-7 and II-8. Further details, including basin physiography and general climatic information for the watersheds each population occupies, are in Appendix C.

Table I-5. Middle-upper Salmon River genetic distance. Pairwise Cavalli-Sforza and Edwards Chord distances above the diagonal. Values below the diagonal are standardized to the maximum value (bolded).

	Sample Location															
Sample Location	**20UPSAL**	**21FRNCH**	**22ALTRC**	**23VALLY**	**24SAWTH**	**25MARSH**	**26CHMBR**	**27BEARV**	**28WFYNK**	**29HERDC**	**30PAHSM**	**31CAMAS**	**32NFSAL**	**33LEMHI**	**34EFSAW**	**35EFSAL**
20UPSAL	--	0.009	0.016	0.002	0.001	0.003	0.022	0.012	0.007	0.008	0.006	0.017	0.011	0.005	0.008	0.011
21FRNCH	0.217	--	0.021	0.009	0.009	0.010	0.028	0.019	0.012	0.020	0.009	0.021	0.014	0.013	0.013	0.019
22ALTRC	0.406	0.537	--	0.018	0.014	0.016	**0.040**	0.030	0.011	0.020	0.021	0.026	0.028	0.023	0.024	0.030
23VALLY	0.055	0.227	0.458	--	0.003	0.005	0.024	0.015	0.009	0.009	0.007	0.024	0.012	0.007	0.013	0.012
24SAWTH	0.035	0.214	0.340	0.071	--	0.004	0.023	0.013	0.006	0.007	0.006	0.016	0.011	0.005	0.007	0.010
25MARSH	0.083	0.247	0.406	0.134	0.111	--	0.026	0.008	0.011	0.012	0.005	0.013	0.012	0.007	0.009	0.014
26CHMBR	0.564	0.695	**1.000**	0.594	0.569	0.642	--	0.028	0.023	0.030	0.021	0.033	0.023	0.018	0.030	0.025
27BEARV	0.302	0.476	0.753	0.383	0.330	0.202	0.710	--	0.023	0.023	0.011	0.014	0.017	0.013	0.012	0.019
28WFYNK	0.179	0.297	0.264	0.214	0.146	0.275	0.569	0.574	--	0.011	0.010	0.022	0.012	0.010	0.015	0.019
29HERDC	0.199	0.499	0.514	0.227	0.184	0.305	0.743	0.589	0.277	--	0.017	0.030	0.024	0.013	0.017	0.019
30PAHSM	0.139	0.229	0.526	0.174	0.146	0.123	0.534	0.287	0.254	0.416	--	0.014	0.009	0.006	0.009	0.014
31CAMAS	0.421	0.526	0.650	0.605	0.403	0.332	0.821	0.360	0.562	0.756	0.363	--	0.020	0.013	0.013	0.028
32NFSAL	0.272	0.363	0.710	0.297	0.287	0.305	0.569	0.423	0.312	0.592	0.217	0.509	--	0.012	0.019	0.015
33LEMHI	0.126	0.320	0.567	0.166	0.131	0.179	0.451	0.327	0.247	0.327	0.159	0.325	0.312	--	0.008	0.015
34EFSAW	0.207	0.327	0.610	0.317	0.169	0.214	0.766	0.310	0.375	0.438	0.217	0.338	0.479	0.204	--	0.013
35EFSAL	0.270	0.466	0.761	0.302	0.259	0.353	0.630	0.469	0.479	0.489	0.360	0.708	0.383	0.380	0.320	--

Historically Occupied Areas

Chinook salmon were extirpated from the Clearwater River and from the Snake River and its tributaries above Hells Canyon Dam (Figure I-4). These areas encompass approximately 50% of the pre-European spawning areas for spring-summer chinook in the Snake River basin (NRC 1996). Although the fish originating in these areas may have been included in the Snake River spring/summer chinook ESU, it is possible that some of these areas may have supported a different ESU. Likewise, there are no data on which to base definitive population delineations for these extirpated areas, so we list major tributaries known to support stream-type chinook salmon. By analogy to other populations identified, it is be reasonable to suppose that these tributaries supported one or more populations, but the lack of data, such as spawning distributions, make it impossible to make those determinations.

- **Clearwater River.** Blocked to chinook in 1927 by the Lewiston Dam, major subbasins in the Clearwater include the ***North Fork Clearwater***, ***Lolo Creek***, ***South Fork Clearwater***, ***Middle Fork Clearwater***, the ***Lochsa River***, and the ***Selway River***.
- **Snake River above Hells Canyon Dam.** Tributaries above Hells Canyon were sequentially blocked by tributary and mainstem dams beginning in the early 1900s and culminating with the construction of the Hells Canyon Dam complex in the 1960s. Important tributaries supporting stream-type chinook include the ***Powder River***, the ***Burnt River***, the ***Weiser River***, the ***Payette River***, parts of the ***Malheur River***, the ***Boise River***, the ***Owyhee River***, the ***Bruneau River***, ***Big Wood River***, ***Salmon Falls Creek*** and ***Rock Creek***.

Monitoring and Evaluation Needs

Our population identification efforts would be greatly improved by the addition of several types of data. As research efforts continue on Snake River spring/summer chinook population structure, we recommend that a priority be placed on the following, in the following order:

- Genetic information, collected at a finer scale. The Upper and Middle Forks of the Salmon River particularly lack samples. Microsatellite data throughout the Snake drainage, and allozyme data from the Salmon River basin, compatible with that already collected in northeastern Oregon, would be especially useful.
- Dispersal and stray rate information. Since dispersal rates and distance underlie true population boundaries, more data about wild chinook homing behavior would be extremely useful. In particular, dispersal information collected at relatively small distances (e.g., 10–50 km) would fill a critical data gap.
- Spawn-timing data. Spring and summer chinook are distinguished on the basis of their adult run-timing. However, few data exist to determine whether these fish represent distinct spawning units based on spawn timing or spawn over a continuous and overlapping time period. This information would help refine the boundaries of populations in areas that include both spring and summer runs.

- Hatchery fish source and outplanting documentation. Because naturally spawning hatchery fish can alter the genetic signal of a population, better documentation of the history of hatchery outplantings throughout the basin would be extremely useful.
- Juvenile life-history data. In several cases, juvenile life-history patterns (particularly outmigration timing) helped determine boundaries between populations at a fine scale. Additional information of this type may contribute to refining population delineations.
- Morphological data, collected on a finer scale. Although there was some morphological data available (particularly length-at-age information), it was typically collected at a very coarse scale (e.g., one sample from each major tributary to the Snake or Salmon Rivers). Finer-scale data collection would give this data type a greater contribution to population identification efforts.

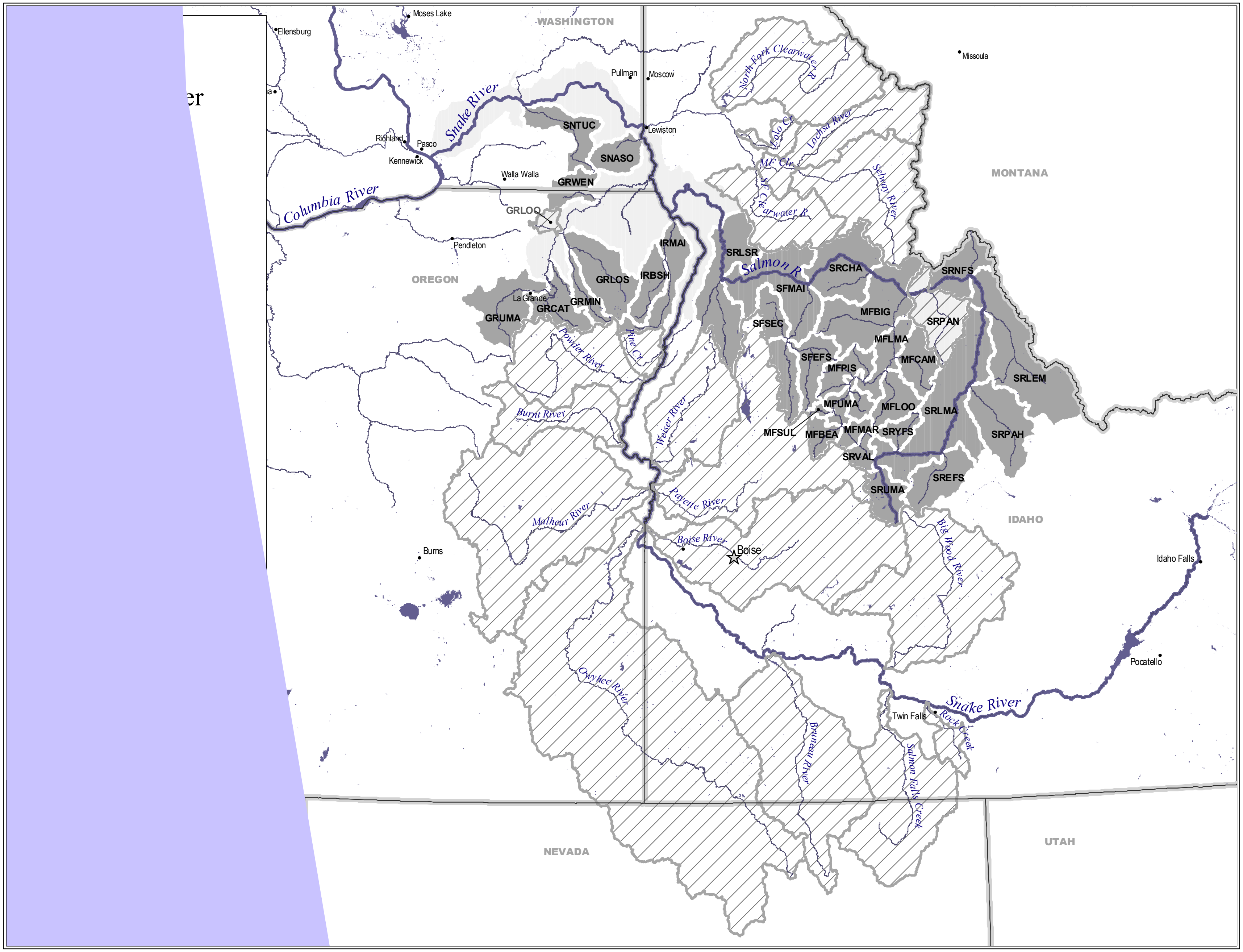


Figure I-4. Extirpated areas possibly affiliated with the Snake River spring/summer chinook ESU.

Table I-6. Snake River spring/summer chinook core spawning areas.

Region	Population	Code	Core Spawning Area Description	Historical Spawning Area Description
Grande Ronde				
	Catherine Creek	GRCAT	Lower 3 miles of the North Fork, lower 2 miles of the South Fork, and the main stem from the forks to 5 miles above the town of Union	
	Wallowa/Lostine River	GRLOS	2.5 miles below forks to Williamson Campground, Wallowa River 4.5 miles above confluence with Hurricane Creek to confluence with Hurricane Creek, and the lower 3 miles of Hurricane Creek	
	Minam River	GRMIN	Main stem from Elk Creek downstream to Little Minam	
	Upper mainstem Grande Ronde River	GRUMA	Mainstem Grande Ronde from 0.5 miles below East Fork to the confluence with Sheep Creek	
	Wenaha River	GRWEN	South Fork from Milk Creek to mouth and the main stem from forks to Crooked Creek	
Imnaha				
	Big Sheep Creek	IRBSH	Road 39-140 bridge to Coyote Creek and lower 3 miles of Lick Creek	
	Imnaha River main stem	IRMAI	Mainstem from Blue hole to Grouse Creek	
Lower Snake tributaries				
	Tucannon River	SNTUC	Spawning mostly occurs from about RM 32 to RM 59.	
	Asotin Creek	SNASO	Spawning is known to occur in the North Fork.	
South Fork Salmon				
	Secesh River	SFSEC	Mainstem Secesh River and Lake Creek	
	South Fork Salmon River	SFMAI	Main stem upstream of East Fork South Fork Salmon (two primary locations: Poverty Flat	

Region	Population	Code	Core Spawning Area Description	Historical Spawning Area Description
			and Stolle Meadows)	
	East Fork South Fork Salmon River/Johnson Creek	SFEFS	Johnson Creek below Trapper Creek, Johnson Creek above Landmark Creek (reestablished by barrier removal, 1985), East Fork South Fork Salmon River above Johnson Creek (reintroduced from McCall Hatchery, 1990s)	East Fork South Fork Salmon River spawning aggregate had been extirpated by mining activities in 1940s; reintroductions began in 1990s.
Salmon River tributaries				
	Chamberlain Creek	SRCHA	Chamberlain Creek above West Fork, West Fork Chamberlain Creek	
	Little Salmon River	SRLSR	Rapid River, Boulder Creek, and Hazard Creek	
Middle Fork Salmon River				
	Bear Valley Creek/Elk Creek	MFBEA	Bear Valley Creek upstream of Fir Creek, Elk Creek	
	Big Creek	MFBIG	Big Creek (primary areas upstream of Monumental Creek (spring run) and downstream of Monumental Creek (summer run), Monumental Creek	
	Camas Creek	MFCAM	Camas Creek upstream of Hammer Creek, South Fork Camas Creek	
	Middle Fork Salmon River below Indian Creek	MFLMA	Mainstem Middle Fork Salmon	
	Pistol Creek	MFPIS	Marble, Indian, and Pistol Creeks; Rapid River	
	Marsh Creek	MFMAR	Marsh Cr eek upstream of Beaver Creek, and Beaver, Cape Horn, Knapp and Creeks	
	Sulphur Creek	MFSUL	Sulphur Creek	
	Loon Creek	MFLOO	Loon Creek upstream of Cold Springs Creek, Warm Springs Creek, Mayfield Creek	
	Middle Fork	MFUMA	Mainstem Middle Fork Salmon	

Region	Population	Code	Core Spawning Area Description	Historical Spawning Area Description
	Salmon River above Indian Creek			
Upper Salmon River				
	Valley Creek	SRVAL	Mouth to Stanley Lake Creek (summer run); main stem and tributaries upstream of Stanley Lake Creek (spring run), Elk Creek,	
	Lemhi River	SRLEM	Primary area in mainstem Lemhi upstream of Hayden Creek, some spawning in Hayden Creek and lower Lemhi River	
	North Fork Salmon River	SRNFS	Mainstem North Fork Salmon	
	Pahsimeroi River	SRPAH	Mainstem Pahsimeroi	
	East Fork Salmon River	SREFS	Mainstem East Fork from mouth to ~3.5 miles below Boulder Creek (summer run); main stem from 3.5 miles below Boulder Creek to headwaters (spring run); Herd Creek	
	Upper mainstem Salmon River			
	above Redfish Lake	SRUMA	Mainstem Salmon River from Redfish Lake Creek to headwaters, Alturas Lake Creek, Pole Creek, Beaver Creek, Frenchman Creek	
	below Redfish Lake	SRLMA	Primary spawning area: mainstem Salmon River between East Fork Salmon and Redfish Lake Creek, some spawning downstream to mouth of Lemhi River	
	Yankee Fork	SRYFS	Mainstem Yankee Fork (from ~1 mile above mouth to headwaters), West Fork Yankee Fork	

Table I-7. Snake River spring/summer chinook salmon populations.

Basin	Population Name	Population Code	Spatial Structure	Within-Population Characteristics		
				Life History	Habitat (Level 4 Ecoregion)	Genetics
Grande Ronde						
	Catherine Creek	GRCAT	Branched continuous	Adults: spring run	Upper reaches Wallowa/Seven Devils Mountains, lower reaches continental zone foothills	
	Wallowa/Lostine River	GRLOS	Branched discontinuous	Adults: spring run	Upper reaches mesic forest, lower reaches Blue Mountain basins	Lostine River samples show consistent genetic signal, with some differentiation from the rest of the Grande Ronde River basin.
	Minam River	GRMIN	Branched discontinuous	Adults: spring run	Upper reaches mesic forest, lower reaches Wallowa/Seven Devils Mountains	
	Upper mainstem Grande Ronde River	GRUMA	Branched discontinuous	Adults: spring run	Maritime-influenced zone	
	Wenaha River	GRWEN	Branched discontinuous	Adults: spring run	Canyons and dissected highlands	
Imnaha						
	Big Sheep Creek	IRBSH	Branched continuous	Adults: spring run	Upper reaches canyons and dissected highlands, lower reaches canyons and dissected uplands	
	Imnaha River main stem	IRMAI	Linear continuous	Adults: spring run	Upper reaches mesic forest, middle reaches canyons and dissected highlands, lower reaches canyons and dissected uplands	
Lower Snake tributaries						
	Tucannon River	SNTUC	Linear continuous	Adults: spring run	Upper reaches canyons and dissected highland, lower reaches	

Basin	Population Name	Population Code	Spatial Structure	Within-Population Characteristics		
				Life History	Habitat (Level 4 Ecoregion)	Genetics
			continuous		dissected loess uplands **	
	Asotin Creek	SNASO	Linear continuous	Adults: spring run	Lower Snake and Clearwater Canyons	
South Fork Salmon						
	Secesh River	SFSEC	Branched discontinuous	Adults: summer run	Southern forested mountains	
	South Fork Salmon River	SFMAI	Branched discontinuous	Adults: summer run	Upper reaches southern forested mountains, lower reaches hot dry canyons	
	East Fork South Fork Salmon River/Johnson Creek	SFEFS	Branched discontinuous	Adults: summer run	Upper reaches southern forested mountains, lower reaches hot dry canyons	
Salmon River tributaries						
	Chamberlain Creek	SRCHA	Branched discontinuous	Adults: spring run	Upper reaches southern forested mountains, lower reaches hot dry canyons	Well-differentiated from all other Snake River populations.
	Little Salmon River	SRLSR	Branched discontinuous	Adults: spring and summer run	Upper reaches in 4 ecoregions, predominantly Wallowa/Seen Devils Mountains, lower reaches canyons and dissected uplands**	
Middle Fork Salmon River						
	Bear Valley Creek/Elk Creek	MFBEA	Branched continuous	Adults: spring run	Southern forested mountains	
	Big Creek	MFBIG	Branched discontinuous	Adults: spring and summer run	Upper reaches southern forested mountains, lower reaches hot dry canyons	
	Camas Creek	MFCAM	Branched continuous	Adults: spring run	Upper reaches southern forested mountains, lower reaches hot dry canyons	
	Middle Fork	MFLMA	Branched	Adults: spring run	Upper reaches southern forested	

Basin	Population Name	Population Code	Spatial Structure	Within-Population Characteristics		
				Life History	Habitat (Level 4 Ecoregion)	Genetics
	Salmon River below Indian Creek		discontinuous		mountains, lower reaches hot dry canyons	
	Pistol Creek	MFPIS	Branched discontinuous	Adults: spring run	Southern forested mountains	
	Marsh Creek	MFMAR	Branched continuous	Adults: spring run. Juveniles: Cape Horn Creek samples significantly later arrival at lower Granite than other Marsh Creek samples.	Upper reaches high glacial drift-filled valleys, lower reaches southern forested mountains	
	Sulphur Creek	MFSUL	Branched continuous	Adults: spring run	Southern forested mountains	
	Loon Creek	MFLOO	Branched discontinuous	Adults: spring and summer run	Southern forested mountains	
	Middle Fork Salmon River above Indian Creek	MFUMA	Branched discontinuous	Adults: spring run	Southern forested mountains	
Upper Salmon River						
	Valley Creek	SRVAL	Branched continuous	Adults: spring and summer run	High glacial drift-filled valleys	
	Lemhi River	SRLEM	Branched discontinuous	Adults: spring run	Upper reaches barren mountains, middle reaches dry gneissic-schistose-volcanic hills, lower reaches dry intermontane sagebrush valleys	
	North Fork Salmon River	SRNFS	Branched discontinuous	Adults: spring run	Upper reaches South Clearwater forested mountains, lower reaches in 4 ecoregions, predominently	

Basin	Population Name	Population Code	Spatial Structure	Within-Population Characteristics		
				Life History	Habitat (Level 4 Ecoregion)	Genetics
					dry partly wooded mountains	
	Pahsimeroi River	SRPAH	Branched discontinuous *	Adults: spring and summer run	Dry intermontane sagebrush valleys	
	East Fork Salmon River	SREFS	Branched discontinuous	Adults: spring and summer run Juveniles: Herd Creek. Samples significantly earlier arrival at lower Granite than other East Fork samples.	Upper reaches dry partly wooded mountains, lower reaches dry gneissic-schistose-volcanic hills**	Herd Creek samples varied from other East Fork samples
	Upper mainstem Salmon River					
	above Redfish Lake	SRUMA	Branched discontinuous	Adults: spring run. Juveniles: Frenchman Creek samples significantly later arrival at lower Granite than Alturas Lake Creek samples.	Upper reaches southern forested mountains, lower reaches high glacial drift-filled valleys	Alturas Lake Creek samples varied from other upper Salmon samples.
	below Redfish Lake	SRLMA	Branched discontinuous	Adults: spring and summer run	Upper reaches southern forested mountains, lower reaches dry partly wooded mountains	
	Yankee Fork	SRYFS	Branched continuous	Adults: spring run	Southern forested mountains	

* The core area, the mainstem Pahsimeroi River, is linear continuous. This population is classified as branched discontinuous because of the small Salmon River tributaries which are included in this population.

** The spawning reaches for this population also span a broader scale, level 3 ecoregion boundary

Table I-8. Snake River spring/summer chinook hatchery influence.

Basin	Population Name	Population Code	Genetic Evidence of Hatchery Introgression	Natural Spawning of Hatchery-Origin Fish	Hatchery Outplants, Last 10 Years		Notes
					Number	Origin	
Grande Ronde							
	Catherine Creek	GRCAT	No evidence	No data	Low	Recent switch from out of ESU to within-population broodstock	Previous (>5 years ago) natural spawning of hatchery-origin fish high
	Wallowa/Lostine River	GRLOS	No evidence	Low	Low	Recent switch from out of ESU to within-population broodstock	Previous (>5 years ago) natural spawning of hatchery-origin fish high
	Minam River	GRMIN	No evidence	Low	None		Previous (>5 years ago) natural spawning of hatchery-origin fish medium
	Upper mainstem Grande Ronde River	GRUMA	No evidence	No data	Low	All releases from in-population broodstock	Previous (>5 years ago) natural spawning of hatchery-origin fish high
	Wenaha River	GRWEN	No evidence	No data	None		Previous (>5 years ago) natural spawning of hatchery-origin fish high
Imnaha							
	Big Sheep Creek	IRBSH	No evidence	No data	None		
	Imnaha River main stem	IRMAI	Affinity to locally-derived broodstock	No data	Medium	All releases from in-population broodstock	

Basin	Population Name	Population Code	Genetic Evidence of Hatchery Introgression	Natural Spawning of Hatchery-Origin Fish	Hatchery Outplants, Last 10 Years		Notes
					Number	Origin	
Lower Snake tributaries							
	Tucannon River	SNTUC	No data	High	Medium	All releases from in-population broodstock	Sharp recent (last five year) increase in natural spawning of hatchery-origin fish
	Asotin Creek	SNASO	No data	No data	None		
South Fork Salmon							
	Secesh River	SFSEC	No evidence	Low	None		
	South Fork Salmon River	SFMAI	Affinity to locally-derived broodstock	Low	High	All releases from in-population broodstock	
	East Fork South Fork Salmon River/Johnson Creek	SFEFS	No evidence	None	Low	All releases from in-ESU broodstock	Recent decrease in hatchery outplants
Salmon River tributaries							
	Chamberlain Creek	SRCHA	No evidence	No data	None		
	Little Salmon River	SRLSR	High, non-local broodstock	No data	High	Majority releases from out of ESU broodstock	
MF Salmon River							
	Bear Valley Creek/Elk Creek	MFBEA	No evidence	None	None		

Basin	Population Name	Population Code	Genetic Evidence of Hatchery Introgression	Natural Spawning of Hatchery-Origin Fish	Hatchery Outplants, Last 10 Years		Notes
					Number	Origin	
	Big Creek	MFBIG	No data	None	None		
	Camas Creek	MFCAM	No evidence	None	None		
	Middle Fork Salmon River below Indian Creek	MFLMA	No data	None	None		
	Pistol Creek	MFPIS	No data	None	None		
	Marsh Creek	MFMAR	No evidence	None	None		
	Sulphur Creek	MFSUL	No data	None	None		
	Loon Creek	MFLOO	No data	None	None		
	Middle Fork Salmon River above Indian Creek	MFUMA	No data	None	None		
Upper Salmon River							
	Valley Creek	SRVAL	Affinity to locally-derived broodstock	None	None		
	Lemhi River	SRLEM	No evidence	None	None		Recent decrease in hatchery outplants
	North Fork Salmon River	SRNFS	No evidence	No data	None		

Basin	Population Name	Population Code	Genetic Evidence of Hatchery Introgression	Natural Spawning of Hatchery-Origin Fish	Hatchery Outplants, Last 10 Years		Notes
					Number	Origin	
	Pahsimeroi River	SRPAH	No evidence	No data	Medium	Recent switch from out of ESU to within-population broodstock	
	East Fork Salmon River	SREFS	No evidence	None	Low	All releases from in-ESU broodstock	Recent decrease in hatchery outplants
	Upper mainstem Salmon River						
	above Redfish Lake	SRUMA	Affinity to locally-derived broodstock	No data	Medium	All releases from in-ESU broodstock	Recent decrease in hatchery outplants
	below Redfish Lake	SRLMA	No data	No data	None		
	Yankee Fork	SRYFS	No evidence	None	None		Recent decrease in hatchery outplants

Hatchery Influence Criteria:

Evidence of hatchery spawning

A. High = Over 25% (average over the last 5 years) of natural spawners are hatchery-origin fish

B. Medium = 10-25% (average over the last 5 years) of natural spawners are hatchery-origin fish

C. High = Less than 10% (average over the last 5 years) of natural spawners are hatchery-origin fish

D. None = No evidence of hatchery-origin spawners

E. No data = No data available

Hatchery outplants

A. High = average of >500,000 fish released per year, last ten years

B. Medium = average of 50,000 to 500,000 fish released per year, last ten years

C. Low = average of <50,000 fish released per year, last 10 years

D. None = No fish released, last 10 years

II. UPPER COLUMBIA RIVER SPRING CHINOOK SALMON

The Upper Columbia River Spring Chinook Salmon ESU includes stream-type fish spawning upstream of Rock Island Dam. Like Snake River spring/summer chinook, these fish rear in freshwater for slightly more than a year before smoltification and seaward migration. In addition to dramatic declines as a result of habitat loss, heavy harvest pressures, and dam construction, this ESU has suffered tremendous artificial propagation impacts as a result of the Grand Coulee Fish Maintenance Project (GCFMP). Briefly, from 1939 to 1943, all spring chinook adults passing upstream of Rock Island Dam were collected and either planted into Nason Creek, the Entiat River, or Methow River or spawned in hatcheries and the progeny released into those areas (Ford et al. 2001, Myers et al. 1998, Chapman et al. 1995). In addition, there were substantial outplants of out-of-basin hatchery stocks until the 1980s (Myers et al. 1998). In response to low abundance, steeply declining trends, and habitat loss, this ESU was listed as endangered in 1999.

As part of a proposal by two public utility districts to develop a Habitat Conservation Plan, a multi-agency group assessed population structure and developed interim recovery goals for this ESU (Ford et al. 2001) as part of the Quantitative Analytical Report (QAR) process. With little new data available to us, we relied heavily on their thorough analysis. However, we do address the question of population status in the Okanogan River, a question the QAR analysis left open.

Table II-1. Available data types and analyses for the Upper Columbia spring chinook salmon ESU.

Data Type	Description
Genetic	Ford et al. (2001) provided a complete analysis of 44 allozyme loci from 6 locations (across 5 years) for the Wenatchee and Methow basins.
Dispersal/distance	Distance between spawning areas calculated using spawning distributions defined by WDFW redd surveys. Wenatchee and Methow-specific straying data contributed to our generalized dispersal distance analysis (Appendix B).
Phenotypic	Length-at-age data analyzed by Ford et al. (2001)
Habitat	EPA-defined ecoregions considered.
Demographic correlation	12 index areas (redds per mile) in the Wenatchee, Entiat, and Methow basins. Length of data sets vary; many cover the time period from the mid-1970s to the mid-1990s. Ford et al. (2001) conducted pair-wise correlations on available time series.

Demographically Independent Populations within the Upper Columbia River Spring Chinook ESU

We identified three independent populations in this ESU. We considered the genetic analyses conducted by Ford et al. (2001) as well as our dispersal curve and distance analysis (Appendix B). Ford et al. (2001) also present analyses of demographic correlation and a describe several habitat features (Table II-1). Due to the relatively small size of the area, we did not identify any major groupings.

Genetic analysis of Washington Department of Fish and Wildlife (WDFW) samples from this ESU suggest that samples from the White River (a tributary to the Wenatchee) and the Twisp River (a tributary to the Methow) contribute the majority of the variation observed between localities (Tables II-2 and II-3). These two sampling locations also showed the greatest differentiation from other areas, based on a UPGMA clustering (Figure II-1). The general lack of differentiation between major tributaries is almost certainly due to the homogenization of stocks during the GCFMP. We identified three populations in this ESU (Figure II-2).

1. ***Wenatchee River (UCWEN).*** This population includes fish in the Wenatchee River and its tributaries, except Icicle Creek. Spawning areas within this basin, with the exception of Peshastin Creek, fell within the 30-km threshold. (Note that Peshastin Creek has recently had only hatchery strays present on the spawning grounds.) Distance to spawning areas outside the Wenatchee basin substantially exceeds 30 km (Table II-4). Demographic trends within this basin were generally more correlated that than trends between drainages, further supporting this designation. However, samples from the White River show consistent genetic differentiation from other Upper Columbia fish (Figure II-1, Ford et al. 2001). This apparent substructure should be considered not only in establishing recovery goals, but also in evaluating management actions.
2. ***Entiat River (UCENT).*** Entiat River spawning areas are well separated from spawning areas in the Wenatchee or Methow Rivers (Table II-4). The Entiat has received very few strays from hatchery programs in either the Wenatchee or Methow Rivers (Ford et al. 2001).
3. ***Methow River (UCMET).*** Like the Wenatchee, the Methow River population includes a location (Twisp River) that supports fish that are substantially differentiated from other localities within the basin (Figure II-1, Ford et al., 2001). However, we treat this as a single population due to the continuous spawning between the Methow and Twisp Rivers. Spawning areas within this watershed are substantially separated from other Columbia River spawning aggregations.

Primary spawning areas, population characterization and hatchery influence for each population are presented in Tables II-5, II-6 and II-7. Further details, including basin physiography and general climatic information for the watersheds in which each population is found, can be found in Appendix C.

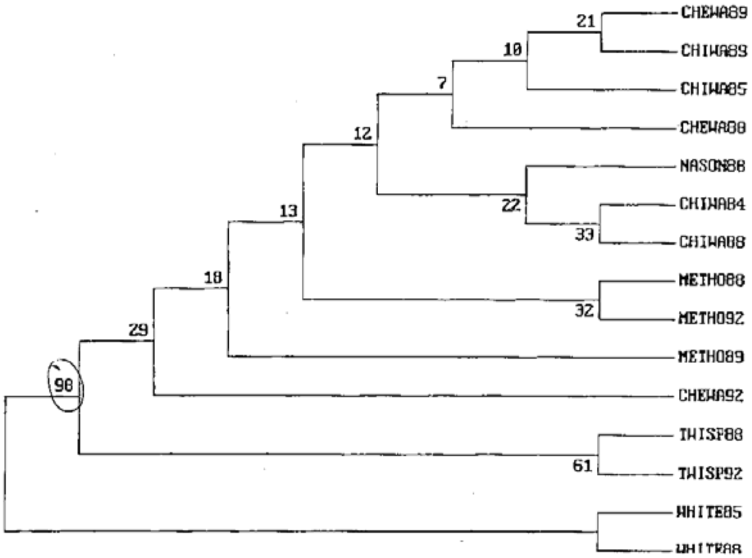


Figure II-1. UPGMA cluster diagram of all broodyear-locality samples with a sample size of 25 or greater from the Upper Columbia spring chinook ESU. Bootstrap percentages from 1,000 replicates are presented at nodes. From Ford et al. 2001.

Table II-2. Hierarchical analysis of genetic variation among samples from the Wenatchee and Methow Rivers within the Upper Columbia spring chinook ESU. From Ford et al. 2001.

	Among Major Tributaries (F_{TP})	**Among Spawning Areas, within Major Tributaries (F_{ST})**	**Among Broodyears, within Spawning Areas (F_{YS})**
Point estimate	0.001859	0.012339	0.016846
95% confidence	0.006257	0.016595	0.020351
interval	-0.002656	0.007308	0.012877

Table II-3: Hierarchical analysis of genetic variation among samples from the Wenatchee and Methow Rivers excluding samples from the White and Twisp Rivers. From Ford et al. 2001

	Among Major Tributaries (F_{TP})	**Among Spawning Areas, within Major Tributaries (F_{ST})**	**Among Broodyears, within Spawning Areas (F_{YS})**
Point estimate	-0.000802	0.002045	0.005823
95% confidence	0.002326	0.003817	0.009292
interval	-0.003669	0.000540	0.002453

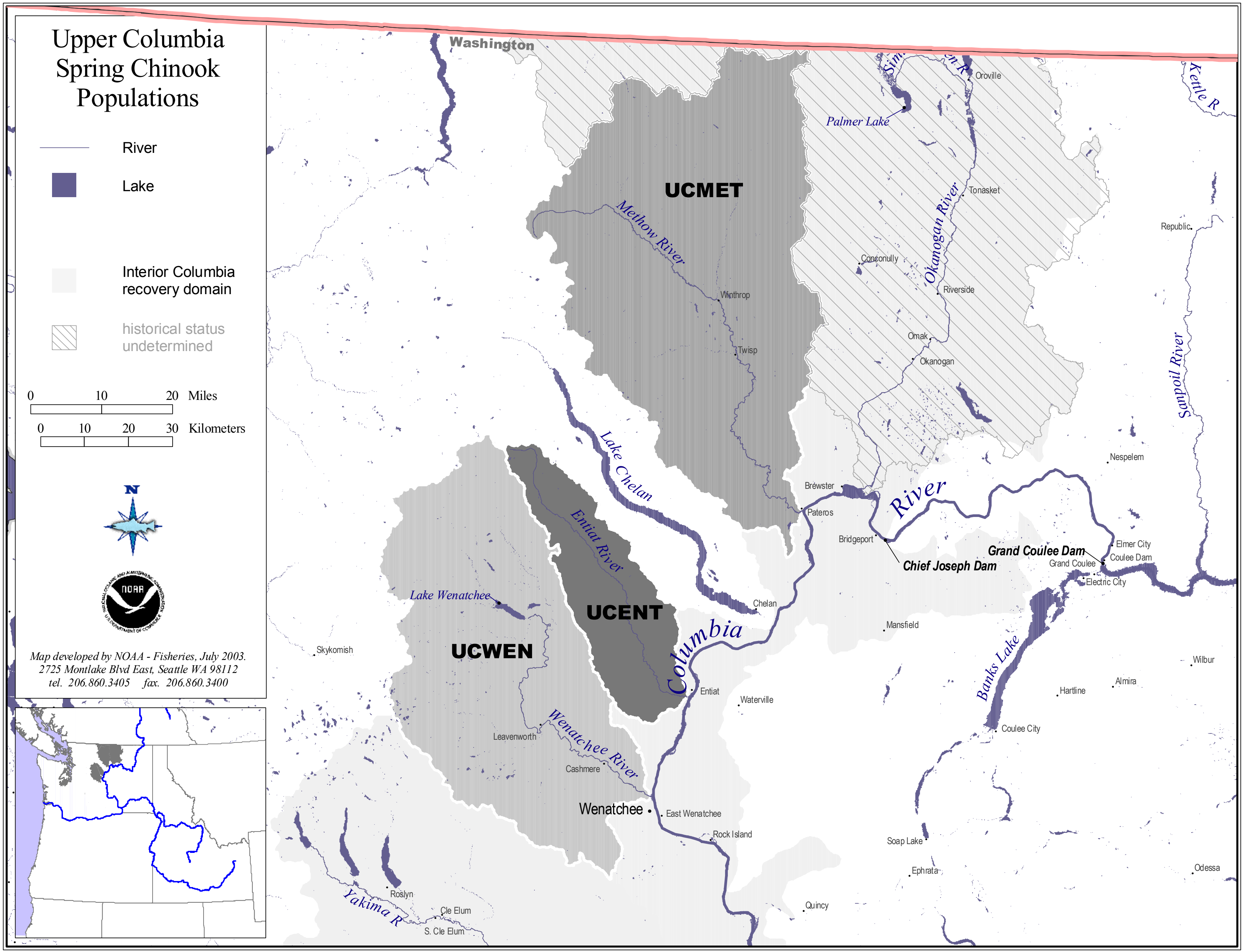


Figure II-2. Upper Columbia River spring chinook salmon extant populations.

Table II-4. Distance matrix for Upper Columbia spring chinook salmon ESU. Distances were computed using 100k scale hydrography from Streamnet; distance units are in kilometers.

	UCWEN	UCENT	UCMET
UCWEN	0		
UCENT	90	0	
UCMET	205	146	0

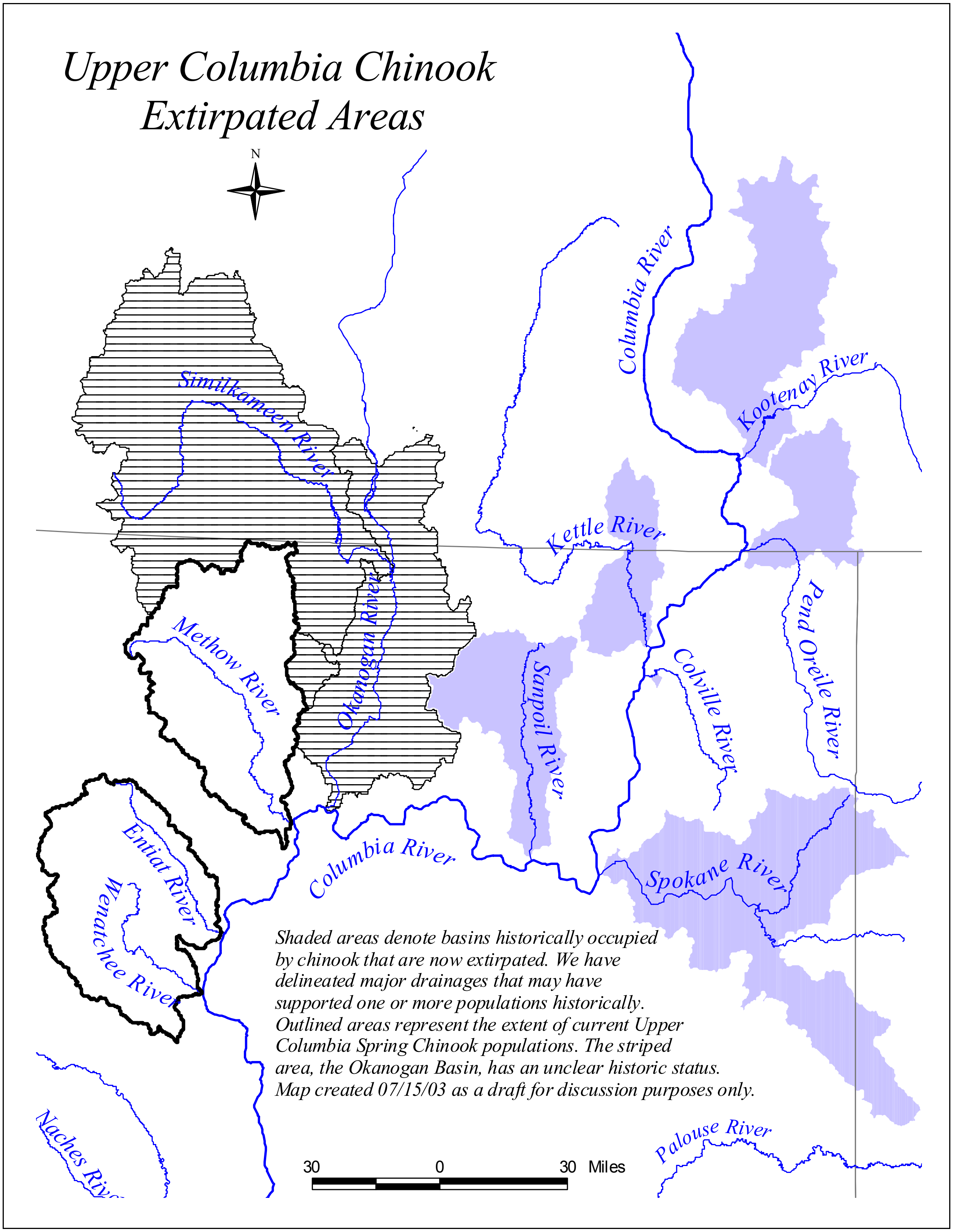
Historically Occupied Areas

Within the current boundaries of the ESU, spring chinook in the Okanogan River are regarded as extirpated (SASSI, 1993). Unfortunately, the historical status of spring-run, stream-type fish belonging to this ESU in the Okanogan drainage is ambiguous. There are some anecdotal references to spring or early summer-running fish in the Okanogan drainage (Confederated Colville Tribes, personal communication). Mullan (1992) did not believe that sufficient habitat exists to support a population of spring-run chinook. However, historically, several tributaries to the Okanogan, including Salmon Creek, Omak Creek, and several in Canada appear to have provided suitable habitat for stream-type chinook spawning and rearing, in quantities similar to that in other populations we have designated (e.g., Asotin Creek, Snake River spring/summer chinook ESU). It is probably impossible to determine definitively whether an independent population of Upper Columbia spring chinook ESU fish historically existed here, but we recognize the possibility that the area may have supported one.

The construction of Grand Coulee Dam in 1939 blocked access to over 50% of the river miles formerly available to Upper Columbia spring chinook (NRC 1996). Although we are unable to define populations in this blocked area with any certainty, we can identify major watersheds that may have supported stream-type chinook likely belonging to this ESU. By analogy, it may be reasonable to suppose that these tributaries supported one or more populations, but the lack of distributional or genetic information makes it impossible to make these determinations definitively.

Tributaries to the Columbia River, above Grand Coulee Dam: Sanpoil River, Spokane River, Colville River, Kettle River, Pend Oreille River, and Kootenai River (Figure II-3).

Figure II-3. Upper Columbia spring chinook salmon extirpated areas.



Upper Columbia Chinook Extirpated Areas

Shaded areas denote basins historically occupied by chinook that are now extirpated. We have delineated major drainages that may have supported one or more populations historically. Outlined areas represent the extent of current Upper Columbia Spring Chinook populations. The striped area, the Okanogan Basin, has an unclear historic status. Map created 07/15/03 as a draft for discussion purposes only.

Monitoring and Evaluation Needs

Our population identification efforts would be enhanced by additional data. As research efforts continue on Upper Columbia spring chinook population structure, we recommend that a priority be placed on the following data needs, in the following order:

- **Additional genetic samples.** Genetic samples were particularly lacking from the Entiat River. In addition, given the past and current hatchery practices in this ESU, continued genetic sampling will be extremely important to ensure that the current population structure has not been compromised by hatchery influences.
- **Dispersal information at a fine-scale**. Generally lacking in our dispersal analysis were areas that had been sampled on a 0–50 km scale. Altering the current hatchery tag recovery program to record the exact location at which hatchery strays were found (rather than the reach in which they were found) would provide excellent information for population delineation. Any dispersal rate information that could be collected with wild fish would also be extremely useful.

Table II-5. Upper Columbia River spring chinook salmon core spawning areas.

Region	Population	Code	Current Core Spawning Areas	Historical Spawning Area
Wenatchee	Wenatchee River	UCWEN	White River – Grasshopper Meadows to Napeequa River; Little Wenatchee – Falls to Lost Creek; Chiwawa – Trinity to Grouse Creek	
Entiat	Entiat River	UCENT	Main stem - Preston Creek downstream to McKenzie Ditch and Diversion Dam (RM 16–23.1)	
Methow	Methow River	UCMET	Lower 15 miles of Twisp, lower 15 miles of the Chewuch, mainstem Methow from Mazama to Winthrop, and lower 1 mile of the Lost River, and Nason Creek – upper railroad bridge to mouth	

Table II-6. Upper Columbia River spring chinook salmon population characterization.

				Within-Population Diversity		
Basin	**Population Name**	**Population Code**	**Spatial Structure**	**Adult Run-Timing**	**Habitat (Level 4 Ecoregion)**	**Genetics**
Methow	Methow River	UCMET	Branched continuous	Spring	Upper reaches Pasayten/ Sawtooth Highlands and Okanogan Pine/Fir Hills, lower reaches Okanogan Valley*	Samples from the Twisp River show consistent differentiation from other basin fish.
Wenatchee	Wenatchee River	UCWEN	Branched discontinuous	Spring	Upper reaches Wenatchee/ Chelan Highlands, lower reaches Chiwaukum Hills and Lowlands	Samples from the White River show consistent differentiation from other basin fish.
Entiat	Entiat River	UCENT	Branched continuous	Spring	Chelan Tephra Hills	

* Spawning areas for this population span a broader-scale, level 3 ecoregion boundary

Table II-7. Upper Columbia spring chinook salmon hatchery influence

Basin	Population Name	Population Code	Genetic Evidence of Hatchery Introgression	Natural Spawning of Hatchery-Origin fish	Hatchery Outplants, Last 10 years		
					Number	Origin	Notes
Wenatchee	Wenatchee River	UCWEN	All ESU fish heavily influenced by the Grand Coulee Fish Mangement Plan, in which all spawners crossing Rock Island Dam were collected. Progeny and adults were outplanted.	High	High	Majority releases from out of ESU broodstock	Previous (>5 years ago) natural spawning of hatchery-origin fish medium
Entiat	Entiat River	UCENT		High	Medium	Majority releases from within population broodstock	Previous (>5 years ago) natural spawning of hatchery-origin fish medium
Methow	Methow River	UCMET		High	High	Majority releases from within population broodstock	Previous (>5 years ago) natural spawning of hatchery-origin fish medium, outplanting history includes seven stocks

Hatchery Influence Criteria:

Evidence of hatchery spawning

A. High = Over 25% (average over the last 5 years) of natural spawners are hatchery-origin fish
B. Medium = 10-25% (average over the last 5 years) of natural spawners are hatchery-origin fish
C. High = Less than 10% (average over the last 5 years) of natural spawners are hatchery-origin fish
D. None = No evidence of hatchery-origin spawners
E. No data = No data available

Hatchery outplants

A. High = average of >500,000 fish released per year, last 10 years
B. Medium = average of 50,000 to 500,000 fish released per year, last 10 years
C. Low = average of <50,000 fish released per year, last 10 years
D. None = No fish released, last 10 years

III. SNAKE RIVER FALL CHINOOK SALMON

This ESU includes fish spawning in the lower main stem of the Snake River, and lower reaches of the Clearwater, Imnaha, Grande Ronde, Salmon, and Tucannon Rivers. The Lyons Ferry Hatchery stock, originally derived from returns to the lower Snake River, was included in the ESU. Unlike the other listed chinook ESUs in the interior Columbia River basin, Snake River fall chinook exhibit a subyearling, ocean-type life history. These fish return to the Snake River basin in September and October and spawn shortly thereafter. In contrast with stream-type fish, juveniles outmigrate the next summer, rather than rearing in freshwater for 13–14 months before outmigrating. Fish with this life history are well-distinguished genetically from stream-type fish (Waples et al. 1991).

This ESU has faced a variety of threats, including extreme loss of habitat due to construction of many dams on the mainstem Snake River, beginning in the early 1900s and culminating with the completion of the Hells Canyon Dam complex in the 1960s. These dams inundated spawning areas and blocked upstream passage, leading to a dramatic decline in numbers (Irving and Bjorrn 1981, Fulton 1968). In fact, after adjusting for spawning/rearing suitability, Dauble (2000) calculated that 20% or less of historical Snake River habitat is currently available to fall chinook. In addition, in the 1980s, these fish faced a genetic threat in the form of straying from hatchery fish of the Upper Columbia River lineage. As a result of this combination of factors, this ESU was listed as threated in 1992 (NMFS 1992). However, these fish were provisionally included in a common ESU with the more robust Deschutes River run in the most comprehensive status review to date of chinook salmon (Myers et al. 1998). In an amended decision, the runs of the Snake and Deschutes Rivers each were granted their presently separate ESU status based on geographic separation, habitat differences, and apparent demographic independence (NMFS 1999). Marshall et al. (2000), in a study of naturally produced juvenile progeny of fall chinook spawning upstream from Lyons Ferry between 1990 and 1994, concluded that distinctive patterns of allelic diversity persisted in naturally produced juveniles in the Snake River that (1) were differentiated from Upper Columbia River populations, and (2) supported earlier conclusions that the Snake River fall chinook ESU remained an important genetic resource. Subsequent analyses of 1995 and 1996 broodyear wild juveniles substantiated these conclusions (A. Marshall, pers. comm.).

Demographically Independent Populations of Snake River Fall Chinook Salmon

Although genetic, life-history, and habitat information to separate fish from this ESU from other ESUs was available, virtually no sampling at a finer scale had been conducted (Table III-1). Primarily on the basis of current spawning distribution and abundance, we identified a single population in this ESU (Figure III-1):

Snake River Main Stem and Lower Tributaries. A majority (58%) of fish in this population spawn in the mainstem Snake River between the top of Lower Granite Reservoir and Hells Canyon Dam, with the remaining fish distributed among lower sections of the major tributaries (Connor et al. 2002). Fish in the mainstem Snake are apparently primarily distributed in a series of aggregates from the Asotin Creek confluence to river km 353, although small numbers have been reported to spawn in the tailraces of the Lower Snake dams (Connor et al. 1993, Dauble et al. 1995). Due to their geographic proximity, and the likelihood that individual tributaries could not support a sufficiently large population, we considered these aggregates and associated reaches in the lower major tributaries to the Snake to be a single population.

Primary spawning areas, population characterization and hatchery influence are presented in Tables III-2, III-3 and III-4. Additional information, including basin physiography, can be found in Appendix C.

Historically Occupied Areas

Before European impact, Snake River fall chinook are believed to have occupied the mainstem Snake River up to Shoshone Falls (Gilbert and Evermann 1894). In particular, the area downstream of Upper Salmon Falls, at rkm 930, was identified by Evermann (1896) as the "... largest and most important salmon spawning ground of which we know in Snake River." After loss of these upstream reaches with construction of Swan Falls Dam in 1920, the reach between Marsing, Idaho, and Swan Falls Dam (rkm 565 to 682) is believed to have been the primary spawning and rearing areas for Snake River fall chinook (Irving and Bjornn 1981; Haas 1965). However, construction of the Hells Canyon Dam complex (1958–1967) cut off anadromous fish access to historical fall chinook habitat upstream of river km 398.6. Additional fall chinook habitat was lost through inundation as a result of the construction of the lower mainstem Snake River dams (Groves and Chandler 1999).

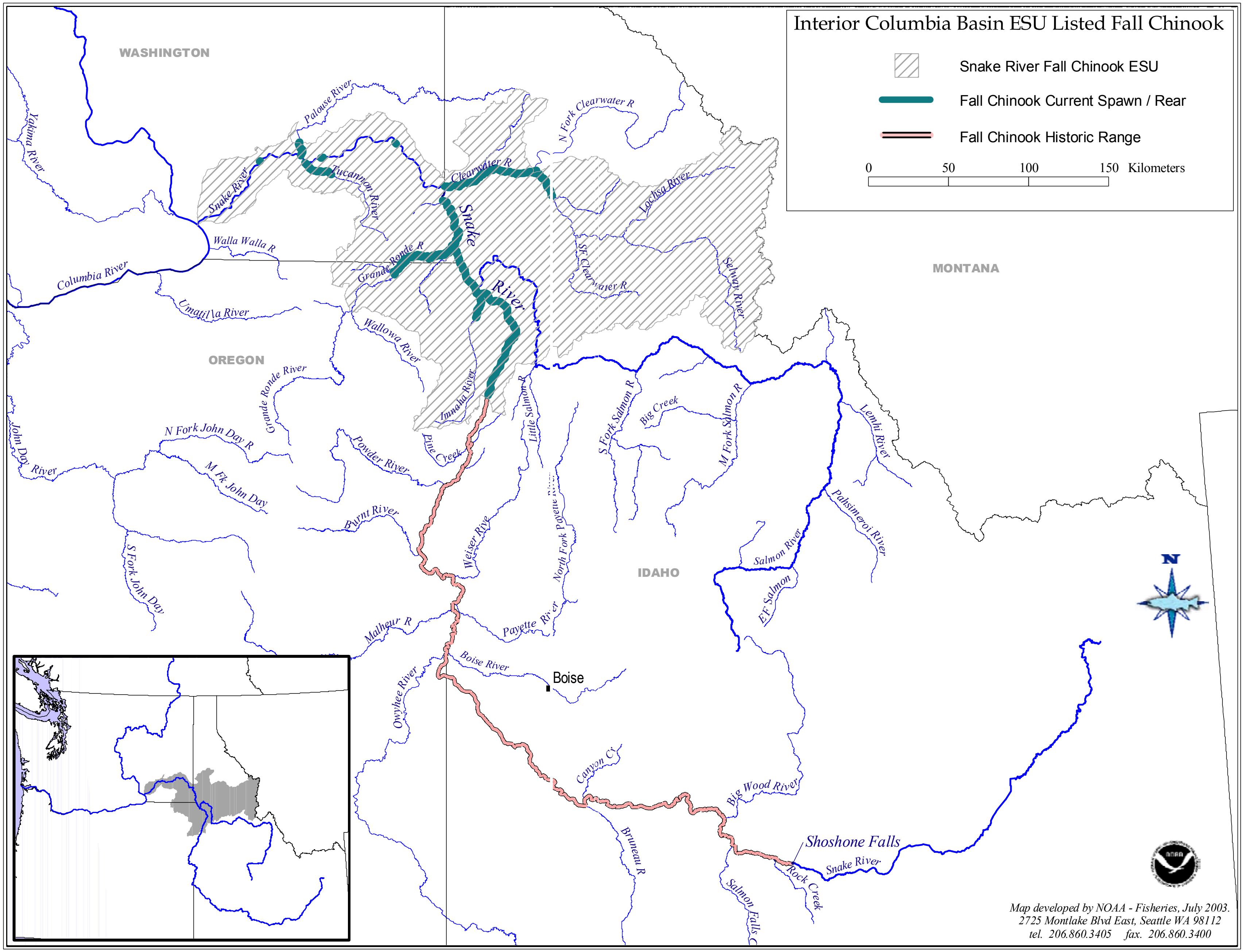
Historical use of the Clearwater River is more ambiguous. If ocean-type fish used the lower Clearwater, they were extirpated after construction of the Lewiston Dam in 1929. However, Tiffan et al. (2001) concluded that there is "no conclusive evidence" as to whether the lower Clearwater River supported the basic subyearling migrant life-history pattern associated with Snake River fall chinook.

Because there are not good data describing the distribution of fall chinook before these human impacts, it is impossible to define historical population structure. However, fish in this ESU currently tend to aggregate in areas of suitable habitat, with scattered spawning between aggregates. We consider it likely that a similar structure extended upstream, with the discontinuous aggregates likely functioning as elements of a metapopulation. Long stretches of unsuitable habitat, such as Hells Canyon (characterized by Parkhurst (1950) as of "... no value to salmon because of steep gradient and bedrock") may have served to more fully isolate some spawning areas from others.

Monitoring and Evaluation Needs

The distribution and abundance of fish in the Snake River fall chinook ESU currently suggests a single population. However, it is possible that there is finer-scale differentiation between spawning areas. Particular information that would be useful includes:

- **Genetic samples** identifiable as mainstem Snake or tributary-derived. These samples would provide information about the degree of differentiation within the spawning aggregate.



Map developed by NOAA - Fisheries, July 2003.
2725 Montlake Blvd East, Seattle WA 98112
tel. 206.860.3405 fax. 206.860.3400

Figure III-1. Current and historical population boundaries and spawning areas for Snake River fall chinook salmon. Table

III-1. Available data types and analyses for the Snake River fall chinook salmon ESU.

Data Type	Description
Genetic	No within-ESU genetic data available.
Dispersal/distance	Distance between spawning aggregates described by Connor et al. (2002).
Phenotypic	No within-ESU data available.
Habitat	EPA-defined ecoregions considered.
Demographic correlation	Aggregate run at Lower Granite Dam.

Table III-2. Snake River fall chinook salmon population characterization.

				Within-Population Diversity		
Basin	**Population Name**	**Population Code**	**Spatial Structure**	**Adult Run Timing**	**Habitat (Ecoregion)**	**Genetics**
Snake River	Snake River	SNMAI	Branched discontinuous	Fall	Mostly canyons and dissected uplands, with lower reaches in lower Snake and lower Clearwater Canyons	

Table III-3. Snake River fall chinook salmon core spawning areas.

Region	Population	Code	Current Core Spawning Areas Description	Historical Spawning Area Description
Snake River	Snake River	SNMAI	32-km section of the mainstem Snake River starting approximately 10 km above the Asotin Creek confluence; lower portions of the Salmon, Clearwater, and Grande Ronde Rivers and Snake River rkm 343 to rkm 353.	Before 1910: Snake River downstream of upper Salmon Falls at rkm 930. After 1910: Snake River between Marsing and Weiser, Idaho (rkm 565 to 682).

Table III-4. Hatchery influence table for the Snake River fall chinook salmon ESU.

Basin	**Population Name**	**Population Code**	**Genetic Evidence of Hatchery Introgression**	**Natural Spawning of Hatchery-Origin Fish**	**Hatchery Outplants, Last 10 years**		**Notes**
					Number	**Origin**	
Snake River	Snake River	SNMAI	Affinity to locally-derived broodstock	High	High	All releases from in-population broodstock	Recent increase in natural spawning of hatchery-origin fish

Hatchery Influence Criteria:

Evidence of hatchery spawning

A. High = Over 25% (average over the last 5 years) of natural spawners are hatchery-origin fish
B. Medium = 10-25% (average over the last 5 years) of natural spawners are hatchery-origin fish
C. High = Less than 10% (average over the last 5 years) of natural spawners are hatchery-origin fish
D. None = No evidence of hatchery-origin spawners
E. No data = No data available

Hatchery outplants

A. High = average of >500,000 fish released per year, last ten years
B. Medium = average of 50,000 to 500,000 fish released per year, last ten years
C. Low = average of <50,000 fish released per year, last 10 years
D. None = No fish released, last 10 years

IV. SNAKE RIVER STEELHEAD

The Snake River Steelhead ESU includes both resident and anadromous *Oncorhynchus mykiss* that spawn in the Snake River and its tributaries. These fish are genetically differentiated from other interior Columbia steelhead populations; they spawn at higher altitudes (up to 2,000 m) and after longer freshwater migrations (up to 1,500 km) (Busby et al. 1996). Like other ESUs in the Snake River basin, these populations have been affected by a wide variety of impacts, from the development of the hydropower corridor to habitat degradation and loss to inadvertent negative effects of hatchery practices. Although total abundance is relatively high, the large majority of these fish are of hatchery origin. In addition, the ESU has suffered dramatic declines in at least the last 20 years. As a result of these factors, this ESU was listed as threatened in 1999.

Like steelhead in other areas, fish in this ESU exhibit a wide range of life-history strategies, including varying times of freshwater rearing or ocean residence, or elimination of an ocean residence altogether. Traditionally, two prominent life-history strategies have been recognized in this area. A-run fish are smaller, on average have a shorter freshwater and ocean residence, and apparently begin their up-river migration earlier in the year. B-run fish are larger, spend more time rearing in both fresh and salt water, and appear to begin their up-river migration later in the year.

Demographically Independent Populations within the Snake River Steelhead ESU

We identified 24 populations in 5 major groupings in this ESU (Figure IV-1). Both genetic distances and distances between spawning aggregates played an important role in defining the major groupings, while life history and habitat or environmental considerations played a larger role at a finer scale (Table IV-1). Importantly, allozyme data (Winans unpublished; Marshall unpublished) suggested that spatial distance was more predictive of differentiation than run-type. In analyses of both A- and B-run fish, within-basin genetic distances are uniformly lower than those between basins (Table IV-2).

Available data across the Snake River basin were patchy. Demographic information was extremely limited, as few spawning ground surveys are conducted due to logistic constraints. In addition to scattered allozyme data from several data sets, genetic data collected at a very fine scale in the Grande Ronde and Imnaha watersheds (Moran 2003) were available. These detailed data provided a useful template for population definition in areas of the Snake and interior Columbia basins for which fine-scale data were not available. Ongoing genetic analyses contracted by the Idaho Department of Fish and Game (IDFG) are anticipated to yield additional information on steelhead population structure in Idaho in the future (A. Byrn, IDFG, and J. Nielsen, USGS, pers. comm.)

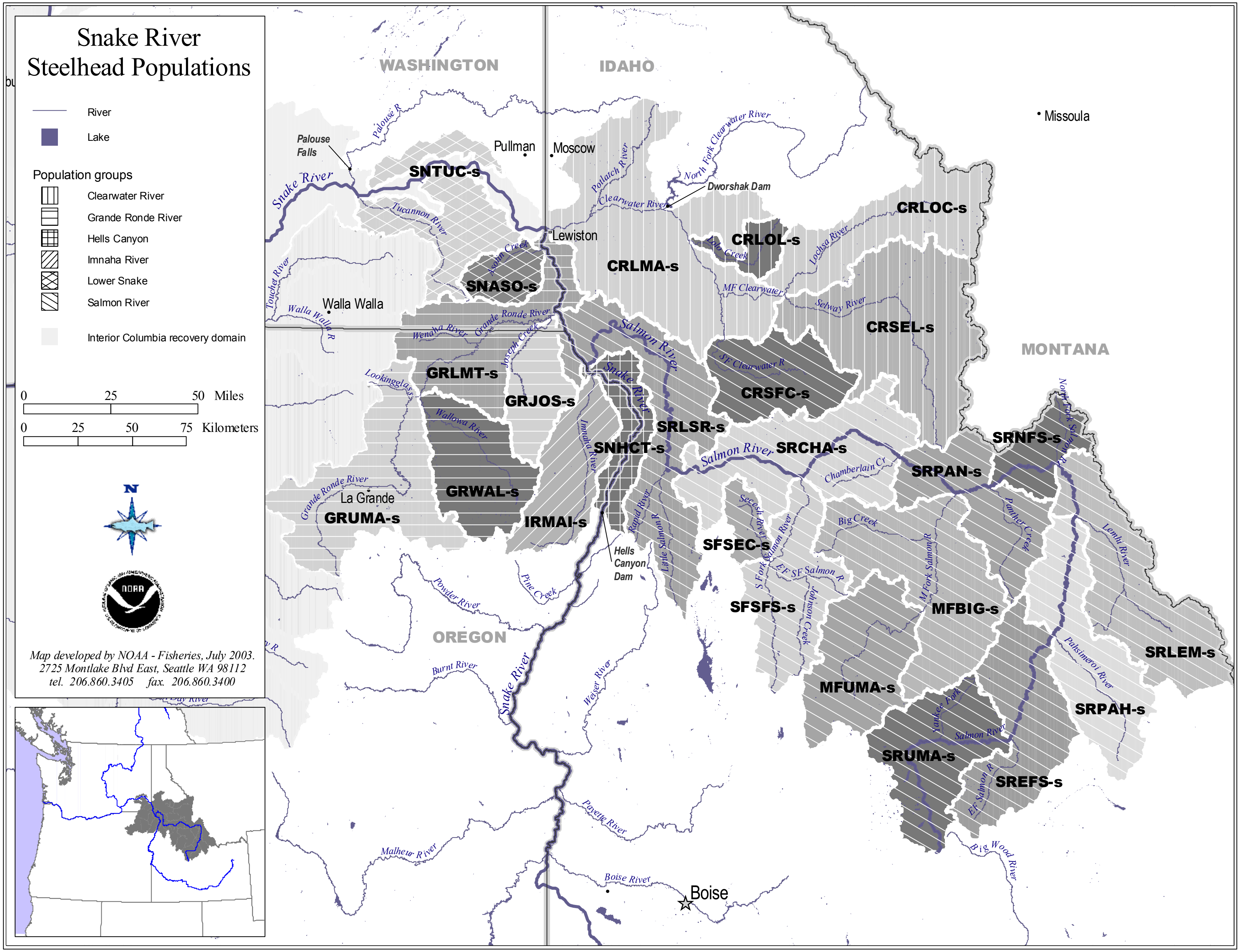


Figure IV-1. Snake River steelhead populations.

Table IV-1. Available data types and analyses for the Snake River steelhead ESU.

Data Type	**Description**
Genetic	Moran (unpub.) provided data from 14 microsatellite loci for 46 samples in the Snake River basin, with the majority of those samples from the Grande Ronde and Imnaha subbasins. We calculated Cavalli-Sforza and Edwards' distances and conducted a PCA with a reduced data set (9 loci), and used Moran's full-data set UPGMA cluster analysis of Fst values. In addition, allozyme data were available from 43 locations for 50 loci (Waples et al. 1993; Waples, unpublished data; and Marshall, unpublished data). (Appendix X)
Dispersal/distance	Distance between spawning areas calculated from Streamnet spawning area maps, updated with ODFW and IDFG data and professional judgment. Steelhead spawning areas are extremely poorly known, so distance information was considered less strongly than in chinook ESUs. Lacking ESU-specific data on dispersal distances, we used the results from the generalized dispersal distance analysis (Appendix B).
Phenotypic	A-run and B-run stream characterizations considered in population delineations (Kiefer et al. 1992). Juvenile and adult passage at Lower Granite Dam from pit tag detections, PSFMC.
Habitat	EPA-defined ccoregions. Level 4 delineations considered in some population identifications.
Demographic correlation	Index (redds per mile) available for four streams in the Grande Ronde basin. Length of data sets vary; many cover the time period from the mid-1960s to the present

In addition to the uneven distribution of data, two more factors complicated our assessment of steelhead population structure. First, the coarse-scale, allozyme data indicated the possible influence of putative straying of Wallowa Hatchery steelhead into other basins (data from Marshall, unpublished). The Wallowa sample shows very low pairwise genetic distances from at least seven other sampling sites (Table IV-3), suggesting considerable influence of strays from this hatchery in these locations. Second was the possible contribution of resident fish to the anadromous component of the population. Several outliers (Figure IV-1) may be showing a strong resident signal; further sampling of resident rainbow trout could help clarify the population structure in these areas.

Major groupings and populations, in order moving upstream from the mouth of the Snake River, are described in the subsections that follow.

Table IV-2. Matrix of steelhead populations (from Marshall, unpublished) having pairwise Nei's distances less than 0.001.

	1	2	3	4	5	6	7	8	9
1-Umatilla									
2-John Day	x								
3-Lower Tucannon									
4-Upper Tucannon		x							
5-Chesnimnus Creek	x		x	x					
6-Deer Creek	x		x	x					
7-Wallowa Hatchery	x	x	x	x	x	x			
8-Little Sheep Hatchery		x	x		x				
9-Asotin Creek			x			x	x		

Lower Snake River

Tributaries in the lower Snake River were grouped on the basis of genetic and geographic similarity as well as proximity. Microsatellite samples (Moran, unpublished) from the Tucannon River and Asotin Creek were very similar (Table IV-2; Figure IV-2; Appendix A), although they showed a high degree of interannual variability. Allozyme data (Marshall, unpublished) also indicated that these two areas were very similar, not only to each other, but also to Wallowa Hatchery samples. In addition, these drainages share ecoregion characteristics, draining the Blue Mountains. We identified two populations:

1. ***Tucannon River (SNTUC-s)*** This population includes the Tucannon River, and nearby streams Alkali, Almohta, Penawawa, and Alpowa Creeks. Genetic samples from the upper and lower Tucannon were extremely similar (Appendix A). We therefore found no basis for further subdivision into demographically independent units. Mitochondrial DNA of westslope cutthroat trout observed in six of 90 wild steelhead from the Tucannon River (K. Brown and G.Thorgaard, unpublished) has been interpreted to reflect an ancient hybridization event in this drainage with a now-extinct cutthroat population. This haplotype has not been found in limited sampling of wild steelhead of adjacent drainages. Should further sampling support these observations, the distinction of Tucannon steelhead from those of other drainages within the ESU is particularly notable.
2. ***Asotin Creek (SNASO-s).*** We separated fish spawning in this waterway from the genetically similar Tucannon River fish on the basis of distance. The 135 km separating spawning areas in the Tucannon River and Asotin Creek is well over our threshold of 30 km.

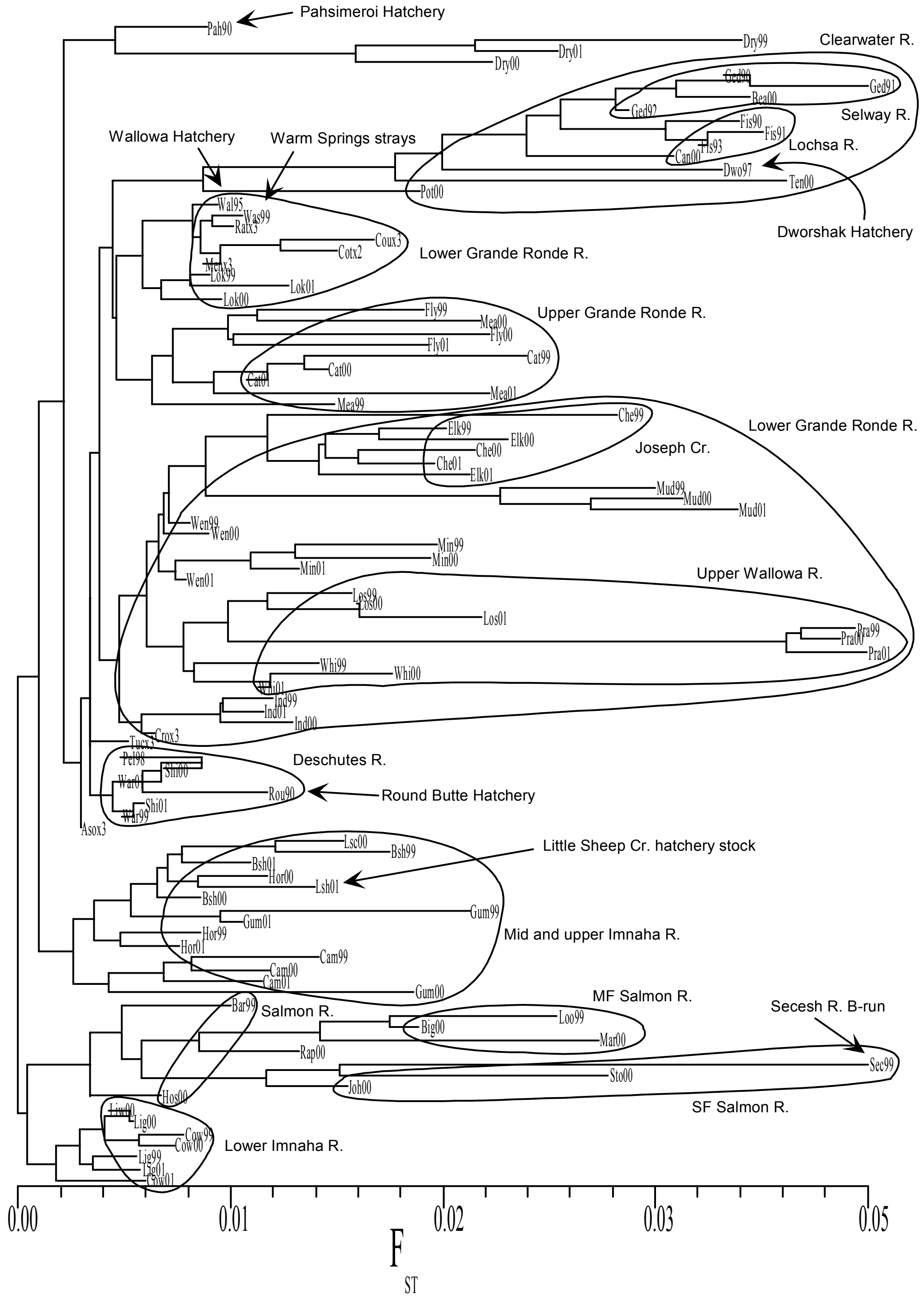


Fig. IV-2. Neighbor joining cluster analysis of pairwise F_{ST} values derived from 16 microsatellite loci (SE Washington samples pooled across years). Reproduced with permission from Moran, 2003.

Clearwater River

Unlike chinook, steelhead were able to maintain access to the Clearwater subbasin after the construction of Lewiston Dam in 1929, and are therefore included in the ESU. Based on geography (basin topography) and several scattered genetic samples (Figure IV-2), we defined fish in this subbasin as a single major grouping. However, the Clearwater River includes substantial life-history diversity, because it supports populations traditionally classified as both A-run and B-run. We identified six extant populations in the Clearwater basin:

3. ***Lower Clearwater River(CRLMA-s).*** This population includes the lower portions of the Middle and South Fork Clearwater River and their tributaries. Fish in these areas are all A-run and are distinguished from the rest of the basin on the basis of this life-history pattern. In addition, a break in habitat characteristics separates it from the North Fork. Clear Creek, a tributary to the lower Middle Fork presumably supported A-run steelhead (due to habitat similarity to lower reaches), but has had recent hatchery influence from Dworshak and Kooskia Hatchery B-run fish. Its placement in any population was less clear; it was grouped with the lower Clearwater on the basis of its assumed historical life history and a lack of data that would include it in any other population.
4. ***South Fork Clearwater River (CRSFC-s)*** We identified the South Fork Clearwater River and its tributaries from Mill Creek upstream as an historically independent population supporting B-run fish. Spawning areas in this population exceed our threshold (Appendix A), and therefore likely preclude substantial straying. However, the South Fork was historically blocked from 1949 to 1963, and the anadromous component of the population was extirpated. The current population is derived from resident rainbow trout, juvenile stocking from Dworshak Hatchery stock, adults trapped at Lewiston Dam (Kiefer et al. 1992), and possibly residualized (resident) endemic *O. mykiss*.
5. ***Lolo Creek (CRLOL-s).*** Few data were available for Lolo Creek: this area was identified as an independent population on the basis of geographic isolation from all but the lower mainstem population (population 2) and basin size. The lower main stem supports A-run fish, whereas this area currently supports B-run steelhead, supporting this division. Which run(s) this population supported historically is unknown.
6. ***Selway River (CRSEL-s).*** Genetic samples from the Lochsa and Selway Rivers are cluster most closely (Table IV-2; Figure IV-2). Although these areas are not well-separated, each basin covers an enormous area (Appendix C). Given the very few genetic samples from the Selway and Lochsa, we have designated each as an independent population. This population includes fish spawning in the main stem and all tributaries to the Selway. There is likely to be substantial substructure within this population.

	SNTUC-s	SNASO-s	CRLMT-s	CRSFC-s	CRLOL-s	CRSEL-s	CRLOC-s	GRLMT-s	GRJOS-s	GRWAL-s	GRUMA-s	SRLSR-s	SFSFS-s	SFSEC-s	SRCHA-s	MFBIG-s	MFUMA-s	SRPAN-s	SRNFS-s	SRLEM-s	SRPAH-s	SREFS-s	SRUMA-s	IRMAI-s	SNHCT-s
SNTUC-s	0																								
SNASO-s	40	0																							
CRLMT-s	36	27	0																						
CRSFC-s	197	187	34	0																					
CRLOL-s	111	102	4	86	0																				
CRSEL-s	183	173	38	93	77	0																			
CRLOC-s	186	176	36	96	74	10	0																		
GRLMT-s	104	74	90	251	165	242	239	0																	
GRJOS-s	80	50	66	227	142	218	215	24	0																
GRWAL-s	209	179	195	356	270	347	344	8	129	0															
GRUMA-s	208	178	194	355	270	346	343	8	128	11	0														
SRLSR-s	118	87	104	265	179	256	253	75	52	180	180	0													
SFSFS-s	324	293	310	471	385	462	459	281	258	386	386	75	0												
SFSEC-s	382	352	368	529	443	520	517	695	718	924	924	134	11	0											
SRCHA-s	252	221	238	399	485	562	559	737	760	966	966	4	13	72	0										
MFBIG-s	462	431	448	609	695	772	769	947	970	1176	1176	209	148	206	76	0									
MFUMA-s	529	498	515	676	762	839	836	1014	1037	1243	1243	276	215	273	142	31	0								
SRPAN-s	400	369	386	547	633	710	707	885	908	1114	1114	134	86	144	13	44	110	0							
SRNFS-s	454	423	440	601	687	764	761	939	962	1168	1168	200	140	198	67	67	133	11	0						
SRLEM-s	486	455	472	633	719	796	793	971	994	1200	1200	233	206	264	133	133	200	77	34	0					
SRPAH-s	564	533	550	711	797	874	871	1049	1072	1278	1278	310	250	308	177	177	244	366	77	40	0				
SREFS-s	611	580	597	758	844	921	917	1095	1118	1324	1324	358	297	355	486	486	553	675	125	88	16	0			
SRUMA-s	670	639	656	817	903	980	977	1155	1178	1384	1384	417	356	414	545	545	612	734	184	147	75	7	0		
IRMAI-s	116	86	103	263	178	254	252	74	57	179	179	25	231	289	159	365	432	303	357	423	467	514	573	0	
SNHCT-s	113	83	99	260	174	251	248	70	54	175	175	21	227	285	155	361	428	299	353	419	463	510	569	9	0

7 ***Lochsa River (CRLOC-s).*** The Lochsa population includes the Lochsa River and all tributaries. We separated it from the Selway River largely on the basis of basin topography and apparent population size. Like the Selway, there is likely to be substantial substructure within this population.

In addition, the Clearwater River includes one historical population from which the anadromous component has been extirpated.

H-1. North Fork Clearwater River (CRNFC-s). The anadromous component of this population was extirpated in the wild, but is represented by the Dworshak Hatchery stock, which was derived from fish returning to the passage-blocking Dworshak Dam. The population also includes resident rainbows above Dworshak Dam. These fish are the most consistently genetically divergent samples from the Clearwater basin (Table IV-2, Figure IV-1), supporting designation of this area as an (historical) independent population.

Grande Ronde River

Steelhead in the Grande Ronde River basin have been sampled at a very fine scale for genetic analysis (Moran, unpublished). These data, coupled with samples from the Imnaha and Salmon Rivers, suggest that the Grande Ronde population forms a relatively coherent group (Figure IV-2). However, three conspicuous outliers—Mudd Creek, Prairie Creek, and Dry Creek—were significantly divergent, not only from other Grande Ronde populations, but also from other Snake River basin samples (Figure IV-1). This extreme differentiation may reflect the influence of resident *O. mykiss* in these areas. Within the Grande Ronde, we identified four populations:

8 ***Lower Grande Ronde (GRLMT-s).*** This population includes the mainstem Grande Ronde River and all tributaries (including the outlier Mudd Creek) upstream to the confluence of the Wallowa River, except the Joseph Creek drainage. Most genetic samples (except Mudd Creek, above) from this region formed a distinct cluster (Figure IV-1), and spawning areas in this population are well-separated from other populations.

9 ***Joseph Creek (GRJOS-s).*** Spawning areas in Joseph Creek are well separated (67 km) from other spawning aggregations. In addition, samples from the tributaries to Joseph Creek (Chesnimnus and Elk Creeks) form a distinct group in a cluster analysis (Figure IV-1).

10 ***Wallowa River (GRWAL-s).*** We defined the Wallowa River, including the Minam River, the Lostine River and several smaller tributaries as an independent population. Spawning within this population currently does not begin until the confluence of the Wallowa and Minam Rivers (population 8), and this population was separated from the lower mainstem on this topographical and distance factor. Genetic samples from the Minam were somewhat differentiated from other Wallowa River samples, but spawning areas from the confluence upstream are in very close proximity to each other. This population includes the outlier Prairie Creek.

11 ***Upper Grande Ronde (GRUMA-s).*** The remainder of the Grande Ronde drainage, including the mainstem upper Grande Ronde and tributaries Lookingglass Creek, Catherine Creek, and Indian Creek we designate as an independent population. Genetic samples from this region form a distinct cluster in a dendrogram (Figure IV-1); the majority of spawning in this population is separated from lower populations by a minimum of 33 km (although spawning and rearing habitat was classified as being closer). Dry Creek, which was an outlier in the genetic analysis (Figure IV-1) is included in this population. Like other outliers, this may reflect the contribution of resident fish to the sample.

Salmon River

Although only a few locations from the Salmon River were sampled for genetic analysis, these samples did form a cohesive group (Figure IV-1). On the basis of this genetic signal and basin topography, we identified the Salmon River as a major grouping in the Snake River Steelhead ESU. Within the Salmon River cluster, there was some geographic signal as Middle Fork Snake River samples clustered together, as did samples from the South Fork. However, samples from the Rapid River and two tributaries to the mainstem Salmon River (Bargamin and Horse Creeks, both classified as A-run streams) were not clearly allied with either group (Figure IV-1). We identified a total of 11 current populations in this major grouping:

12 ***Little Salmon and Lower Salmon tributaries (SRLSR**-s). This population of A-run fish includes the Little Salmon River and its tributaries, as well as steelhead-supporting tributaries to the lower Salmon River, downstream from the mouth of the Little Salmon (Whitebird Creek, Skookumchuck Creek, Slate Creek, and several smaller tributaries). These spawning areas were grouped on the basis of their shared life history and available spawning habitat—the lower tributaries were not judged to be large enough to support an independent population alone. The population as a whole is separated from other upstream spawning areas by 75 km, a distance likely to preclude significant straying between areas.

13 ***South Fork Salmon River (SFMAI-s)***. This B-run population was defined on the basis of geographic and genetic characteristics. The population includes the South Fork Salmon River and all its tributaries except the Secesh River. These areas are geographically well separated from other spawning aggregates except the Secech (Table IV-3) and genetic samples from the South Fork Salmon River are distinct from those in the Secesh (Table IV-2). French, Sheep and Crooked Creeks and the Wind River, which would have been grouped with this population following the “nearest upstream population” rule were excluded, however, because these streams are classified as A-run. They were grouped with Chamberlain Creek (population 15), the nearest A-run population instead.

14 ***Secesh River (SFSEC-s).*** This population, including the mainstem Secesh and its tributaries, was defined primarily on the basis of genetic information. Microsatellite samples from the Secesh were highly differentiated from other South Fork Salmon River samples (Table IV-2).

15 ***Chamberlain Creek (SRCHA-s)***. This population, which includes fish spawning in French, Sheep Crooked, Bargamin, and Sabe Creeks, the Wind River and Chamberlain Creek was delineated on the basis of life history and basin topography. All streams in this population are classified as A-run (Kiefer et al. 1992), whereas the populations immediately downstream (South Fork Salmon River) and upstream (lower Middle Fork Salmon River) are classified as B-run. No genetic samples were available from Chamberlain Creek.

16 ***Lower Middle Fork Salmon River (MFBIG-s).*** The lower Middle Fork Salmon River and tributaries, up to and including Loon Creek, were identified as an independent steelhead population. Genetic samples from Big and Loon Creeks (both in the lower Middle Fork Salmon River) were more closely allied than either was to samples from Rapid River and Marsh Creek (Figure IV-1). Although the extent of steelhead spawning in the main stem of the Middle Fork Salmon River is uncertain, there is a significant habitat break between the lower and upper Middle Fork.

17 ***Upper Middle Fork Salmon River (MFUMA-s).*** Geographically separated from other spawning areas (Table IV-3), this population delineation was also supported by genetic distance from lower Middle Fork Salmon River samples and a significant habitat break between the two populations. The population includes fish spawning in the Middle Fork main stem and tributaries upstream from Loon Creek.

18 ***Panther Creek.*** This population includes both the Panther and Owl Creek drainages. Anadromous *O. mykiss* in Panther Creek were likely extirpated due to mining impacts by the 1950s. However, Owl Creek was not affected by these activities (and may in recent times have received strays from other Salmon River populations such as the North Fork). This area was judged to be of sufficient size to maintain an independent population.

19 ***North Fork Salmon River (SRNFS-s).*** Few data were available for this population. Designation of this population, which includes Indian Creek, was based primarily on geographic distance of the primary spawning areas from other spawning aggregates and basin topography.

20 ***Lemhi River (SRLEM-s).*** Lemhi River steelhead were virtually eliminated by a water diversion dam used for hydroelectric power generation at the mouth of the Lemhi (Bjornn 1978), although it is possible that some steelhead gained access to the river during high flows. Steelhead currently found in the Lemhi River drainage are presumably primarily derived from several hatchery stocking efforts. We classified the Lemhi as an independent population based on the distance of spawning aggregates to other Salmon River spawning areas (34 km). In addition, the Lemhi River flows primarily through a dry intermontane sagebrush valley (EPA ecoregion, level 4), a markedly different habitat type than other watersheds within the Salmon River basin (except the Pahsimeroi River, below). This population includes all tributaries to the Salmon from the mouth of the North Fork Salmon River to the mouth of the Lemhi, as well as the Lemhi River drainage.

20. Pahsimeroi River (SRPAH-s). This population includes the Pahsimeroi River and its tributaries, as well as all tributaries to the Salmon River from the mouth of the Lemhi upstream to the Pahsimeroi. Like the Lemhi River, the Pahsimeroi falls within the dry intermontane sagebrush valley ecoregion (EPA, level 4). It is separated from spawning aggregates by a minimum of 40 km and was identified as an independent population on this basis.

21. ***East Fork Salmon River (SREFS-s).*** Spawners in the East Fork Salmon River population, including Herd Creek are geographically close to those in the upper main stem of the Salmon River (7 km). However, there is a significant habitat break at the confluence of the East Fork and mainstem Salmon that was the basis of defining this population.
22. ***Upper Mainstem Salmon River (SRUMA-s).*** As above, this population, which includes **xxx**, is separated from its nearest neighbor, the East Fork Salmon River population, based on a significant break in habitat type. This population is separated from all other steelhead spawning aggregates by a minimum of 75 km.

Imnaha River

The Imnaha River supports steelhead spawning in the upper main stem and a variety of tributaries including Cow, Lightning, Horse, Big Sheep, and Gumboot Creeks.

23. ***Imnaha River (IRMMT-s).*** This population includes steelhead spawning in the mainstem Imnaha River and all its tributaries. These spawning aggregates are all in close proximity to each other; the greatest geographic distance between two spawning areas is 19 km between the mouth of Horse Creek and the mouth of Big Sheep Creek. Genetic samples have been taken from seven spawning areas. A cluster analysis (Figure IV-1) indicates that while there are two distinct clusters of Imnaha spawners, they do not neatly correspond to geographic segments of the drainage (Moran 2003). Given the lack of clear genetic or geographic delineation, we defined a single population.

Hells Canyon

Steelhead spawning is supported in a number of small tributaries to the Snake River in the Hells Canyon region, including Captain John, Granite, and Sheep Creeks. The main stem does not support spawning, but it does provide rearing habitat. Although these streams are geographically separated from other major spawning areas, none of these tributaries appears to be large enough to support an independent population. It is likely that, historically, spawning in this area was maintained in the long-term by straying from larger (likely upstream) populations. Currently, it is likely that strays from the Hells Canyon National Fish Hatchery support these areas. We identified a single group of dependent tributaries:

24. ***Hells Canyon tributaries (SNHCT-s).*** This dependent area includes tributaries to the mainstem Snake in the Hell’s Canyon reach, including Granite Creek, Sheep Creek, Deep Creek and others designated as supporting steelhead spawning or rearing. This area does not fit the definition of an independent population. However, maintaining this area may be important for ESU viability or other recovery goals.

Population primary spawning areas, characterization and hatchery influence can be found in Tables IV-4, IV-5, and IV-6. Further details about each population, including basin physiography and general climatic information for the watersheds in which each population is found, are in Appendix C.

Historically Occupied Areas

Like Snake River spring/summer chinook, Snake River steelhead were blocked from portions of the upper Snake River beginning in the late 1800s and culminating with the construction of the Hells Canyon Dam in the 1960s. We identify major tributaries in which steelhead spawning is known or strongly believed to have occurred. By analogy, it may be reasonable to suppose that these tributaries supported one or more populations, but the lack of distributional or genetic information makes it impossible to make these determinations definitively.

Snake River and Tributaries above Hells Canyon Dam

Tributaries above Hells Canyon were sequentially blocked by tributary and mainstem dams beginning in the early 1900s and culminating with the construction of the Hells Canyon Dam complex in the 1960s. Important likely anadromous *O. mykiss* supporting tributaries include the ***Powder River***, the ***Burnt River***, the ***Weiser River***, the ***Payette River***, parts of the ***Malheur River***, the ***Boise River***, the ***Owyhee River***, the ***Bruneau River***, ***Big Wood River***, ***Salmon Falls Creek*** and ***Rock Creek*** Figure IV-3). Interestingly, Leary (2001) found little genetic divergence between Oxbow and Pahsimeroi steelhead hatchery stocks and resident *O. mykiss* populations in the Powder River and other small tributaries just above the impassable dams in the mainstem Snake River, suggesting that the anadromous gene pool may still be represented in this historically accessible area.

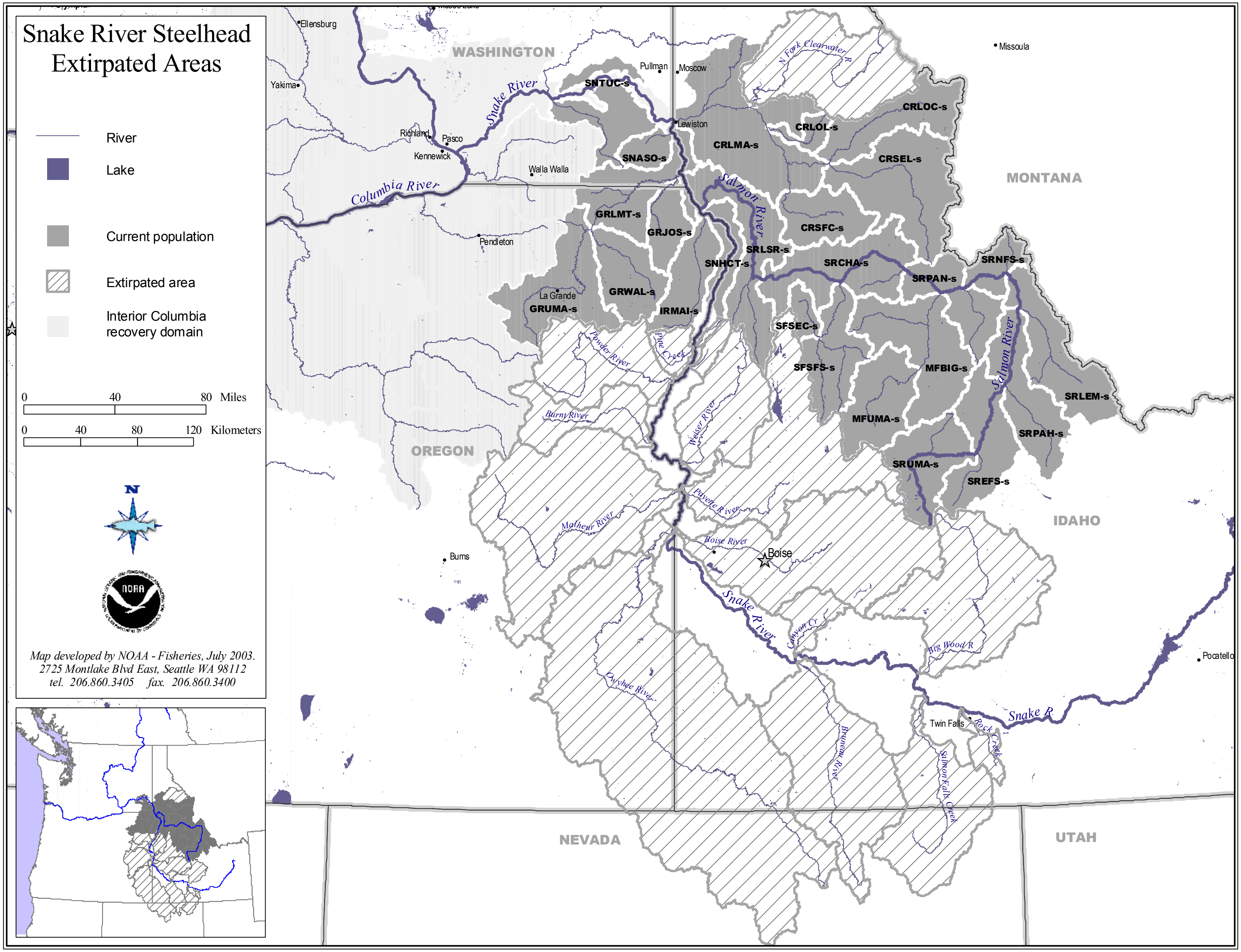


Figure IV-3. Snake River steelhead historical areas that are now extirpated.

Monitoring and Evaluation Needs

Population identification for steelhead in the Snake River could be substantially improved with additional data. We identified the following data needs, in order of priority:

- **Distribution of spawners, particularly in mainstem areas.** In order to determine the distance between spawning aggregates, we used spawning areas as identified in Streamnet (2003), modified in a few cases by local data. Real data on the current spatial and temporal distribution of steelhead spawners is sorely lacking, and is fundamental to determining population structure.
- **Stray rates.** Similarly, empirical estimates of stray distances and rates of wild and hatchery fish in natural settings would give us greater confidence in establishing population boundaries and influence of hatchery straying.
- **Genetic information—broad-scale sampling.** Although Moran (unpublished) sampled the Grande Ronde and Imnaha basins extensively, genetic data from the Clearwater and Salmon Rivers and their tributaries have only been collected at a very coarse scale. More fine-scale sampling, consistent with that conducted in northeastern Oregon, would help immensely in refining population delineations.
- **Genetic information—resident and anadromous fish sampling.** Determining the degree to which the resident component of *O. mykiss* populations contributes to the anadromous component (and vice versa) can provide important insight into population structure and connectivity. In addition, a better characterization of the resident component would allow a more accurate assessment of apparent outlier populations, such as Mud, Prairie, and Dry Creeks in the Grande Ronde basin.
- **Life-history characteristics.** Very little life-history information has been collected that would allow comparison of fish from different streams or basins. Of particular interest is information distinguishing A-run and B-run streams; however, all life-history characteristics, from age structure to juvenile migration patterns, are of interest.
- **Local area counts and run size.** Currently, population or stream-level counts are only conducted for a few streams in northeastern Oregon. Improved information about local run sizes would help substantially in determining whether an area could be considered an independent population.

Table IV-4. Snake River steelhead core spawning areas.

Region	Population	Code	Current Core Spawning Areas Description	Historical Spawning Area Description
Lower Snake	Tucannon River	SNTUC-s	Main stem upstream of Highway 12 bridge, Cummings Creek, the Little Tucannon River, and lower Panjab Creek	
	Asotin Creek	SNASO-s	George Creek, Pintler Creek, mainstem Asotin from George Creek upstream, North and South Forks and Charlie Creek	
Clearwater	Lower Clearwater	CRLMA-s		
	South Fork	CRSFC-s		
	Lolo Creek	CRLOL-s		
	Lochsa River	CRLOC-s		
	Selway River	CRSEL-s		
Grande Ronde	Lower Grande Ronde	GRLMT-s		
	Joseph Creek	GRJOS-s		
	Wallowa River	GRWAL-s		
	Upper Grande Ronde	GRUMA-s		
Salmon River	Little Salmon	SRLSR-s		

Region	Population	Code	Current Core Spawning Areas Description	Historical Spawning Area Description
River	South Fork	SFMAI-s	Main stem from Krassel Creek to Nasty Creek and from Nickle Creek to Rice Creek. East Fork South Fork from Williams Creek to Parks Creek. Johnson Creek from Porcupine Creek to Bear Creek. Burntlog Creek from Mouth to RM 3.5	
	Secesh River	SFSEC-s	Main stem from Alex Creek to Grouse Creek, Lick Creek from mouth to RM 5	
	Chamberlain Creek	SRCHA-s		
	Big, Camas, and Loon	MFBIG-s	Big Creek – main stem from Rush Creek to Lime Creek, Logan Creek to Jacob's Ladder Creek. Crooked Creek from mouth to Bismark Creek. Monumental Creek from mouth to Rainbow Creek. Camas Creek – main stem from Anvil Creek to South Fork. Yellowjacket Creek below Beagle Creek. Loon Creek – main stem from Cold Spring Creek to Cabin Creek. Warm Spring Creek from mouth to Parker Creek.	

Region	Population	Code	Current Core Spawning Areas Description	Historical Spawning Area Description
	Upper Middle Fork	MFUMA-s	Marble Creek – main stem from Spring Creek to Safety Creek. Indian Creek- main stem from East Fork to Wampum Creek. Pistol Creek – main stem from 32 Creek to Luger Creek. Rapid River – main stem from Hardscrabble Creek to Sulphur Creek (2). Sulphur Creek (1) – main stem from mouth to North Fork. Bear Valley Creek – mainstem from mouth to Cache Creek. Elk Creek from mouth to West Fork. Marsh Creek – main stem from Cape Horn Creek to Flat Creek. Cape Horn Creek from mouth to Banner Creek. Beaver Creek from mouth to Winnemucca Creek. Knapp Creek from mouth to RM 8.	
	Panther Creek	SRPAN-s		
	North Fork	SRNFS-s		
	Lemhi River	SRLEM-s		
	Pahsimeroi River	SRPAH-s		
	East Fork	SREFS-s		
	Upper main stem	SRUMA-s		
Imnaha	Imnaha River	IRMMT-s		
Hells Canyon	Hells Canyon	SNHCT-s		

Table IV-5. Snake River steelhead population characterization.

Basin	Population Name	Population Code	Spatial Structure	Within-Population Diversity		
				Life History	Habitat (Level 4 Ecoregion)	Genetics
Lower Snake	Tucannon River	SNTUC-s	Branched discontinuous	Adults: A-run	Upper reaches canyons and dissected highlands, lower reaches dissected loess uplands**	MtDNA may reflect ancient hybridization event with now-extinct cutthroat (K. Brown and G. Thorgaard, unpublished)
	Asotin Creek	SNASO-s	Branched continuous	Adults: A-run	Lower Snake and Clearwater Canyons	
Clearwater	Lower Clearwater	CRLMA-s	Branched discontinuous	Adults: A-run	Upper reaches northern Idaho hills and lower relief mountains, lower reaches Lower Clearwater canyons**	
	South Fork	CRSFC-s	Branched discontinuous	Adults: B-run; juveniles: American River samples significantly later arrival at lower Granite than rest of South Fork samples	South Clearwater forested mountains	
	Lolo Creek	CRLOL-s	Branched continuous	Adults: B-run	Upper reaches Clearwater mountains and breaks, middle reaches Weippe Prairie, lower reaches lower Clearwater canyons	

Basin	Population Name	Population Code	Spatial Structure	Within-Population Diversity		
				Life History	Habitat (Level 4 Ecoregion)	Genetics
	Lochsa River	CRLOC-s	Branched discontinuous	Adults: B-run; juveniles: Colt Kill and Stormy Creek samples significantly later arrival at Lower Granite than rest of Lochsa samples	Limited upper reaches Clearwater mountains and breaks, lower reaches Lochsa-Selway-Clearwater canyons**	
	Selway River	CRSEL-s	Branched discontinuous	Adults: B-run	Limited upper reaches in south Clearwater forested mountains, lower reaches Lochsa-Selway-Clearwater canyons	
Grande Ronde	Lower Grande Ronde	GRLMT-s	Branched discontinuous	Adults: A-run	Upper reaches canyons and dissected highlands, lower reaches canyons and dissected uplands	Mudd Creek was an outlier in NE Oregon.
	Joseph Creek	GRJOS-s	Branched discontinuous	Adults: A-run	Upper reaches canyons and dissected highlands, lower reaches canyons and dissected uplands	
	Wallowa River	GRWAL-s	Branched discontinuous	Adults: A-run	Upper reaches mesic forest, lower reaches split between Wallowa/Seven Devils Mountains and Blue Mountain basins	Minam and Wallowa River samples were well differentiated. Prairie Creek was an outlier in NE Oregon.
	Upper Grande Ronde	GRUMA-s	Branched discontinuous	Adults: A-run	Primarily maritime-influenced zone, with limited mesic forest, Blue Mountain basins and Wallowa/Seven Devils Mountains	Dry Creek was an outlier in NE Oregon.

Basin	Population Name	Population Code	Spatial Structure	Within-Population Diversity		
				Life History	Habitat (Level 4 Ecoregion)	Genetics
Salmon River	Little Salmon	SRLSR-s	Branched discontinuous	Adults: A-run; juveniles: White Bird Creek samples significantly later arrival at Lower Granite than Rapid River samples	Upper reaches include 4 ecoregions, predominantly Wallowa/Seven Devils Mountains, lower reaches canyons and dissected uplands**	
	South Fork	SFMAI-s	Branched discontinuous	Adults: B-run	Upper reaches southern forested mountains, lower reaches hot dry canyons	
	Secesh River	SFSEC-s	Branched continuous	Adults: B-run	Southern forested mountains	
	Chamberlain Creek	SRCHA-s	Branched discontinuous	Adults: A-run	Upper reaches southern forested mountains, lower reaches hot dry canyons	
	Big, Camas, and Loon	MFBIG-s	Branched discontinuous	Adults: B-run	Upper reaches southern forested mountains, lower reaches hot dry canyons	
	Upper Middle Fork	MFUMA-s	Branched discontinuous	Adults: B-run	Southern forested mountains, with limited high glacial drift-filled valleys in upper reaches	
	Panther Creek	SRPAN-s	Branched discontinuous	Adults: A-run	Southern forested mountains, limited hot dry canyons in lower reaches	
	North Fork	SRNFS-s	Branched discontinuous	Adults: A-run	Predominently south Clearwater forested mountains, limited areas in 4 other ecoregions	

Basin	Population Name	Population Code	Spatial Structure	Within-Population Diversity		
				Life History	Habitat (Level 4 Ecoregion)	Genetics
	Lemhi River	SRLEM-s	Branched discontinuous*	Adults: A-run	Upper reaches barren mountains, middle reaches dry gneissic-schistose-volcanic hills, lower reaches dry intermontane sagebrush valleys	
	Pahsimeroi River	SRPAH-s	Branched discontinuous	Adults: A-run	Dry intermontane sagebrush valleys	
	East Fork	SREFS-s	Branched discontinuous	Adults: A-run	Upper reaches dry partly wooded mountains, lower reaches dry gneissic-schistose-volcanic hills**	
	Upper Main stem	SRUMA-s	Branched discontinuous	Adults: A-run	Upper reaches high glacial drift-filled valleys, lower reaches southern forested mountains	
Imnaha	Imnaha River	IRMMT-s	Branched discontinuous	Adults: A-run	Upper reaches canyons and dissected highlands with limited mesic forest, lower reaches canyons and dissected uplands	Big Sheep, Little Sheep and Horse Creeks samples clustered together, distinct from Cow and Lightning Creeks: samples
Hells Canyon	Hells Canyon	SNHCT-s	Branched discontinuous	Adults: A-run	Canyons and dissected uplands	

* The core area, the mainstem Pahsimeroi River, is linear continuous. This population is classified as branched discontinuous because of the small downstream Salmon River tributaries, which are included in this population.

** The spawning reaches for this population span a broader-scale, level 3 ecoregion boundary

Table IV-6. Snake River steelhead hatchery influence.

Basin	Population Name	Population Code	Genetic Evidence of Hatchery Introgression	Natural Spawning of Hatchery-Origin Fish	Hatchery Outplants, Last 10 years		
					Number	Origin	Notes
Lower Snake							
	Tucannon River	SNTUC-s	High, non-local broodstock	High	Medium	Majority releases from out-of-ESU broodstock	Outplanting history includes seven stocks
	Asotin Creek	SNASO-s	High, non-local broodstock	No data	Low	Majority releases from out-of-ESU broodstock	
Clearwater	Lower Clearwater	CRLMA-s	Affinity to locally-derived broodstock	No data	High	Majority releases from within-ESU broodstock	
	South Fork	CRSFC-s	No data	No data	High	Majority releases from within-ESU broodstock	Recent increase in hatchery outplants
	Lolo Creek	CRLOL-s	No data	No data	Low	Majority releases from within-ESU broodstock	
	Lochsa River	CRLOC-s	No evidence	No data	None		History of within-ESU outplants
	Selway River	CRSEL-s	No evidence	No data	None		
Grande Ronde	Lower Grande Ronde	GRLMT-s	Affinity to locally-derived broodstock	No data	Medium	Majority releases from within-ESU broodstock	
	Joseph Creek	GRJOS-s	No evidence	None	None		
	Wallowa River	GRWAL-s	No data	No data	High	Majority releases from within-population broodstock	
	Upper Grande Ronde	GRUMA-s	No evidence	Medium	Low	Majority releases from within-ESU broodstock	

	Ronde					within-ESU broodstock	
Salmon River	Little Salmon	SRLSR-s	Relevant hatchery stock not sampled	No data	High	Majority releases from within-ESU broodstock	Outplanting history includes seven stocks
	South Fork	SFMAI-s	No evidence	No data	None		History of within-ESU outplants
	Secesh River	SFSEC-s	No evidence	No data	None		
	Chamberlain Creek	SRCHA-s	No data	No data	None		
	Big, Camas, and Loon	MFBIG-s	No evidence	No data	None		
	Upper Middle Fork	MFUMA-s	No evidence	No data	None		
	Panther Creek	SRPAN-s	No data	No data	None		History of within-ESU outplants
	North Fork	SRNFS-s	No data	No data	Medium	Majority releases from within-ESU broodstock	
	Lemhi River	SRLEM-s	No data	No data	Medium	Majority releases from within-ESU broodstock	
	Pahsimeroi River	SRPAH-s	No data	No data	High	Majority releases from within-population broodstock	
	East Fork	SREFS-s	No data	No data	Medium	Majority releases from within-ESU broodstock	Recent decline in hatchery outplants
	Upper Mainstem	SRUMA-s	No data	No data	High	Majority releases from within-ESU broodstock	Outplanting history includes six stocks
Imnaha	Imnaha River	IRMMT-s	Affinity to locally-derived broodstock	Medium	Medium	Majority releases from within-population broodstock	

Hells Canyon	Hells Canyon	SNHCT-s	No data	No data	High	Majority releases from within-ESU broodstock

Hatchery Influence Criteria:

Evidence of hatchery spawning
A. High = Over 25% (average over the last 5 years) of natural spawners are hatchery-origin fish
B. Medium = 10-25% (average over the last 5 years) of natural spawners are hatchery-origin fish
C. High = Less than 10% (average over the last 5 years) of natural spawners are hatchery-origin fish
D. None = No evidence of hatchery-origin spawners
E. No data = No data available

Hatchery outplants
A. High = average of >500,000 fish released per year, last 10 years
B. Medium = average of 50,000 to 500,000 fish released per year, last 10 years
C. Low = average of <50,000 fish released per year, last 10 years
D. None = No fish released, last 10 years

V. UPPER COLUMBIA RIVER STEELHEAD

The Upper Columbia River steelhead ESU includes anadromous and resident *O. mykiss* fish in anadromous-accessible regions upstream of Rock Island Dam. It was listed as endangered in 1998 as a result of steep declines in abundance of naturally produced fish, heavy harvest pressures, habitat loss, and large hatchery impacts. In fact, since 1985, between 71 and 90% of the steelhead passing Priest Rapids Dam were hatchery produced.

Determining population structure within this ESU is complicated by the effects of the Grand Coulee Fish Maintenance Project (GCFMP) and subsequent supplementation efforts. From 1939 to 1943, steelhead passing upstream of Rock Island Dam were collected for broodstock. However, mixing of populations above the dam was probably not complete because nonanadromous and 5+-year-old anadromous *O. mykiss* were not trapped (Fish and Hanavan 1948; described in Chapman et al. 1994). After the GCFMP, extensive artificial propagation of steelhead resumed in the 1960s. Currently, separate hatchery programs for steelhead in the Wenatchee and Methow Rivers are in place.

In response to a proposal by two public utility districts to develop a Habitat Conservation Plan, the Quantitative Analytical Report (QAR) process was initiated. This multi-agency group assessed population structure and developed interim recovery goals for this ESU (Ford et al. 2001). With little new data available to us, we relied heavily on their thorough analysis. However, we address the current and historical status of steelhead in the Okanogan River, a question the QAR process left open.

Demographically Independent Populations within the Upper Columbia River Steelhead ESU

In delineating populations, we considered several data types (Table V-1). We first examined the genetic analyses conducted by Chapman et al. (1994) and Ford et al.'s re-analysis of Chapman's data (2001). These analyses indicated that there was substantial variation between sampling localities, but that there was no clear geographic pattern to that variation (Table V-2). Thus we relied heavily on spawning distributions and our dispersal curve analysis (Appendix B). Habitat types also played a role in our population delineations. Due to the relatively small size of the area, we did not identify any major groupings. We identified four historically independent populations in this ESU (Figure V-1). Data do not exist to assess the contribution of resident fish to these populations.

21 ***Wenatchee River (UCWEN-s).*** This population includes all steelhead spawning in the Wenatchee River and its tributaries. Spawning areas within the Wenatchee are relatively contiguous, and are 59 km from those in the Entiat River.

22 ***Entiat River (UCENT-s).*** Entiat River spawning areas are well separated from spawning areas in both the Wenatchee and Methow Rivers (Table V-2). The Entiat

River has no targeted hatchery program at this time. ***Methow River (UCMET-s).*** Steelhead in the Methow and Twisp Rivers and all tributaries are included in this population. Like the other populations in this ESU, it was defined primarily on the basis of its separation from other spawning areas.

23 ***Okanogan River (UCOKA-s).*** The current status of steelhead endemic to the Okanogan is unknown. Currently, low numbers of natural steelhead return to this system, but may be offspring from hatchery returns. However, the Okanogan appears to have supported an independent population of steelhead historically. Although habitat conditions for rearing are highly degraded in the system, the Okanogan and its tributaries in the U.S. and Canada appear to have contained sufficient habitat to have supported an independent population of steelhead. In addition, the Okanogan is found in a substantially different habitat than other populations in this ESU, further supporting delineation of this population.

Primary spawning areas, characterization and hatchery influence for each population are presented in Table V-4, V-5, and V-6. Further details, including basin physiography and general climatic information for the watersheds in which each population is found, can be found in Appendix C.

Historically Occupied Areas

The construction of Grand Coulee Dam in 1939 blocked access to over 50% of the river miles formerly available to Upper Columbia steelhead (NRC 1996). Although we are unable to define populations in this blocked area with any certainty, we can identify major watersheds that appear to be capable of supporting anadromous *O. mykiss* and likely belonged to this ESU. By analogy, it may be reasonable to suppose that these tributaries supported one or more populations, but the lack of distributional or genetic information makes it impossible to make these determinations definitively.

Tributaries to the Columbia River, above Grand Coulee Dam: Sanpoil River, Spokane River, Colville River, Kettle River, Pend Oreille River, and Kootenai River (Figure V-2).

Monitoring and Evaluation Needs

Our population identification efforts would be enhanced by additional data. As research efforts continue on Upper Columbia steelhead population structure, we recommend that a priority be placed on the following data needs, in the following order:

- **Dispersal information.** Generally lacking in our dispersal analysis were strong data for steelhead as well as fine-scale (0–50 km) dispersal information. A better understanding of the likelihood and distance of steelhead spawning would greatly increase the strength of our population delineations. Importantly, radio-tagging data for Upper Columbia River steelhead intercepted at Rock Island Dam (Bickford, unpubl. data) suggest that there is substantial straying among basins that may affect the ESU's genetic structure. A clearer picture of hatchery- and natural-origin straying in this region would also be helpful in evaluating population boundaries.

- **Wild fish spawning distributions.** Accurate information about the distribution of steelhead spawning in the ESU is extremely important for drawing appropriate boundaries. While recent radio-tracking studies are improving our understanding of steelhead behavior and distribution, these studies primarily focus on hatchery-origin fish (see also below).
- **Additional genetic samples**. Additional genetic sampling, particularly sampling conducted two or more generations after the initiation of basin-specific hatchery programs, would be useful to assess the degree of genetic differentiation between locations. In addition, samples of resident and anadromous fish would be extremely helpful in assessing the degree to which resident fish contribute to the anadromous component of the population.
- **Reproductive success at particular spawning locations.** Recent radio-tracking studies following primarily hatchery-origin fish show spawning in areas that may not be suitable for rearing. If this is the case, these spawners may contribute little or nothing to the population. A better understanding of the suitability of habitats used by steelhead would provide insight into the realized composition of populations.

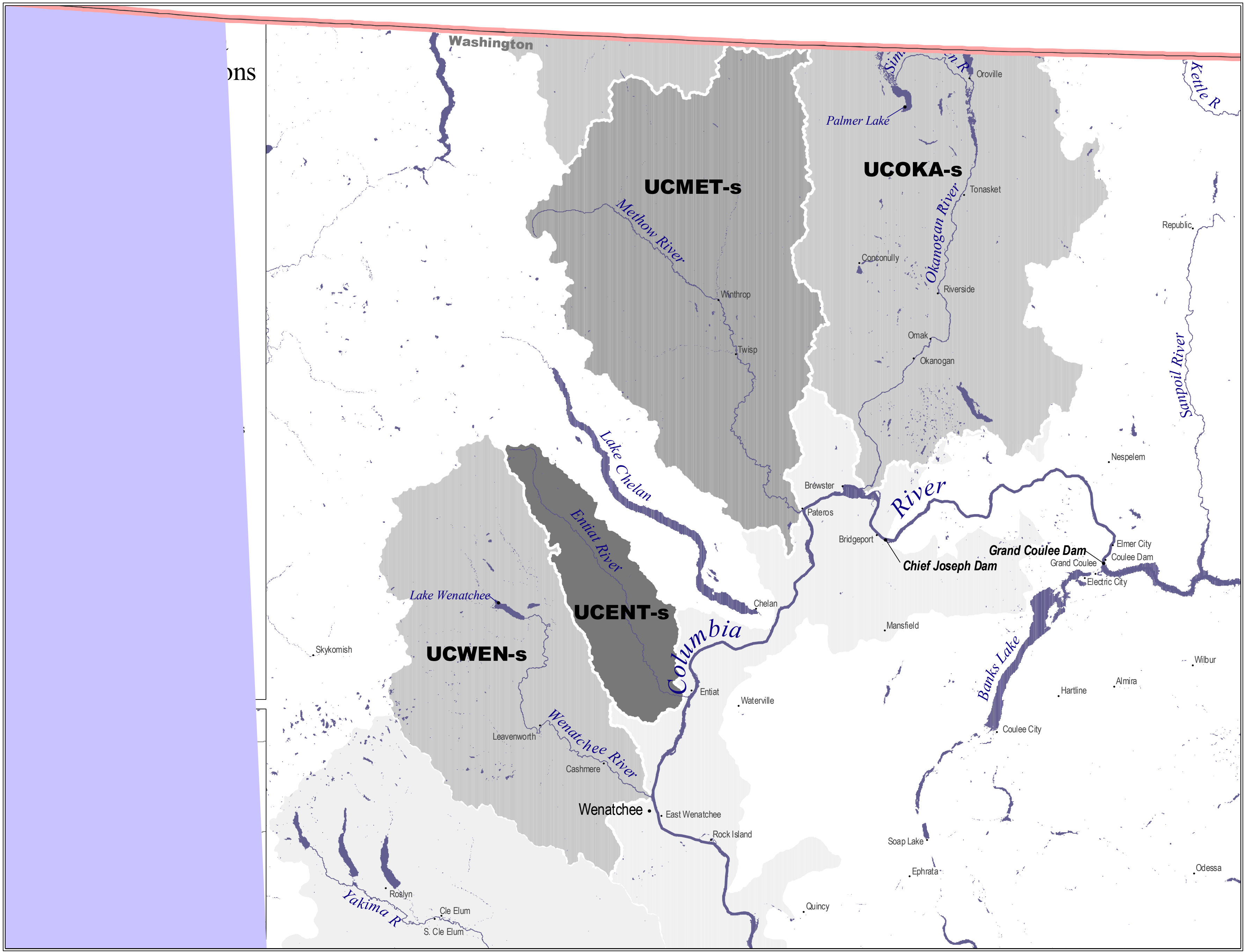
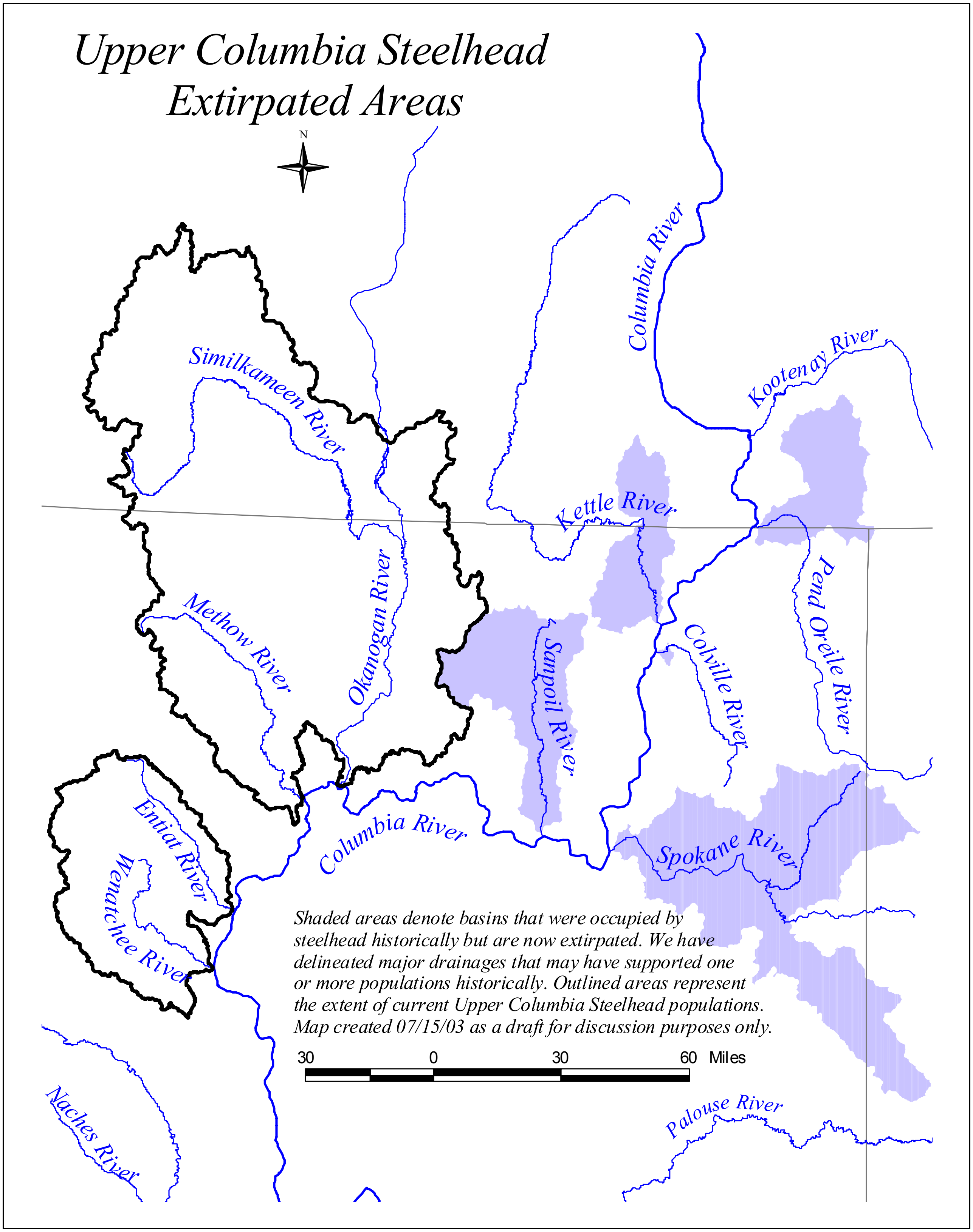


Figure V-1. Upper Columbia steelhead populations.



Shaded areas denote basins that were occupied by steelhead historically but are now extirpated. We have delineated major drainages that may have supported one or more populations historically. Outlined areas represent the extent of current Upper Columbia Steelhead populations. Map created 07/15/03 as a draft for discussion purposes only.

Figure V.2. Upper Columbia steelhead extirpated areas.

Table V-1. Available data types and analyses for the Upper Columbia steelhead ESU.

Data Type	**Description**
Genetic	Chapman et al. (1994) and Ford et al. (2001) calculated Fst statistics for available allozyme data from the Methow, Entiat, and Wenatchee Rivers.
Dispersal/distance	Distance between spawning areas calculated using spawning distributions defined by Mullen et al. (1992) and Chapman et al. (1994). Lacking ESU-specific data on dispersal distances, we used the results from the generalized dispersal distance analysis (Appendix A).
Phenotypic	None available.
Habitat	EPA-defined ecoregions considered in population designations.
Demographic correlation	No data available.

Table V-2. Estimates of Fst for Upper Columbia steelhead. From Ford et al. 2001.

Fst	**All Wild Samples from 1985** [1]	**1984 and 1985 Wenatchee River Samples**[2]	**1983 and 1985 Entiat River Samples**[3]	**1983 and 1985 Methow River Samples**[4]
Estimate	0.0307	0.0140	0.0197	0.0074
95% confidence interval	0.0141	-0.0004	0.0046	-0.0073
	0.0541	0.0344	0.0340	0.0340

[1] Samples 1, 2, 3, 4, 6, 7, 8, 10, and 14 from Chapman et al. (1994, Table 2). 1985 refers to the broodyears; fish were collected in 1986 (Hershberger and Dole 1987).

[2] Samples 14 and 15.

[3] Samples 4 and 5.

[4] Samples 8 and 9.

Table V-3. Distance matrix for Upper Columbia steelhead. Distances were computed using 100k-scale hydrography from Streamnet; distance units are in kilometers.

	UCWEN-s	**UCENT-s**	**UCMET-s**	**UCOKA-s**
UCWEN-s	0			
UCENT-s	59	0		
UCMET-s	118	86	0	
UCOKA-s	149	117	48	0

Table V-4. Upper Columbia steelhead core spawning areas.

Region	Population	Code	Current Core Spawning Areas Description	Historical Spawning Area Description
Wenatchee	Wenatchee River	UCWEN-s	Mainstem from Lake Wenatchee to Mission Creek, lower Chiwawa River and lower Chumstick Creek	
Entiat	Entiat River	UCENT-s	Preston Falls downstream to the mouth, lower Mad River	
Methow	Methow River	UCMET-s	Mainstem Methow from Mazama to Black Canyon, the lower 10 miles of the Chewuch River, and the lower 8 miles of the Twisp River	
Okanogan	Okanogan River	UCOKA-s	Unknown	

Table V-5. Upper Columbia steelhead population diversity.

				Within-Population Diversity		
Basin	Population Name	Population Code	Spatial Structure	Adult Run Timing	Habitat (Level 4 Ecoregion)	Genetics
Wenatchee	Wenatchee River	UCWEN-s	Branched discontinuous	Summer	Upper reaches Wenatchee/Chelan highlands, lower reaches Chiwaukum Hills and lowlands	
Eniat	Entiat River	UCENT-s	Branched continuous	Summer	Chelan Tephra Hills	
Methow	Methow River	UCMET-s	Branched continuous	Summer	Upper reaches Pasayten/Sawtooth highlands and Okanogan pine/fir hills, lower reaches Okanogan Valley*	
Okanogan	Okanogan River	UCOKA-s	Unknown	Summer	Unknown	

* Spawning areas for this population span a broader-scale, level 3 ecoregion boundary

Table V-6. Upper Columbia steelhead hatchery influence.

Basin	Population Name	Population Code	Genetic Evidence of Hatchery Introgression	Natural spawning of hatchery-origin fish	Hatchery Outplants, last 10 years		
					Number	**Origin**	**Notes**
Wenatchee	Wenatchee River	UCWEN-s	All ESU fish heavily influenced by the Grand Coulee Fish Mangement Plan, in which all but 5+ year spawners crossing Rock Island Dam were collected. Progeny and adults were outplanted	High	Medium	Majority releases from in-ESU broodstock	Outplant history includes six stocks
Entiat	Entiat River	UCENT-s		High	Low	All releases from in-ESU broodstock	
Methow	Methow River	UCMET-s		High	Medium	All releases from in-ESU broodstock	
Okanogan	Okanogan River	UCOKA-s		No data	Medium	All releases from in-ESU broodstock	

Hatchery Influence Criteria:

Evidence of hatchery spawning
A. High = Over 25% (average over the last 5 years) of natural spawners are hatchery-origin fish
B. Medium = 10-25% (average over the last 5 years) of natural spawners are hatchery-origin fish
C. High = Less than 10% (average over the last 5 years) of natural spawners are hatchery-origin fish
D. None = No evidence of hatchery-origin spawners
E. No data = No data available

Hatchery outplants
A. High = average of >500,000 fish released per year, last 10 years
B. Medium = average of 50,000 to 500,000 fish released per year, last 10 years
C. Low = average of <50,000 fish released per year, last 10 years
D. None = No fish released, last 10 years

VI. MID-COLUMBIA RIVER STEELHEAD

The Mid-Columbia Steelhead ESU includes *O. mykiss* that spawn in tributaries to the Columbia generally in the Columbia Plateau region: Rock Creek and the White Salmon, Klickitat, and Yakima Rivers on the northern side of the Columbia and Fifteenmile Creek and the Deschutes, John Day, Umatilla, and Walla Walla Rivers on the southern side. Like other steelhead, these fish show a range of life-history strategies; this ESU includes both summer and winter spawning runs.

Also like other steelhead, this ESU has felt a variety of impacts. Harvest, habitat alteration (particularly due to irrigation), inadvertent negative effects of hatchery practices and dam construction have all changed the abundance, distribution and survival of fish in this ESU. As a result, declining runs and a reduction in available habitat led to the listing of this ESU as threatened in 1999. This is the only anadromous salmonid ESU listed in this region.

Demographically Independent Populations within the Mid-Columbia River Steelhead ESU

We identified sixteen populations in four major groupings and one unaffiliated area in this ESU (Figure VI-1), largely on the basis of basin topography and habitat similarity, since data tended to be patchily distributed across the region (Table VI-1). In particular, genetic studies in this ESU tended to be locally focused, with few overlapping loci to allow comparison across the broader geographic area, although some information was available within our groupings. Uncertainties about hatchery straying and interbreeding also limited our ability to draw definitive conclusions from genetic data. We delineated a total of 16 populations in this ESU.

Cascades Eastern Slope Tributaries

Populations in this major grouping are united primarily by geographic proximity. The habitats they occupy are diverse, but the constituent rivers generally drain the eastern slope of the Cascades and the dry Columbia Plateau. This group contains four extant and one extirpated population, as well as a large area that is currently blocked to anadromous fish passage.

1. ***Klickitat River (MCKLI-s).*** This population was defined largely on the basis of genetic information. A recent analysis (Phelps et al. 2000) indicated that both resident fish and presumed native Klickitat steelhead showed allele frequencies between coastal and inland lineages, suggesting a distinct lineage of resident and anadromous *O. mykiss* in this basin (Figure VI-2). The population is moderately separated (22 km) from the nearest spawning aggregate in Fifteenmile Creek, which is on the Oregon side of the Columbia. We included both winter- and summer-run steelhead in the Klickitat River and its tributaries in this population because spawning areas overlap and samples from the sport fishery do not show strong segregation. Genetic

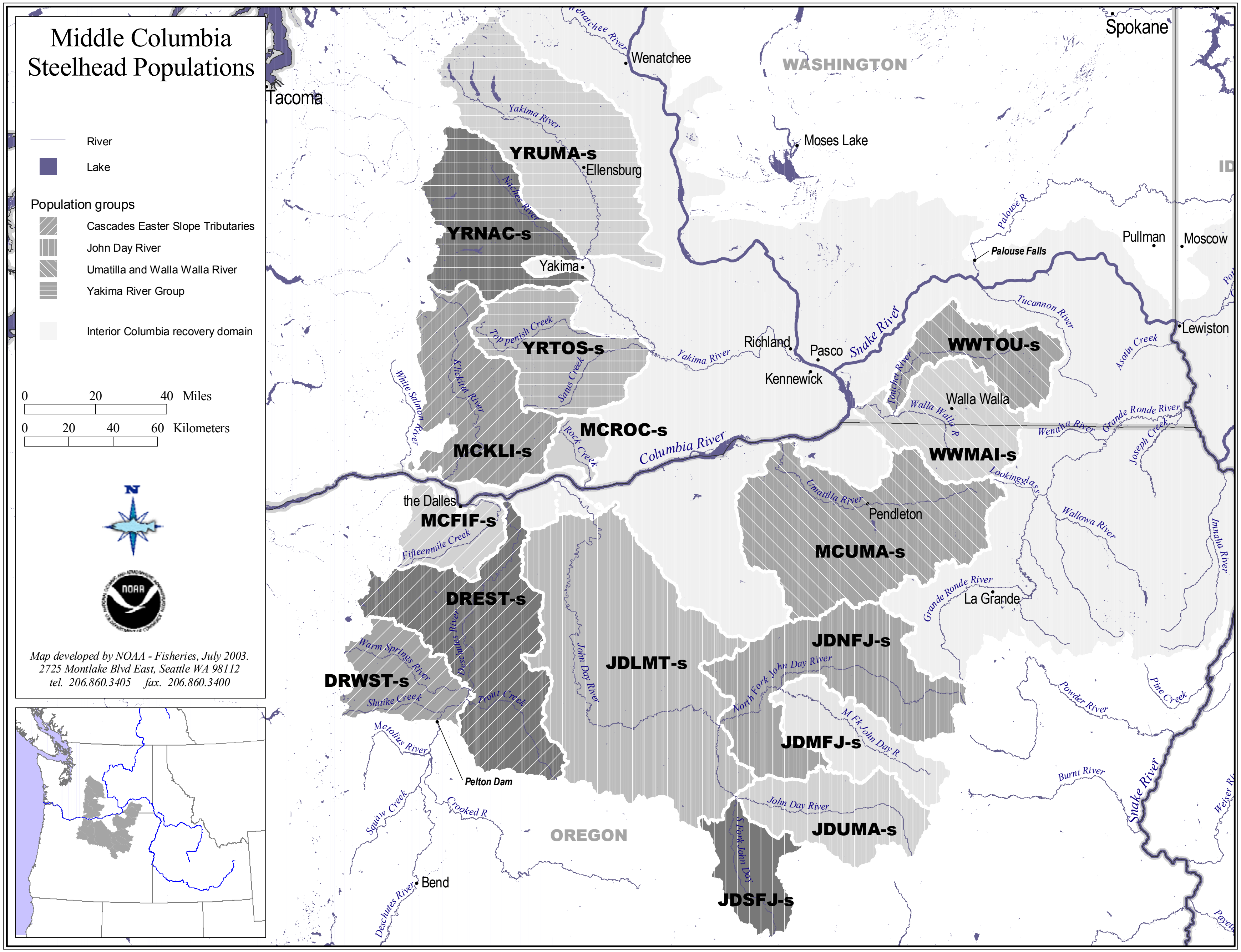


Figure VI-1. Mid-Columbia steelhead populations.

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                                                                 Distance
.20       .18       .16       .14       .12       .10       .08       .06       .04       .02       .00
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+
                                                                              *********************** SATUS DRY CK
                                                                            ***
                                                               ************** *********************** SATUS CREEK
                                                               *            *
                                                           *****            ************************* SATUS LOGY CK
                                                           *   *
                                                           *   ************************************** TOPPENISH CK
                                                           *
                                                           *               ************************** LITTLE NACHES R
                                                       *****          ******
                                                       *   *          *    ************************** RATTLESNAKE CK
                                                       *   *  *********
                                                       *   *  *       *       *********************** WAPATOX TRAP
                                                       *   *  *       *   *****
                                          **************   ****       *****   *********************** CHANDLER TRAP
                                          *            *      *           *
                                          *            *      *           *************************** ROZA TRAP
                                          *            *      *
                                          *            *      *************************************** TEANAWAY R
                                          *            *
                                          *            ********************************************** WELLS SUMMER RUN
                                          *
                                          *                 ***************************************** YAKIMA HATCHERY
                                          *                **
                                          *                **   ************************************* SUMMIT CREEK
                                          *                ******
                                          *                *    *    ******************************** BOWMAN CREEK
                                          *     ************    ******
                                          *     *          *         ******************************** LITTLE KLICKITAT
                                          *     *          *
                                          *     *          *    ************************************* TROUT CREEK
                                          *     *          ******
                                          *******               * *********************************** WHITE CREEK
                                                *               ***
                                                *                 *********************************** SWALE CREEK
                                                *
                                                *    ************************************************ SKAMANIA SUMMER
                                                ******
                                                     ************************************************ SKAMANIA WINTER
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+
.20       .18       .16       .14       .12       .10       .08       .06       .04       .02       .00
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Figure VI-2. UPGMA cluster analysis of samples from the Klickitat and Yakima Rivers. Dendrogram based on Cavalli-Sforza and Edwards’ chord distances calculated across 32 loci. Data from Phelps et al. (2000).

Table VI-1. Available data types and analyses for the Mid-Columbia steelhead ESU.

Data Type	Description
Genetic	Allozyme data were available from a variety of sources. We used 24 loci sampled from 50 locations throughout Oregon (Currens 1997), particularly focusing on the Deschutes River and nearby drainages. In addition, we considered the analyses presented in Currens and Schreck (1987) for the John Day River. In the Klickitat and Yakima drainages we used 32 polymorphic loci from 21 locations (Phelps et al. 2000). In the Walla Walla and Umatilla drainages, Narum et al. (unpub.) provided data from16 microsatellite loci for 3 sampling locations. Sampled loci were not compatible across sub-areas. Therefore, for each sub-area we calculated Cavalli-Sforza and Edwards' distances, which we then used in a UPGMA cluster analysis. In addition, we conducted a principal components analysis using data from Currens (1997). (Appendix)
Dispersal/distance	General steelhead dispersal distance analysis (Appendix A). Distance between spawning areas calculated from Streamnet spawning area maps, updated with ODFW and WDFW data and professional judgment. Lacking ESU-specific data on dispersal distances, we used the results from the generalized dispersal distance analysis (Appendix A)
Phenotypic	Qualitative spawn timing and juvenile outmigration data for Deschutes River spawning areas (ODFW, unpublished).
Habitat	EPA-defined ecoregions. Level 4 delineations considered in some population identifications.
Demographic correlation	35 index areas (redds per mile) available for John Day basin. Length of data sets vary; many cover the time period from the mid-1960s to the present. We conducted pairwise correlations on available time series.

information (Phelps et al. 2000) does indicate some degree of genetic differentiation between tributaries to the Klickitat River, with the Upper Klickitat, White Creek, and Trout Creek appearing to be most different from Skamania Hatchery stock. Both this life-history diversity and genetic substructure should be considered when evaluating management actions.

2 ***Fifteenmile Creek (MCFIF-s).*** This population includes Fifteenmile Creek and its tributaries in Eightmile and Ramsey Creeks. Spawning areas in these creeks are characterized as continuous, and there is little environmental variation in the basin. It is moderately segregated from other populations (22 km from the Klickitat and 37 km from the nearest spawning in the Deschutes River), and occupies somewhat different habitat. These characteristics, coupled with basin size, genetic differentiation (Figures VI-3 and VI-4) and apparent capacity led us to designate this as a separate population. Fifteenmile Creek is the easternmost distribution of winter steelhead in the Columbia basin. Within the population, genetic samples from Eightmile Creek (Currens 1997)

were highly divergent from samples from Fifteenmile Creek, the Deschutes River, and the Lower Columbia ESU (see Appendix A). These Eightmile Creek samples appear to represent a resident redband rainbow population with little or no interbreeding with anadromous fish (Currens, pers. comm..).

3 ***Deschutes River Eastside Tributaries (DREST-s).*** This population encompasses the mainstem Deschutes River from its mouth to the confluence of Trout Creek, and the tributaries entering the Deschutes from the east: Buck Hollow, Bakeoven, and Trout Creeks. Because of uncertainty concerning the relationship of mainstem spawners in the Deschutes Rivers and tributary populations, mainstem reaches were grouped with their respective tributary populations. It was separated from other Cascade eastern slope populations by geographic distance (37 km to Fifteenmile Creek) and run timing (Deschutes steelhead are exclusively summer run fish), and from the Deschutes River westside tributaries population (see population 4) on the basis of marked habitat differences, coupled with life-history differences. Eastside tributaries drain drier, lower-elevation areas than the westside tributaries; consequently, flow patterns and water temperatures are quite different between the two areas. Steelhead in the two regions are temporally segregated, with eastside tributary fish spawning between January and April, and westside tributary fish spawning between April and May (Olsen et al. 1992).

4 ***Deschutes River Westside Tributaries (DRWST-s).*** The westside Deschutes River tributaries are separated from the eastside tributary population on the basis of habitat and life history characteristics (see population 3). Included in this population are mainstem spawners from the mouth of Trout Creek upstream to Pelton Dam (current upstream barrier to anadromous fish), and the Warm Springs River and Shitike Creek. Recent work suggests that anadromous and resident females in this area are spatially isolated (Zimmerman and Reeves 2002), although males may not follow this pattern.

This region also includes areas that were historically accessible to anadromous fish but now are blocked. We were able to identify one extirpated population and one area that likely supported one or more populations historically (Figure VI-6):

H-1. White Salmon River. Condit Dam, constructed in 1913, blocked passage to the White Salmon River. This river is separated from other steelhead spawning aggregates by 22 km and appears to have sufficient habitat to support an independent population.

H-2. Deschutes River above Pelton Dam. The population structure of steelhead in the area now blocked by Pelton Dam is ambiguous. It may have included multiple life histories, including spring-run fish (Nehlsen 1995). Historically, steelhead were found upstream to Big Falls (RM 132), in Squaw Creek and the Crooked River, and possibly in the Metolius River, with Squaw Creek and the Crooked River being particularly productive. The current resident population in this area may include remnant, residualized steelhead. It is likely that this area supported at least one independent population; in fact, genetic samples from the Crooked River are quite distinct from those from other areas of the Deschutes (Currens 1997).

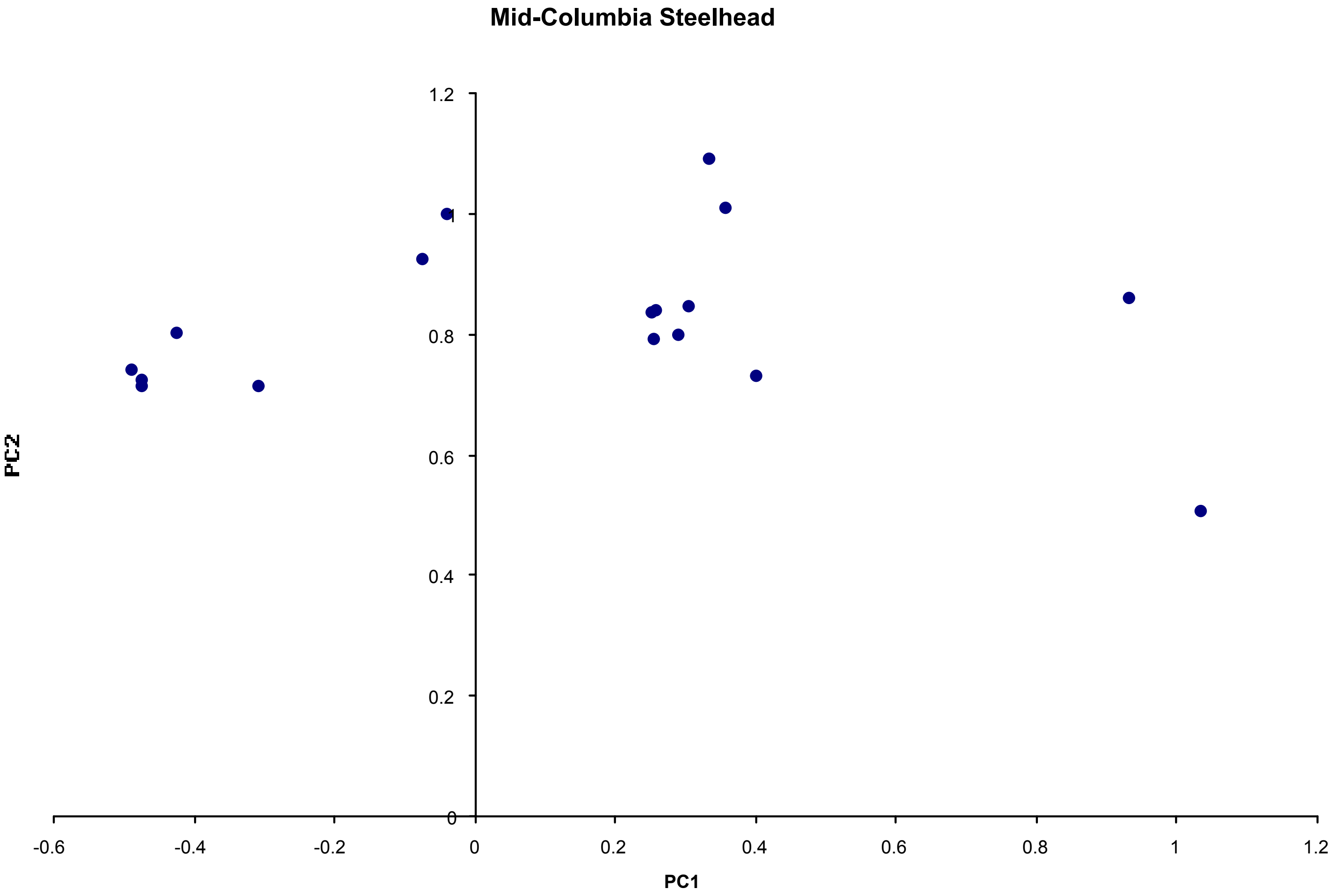


Figure VI-3. Principal components analysis of allozyme data from the Deschutes River, Fifteenmile Creek, and the Lower Columbia. Data from Currens (1997).

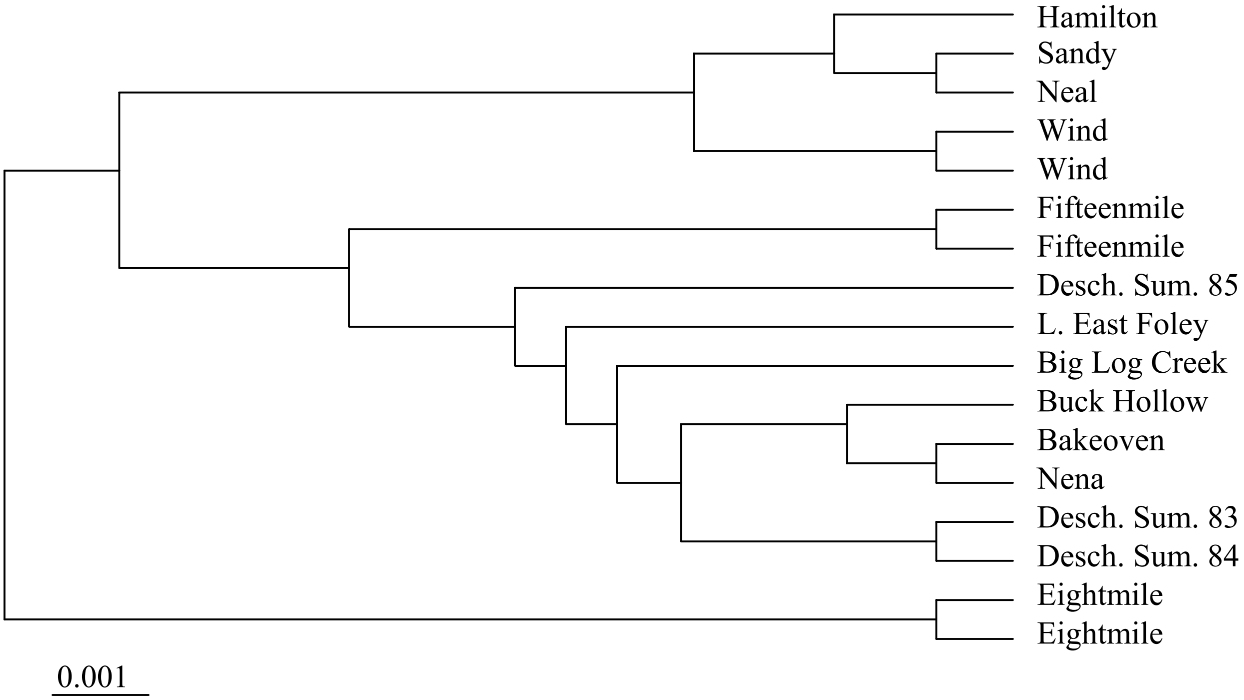


Figure VI-4. UPGMA dendrogram of Lower Columbia and Deschutes River steelhead based on CSE chord distances. Data from Currens (1997).

John Day River

We defined the John Day River as a major grouping based primarily on basin topography and distance from other spawning aggregates. This subbasin is one of the few remaining summer steelhead populations in the interior Columbia basin that have had little influence from introduced hatchery fish and that have more recently been classified as strong or healthy (Lee et al. 1997, Huntington et al. 1994). Within this major grouping we defined five populations on the basis of genetic information, demographic correlations, and habitat/ecoregion data. Spawning areas are widely distributed across tributary and mainstem habitats but are not well-documented.

5 ***Lower Mainstem John Day (JDLMT-s).*** This population includes steelhead-supporting tributaries to the John Day downstream of the South Fork John Day River, including Pine Creek, Bologna Creek, and Grass Valley Canyon. This widespread population is the most differentiated ecologically from other populations, occupying the lower, drier, Columbia Plateau ecoregion. This habitat divergence was a primary factor in delineating this population.

6 ***North Fork John Day (JDNFJ-s).*** We defined this population on the basis of habitat characteristics, basin topography, and demographic patterns. The North Fork occupies the highest elevation, wettest area in the John Day basin. In addition, it encompasses sufficient habitat to support an independent population. Finally, Chilcote (2001) investigated population trajectories in the John Day (and other Oregon rivers). He found that the upper North Fork index count was the most divergent of the John Day

stocks. This combination of factors supports this population's delineation. It includes the main stem and tributaries of the North Fork John Day River.

7 ***Middle Fork John Day (JDMFJ-s).*** Spawning areas in the Middle Fork John Day River are well-separated from all other spawning areas but the North Fork John Day (Table VI-2). This distance, coupled with habitat differences between this population and the North Fork population (see above), and general basin topography led to independent population designation for this area. The population includes the Middle Fork John Day and all its tributaries.

8 ***South Fork John Day (JDSFJ-s).*** Genetic data indicate that *O. mykiss* samples from the South Fork John Day River that may include the anadromous form are differentiated from those in other parts of the John Day (Currens et al. 1985) (Figure VI-4). We delineated this as an independent population on the basis of this genetic information as well as basin topography. The species assemblage in the South Fork is also unique.

9 ***Upper Mainstem John Day (JDUMA-s).*** The upper mainstem John Day River population includes the mainstem John Day River and tributaries upstream from the South Fork. It is separated from the lower main stem on the basis of habitat differences (see population 5), and from the South Fork on the basis of topography.

Although the lower reaches of spawning areas in these populations are in close proximity, we generally felt that separate population status was warranted due to the distribution of fish within each branch of the John Day (with relatively small proportions of available spawning habitat present at the lower reaches) and the size of each basin (large enough to support independent populations), as well as the river branching patterns.

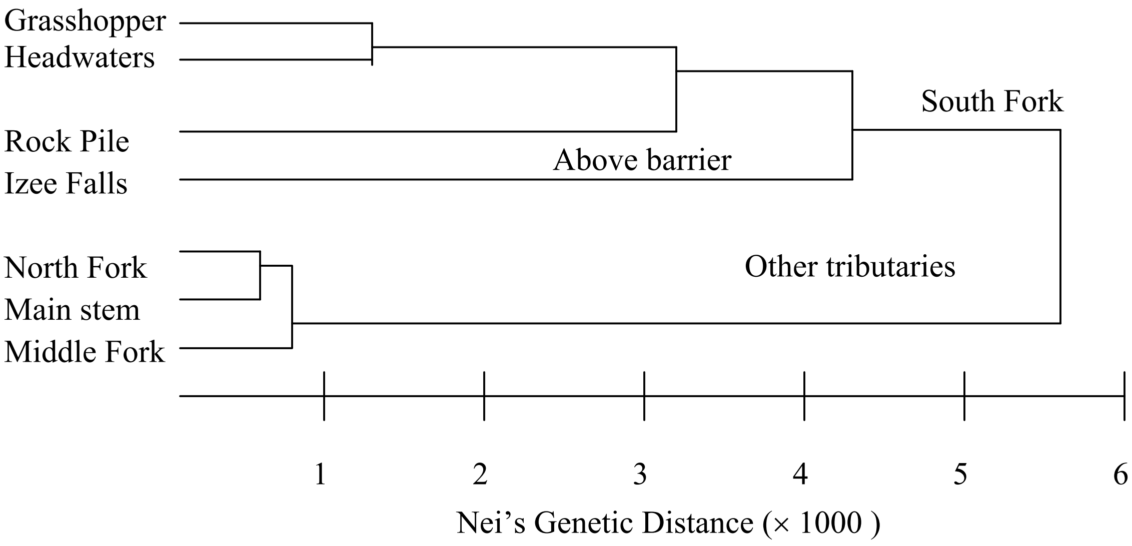


Figure VI-5. Dendrogram based on Nei's genetic distances of *O. mykiss* samples in the John Day River, Oregon. From Currens et al. 1987.

Table VI-2. Distance matrix for Mid-Columbia steelhead.

	UCWSA-s	UCKLI-s	UCFIF-s	DREST-s	DRWST-s	JDLMT-s	JDNFJ-s	JDMFJ-s	JDSFJ-s	UCROC-s	UCUMA-s	WWMAI-s	WWTOU-s	YRTOS-s	YRNAC-s	YRUMA-s
UCWSA-s	0															
UCKLI-s	3	0														
UCFIF-s	40	22	0													
DREST-s	76	57	37	0												
DRWST-s	193	174	155	5	0											
JDLMT-s	114	95	75	72	189	0										
JDNFJ-s	384	365	345	342	459	270	0									
JDMFJ-s	432	413	393	390	507	318	10	0								
JDSFJ-s	417	398	378	375	492	503	50	111	0							
UCROC-s	103	85	65	62	179	190	322	370	357	0						
UCUMA-s	217	199	179	176	293	304	437	485	472	122	0					
WWMAI-s	287	268	248	245	362	373	505	553	541	192	118	0				
WWTOU-s	342	324	304	301	418	429	561	609	597	248	174	101	0			
YRTOS-s	409	391	371	368	485	496	628	676	683	314	241	231	286	0		
YRNAC-s	461	444	424	421	538	549	681	729	736	367	294	283	339	113	0	
YRUMA-s	495	477	457	454	571	582	714	762	769	400	327	317	373	146	40	0

Rock Creek (Unaffiliated Area)

We designated Rock Creek as an unaffiliated, independent population of Mid-Columbia steelhead. Rock Creek is designated as a SASSI stock (WDFW 1992). This stream is geographically well separated from all other populations (distance to nearest spawning area = 62 km), and has sufficient habitat (gauged by professional judgment) to support an independent population. No additional data were available (Rawding, pers. comm.).

10 ***Rock Creek (MCROC-s).*** This population includes Rock Creek and its tributaries, Squaw and Quartz Creeks.

Walla Walla and Umatilla Rivers

The Walla Walla and Umatilla Rivers form a major grouping on the basis of shared ecological characteristics and geographic proximity. They both drain the northwestern slopes of the Blue Mountains, with lower reaches in the warmer, drier habitats of the Columbia Plateau. Within this major group, genetic information, distance between spawning aggregates and ecoregional classifications contributed to our population delineations.

11 ***Umatilla River (MCUMA-s).*** We designated the Umatilla River and its tributaries as an independent population. Both genetic analysis (Narum and Powell 2002) and distance supports separation of this river from the Walla Walla (Table VI-2). Within the Umatilla River basin, there appears to be little genetic differentiation between anadromous or resident fish from several production areas within the basin, with the exception of resident fish in McKay Creek (that may reflect introgression from non-native hatchery stock). (Currens and Schreck (1994) and Currens (1997). In addition, there is connectivity between spawning areas through the main stem from Buckaroo Creek upstream through all the major tributary spawning locations including Squaw Creek, Meacham Creek, South Fork Umatilla, and North Fork Umatilla. This information, combined with the similar habitat across the Umatilla basin supports the designation of a single population for this river.

12 ***Walla Walla River (WWMAI-s).*** Several genetic analyses indicate that *O. mykiss* in the Touchet River are genetically distinct from those elsewhere in the Walla Walla basin (Currens 1985, Currens 1997, Narum et al. in review, Kassler et al. in review) (Table VI-3). In addition, spawners in the mainstem Walla Walla River and its tributaries are geographically distant (101 km) from those in the Touchet and those in the Umatilla River. The Walla Walla River and its tributaries (except the Touchet River) are designated as an independent population.

13 ***Touchet River (WWTOU-s).*** On the basis of genetic and geographic separation, we designated the Touchet River as an independent population (Table VI-2, see also population 12).

Yakima River

We treat the Yakima River as a major grouping. Not only is this river geographically separated from other steelhead spawning areas in this ESU, but recent genetic analysis (Phelps et al. 2000) indicates that steelhead from various locations in the Yakima drainage cluster together more closely than they do with samples from the Klickitat or Deschutes Rivers (Figure VI-2). Within the Yakima, we used available genetic information (Phelps et al. 2000, Utter 1998), spawner distribution and historical basin characteristics. We identified three populations within the Yakima River:

14 ***Satus and Toppenish Creeks (YRTOS-s)***. Satus and Toppenish Creeks are separated from other Yakima River spawning areas by a minimum of 30 km. Genetic samples within Satus Creek cluster loosely with adjacent Toppenish Creek samples (Figure VI-2). We considered treating each of these creeks as a separate population. However, the geographic separation of these creeks is recent, due to human hydrographic modifications. Historically, the creeks joined upstream of their confluence with the Yakima River. Based on this historical joining and genetic similarity, we treat the two creeks as a single population. Importantly, Toppenish Creek samples were divergent from those in Satus Creek, and the current separation likely allows greater opportunity for differentiation than was previously present. This substructure is an important component of this population. Pearsons et al. (2003) and Phelps et al. (2000) found little evidence supporting interbreeding between resident and anadromous fish in these drainages.

15 ***Naches River (YRNAC-s)***. We designated the Naches River as an independent population based on its geographic separation from other spawning areas (40 km), and genetic coherence of samples within the Naches (Figure VI-2).

Table VI-3. Pairwise Fst values for the Walla Walla, Touchet, and Umatilla Rivers. Data from Currens (1997).

	Walla Walla	**Touchet**	**Umatilla**
Walla Walla main stem n=118, 1998 & 1999			
Touchet River n=59, 1999 & 2000	0.010*		
Umatilla River n=94, 2000	0.006*	0.008*	
Snake River n=54, 2000	0.013*	0.009*	0.004

*p <0.05 (with Bonferonni corrections)

16 ***Upper Yakima (YRUMA-s)***. This population includes the Upper Yakima and its tributaries, the Kachess, Cle Elum, and Teanaway Rivers, with the Teanaway and its tributaries supporting the majority of fish returning to this region. Geographic separation from other Yakima River populations (40 km) and genetic separation from Naches River samples (Figure VI-2) support designation of this area as an independent population. Importantly, genetic studies in the Teanaway (Pearsons et al. in review, Busack and Phelps 1996) suggest that there is substantial gene flow between resident and anadromous *O. mykiss* in this region. Phelps et al. (2000) suggest that genetic population structure in the upper Yakima may be confounded by hatchery introgression, but Utter 1998 suggests that allele frequencies seen in this area could reflect natural post-Pleistocene introgression arising from more ancient admixtures following glacial recession.

Primary spawning areas, population characteristics, and hatchery influence are presented in Tables VI-4, VI-5 and VI-6. Additional information about each population, including basin characteristics, can be found in Appendix C.

Monitoring and Evaluation Needs

A lack of data consistently collected across the Mid-Columbia ESU hampered our ability to define populations rigorously. We have identified several data types that would greatly enhance our ability to define and characterize populations. In decreasing order of importance:

- **Spawner distributions.** Accurate, comprehensive spawner distributions, particularly in mainstem areas are lacking in most areas in the ESU. Distances between spawning aggregates are an extremely important component of our efforts to delineate populations. Better distributional data, particularly for mainstem areas will allow greater ability to assess connectivity between areas. In addition, a better understanding of historical spawner distribution and connectivity would be extremely useful.

- **Genetic samples**. Additional genetic samples aimed at three questions would be very useful:
    a. *ESU-substructure*. A lack of congruent samples across the ESU hampered our ability to assess substructure at a large scale within the ESU. This is particularly important for determining major groupings, which are likely to play a role in ESU viability criteria.
    b. *Fine-scale structure*. Genetic samples at a fine-scale in the John Day basin would improve our population definitions in that region greatly.
    c. *Resident and anadromous contribution to population*. Paternity analyses aimed at determining the contribution of resident fish to these populations would increase our understanding of population boundaries, and outlier populations, and could contribute substantially to viability assessments.
- **Dispersal/stray rate information.** Generally lacking in our dispersal analysis were strong data for steelhead as well as fine-scale (0–50 km) dispersal information. A better understanding of the likelihood and distance of steelhead spawning would greatly increase the strength of our population delineations.
- **Residence times and distribution of hatchery strays in the Deschutes River.** The Deschutes River appears to act as a thermal refugium for steelhead migrating through the John Day Reservoir. While many of these fish return to their upstream migration, a substantial number of hatchery strays appear to remain in the drainage and spawn. A better understanding of their distribution and reproductive success would provide insight into the population structure in this basin.

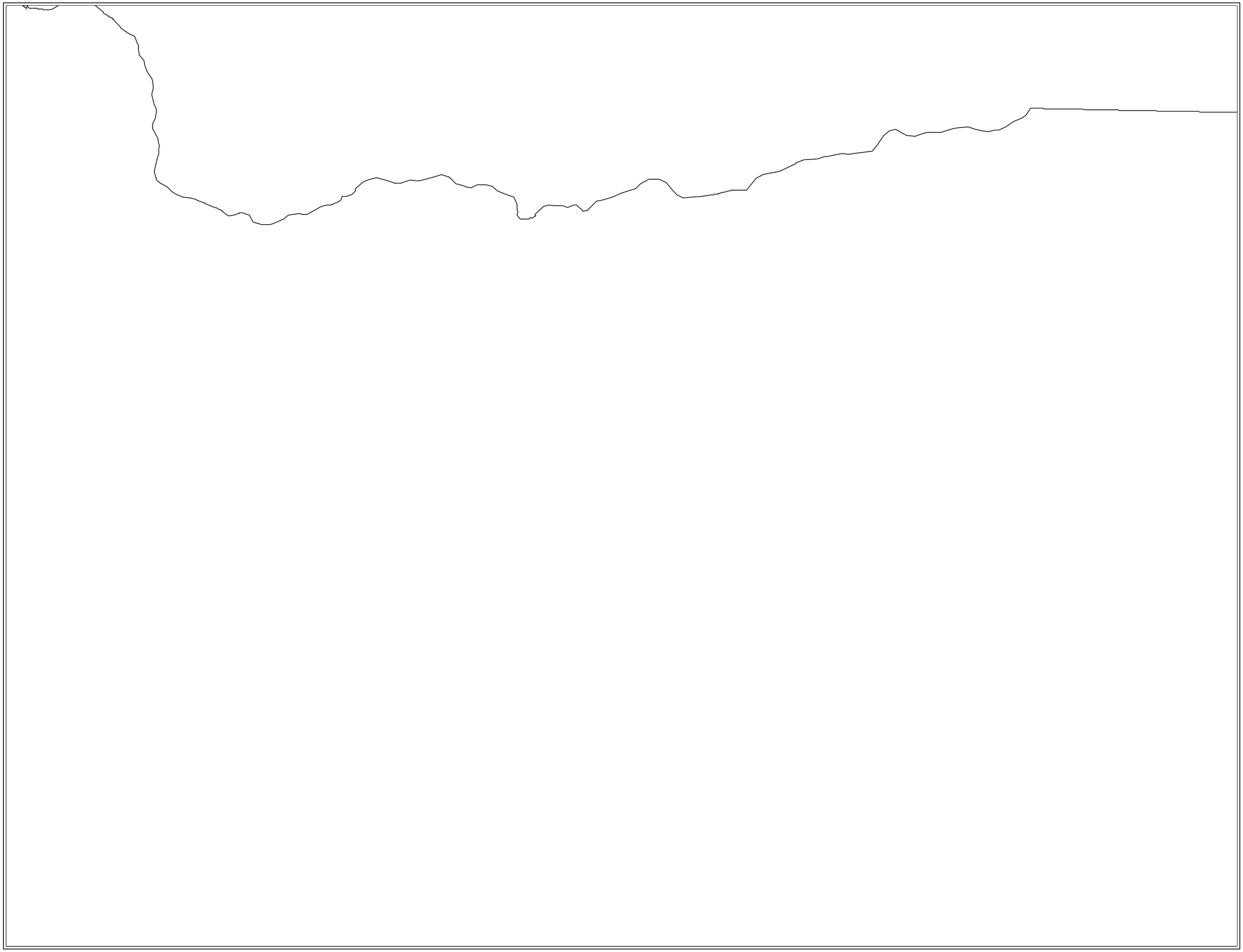


Figure VI-6. Extirpated areas possibly affiliated with the Middle Columbia steelhead ESU.

Table VI-4. Middle Columbia steelhead populations.

				Within-Population Diversity		
Basin	**Population Name**	**Population Code**	**Spatial Structure**	**Adult Run Timing**	**Habitat (Level 4 Ecoregion)**	**Genetics**
Fifteenmile	Fifteenmile Creek	MCFIF-s	Branched discontinuous	Winter	Upper reaches include 3 ecoregions, predominently oak/conifer foothills, lower reaches Pleistocene lake basins.*	The Eightmile and Fifteenmile samples were highly diverged, although possibly due to residents
Klickitat	Klickitat River	MCKLI-s	Branched continuous	Summer and winter	Upper reaches Yakima Plateau and slopes, lower reaches oak/conifer foothills.	
Deschutes	Westside	DRWST-s	Branched discontinuous	Summer	Upper reaches include 3 ecoregions, predominently Ponderosa pine/bitterbrush woodlands, lower reaches predominently John Day/Clarno uplands.*	Abundant resident form present in mainstem reaches
	Eastside	DREST-s	Branched discontinuous	Summer	Upper reaches John Day/Clarno uplands and Umatilla Plateau, lower reaches John Day/Deschutes canyons.*	Abundant resident form present in mainstem reaches
Columbia	Rock Creek	MCROC-s	Branched continuous	Summer	Upper reaches predominently oak/conifer foothills, lower reaches Pleistocene lake basins.*	
John Day	Lower main stem	JDLMT-s	Branched discontinuous	Summer	Upper reaches John Day/Clarno uplands, lower reaches Umatilla Plateau and John Day/Deschutes canyons.*	
	Upper main stem	JDUMA-s	Branched discontinuous	Summer	Upper reaches John Day/Clarno highlands and melange, lower	

				Within-Population Diversity		
Basin	Population Name	Population Code	Spatial Structure	Adult Run Timing	Habitat (Level 4 Ecoregion)	Genetics
					reaches John Day/Clarno uplands.	
	North Fork	JDNFJ-s	Branched discontinuous	Summer	Upper reaches include 4 ecoregions, including melange and maritime-influenced zone, lower reaches John Day/Clarno highlands and uplands.	
	Middle Fork	JDMFJ-s	Branched discontinuous	Summer	Upper reaches melange, lower reaches John Day/Clarno highlands and uplands.	
	South Fork	JDSFJ-s	Branched continuous	Summer	Upper reaches include 3 ecoregions including continental zone highlands, lower reaches John Day/Clarno highlands.	Resident forms above Izee Falls, a barrier to steelhead, contributed to differentiation among samples
Umatilla	Umatilla River	MCUMA-s	Branched discontinuous	Summer	Upper reaches include 4 ecoregions, notably maritime-influenced zone and Umatilla dissected uplands, lower reaches Umatilla Plateau.*	
Walla Walla	Touchet River	WWTOU-s	Branched discontinuous	Summer	Upper reaches mesic forest and maritime-influenced zone, lower reaches deep loess foothills.*	
	Walla Walla River	WWMAI-s	Branched discontinuous	Summer	Upper reaches include3 ecoregions, notably mesic forest, lower reaches include 2 ecoregions, including deep loess foothills.*	
Yakima	Upper main stem	YRUMA-s	Branched discontinuous	Summer	Upper reaches predominently Chiwaukum Hills and lowlands, lower reaches mainly Pleistocene lake basins.*	Resident and anadromous forms interbreed.

				Within-Population Diversity		
Basin	**Population Name**	**Population Code**	**Spatial Structure**	**Adult Run Timing**	**Habitat (Level 4 Ecoregion)**	**Genetics**
	Naches River	YRNAC-s	Branched discontinuous	Summer	Upper reaches grand fir mixed forest and Yakima Plateau and slopes, lower reaches Yakima folds and Pleistocene lake basins.*	
	Toppenish and Satus Creeks	YRTOS-s	Branched discontinuous	Summer	Toppenish Creek is Yakima Plateau and slopes; Satus Creek is Yakima folds.*	Toppenish and Satus Creeks are relatively genetically differentiated.

*Spawning areas for this population span a broader-scale, level 3 ecoregion boundary

Table VI-5. Middle Columbia steelhead core spawning areas.

Region	Population	Code	Current Core Spawning Areas Description	Historical Spawning Area Description
Fifteenmile	Fifteenmile Creek	MCFIF-s	Main stem–upstream from highway 197, Ramsey--mouth to 2 mi. above FS boundary, 8mile--197 to 3 mi. above FS boundary, 5mile–197 to 1.5 mi. above FS boundary	
Klickitat	Klickitat River	MCKLI-s	Main stem spawning distribution is concentrated between RM 5.2 and RM 50.0, lower Swale, Wheeler, Summit, and White creeks and the upper Little Klickitat River.	
Deschutes	Westside	DRWST-s		
	Eastside	DREST-s	Main stem – from Whitehorse rapid (RM 76) to Trout Creek, Buck Hollow from the mouth upstream to Bronx Canyon, Bakeoven from the mouth upstream to Deep Creek, Trout Creek from the mouth to the Forest Service Boundary (at Augar Creek) including the lower 2 miles of Ward Creek	
Columbia	Rock Creek	MCROC-s		
John Day	Lower main stem	JDLMT-s		
	Upper main stem	JDUMA-s		
	North Fork	JDNFJ-s		
	Middle Fork	JDMFJ-s		
	South Fork	JDSFJ-s		

Region	Population	Code	Current Core Spawning Areas Description	Historical Spawning Area Description
Umatilla	Umatilla River	MCUMA-s		
Walla Walla	Touchet River	WWTOU-s	Touchet River upstream of Dayton, the North Fork, South Fork, Wolf Fork, Robinson Fork, and Coppei Creek	
	Walla Walla River	WWMAI-s	Mainstem Walla Walla and tributaries from Oregon state line upstream, Mill Creek above Bennington Dam	
Yakima	Upper main stem	YRUMA-s	Unknown	
	Naches River	YRNAC-s	Mainstem Naches majority (70.5%) spawning from RKm 24.0 to 69.2. Bumping River from RKm 14.5 to RKm 16.1. Little Naches River within the lower 5 RKm*	
	Toppenish and Satus Creeks	YRTOS-s	Satus Creek: mainstem majority (83.3%) spawning RKm 27.0 to 72.4, Dry Creek majority (90.9%) spawning RKm 8.0 to 33.8. Logy Creek majority (75.0%) spawning RKm 6.0 to 12.9. Spawning in Wilson and Charlie Creek is within the lower 2 RKm. Toppenish Creek: mainstem majority (83.3%) spawning RKm 48.3 to RKm 90.1 *	

* From: Hockersmith, E., J. Vella, L. Stuehrenberg, R. N. Iwamoto, and G. Swan. 1995. Yakima River radio-telemetry study: steelhead, 1989-93, Bonneville Power Administration, Portland, Oregon.

VII. SNAKE RIVER SOCKEYE SALMON ESU

The Snake River Sockeye Salmon ESU had the dubious distinction of being the first Pacific Northwest salmon species to be listed under the Endangered Species Act. Once abundant in a variety of lakes in the Snake River drainage, beginning in the late nineteenth century anadromous sockeye salmon (*Oncorhynchus nerka*) were affected by heavy harvest pressures, unscreened irrigation diversions, and dam construction (see Bjornn et al. 1968). In addition, in the 1950s and 1960s, the Idaho Department of Fish and Game actively eradicated sockeye salmon from some locations. As a result of these varied impacts, and the consequent drop in abundance, Snake River sockeye salmon were listed as endangered in November 1991 (NMFS 1991).

O. nerka in general show a great diversity of life histories. In the Snake River basin, three forms are currently recognized: an anadromous form, beach-spawning resident/residual fish, and resident kokanee (Brannon et al. 1994). A number of genetic studies have been conducted to determine the relationships between the variety of life-history types and stocks in the interior Columbia River basin (Monan 1991; Winans et al. 1996; Waples et al. 1997; Faler and Powell 2003). These analyses indicate that in the Sawtooth Valley *O. nerka* are genetically distinct from all other kokanee and sockeye salmon sampled in Idaho, Washington, and British Columbia. Waples et al. (1997) allozyme-based analysis further indicates that Redfish Lake sockeye and beach spawners are distinct from Redfish Lake kokanee (Figure VII-1). Importantly, although the residual sockeye salmon are morphologically most similar to kokanee (small size), they spawn in the same location and at the same time as anadromous sockeye, whereas kokanee spawning is segregated both temporally and spatially from the anadromous fish (Brannon et al. 1994). Otolith microchemistry analyses (Rieman et al. 1994) revealed that some Redfish Lake *O. nerka* outmigrants were progeny of resident females. Based on this information, the Snake River sockeye salmon ESU was determined to include Redfish Lake anadromous sockeye and residual/resident beach spawners (Waples et al. 1991, BRT 2003).

Table VII-1. Available data types and analyses for the Snake River sockeye salmon ESU.

Data Type	**Description**
Genetic	We relied on previously conducted analyses of *O. nerka* throughout the Snake River basin (Monan 1991; Winans et al. 1996; Waples et al. 1997; Faler and Powell 2003)
Dispersal/distance	N/A
Phenotypic	Major life-history forms (resident, anadromous, stream-spawning, beach-spawning) considered.
Habitat	EPA-defined ecoregions considered for historically occupied areas
Demographic correlation	N/A

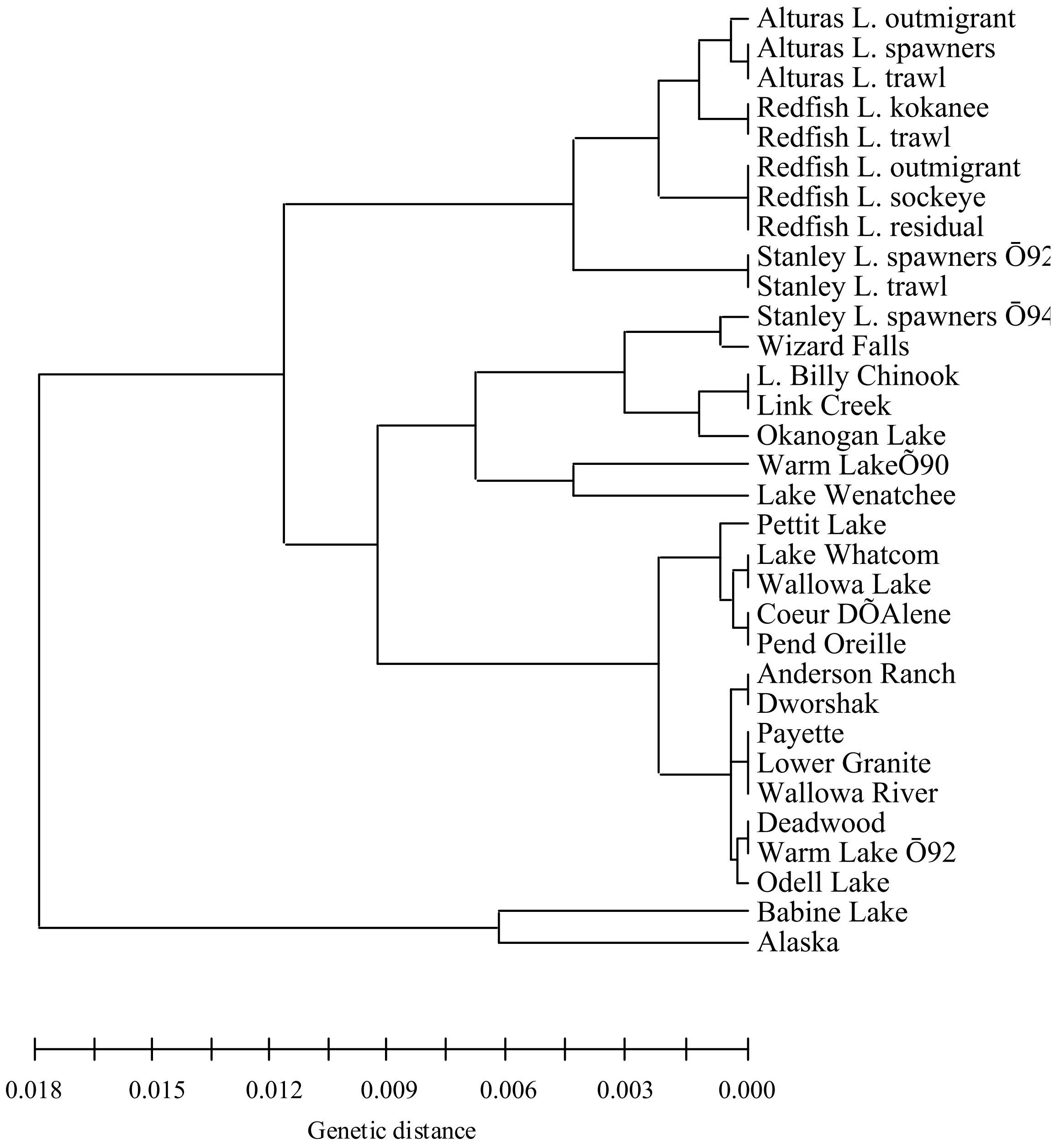
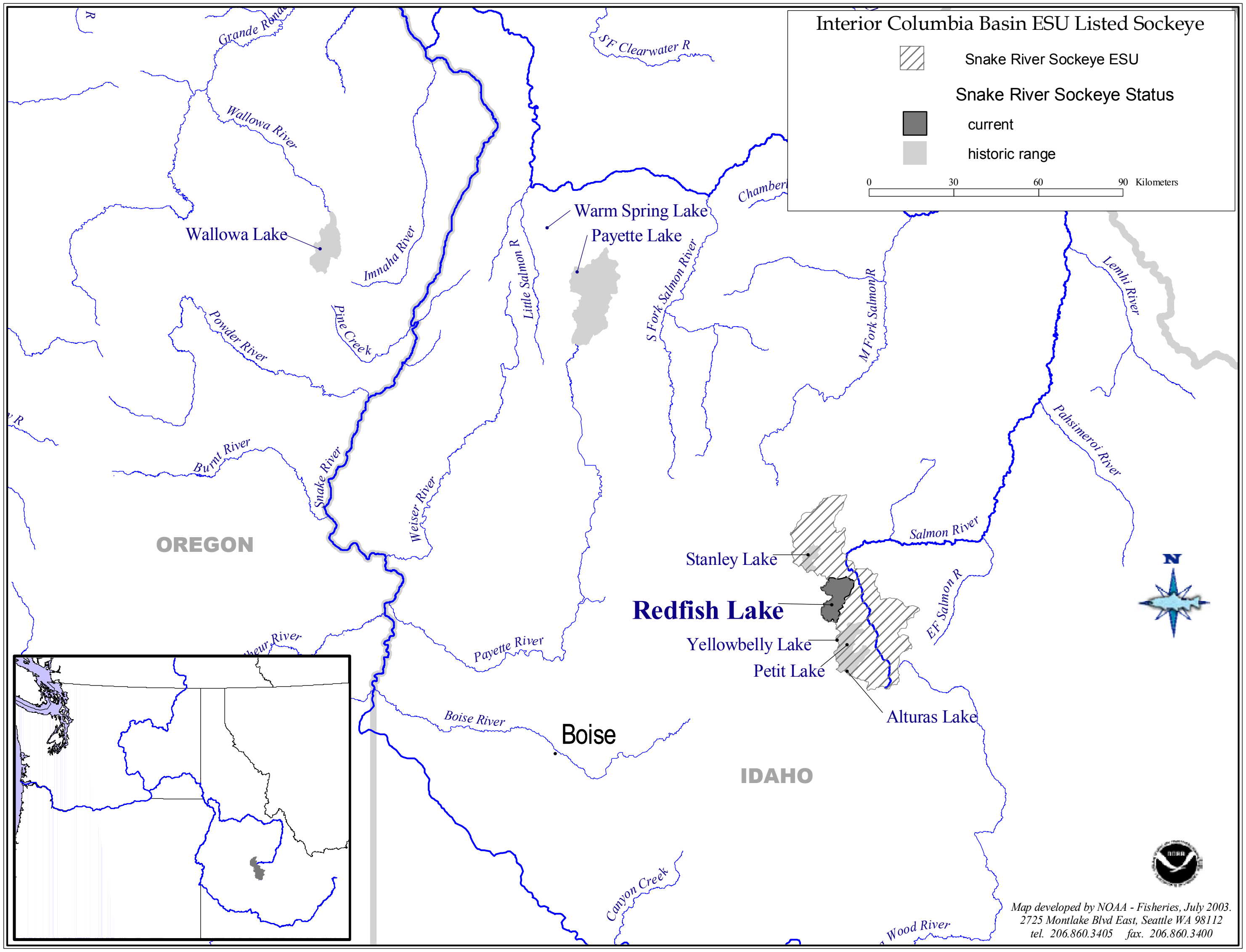


Figure VII-1. Dendrogram of genetic relationships among 32 populations of *Oncorhynchus nerka* from the Pacific Northwest, based on variation at 64 gene loci. Clustering used the UPGMA method based on a matrix of Nei's (1978) unbiased estimates of genetic distance between each pair of samples. From Waples et al. 1997.



Map developed by NOAA - Fisheries, July 2003.
2725 Montlake Blvd East, Seattle WA 98112
tel. 206.860.3405 fax. 206.860.3400

Figure VII-2. Snake River sockeye salmon ESU.

The anadromous component of this ESU travels a greater distance from the sea (approximately 900 miles) to a higher elevation (6,500 feet) than any other sockeye salmon population.

Demographically Independent Populations of Snake River Sockeye

Using available data and analyses (Table VII-1), we identified a single population in this ESU (Figure VII-2):

> ***Redfish Lake Sockeye.*** This population includes all the fish in this ESU. Returns to this population have been extremely low for many years, and a captive broodstock program was begun in 1992 to aid in recovery efforts. This program took all 16 anadromous fish that returned to Redfish Lake between 1992 and 1998 into its broodstock program, and maintained progeny throughout their life cycle. In addition, this program has produced outplants of eggs, fry, and adults for Redfish Lake.

Progeny from captive broodstock have also been released into Alturas and Pettit Lakes. Given the dependence of these areas on the broodstocking program (and consequent close relationship of the fish in all three lakes), we did not define them as separate populations. However, they do provide important spatial structure (distribution) for this population. Sockeye in separate lakes are typically well-differentiated (Wood 1994), suggesting that there may be opportunity for future diversification.

Primary spawning areas, population characteristics, and hatchery influence are presented in Tables VII-2, VII-3, and VII-4. Further information, including basin physiography, can be found in Appendix C.

Historically Occupied Areas

Anadromous sockeye were historically found in several lakes throughout the Snake River basin. In the Sawtooth Valley, the following lakes historically contained sockeye salmon: Alturas, Pettit, Redfish, Stanley, and Yellowbelly (Bjornn et al. 1968). It is generally believed that adults were prevented from returning to the Sawtooth Valley from 1910 to 1934 by Sunbeam Dam, which was constructed on the Salmon River approximately 20 miles downstream of Redfish Lake. Whether or not Sunbeam Dam was a complete barrier to adult migration remains unknown. It has been hypothesized that some passage occurred while the dam was in place, allowing the Sawtooth Valley population or populations to persist (see Bjornn et al. 1968, Waples et al. 1991). Adult returns to Redfish Lake during the period 1954 through 1966 ranged from 11 to 4,361 fish (Bjornn et al. 1968). Sockeye salmon in Alturas Lake were extirpated in the early 1900s as a result of irrigation diversions, although residual sockeye may still exist in the lake (Chapman and Witty 1993); genetic samples from Alturas Lake are closely allied with those from Redfish Lake (Figure VII-1). From 1955 to 1965, the Idaho Department of Fish and

Game eradicated sockeye salmon from Pettit, Stanley, and Yellowbelly Lakes, and built permanent structures on each lake outlet that prevented reentry of anadromous sockeye salmon (Chapman and Witty 1993).

The now-extinct anadromous sockeye salmon runs beyond the Sawtooth Valley (Wallowa, Payette, and Warm Lakes) have a varied history. Wallowa Lake sockeye salmon were considered extinct by 1905 as a result of heavy exploitation, unscreened irrigation diversions, and the eventual construction of a dam to store water in the lake (Chapman and Witty 1993). Black Canyon Dam, constructed on the Payette River in 1924, extirpated sockeye salmon returns to Payette Lake. An anecdotal reference to the Warm Lake sockeye population suggests that "blueback" salmon were trapped in the lake by a land upheaval in the early twentieth century and persisted as a resident population (Humphreys 1983).

Interestingly, remnants of native *O. nerk*a populations may have persisted in several of these locations. For instance, two gene pools of kokanee were identified in Stanley Lake (BRT 2003 draft). One appears to have originated from introductions of Wizard Falls Hatchery (Oregon) kokanee and the other may be a remnant of an *O. nerka* population that survived rotenone treatments in the 1950s and 1960s. Similarly, the 1990 Warm Lake collection of resident fish represents a beach spawning and presumably native population, contrasted with the 1992 collection from a 1990 yearling plant of tributary-spawning kokanee (Waples et al. 1997). The beach spawners are distinguished from all other *O. nerka* populations sampled from Idaho, Washington, and British Columbia, based both on nuclear and mtDNA data (Figure VII-2, Table VII-X). The stream-spawning, introduced kokanees' persistence is uncertain, although the absence of suitable stream-spawning habitat in Warm Lake makes it unlikely that they will leave descendants (Waples et al. 1997). Payette Lake supports a beach-spawning population that has not yet been sampled for genetic analysis. This population may represent descendants of what was once the largest sockeye run in the Snake River basin.

Table VII-2. Snake River sockeye salmon core spawning areas.

Region	Population	Code	Current Core Spawning Areas Description	Historical Spawning Area Description
Snake River	Redfish Lake	SRRED	Redfish Lake, hatchery outplants in Alturas and Pettit Lakes	Redfish, Alturas, Pettit, Yellow Belly, Stanley, Warm, Payette, and Wallowa Lakes

Table VII-3. Snake River sockeye salmon populations.

Basin	Population Name	Population Code	Spatial Structure	Within-Population Diversity		
				Spawning/residence	Habitat (Ecoregion)	Genetics
Salmon River	Redfish Lake	SRRED	Redfish Lake only	Resident and anadromous forms	High glacial drift-filled valleys	Resident and anadromous closely related; kokanee more distinct

Table VII-4. Snake River sockeye salmon hatchery influence.

Basin	Population Name	Population Code	Genetic Evidence of Hatchery Introgression	Natural Spawning of Hatchery-Origin Fish	Hatchery Outplants, Last 10 years		
					Number	**Origin**	**Notes**
Salmon River	Redfish Lake	SRRED	All spawners involved in captive broodstock program	All spawners involved in captive broodstock program	Medium	Majority releases from in-population broodstock	Recent increase in hatchery outplants

Hatchery Influence Criteria:

Evidence of hatchery spawning

A. High = Over 25% (average over the last 5 years) of natural spawners are hatchery-origin fish.
B. Medium = 10-25% (average over the last 5 years) of natural spawners are hatchery-origin fish.
C. High = Less than 10% (average over the last 5 years) of natural spawners are hatchery-origin fish.
D. None = No evidence of hatchery-origin spawners.
E. No data = No data available

Hatchery outplants

A. High = average of >500,000 fish released per year, last 10 years.
B. Medium = average of 50,000 to 500,000 fish released per year, last 10 years.
C. Low = average of <50,000 fish released per year, last 10 years.
D. None = No fish released, last 10 years.

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APPENDIX A
GENETICS

Introduction

Since the late 1960s, the use of molecular genetic markers at individual gene loci (singular - locus) has revolutionized understandings of population structure within species. Nuclear genes (or loci) such as those detected by microsatellite DNA or directly reflected by allozymic proteins (the two marker types primarily used by the TRT) are inherited from each parent in a simple (Mendelian) manner. Expression of variant forms (alleles) at a particular locus permits individual identification of homozygotes when the same allele is inherited, or heterozygotes when different alleles are inherited. Enumerations and analyses of such genotypes and the resulting allelic frequencies for many loci provide a basis for intraspecific genetic characterizations of individuals and populations.

Four evolutionary forces—selection, mutation, migration and drift—interact among conspecific populations as they diverge and sometimes merge over varying time scales. Though commonly operative on phenotypic characters, selection can be safely disregarded in interpreting data from the large suites of neutral or nearly neutral allozyme or microsatellite loci available for anadromous salmonids in the interior Columbia River basin (Utter et al. 1993). Likewise, recent divergence times among populations (usually $<10^4$ years) permit disregarding mutation within ESUs (although substantially higher numbers of alleles accumulated over larger intervals through higher mutation rates increase the discriminatory power of microsatellites at the ESU level).

Thus, drift and migration remain the primary evolutionary forces under consideration when interpreting allelic data within anadromous salmonid ESUs. Under natural conditions, these opposing forces maintain distinction and cohesion within ESUs. Highest in small populations, drift promotes divergence among populations as estimated by measures of genetic distance. Greatest among proximal anadromous populations, migration (effective straying) maintains similarity in a somewhat hierarchical basis commonly permitting inferences of geographic structure from projections of genetic distances (refs.).

This appendix details genetic analyses of available allelic data based on the above understandings. Superimposed on natural patterns of variability among and within populations, the potentially confounding effects of hatchery operations and outplantings are considered where data are available.

METHODS

Samples

Sample details can be found in the original documents describing each set of analyses. See specific ESU descriptions for relevant citations.

Because each broodyear represents only a fraction of the breeding population at a given location, we pooled allelic data over multiple year classes when available to reduce the potential sampling biases. These pooled samples provide the best estimate of the overall population (Waples et al. 1993) and were used in all subsequent analyses.

Genetic Markers

Most analyses were based on allele frequencies at either allozyme or microsatellite loci. Mitochondrial DNA data were also available for Snake River sockeye salmon. Summaries of data types and the corresponding references are provided in tabular format for each ESU. Details of methodological procedures can be found within the references describing each data set.

Data Analysis

Allele frequencies, exact probabilities for conformity with Hardy-Weinberg proportions, F-statistics, and expected heterozygosities were calculated using GENEPOP (version 3.1a; Raymond and Rousset 1995).

At each locus, observed genotypes of individual collections were compared to those expected from multinomial expansions of allelic frequencies (i.e., Hardy-Weinberg expectations). Significant deviations from expected values provided insights into nonconformance to conditions of an “ideal” population (e.g., nonrandom mating, small size, immigration, admixture).

We used PHYLIP (Felsenstein 1992) or Biosys (Swofford and Selander 1988) to calculate Cavalli-Sforza and Edwards’ (1967) chord distance (D_{CSE}) between all pairs of populations. We used the resulting pair-wise distance matrix to construct dendrograms using the UPGMA option of PHYLIP or Biosys. Dendrograms were visualized using TreeView PPC (Page 1996).

To project the relationships among populations without the limitations of a bifurcating tree, we used MINITAB (release version 11) to conduct principal components analysis (PCA). We computed the PC scores based on the covariance among allele frequencies, omitting the largest allele at each locus to account for the nonindependence of allele frequencies within each locus. We then plotted the first two principal component scores to estimate genetic divergence as the relative linear distance between points representing each population.

Designation of Major Groupings

To begin our definition of populations, we sought to identify “major groupings”. Our goal in designating these units was to recognize the larger regions for which there would be negligible opportunity for contemporary exchange among spawning aggregates. All identified spawning aggregates within any major grouping were then compared to all other aggregates within that major grouping. However, no further comparisons between spawning aggregates from different major groupings were made. We designated major groupings by identifying genetically similar samples corresponding to geographic divisions or basins.

GLOSSARY
(Modified from Hallerman 2003)

Allele An alternate form of a gene (or locus) differing from other alleles in DNA sequence.

Allozyme Allelic form of enzyme coding loci often used to estimate allelic and genotypic frequencies within populations. Allozyme alleles are distinguished from one another based on differences in electrophoretic mobility due to differences in net charge or molecular weight.

Dendrogram A branching diagram reflecting genetic difference in which the linear distance between two taxa and the node connecting them is indicative of the level of genetic difference.

F-statistics A suite of hierarchical tests designed to estimate genetic population structure.

F_{ST} The proportion of total genetic variation attributable to population subdivision.

Gene A heritable genetic unit. Genes correspond to a specific location (locus) within the genome and are the physical entity transmitted from parent to offspring.

Gene flow (see **migration**)

Genetic distance An index of the amount of genetic differentiation between samples.

Genetic drift Random changes in allelic frequencies due to natural sampling errors in finite populations. The rate of change due to genetic drift increases as population size decreases.

Genome All of the genetic information found within an organism.

Genotype The alleles present for one or more genes in an organism.

Heterozygosity An estimate of the amount of genetic variation found within a population. Observed heterozygosity is calculated as the proportion of individuals that are heterozygous at a locus. Expected heterozygosity is calculated based on allele frequencies and assuming Hardy-Weinberg proportions.

Hardy-Weinberg proportions The expected binomial relationship between allele frequencies and genotypic frequencies in an ideal population. Ideal populations are those that are not influenced by natural selection, mutation, random genetic drift, nonrandom mating, or migration.

Heterozygous Having two different allelic variants at a locus.

Homozygous Having two copies of the same allele at a locus.

Ideal population An infinitely large group of random-mating individuals. Such a population does not experience any selection, mutation, or migration.

Locus (plural, loci) A specific location within the genome.

Mendelian inheritance Mode of inheritance in which individuals receive one allele from each of their parents. Thus, each individual contains two alleles at each nuclear locus.

Microsatellites Highly repetitive DNA sequences commonly used to estimate allele frequencies within populations. Microsatellites are noncoding stretches of a simple repeated array of nucleotides (e.g., …CACACACA…).

Migration In genetic usage, the exchange of alleles among populations.

Mitochondrial DNA (mtDNA) The maternally inherited cytoplasmic circular DNA fragment found within the mitochondria. MtDNA can be used to infer population structure.

Mutation The processes through which an organism acquires heritable genetic changes.

Neutral loci Loci in which alternate alleles have no effect on the fitness of the carrier.

Nuclear genes Biparentally inherited genes found in the nucleus of eukaryotic organisms.

Phenotypic characters Combined physical expression of genotype and environment. For example, morphological characteristics or life-history attributes of an individual.

Principle Components Analysis (PCA) A statistical approach to visualize nonhierarchical relationships among populations along multiple axes.

dendrogram

Selection Differential survival and reproductive success of alternate genotypes as expressed through the phenotype

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APPENDIX B
DISPERSAL RATE AND DISTANCE ASSESSMENT FOR POPULATION DELINEATION

Introduction

Anadromous Pacific salmon (*Oncorhynchus* spp.) are extraordinary in their ability to spend years feeding in the ocean and then migrate, sometimes hundreds of miles, back not only to their home stream, but to their specific spawning or rearing grounds (Donaldson and Allen 1957, Bentzen et al. 2001). Yet, a fraction of returning fish "stray" and end up somewhere other than their natal stream (e.g., Quinn et al. 1991). This straying allows fish to colonize novel streams which may have favorable habitat (Milner and Bailey 1989) or to access alternative spawning grounds should conditions not be suitable in their home stream (Leider 1989). Quinn (1993) explains that several factors may influence salmon stray rates including species, the time of year released, and local conditions. Water levels, water temperature, or sediment load could be unfavorable in certain areas at the time of returning, which could prompt adult fish to search elsewhere for appropriate spawning grounds. Furthermore, fish reared in and released from a hatchery may stray more than wild fish (Jonsson et al. 1991) because they are subjected to many confusing odors and unnatural events during the artificial rearing procedure which can confound the imprinting process in juvenile salmon.

In defining demographically independent populations, quantifying the rate of straying is an important consideration, since a significant amount of straying between two spawning areas will couple the dynamics of those two locations. While the exact level of reproductive isolation that is required for a popluation to have substantially independent dynamics is not well understood, some theoretical work suggests that substantial independence will occur when the proportion of a population that consists of migrants is less than about 10% (Hastings 1993).

In this appendix, we use available data to assess the relationship between distance from a natal stream or release point and the stray rate of adult chinook (*O. tshawytscha*) and steelhead (*O. mykiss*) salmon in the interior Columbia River basin as they return to freshwater. We analyzed the data to determine whether a general pattern existed that could be used to characterize levels of straying between production areas as a function of the distance between areas. Given the limited nature of the available data, we concentrated on identifying a general distance, below which the rate of straying between production areas would be relatively high, and a second distance, above which the probability of straying would be very low. The range of distances between these two values was classified as being associated with a moderate potential for straying. The 10% rule of thumb (Hastings 1993) for evaluating the independence of a population would correspond to the aggregate input into a population from outside sources. Because data do not exist to evaluate the input into a population, our analysis focused on the dispersion of returning adults from a given release and acclimation (or natal) area. We estimated the distance associated with a 5% stray rate from a natal or release area, assuming that relatively small numbers of fish would be likely to stray beyond this distance.

Because we seek to identify natural patterns of population connectivity, data representing wild fish within the interior Columbia River basin would be of most use. Second-most informative would be data from locally derived hatchery stocks acclimated in the natal stream before release. Third most useful would be other hatchery fish studies. Unfortunately, little information is available on wild fish. Hatchery systems frequently offer more thorough release and recapture data through their use of coded-wire tags (CWTs) and organized efforts to document the source of onstation returns. Here, we considered three data sets involving spring chinook and one using steelhead. The spring chinook data sets were:

2. a CWT-based carcass study of wild spring chinook in the John Day River;
3. spring chinook supplementation monitoring results from two major upper Columbia tributaries, using mostly local stock that have been acclimated in waters from their home stream, and
4. hatchery releases of chinook from local broodstock in the mid-Columbia and Snake Rivers.

Much less information is available for steelhead – our analysis was limited to a comparison of stray rates of releases from steelhead hatcheries in the Columbia River basin.

Methods

All three data sets were derived from a similar combination of events: chinook or steelhead were tagged with CWTs and released at specific, known locations. Subsequently, some method was used to determine the proportion of adult returns from those releases to particular locations, including the release area. Spawning ground survey information was used to determine the distribution of returns in natural spawning areas. Returns to hatchery facilities were also used in the analysis. Typically, adult recoveries on the spawning ground could not be assigned individual recovery locations. Recoveries were most often based on data obtained from carcasses found during spawning ground surveys. Such recoveries are generally recorded by river reach, typically a major subtributary or a contiguous section of a main stem. We calculated the distances between the release point and an average distance calculated for each spawner recovery location. We also calculated the proportion of total recoveries for each tagged release group reported for each recovery reach used in the analysis. When the data supported it, we plotted the proportion of fish recovered at each spawning site against the distance between release and recovery locations, and conducted a regression analysis to create a dispersal curve. Using the resulting equation, we determined the distance at which the expected stray rate would be 5% or less. We used the standard error estimate from the regression analysis to generate confidence estimates associated with the 5% straying rate estimates.

Data Set 1*:* Wild Fish—John Day River

The John Day is a tributary to the Columbia River, just upstream of John Day Dam (Fig. 1). For this analysis we used data from a study done in the John Day River between 1978 and 1985 (Lindsay et al. 1986). They captured 75,794 wild spring chinook fingerlings and 11,868 smolts at three traps, one each in the upper Middle and North Fork John Day and in Granite Creek, a tributary to the North Fork, between 1978 and 1982 and marked them with CWTs and adipose fin clips. All known spawning areas were surveyed from 1978 to 1985, and redd counts were conducted on foot. The total spawning population was estimated by multiplying redd counts by 3.0, which they calculated to be the average number of adults per redd. Any carcasses were collected and checked for the incidence of a CWT. If a tag was present, they noted the original release point. Redd counts and carcass survey results were tabulated by major spawning reach—usually several kilometers in length. Carcass sample rates averaged 12%, 18%, and 22% of the total estimated spawner population for the Middle Fork, North Fork, and Granite Creek, respectively.

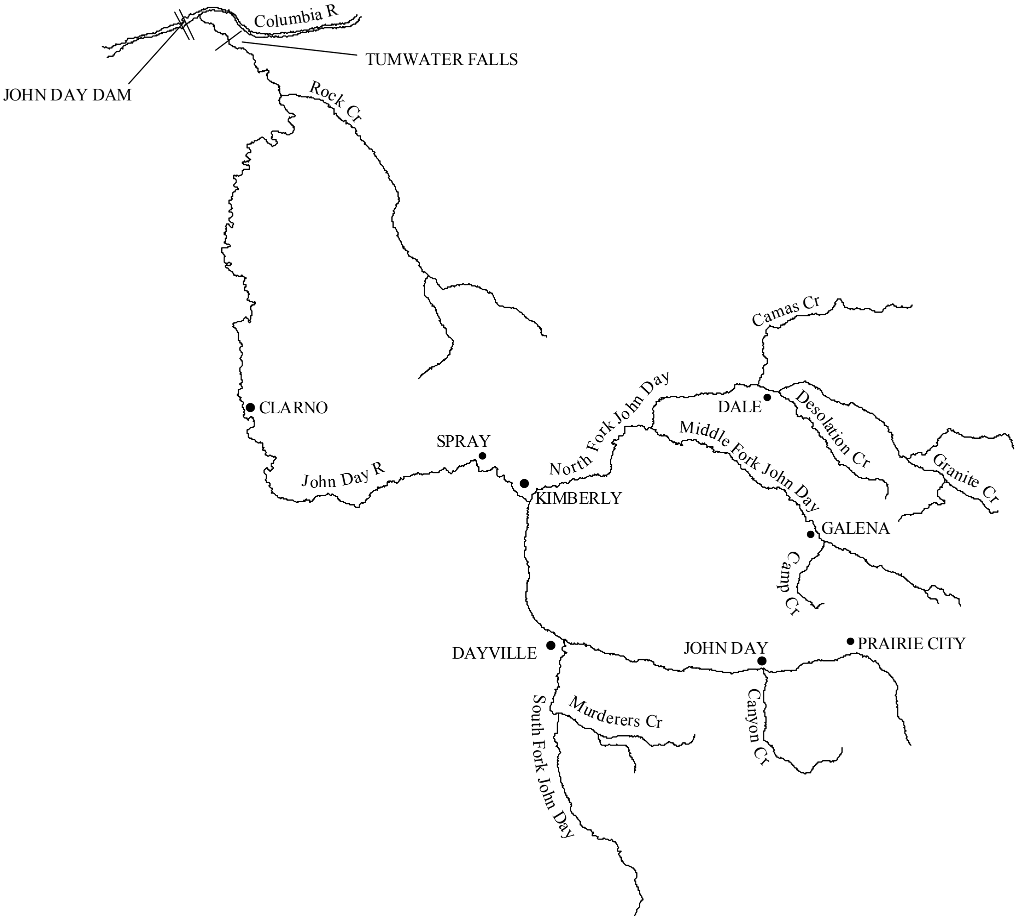

Figure 1. Map of the John Day River basin, Oregon. From Lindsay et al. (1986).

We calculated “weighted distances” between these three major tributaries of the John Day using redd count information from Lindsay et al. (Table 1). In the report, the exact positions of carcass recoveries in particular tributaries were not recorded. Redd counts and carcass recoveries were recorded by spawning reaches within each tributary. Under the assumption that carcass recoveries within a given spawning reach represent the distribution of redds within that reach, the redd count information was used to calculate the average distance that marked spawners were recovered relative to the mouth of the tributary of recovery. We calculated the distance from the midpoint of each spawning area to the confluence of its tributary with the mainstem John Day. We then found the proportions of redds in each tributary that fall in the different spawning reaches. For each reach within a given tributary (e.g., Granite Creek), we multiplied the average distance by the proportion of redds. Summing over the reaches within a tributary resulted in an estimate of the weighted average distance for recoveries relative to the tributary confluence. The distance between the marking point and recoveries for a particular tributary was calculated by adding together the stream distance from the marking point to the confluence of the selected tributary and the average distance of mark recovery from the confluence (Table 1).

Table 1. Weighted distances between release and recovery areas in the John Day River basin.

	CWT Tagging Stream		
Recovery Stream	**Middle Fork**	**North Fork**	**Granite Creek**
Middle Fork	0 km	212 km	215 km
North Fork	128 km	0 km	18 km
Granite Creek	156 km	13 km	0 km

Data Set 2: Acclimated Hatchery Releases of Mostly Local Broodstock - Upper Columbia River

In recent years, ambitious natural stock supplementation programs were developed and implemented in the Wenatchee and Methow subbasins. These programs provide an opportunity to evaluate homing and stray rates from fixed-point acclimation facilities in each tributary. While these experiments are not specifically done on naturally spawning and rearing populations, they are arguably closer surrogates than measurements of straying between major hatchery facilities.

Each data set described and analyzed below consists of three basic components: tag releases or tagging from a fixed acclimation pond or of fish from a distinct section of the spawning/rearing habitat in a major drainage; estimates of returning adults to specific sections of the drainage (redd counts expanded by fish per redd), carcass samples with CWTs identified from specific sections of the drainage.[1]

Spawning ground surveys have been conducted throughout each of the upper Columbia tributaries since the mid-1950s. Survey methods were expanded and strengthened in the mid-1980s. In recent years, virtually the entire system has been assessed to estimate the number of spawners and their distribution among the major tributaries. In the Mid-Columbia, spawner

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[1] Data for the Wenatchee obtained by Kristine Petersen (NMFS) from WDFW staff. Data for the Methow obtained from Joel Hubbell, Yakama Fisheries. Data for 2000 and 2001 are preliminary. Finalized data will be part of future reports from YIN and WDFW.

estimates are based on extensive redd surveys and an assumption regarding the average number of spawners per redd. Carcass recoveries during the spawning ground survey provide a means of recovering CWTs representative of the point release group.

Point releases of juveniles reared from natural broodstock are used as a starting point for the analysis. Returns from the annual point releases are collected and compared to samples taken from major spawning reaches throughout each drainage.

The Wenatchee is a tributary to the Columbia, entering above Rock Island Dam and below Rocky Reach Dam (Fig. 2). Natural production of spring chinook in the basin occurs primarily in the upper basins. Two different hatchery programs for spring chinook are under way in the basin; an onstation mitigation program at Leavenworth National Fish Hatchery and a separate directed natural stock supplementation program, using the Eastbank Hatchery for early rearing, along with collection/acclimation facilities near the mouth of the Chiwawa River. In recent years, relatively large numbers of tagged adults (>30) from this program have been recovered on the spawning grounds. We used returns from the 1997, 2000, and 2001 return years in this analysis.

The Chiwawa supplementation program began in 1991 with relatively small releases of 1989 brood yearlings (Peterson et al. 2000). Adult broodstock are collected at a weir in the Chiwawa River (major tributary to the Wenatchee). The weir is located just upstream of the confluence of the Chiwawa with the Wenatchee main stem. The adults are taken to Eastbank Hatchery for spawning. Incubation and early rearing occurs at the Eastbank facility. In the fall, juveniles are transported to an acclimation pond adjacent to the weir site in the lower Chiwawa River. Juveniles are reared on a combination of Chiwawa and mainstem Wenatchee River water until release during the spring high river flows (Peterson et al. 2000). Recovery data from the Wenatchee included the results of spawning ground surveys. Sampling information for the recovery years used in this analysis are summarized in Table 2.

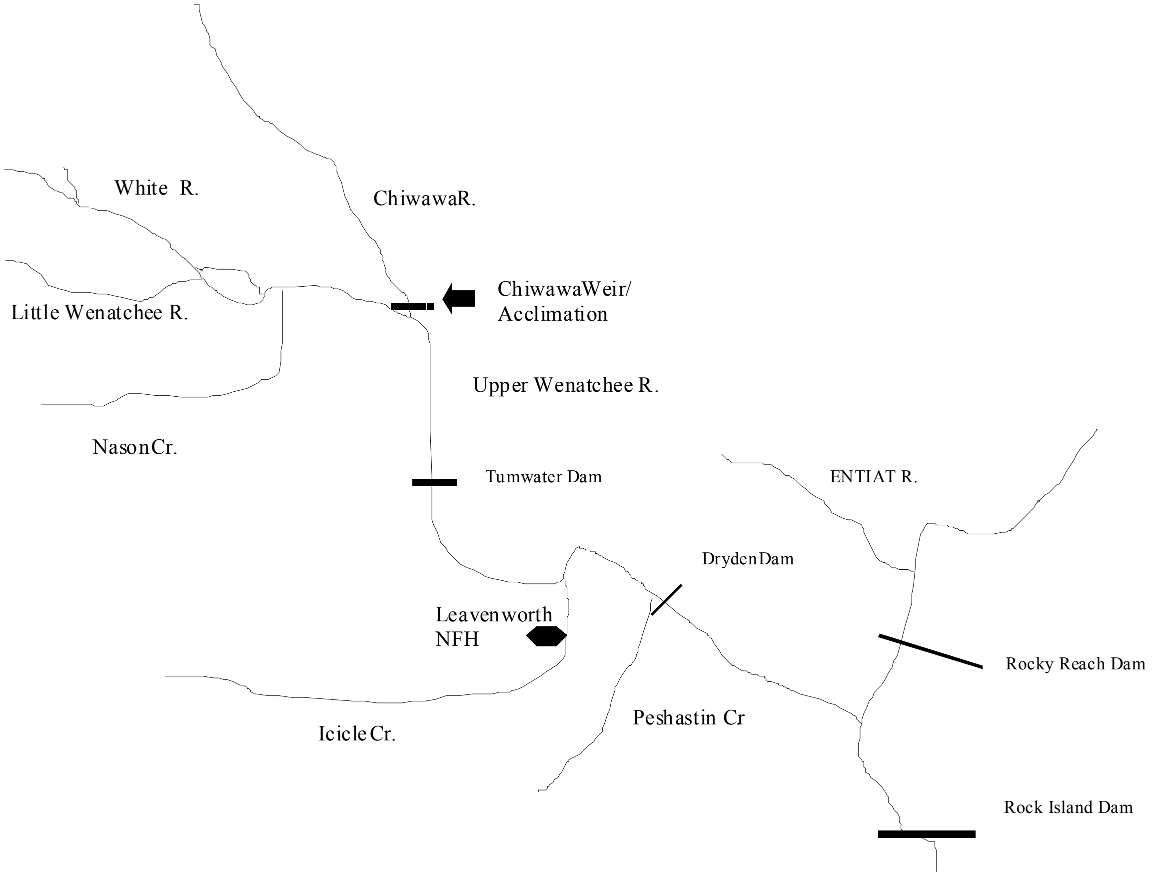

Figure 2. Map of the Wenatchee River basin rearing and release points.

Table 2: Spawning ground sampling rates for production areas within the Wenatchee system. Entries in the table are (carcasses recovered minus unidentifiable) divided by (estimated adult escapement) = proportion of adult escapement sampled.

Tributary	1997	2000	2001
Chiwawa River	16/108 = 0.09	114/262 = 0.40	710/2301 = 0 .31
Nason Creek	39/121 = 0.32	100/220 = 0.45	358/823 = 0.44
Upper Wenatchee River	4/33 = 0.12	31/81 = 0.38	177/473 = 0.37
Little Wenatchee	3/18 = 0.17	8/20 = 0.40	65/163 = 0.40
White	8/33 = 0.24	0/18	66/229 = 0.29
Icicle Creek	26/73 =0.36	51/150 = 0.34	149/194 = 0.72

The Methow enters the Columbia just upstream of Wells Dam (Fig. 3). In the Methow Hatchery, spring chinook are collected from three major spawning areas in the basin: the Chewuch, Twisp, and upper mainstem Methow Rivers. Spawning also occurs in major side tributaries including the Lost River and Early Winters Creek. Adult broodstock are collected from the respective tributaries and spawned at the Methow Hatchery. Broodstock separation is maintained through the incubation and early rearing stage at the hatchery. Juveniles from each broodstock receive CWTs and are moved back to acclimation ponds located in their respective natal streams a few weeks before release. Sufficient recovery information was available to do an analysis for the 2001 return year. The distances between release and recovery sites were found using information from Mullan (1992). As in the John Day analysis, we calculated distances weighted with redd counts to stray sites in the Wenatchee and Methow, since recovery sites were identified in the upper Columbia only to the stream reach, not to specific recovery points (Table 3).

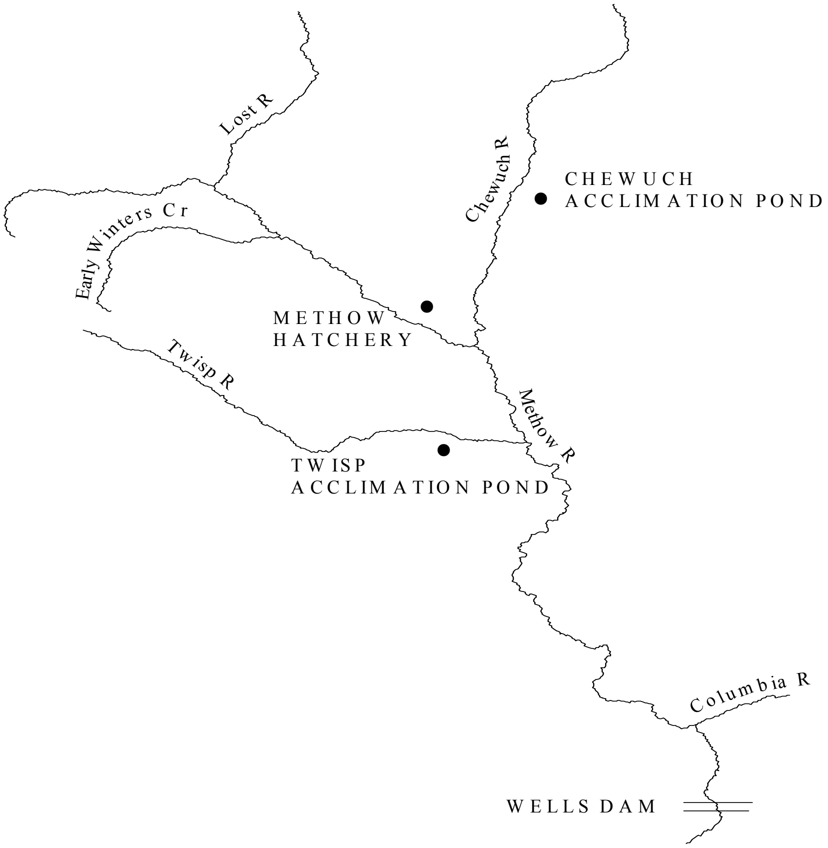

Figure 3. Methow River system with spring chinook spawning areas/release sites identified.

Table 3. Distances from release points to the confluences of major tributaries in the upper Columbia.

	Confluence with Columbia (RKm)	From Chiwawa Pond (km)	From Methow Hatchery (km)
Wenatchee	753	0	290
Entiat	779	138	151
Methow	843	290	0

Weighted recovery distances were calculated as the sum of the distance upstream of the confluence of a specific tributary and the distance of that confluence from the release point

(Table 4). Returns from all annual point releases are collected at the release site and in surveys of major spawning reaches throughout all three drainages (Wenatchee, Entiat, and Methow Rivers).

Table 4. Sampling information for the Methow River basin in 2001, by major spawning area, including number of carcasses taken, and the percent of the estimated number of spawners sampled as carcasses.

Tributary Reach	Estimated Redds	Adults (@2.2/redd)	Carcass Sample (excluding unknowns)	Sampling Fraction
Chewuch River	1,037	2,281	382	0.17
Lost River	73	161	6	0.04
Methow main stem	3,073	6,761	1,118	0.17
Twisp River	370	814	116	0.14

Data Set 3*:* Coarse-scale, Local Broodstock Hatchery Fish—Mid-Columbia and Snake Rivers

We obtained release and recovery data on hatchery chinook and steelhead using CWT information in the Regional Mark Information System database maintained by the Pacific States Marine Fisheries Commission (PSMFC 2002). The PSMFC tracks fish that have been implanted with CWTs by various fisheries agencies in the interior Columbia River basin.

For chinook, we searched for releases and subsequent recoveries of hatchery fish marked with CWTs. We focused onfish released from five hatchery programs that use local wild broodstock (Sawtooth, Tucannon, Warm Springs, McCall, and Lookingglass) for the approximate years of 1986 to 2001 (Fig. 4). A total of 17,626 fish were included in this group. McCall and Lookingglass Hatcheries are special cases: while McCall is on Payette Lake and Lookingglass is on Lookingglass Creek, the hatcheries use broodstock from the South Fork Salmon and Imnaha Rivers, respectively, and the fish are then returned to those locations for release (Table 5).

For steelhead, we used data from hatcheries that use local broodstock and had many years of CWT data as well as comprehensive data on spawner returns. We used data from Big Canyon, Little Sheep, Spring Creek, Sawtooth, Pahsimeroi, and Clearwater, for a total of 16,769 fish (17,765 including Deschutes recaptures) for the years 1975-2002. (Table 6, Fig. 4). For this species, we generally excluded data from recoveries in the Deschutes River basin. The relatively cold outflow from the Deschutes River provides a thermal refuge for steelhead migrating upstream in the Columbia River main stem. Tagging data indicate that many hatchery steelhead originating from Snake River facilities enter the Deschutes during summer migration. While radio tracking studies infer that a significant portion of these fish migrate out of the Deschutes before spawning, recoveries during the spawning period in the Deschutes indicate that many remain in the system. Therefore, including data for Deschutes recoveries could exaggerate stray rates under more common conditions, although we have presented some results that include those fish in order to demonstrate the effect these data have.

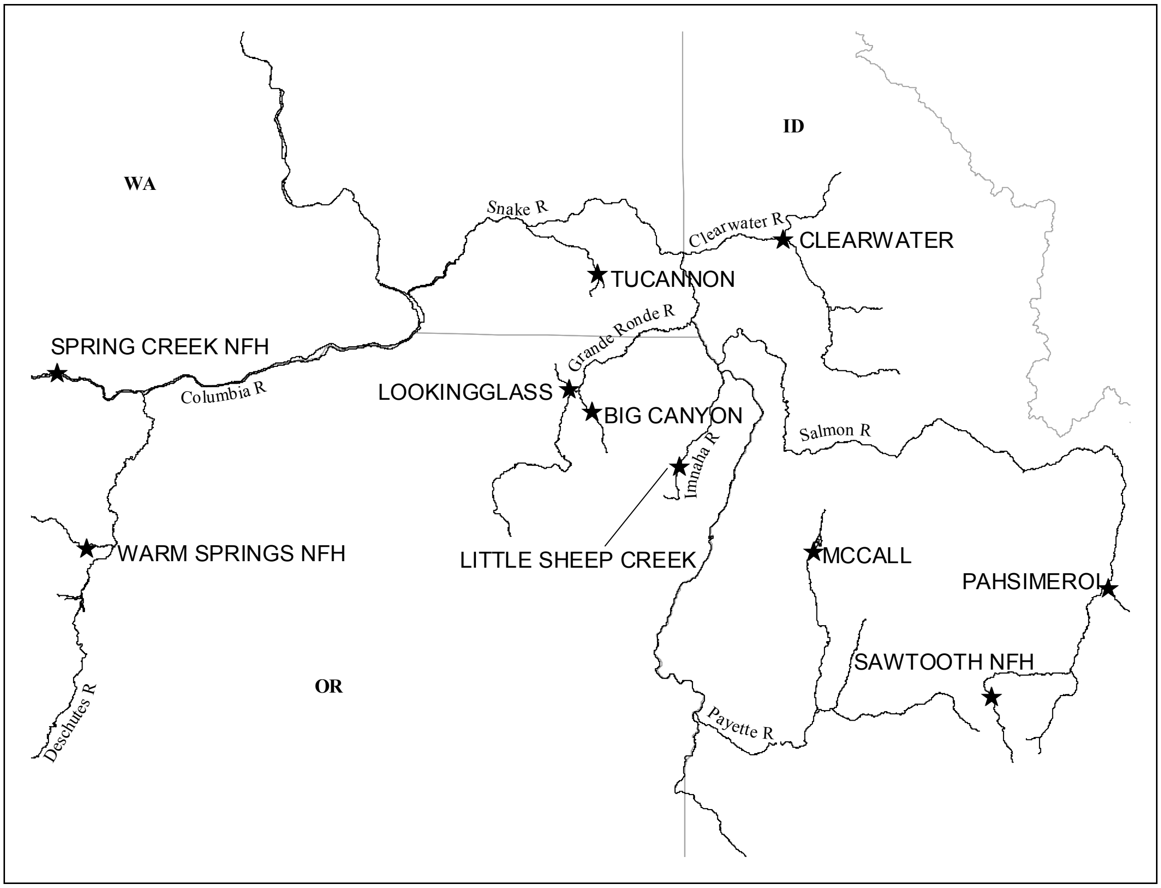

Figure 4. Map of hatcheries used for chinook and steelhead analyses.

A recovery location was defined as an area of probable spawning, such as hatchery racks, freshwater traps, or on spawning grounds. We took these recoveries and calculated the proportion found at each location for each release group. No comprehensive recovery program is conducted specifically for these CWTed fish. Rather, when these fish turn up at ongoing monitoring locations, the individual is entered incidentally into any existing database being used.

Table 5. Hatcheries, broodstock origin, final release point, and number of fish used for chinook analysis.

Hatchery	**Broodstock/ Release Location**	***n***
Lookingglass	Imnaha River	2,453
McCall	South Fork Salmon River	5,417
Sawtooth	Upper Salmon River	1,127
Tucannon	Tucannon River	319
Warm Springs	Warm Springs River	8,310

Table 6. Hatcheries, broodstock origin, final release point, and number of fish used for steelhead analysis.

		n	
Hatchery	**Broodstock/Release Location**	**W/O Deschutes**	**W/ Deschutes**
Big Canyon	Big Canyon Creek	1,193	1,489
Clearwater	Clearwater River	6,667	6,670
Little Sheep	Little Sheep Creek	2,041	2,089
Pahsimeroi	Pahsimeroi River	3,838	3,921
Sawtooth	Upper Salmon River	825	836
Spring Creek	Mid Columbia River	2,205	2,760

We plotted distance versus proportion for all hatcheries on the same graph. Distances between chinook spawning areas were calculated in ArcView using a 1:100,000 scale hydrography map from the National Hydrography Data Set web site (2002). The distance used was the shortest possible water route from the beginning or end node of one spawning area to closest end of the next area. We used spawning and rearing areas as defined by the Streamnet website (2002,) then refined them using the local knowledge of TRT members. If spawning areas were connected to each other, they were all counted as one spawning area. Because steelhead spawning areas are extremely variable from year to year, we did not find the distances between steelhead spawning areas.

Results

Even though analytical methods used on the three data sets were not the same and had differing strong and weak points, we found that the results were fairly uniform across all data sets. In all cases, stray rates dropped to very low rates more than 30 km from the natal area or release point, and straying was highest less than 10 km away.

Data Set 1*:* Wild Fish - John Day

No straying was detected between major subbasins of the John Day; the only straying that Lindsay et al. (1986) observed was between sites within the North Fork John Day (Table 7).

Table 7. Proportions of wild spring chinook groups released at different locations in the John Day River basin that were recovered at various sites.

	CWT Tagging Area		
Recovery Area	**Middle Fork**	**North Fork**	**Granite Creek**
Middle Fork	1	0	0
North Fork	0	0.77	0.08
Granite Creek	0	0.23	0.92

The mean straying distance, and the 95% confidence bound on that mean, was found to be about 30 km across all river sections for which this statistic was determined, including the Upper Columbia River (Table 8).

Table 8. Results of statistical analyses performed on straying data from the John Day and Upper Columbia Rivers. CI = confidence interval

	Stray Rate # 5%		
Data Set	**Mean (km)**	**95% CI Mean (km)**	**95% CI Estimate (km)**
Wenatchee and Methow	20	30	134
John Day	30	36	55
John Day and Upper Columbia	26	29	105

Here, the best source of data was used: wild fish spawning naturally. This is the ideal resource to use, since wild fish have evolved over many generations to be perfectly suited to many of the nuances of living in their particular stream. Hatchery fish come from stock that is limited in its genetic diversity and is often not originally from the particular stream in question. This analysis did, however, examine a somewhat limited area: only one river basin. Also, the sampling was performed at a fairly coarse scale; there were only three origins that a smolt could have in the analysis: the North Fork, the Middle Fork, and Granite Creek. This results in a picture that is not quite as sharp as it could have been had there been more discrimination in the definition of natal areas.

Data Set 2: Acclimated Hatchery Releases, Fine-scale Sampling, Semi-Local Broodstock - Upper Columbia River

Most fish returned close to the vicinity of their release point (Fig. 5). The farthest recorded recovery was 290 km. For the Chiwawa acclimation pond, most recoveries were at the weir, with some in the mainstem Wenatchee River and in nearby Nason Creek. Few were found in the Little Wenatchee River, and there were no retrievals outside the Wenatchee basin. No fish released in the Methow system were found outside the basin.

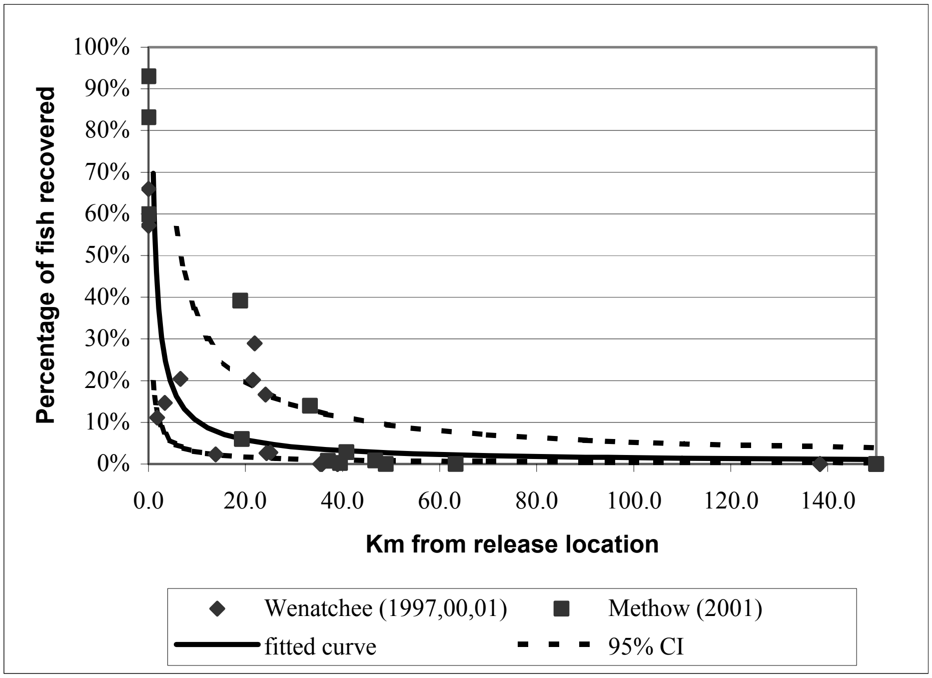

Figure 5. Dispersal curve for the Upper Columbia River , with Wenatchee and Methow recoveries with 95% confidence interval.

This data set has a slightly larger scope than the John Day analysis, looking at two, albeit smaller, river basins. Like the John Day study, only a handful of release points were used: two in the Wenatchee and three in the Methow. While fish were acclimated to their natal streams for a period before release, incubation and early rearing was at a central facility. This may have influenced the degree of straying. These drawbacks in the data set used could inflate stray rates higher than those expected for wild fish.

Analysis 3: Coarse-scale, Local Broodstock Hatchery - Mid-Columbia and Snake River

Chinook

The farthest recovery for chinook was 1,284 km. An exponential curve fit to the data had a moderate fit ($R^2 = 0.600$), and the point estimate of the distance associated with a 5% stray rate was 55 km, with an upper confidence limit of 110 km.

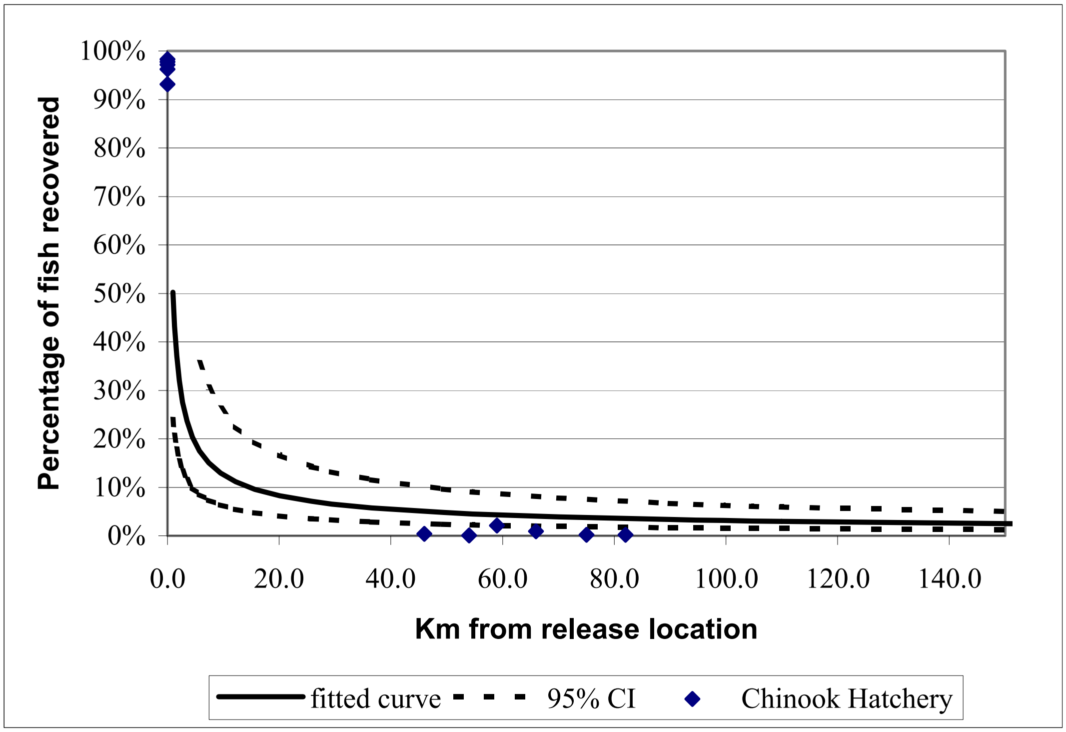

Figure 6. Dispersal curve for interior Columbia spring/summer chinook, based on coded-wire tag recoveries. Data are from Sawtooth, Tucannon, Warm Springs, McCall, and Lookingglass Hatcheries.

Steelhead

The farthest recovery for steelhead was 1091 km. The dispersal curve has a better fit to the data than the curve for chinook ($R^2 = 0.7973$). The estimated distance at which a 5% stray rate can be expected is 37 km (upper confidence limit: 105 km, Fig. 7).

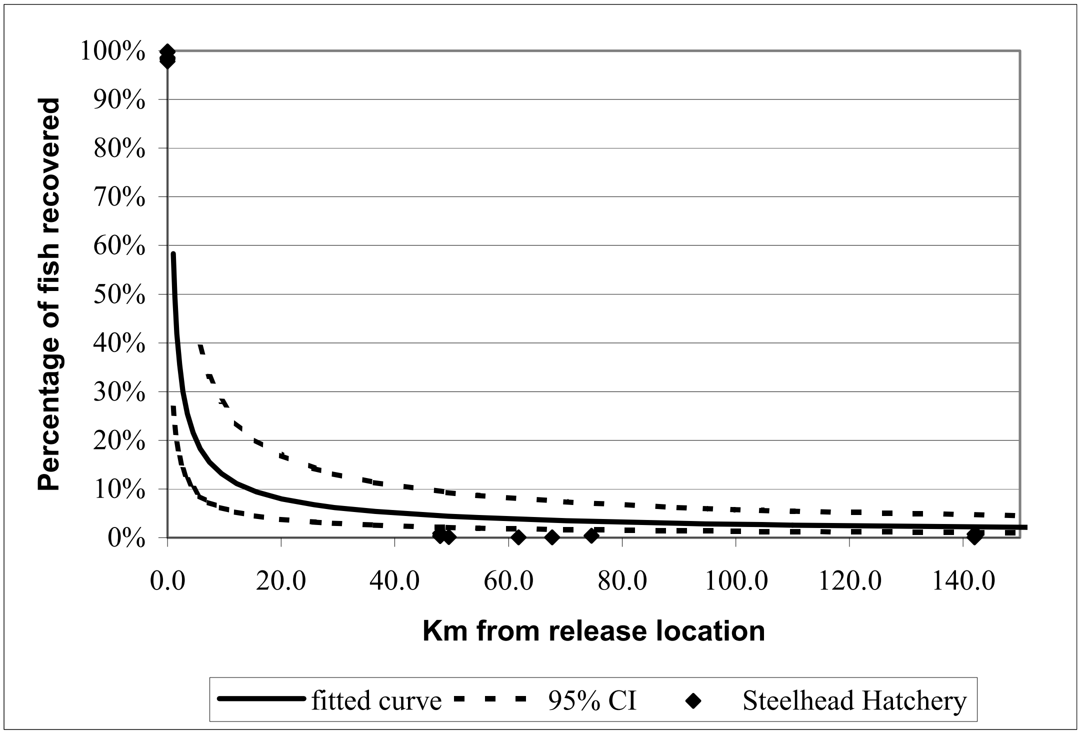

Figure 7. Dispersal curve for interior Columbia steelhead, based on coded-wire tag recoveries. Results do not include Deschutes River recoveries. Data are from Big Canyon, Little Sheep, Spring Creek, Sawtooth, Pahsimeroi, and Clearwater Hatcheries.

The sampling supporting this data set was unsystematic and on a coarse scale, but all hatchery fish examined were the progeny of local broodstock. The lack of data points between 5 and 40 km from release points hampers this analysis. The curve produced by fitting these data is driven by the high proportions recovered at the release point and the lack of recoveries at some distance (>50 km) from release points. The data and relative shape of the curve support the assumption that stray rates would be less than 5% for distances less than 40–50 km.

Discussion

These three data sets have different strengths and weaknesses in their methods. However, uniting all three analyses is the strong trend of decreasing recoveries with increasing distance. A general pattern seen is that most recoveries occur less than ten km from the release site, and there are few to none farther than thirty km away. These numbers are broad estimates deduced from studying a large amount of different types of data from throughout the Columbia River basin. For the purposes of population identification, spawning areas that are less than ten km from each other we classify as likely to receive strays from one another, and those farther than thirty km away from each other as unlikely to share a significant number of spawners.

We compiled a list of spawning areas for upper Columbia spring chinook (Table 9) and Snake River spring/summer chinook (Table 10) and indicated the distance from each of them to their closest spawning grounds. In general, we did not find much information on spawning areas for the moderate straying distances between ten to thirty km, so in order to define populations for these we considered other types of data including life history, morphology, and genetics.

The R-squared values found in the third analysis indicate that steelhead (not counting those that stray into the Deschutes) are less prone to distraction during their homing migration than chinook salmon, with distance between release location and spawning grounds accounting for 80% of spawning area choice, as opposed to only 60% for chinook. This conclusion has to be tempered by the fact that there are no observations at short distances. Chinook recoveries within this distance range were highly variable.

The Wenatchee and Methow stray rate information in the second analysis should be interpreted with the specifics of the two rearing programs in mind. In each case, due to different reasons, rearing practices involved may have influenced stray rate estimates. For the Wenatchee information, release groups are reared at a single site, within the Chiwawa River and near the confluence of that drainage with the mainstem Wenatchee River. River water from the Wenatchee main stem is brought into the rearing facility and used in early rearing. There are spawning areas in the upper Wenatchee main stem and in nearby Nason Creek. Substantial returns of the Chiwawa releases to these other areas could be the result of returning adults that are imprinting on upper mainstem waters. In the Methow, the fact that releases into all three acclimation ponds are extensively reared at the central Methow facility may affect stray rates among production areas. Both the Twisp and Chewuch releases are fish released at those sites that had been reared at the facility on the Methow main stem before being transferred to the acclimation sites for a short period before release. This rearing practice likely increased the propensity of returning adults to home back to the Methow, rather than acclimation/release reaches (Candy and Beacham 2000).

Similar analyses were conducted by the Puget Sound and Willamette/Lower Columbia TRTs. Both groups also used the PSMFC CWT database. The Puget Sound TRT looked at hatchery chinook from hatcheries using local wild broodstock or broodstocks that were genetically similar to the local wild population. They found that the steepest decline in their dispersal curve occurred between zero and 75 km from the release site. The Willamette/Lower Columbia TRT also discovered that a steep drop in recoveries occurred the farther away the fish were from the release site, which resulted in negligible recoveries more than 50 km away. These findings correspond with our results, as well as studies done outside the Columbia River basin (e.g., Schroeder et al. (2001) on coastal Oregon steelhead).

When looking at a dispersal curve to gain a picture of straying trends, a possible problem is that the farther along the x-axis a point is, the more area that is being accounted for by that distance from the release point due to stream branching. So it could potentially seem like there is a rise in the number of fish spawning at farther distances, simply because with more stream area accounted for at a number of kilometers, the more likely a fish is to be found within that circle. Our curves show no such climb after the initial sharp drop; there are still very few fish recovered very far from the release site. It is unlikely that this phenomenon had much effect on our data.

A caveat about the distances between spawning areas calculated above is that using a 1:100,000 stream map results in slightly shorter stream distances since some sinuosity is lost at this scale, but relative distances can be obtained with confidence. Our findings are important in our goal to identify populations within the Columbia River basin because if fish from one spawning area are likely to stray to another spawning reach, it is much more likely that these fish groups will be related and could affect each other. When combined with other data types, such as morphology, life history, and genetics, this knowledge can be an influential component of the population-identifying process.

Table 9. Upper Columbia spring chinook spawning areas and the distance to the nearest spawning area. Those areas that are within the likely stray distance of 10 km to another spawning area have their distances in bold; those that are more than the unlikely stray distance of 30 km have their distances in italics.

Spawning Area	**Closest Spawning Area**	**Distance (km)**	**Notes**
Chiwawa River	Wenatchee River	**7.3**	
Entiat/Mad River	Peshastin Creek (Wenatchee)	*77.3*	a
Little Wenatchee River	White River (Wenatchee)	22.2	
Methow River and tributaries	Twisp River and tributaries	11.8	
Peshastin Creek (Wenatchee)	Entiat/Mad River	*77.3*	a
Twisp River and tributaries	Methow River and tributaries	11.8	
Wenatchee River/Nason Creek	Chiwawa River	**7.3**	
White River (Wenatchee)	Little Wenatchee River	22.2	

[a] Peshastin Creek is mostly occupied by hatchery outplants

Table 10. Snake River spring/summer chinook spawning areas and the distance to the nearest spawning area. Those areas that are within the likely stray distance of 10 km to another spawning area have their distances in bold; those that are more than the unlikely stray distance of 30 km have their distances in italics.

Spawning Area	Closest Spawning Area	Distance (km)	Notes
Upper Alturas Lake Creek and tributaries	Upper Salmon River and tributaries	**3.2**	a
Bargamin Creek and tributaries	Hot Springs Creek (Salmon)	14.9	
Basin Creek (Salmon) and tributary	Big Casino Creek (Salmon)	**4.7**	
Bear Creek (Wallowa)	Upper Wallowa/Lostine River and tributaries	14.9	
Berg Creek (Salmon)	Van Creek (Salmon)	10.8	
Big Casino Creek (Salmon)	Basin Creek (Salmon) and tributary	**4.7**	
Big Creek (Middle Fork Salmon)	Lower Loon Creek (Middle Fork Salmon)	*44.0*	b*
Upper Big Creek (Middle Fork Salmon) and tributaries	Monumental Creek (Big)	**0.3**	
Big Sheep Creek (Imnaha)	Upper Imnaha	*55*	c
Cabin Creek (Big)	Rush Creek (Big)	**7.7**	
Captain John Creek (Snake)	Deep Creek (Salmon)	*75.2*	
Catherine Creek (Grande Ronde) and tributaries	Indian Creek (Grande Ronde)	*92.3*	
Challis Creek (Salmon)	Morgan Creek (Salmon)	**5.7**	
Chamberlain Creek (Salmon) and tributaries	Hot Springs Creek (Salmon)	29.7	
Cottonwood Creek (Loon)	Warm Springs Creek (Loon)	13.2	
Crooked Creek (Salmon) and tributary	Warren Creek (Salmon)	**7.9**	
Crooked Creek (Valley)	Upper Valley Creek (Salmon) and tributaries	**2.5**	
East Fork Salmon and tributaries	Road Creek (East Fork Salmon) and tributaries	**4.7**	
East Fork Salmon River	Upper Salmon River #3	**6.8**	d*
Eightmile Creek (Fifteenmile)	Fifteenmile Creek (Columbia)	*47.3*	
Fivemile Creek (Salmon)	Warren Creek (Salmon)	13.2	
Garden Creek (Salmon)	Challis Creek (Salmon)	19.3	

Goat/Meadow Creek (Valley)	Iron Creek (Valley)	**0.8**	
Upper Grande Ronde River	Catherine Creek (Grande Ronde) and tributaries	*91*	e
Granite Creek (Snake)	Sheep Creek (Snake)	16.2	
Horse Creek (Salmon)	Hot Springs Creek (Salmon)	*30.8*	
Hot Springs Creek (Salmon)	Bargamin Creek and tributaries	14.9	
Upper Imnaha	Big Sheep Creek (Imnaha)	*55*	c
Indian Creek (Grande Ronde)	Lookingglass Creek (Grande Ronde) and tributaries	*31.2*	
Indian Creek (Salmon)	Squaw Creek (Salmon)	**0.2**	
Iron Creek (Salmon)	Morgan Creek (Salmon)	*46.1*	
Iron Creek (Valley)	Goat/Meadow Creek (Valley)	**0.8**	
John Day Creek (lower Salmon)	Slate Creek (lower Salmon) and tributaries	**9.5**	
Kelly Creek (Salmon)	Van Creek (Salmon)	**0.4**	
Kinnikinic Creek (Salmon)	Squaw Creek (upper Salmon) and tributaries	**5.7**	
Lemhi River/Hayden Creek and tributaries	North Fork Salmon River and tributaries	*85.1*	
Little Salmon River	Berg Creek (Salmon)	13.1	
Lookingglass Creek (Grande Ronde) and tributaries	Indian Creek (Grande Ronde)	*31.2*	
Lower Loon Creek (Middle Fork Salmon)	Upper Loon Creek (Middle Fork Salmon)	**2.7**	f*
Upper Loon Creek and tributaries	Cottonwood Creek (Loon)	11.8	g
Upper Loon Creek (Middle Fork Salmon)	lower Loon Creek (Middle Fork Salmon)	**2.7**	f*
Minam River and tributaries	Bear Creek (Wallowa)	*58.3*	
Monumental Creek (Big)	Upper Big Creek (Middle Fork Salmon) and tributaries	**0.3**	
Morgan Creek (Salmon)	Challis Creek (Salmon)	**5.7**	
Pahsimeroi River	Upper Salmon River #1	15.9	h*
Panther Creek (Salmon) and tributaries	Squaw Creek (Salmon)	26.5	
Rapid River (Little Salmon) and tributaries	Lower South Fork Salmon River	*81.1*	i *

Redfish Lake Creek	Upper Salmon River and tributaries	**6**	
Road Creek (East Fork Salmon) and tributaries	East Fork Salmon and tributaries	**4.7**	
Rush Creek (Big)	Cabin Creek (Big)	**7.7**	
Upper Salmon River #1	Upper Salmon River #2	**5.1**	j*
Upper Salmon River #2	Upper Salmon River #1	**5.1**	k*
Upper Salmon River #3	East Fork Salmon River	**6.8**	d*
Upper Salmon River and tributaries	Upper Alturas Lake Creek and tributaries	**3.2**	
Upper Middle Fork Salmon River and tributaries	Rush Creek (Big)	20.4	l
North Fork Salmon River and tributaries	Indian Creek (Salmon)	16.8	
Lower South Fork Salmon River	South Fork /East Fork South Fork Salmon River and tributaries	**9.1**	m*
South Fork/East Fork South Fork Salmon River and tributaries	Lower South Fork Salmon River	**9.1**	m*
Upper South Fork Salmon River	South Fork/East Fork South Fork Salmon River and tributaries	29.5	n*
Sheep Creek (lower Salmon)	Wind River (Salmon)	10.7	
Sheep Creek (Snake)	Granite Creek (Snake)	16.2	
Slate Creek (lower Salmon) and tributaries	John Day Creek (lower Salmon)	**9.5**	
Slate Creek (Salmon)	Thompson Creek (Salmon)	**4.8**	
Squaw Creek (Salmon)	Indian Creek (Salmon)	**0.2**	
Squaw Creek (upper Salmon) and tributaries	Kinnikinic Creek (Salmon)	**5.7**	
Thompson Creek (Salmon)	Slate Creek (Salmon)	**4.8**	
Trout Creek (Salmon)	Bargamin Creek and tributaries	16	
Tucannon River	Captain John Creek (Snake)	*197.5*	
Upper Valley Creek (Salmon)	Crooked Creek (Valley)	**2.5**	
Van Creek (Salmon)	Kelly Creek (Salmon)	**0.4**	
Upper Wallowa/Lostine River and tributaries	Bear Creek (Wallowa)	14.9	
Warm Springs Creek (Loon)	Cottonwood Creek (Loon)	13.2	
Warm Springs Creek (Salmon)	Slate Creek (Salmon)	11.3	

Warren Creek (Salmon)	Crooked Creek (Salmon) and tributary	**7.9**
Wenaha River and tributaries	Lookingglass Creek (Grande Ronde) and tributaries	*71.8*
White Bird Creek (Salmon)	Slate Creek (lower Salmon) and tributaries	19.9
Wind River (Salmon)	Sheep Creek (lower Salmon)	10.7
Yankee Fork and tributaries	Warm Springs Creek (Salmon)	13

* Summer chinook spawning grounds

[a] Tributaries of upper Salmon R include lower Alturas Lake Creek

[b] Lower Loon Creek : mouth to Cottonwood Creek

[c] Upper Imnaha: above Dunn Creek

[d] East Fork Salmon: below Herd Creek ; upper Salmon River #3: above Kinikinnic Creek

[e] Upper Grande Ronde: Winter Canyon and above

[f] Lower Loon: below Cottonwood Creek ; upper Loon: above Shell Creek

[g] Upper Loon Creek : Mayfield Creek and above (inclusive)

[h] Upper Salmon: between Morgan Creek , Pennel Gulch

[i] Lower South Fork: below Station Creek

[j] Upper Salmon #1: between Morgan Creek , Pennel Gulch; upper Salmon #2: between Birch Creek , Bayhorse Creek

[k] 1st upper Salmon: between Birch Creek , Bayhorse Creek ; 2nd upper Salmon: between Morgan Creek , Pennel Gulch

[l] Middle Fork Salmon: above Soldier Creek

[m] Lower South Fork Salmon: below Station Creek ; South Fork Salmon: from Chicken Creek to East Fork South Fork (inclusive)

[n] Upper South Fork: above Blackmare Creek ; South Fork Salmon: from Chicken Creek to East Fork South Fork (inclusive)

Abbreviations Used in this Paper

CWT	Coded-wire tag
NFH	National Fish Hatchery
NMFS	National Marine Fisheries Service
PSMFC	Pacific States Marine Fisheries Commission
PUD	Public Utility District
TRT	Technical Recovery Team
YIN	Yakama Indian Nation

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Streamnet web site: **http://www.streamnet.org**

APPENDIX C

PHYSIOGRAPHIC SUMMARIES

Snake River Summer and Spring Chinook

				Spawn / Rear Stream Length (M)		Population Basin Climate					Elevation (M)					
							Mean Temperature (°C × 100)					Spawn/Rear Stream Elevation				
Id	Population Name	Code	Basin Area Acres / Km^2	Sum.	Spr	Mean Annual Precip. (mm)	Jan. Max.	Jan. Min.	Jul. Max.	Jul. Min.	Basin Mean	Su.m Max.	Sum. Min.	Spr. Max.	Spr. Min.	Ecoregion Per Population Basin Level 3 (%)
1	Tucannon River	SNTUC	321940/ 1302.85		42993	617	400	-415	2687	1108	830			1060	445	BM (028) CP (072)
2	Asotin Creek	SNASO	208329/ 843.08		14964	514	325	-449	2591	1076	1020			559	943	BM (032) CP (068)
3	Wenaha River	GRWEN	189076/ 765.17		46353	1115	167	-711	2358	707	1313			1066	575	BM (100)
3	Methow River	UCMET	1164315/ 4711.84	267870		860	-188	-788	2084	732	1416	1152	262			CP (015) NC (085)
4	Lostine River	GRLOS	458861/ 1856.95		99052	719	67	-860	2332	531	1491			1637	915	BM (100)
5	Minam River	GRMIN	153340/ 620.55		45291	1113	-42	-642	2154	681	1736			1480	1034	BM (100)
6	Catherine Creek	GRCAT	288685/ 1168.27		58576	718	176	-552	2559	866	1249			1453	848	BM (100)
7	Grande Ronde	GRUMA	478193/ 1935.19		52377	695	192	-638	2446	781	1355			1439	1007	BM (100)

Id	Population Name	Code	Basin Area Acres / Km^2	Spawn / Rear Stream Length (M)		Population Basin Climate					Elevation (M)					Ecoregion Per Population Basin Level 3 (%)
						Mean Annual Precip. (mm)	Mean Temperature (°C × 100)				Basin Mean	Spawn/Rear Stream Elevation				
				Sum.	Spr		Jan. Max.	Jan. Min.	Jul. Max.	Jul. Min.		Su.m Max.	Sum. Min.	Spr. Max.	Spr. Min.	
	River upper mainstem															
8	Imnaha River mainstem	IRMAI	325333/ 1316.58		58562	710	92	-553	2327	968	1462			1620	827	BM (100)
9	Big Sheep Creek	IRBSH	219026/ 886.37		24129	633	79	-675	2228	798	1513			1663	1111	BM (100)
10	Little Salmon River	SRLSR	673428/ 2725.28	47286	154403	879	61	-850	2485	746	1509	2468	594	1972	436	BM (050) IB (050)
11	South Fork Salmon River mainstem	SFMAI	909958/ 3682.49	136817	91460	892	-25	-1219	2279	431	1817	2245	642	2257	531	BM (001) IB (099)
12	Secesh River	SFSEC	157192/ 636.14	109290		1159	-107	-1165	2136	435	2045	2353	1104			IB (100)
13	East Fork South Fork Salmon River	SFEFS	270248/ 1093.66	139782		1079	-133	-1345	2007	317	2163	2209	1110			IB (100)
14	Chamberlain Creek	SRCHA	522141/ 2113.04		94642	841	-55	-1324	2305	335	1824			2201	676	IB (100)
15	Big Creek	MFBIG	697796/ 2823.89	38445	163882	776	-137	-1331	2339	316	2036	1401	1041	2105	868	IB (100)
16	Middle Fork	MFLMA	240495/ 973.25		77365	618	-110	-1292	2504	430	1996			1408	1071	IB (100)

Id	Population Name	Code	Basin Area Acres / Km^2	Spawn / Rear Stream Length (M)		Population Basin Climate					Elevation (M)					Ecoregion Per Population Basin Level 3 (%)
						Mean Annual Precip. (mm)	Mean Temperature (°C × 100)				Basin Mean	Spawn/Rear Stream Elevation				
				Sum.	Spr		Jan. Max.	Jan. Min.	Jul. Max.	Jul. Min.		Su.m Max.	Sum. Min.	Spr. Max.	Spr. Min.	
	Salmon River below Indian Creek															
17	Camas Creek	MFCAM	254541/ 1030.10		104849	651	-238	-1359	2468	389	2248			2739	1154	IB (100)
18	Loon Creek	MFLOO	227436/ 920.41	36335	72215	724	-183	-1254	2147	381	2283	1751	1229	2408	1525	IB (100)
19	Pistol Creek	MFPIS	288395/ 1167.10		180251	947	-125	-1350	2153	261	2204			2685	1351	IB (100)
20	Sulphur Creek	MFSUL	32438/ 131.27		28364	1226	-171	-1353	2023	274	2170			2396	1689	IB (100)
21	Bear Valley Creek	MFBEA	122609/ 496.18		148187	1075	-92	-1230	2224	411	2156			2353	1874	IB (100)
22	Marsh Creek	MFMAR	95353/ 385.88		100652	1001	-135	-1244	2147	345	2287			2422	1872	IB (100)
23	Middle Fork Salmon River above Indian Creek	MFUMA	113635/ 459.87		67245	997	-111	-1309	2175	328	2157			2010	1401	IB (100)
24	North Fork Salmon River	SRNFS	308104/ 1246.86		67655	601	-201	-1083	2536	745	1889			2311	1058	IB (090) MR (010)
25	Lemhi	SRLEM	942084/		99483	460	-210	-1331	2307	673	2106			2608	1559	IB (004) MR

Id	Population Name	Code	Basin Area Acres / Km^2	Spawn / Rear Stream Length (M)		Population Basin Climate					Elevation (M)					Ecoregion Per Population Basin Level 3 (%)
						Mean Annual Precip. (mm)	Mean Temperature (°C × 100)				Basin Mean	Spawn/Rear Stream Elevation				
				Sum.	Spr		Jan. Max.	Jan. Min.	Jul. Max.	Jul. Min.		Su.m Max.	Sum. Min.	Spr. Max.	Spr. Min.	
	River		3812.50													(096)
26	Pahsimeroi River	SRPAH	530347/ 2146.25	48856		452	-191	-1301	2234	666	2247	1739	1413			MR (100)
27	Salmon River lower mainstem below Redfish Lake	SRLMA	1075793/4353.60	94986	147245	509	-160	-1139	2409	659	2134	1994	1413	2875	1333	IB (054) MR (046)
28	East Fork Salmon River	SREFS	352780/ 1427.65	16603	155989	627	-234	-1160	2095	596	2455	1762	1632	2591	1715	IB (062) MR (038)
29	Yankee Fork	SRYFS	121579/ 492.01		107079	765	-183	-1038	1937	554	2431			2662	1884	IB (100)
30	Valley Creek	SRVAL	93802/ 379.60	9853	115010	775	-166	-1316	2231	356	2225	1953	1896	3153	1902	IB (100)

Ecoregion codes: BM = Blue Mountains, CM = Cascades, CP = Columbia Plateau, ECSF = Eastern Cascades Slopes and Foothills, IB = Idaho Batholith, MR = Middle Rockies, NC = North Cascades, NR = Northern Rockies

				Spawn / Rear Stream Length (M)		Population Basin Climate					Elevation (M)					
							Mean Temperature (°C × 100)					Spawn/Rear Stream				
Id	**Population Name**	**Code**	**Basin Area Acres / Km^2**	**Sum.**	**Spr.**	**Mean Annual Precip. (mm)**	**Jan. Max.**	**Jan. Min.**	**Jul. Max.**	**Jul. Min.**	**Basin Mean**	**Sum. Max.**	**Sum. Min.**	**Spr, Max.**	**Spr. Min.**	**Ecoregion Per Population Basin Level 3 (%)**
1	Wenatchee River mainstem	UCWEN	851017/ 3443.96		131005	1522	-60	-664	2256	880	1198			827	430	CP (003) ECSF (001) NC (096)
2	Entiat River	UCENT	267465/ 1082.40		43131	1032	-1	-541	2144	966	1288			726	359	CP (003) NC (097)
3	Methow River	UCMET	1164309/ 4711.81		167645	860	-188	-788	2084	732	1416			1230	477	CP (015) NC (085)

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Id	Population Name	Code	Basin Area Acres / Km^2	Spawn / Rear Stream Length (M)	Population Climate (By linear spawn / rear reach segments					Elevation (M)			Ecoregion Per Population Basin Level 3 (%)
					Mean Annual Precip. (mm)	Mean Temperature (°C × 100)				Reach Mean	Spawn/Rear Stream		
						Jan. Max.	Jan. Min.	Jul. Max.	Jul. Min.		Fall Min	Fall Max	
1	Snake River	SNMAI	NA / NA	380327	388	422	-332	2918	1206	309	134	488	

Id	Population Name	Code	Basin Area Acres / Km^2	Spawn / Rear Stream Length (M)		Population Basin Climate					Elevation (M)					Ecoregion Per Population Basin Level 3 (%)
				Sum.	Wtr.	Mean Annual Precip. (mm)	Mean Temperature (°C × 100)				Basin Mean	Spawn/Rear Stream				
							Jan. Max.	Jan. Min.	Jul. Max.	Jul. Min.		Sum. Max.	Sum. Min.	Wtr, Max.	Wtr. Min.	
1	Tucannon River	SNTUC-s	699561/ 2831.03	177230		521	408	-364	2820	1162	703	1385	194			BM (013) CP (087)
2	Asotin Creek	SNASO-s	208329/ 843.08	105567		514	325	-449	2591	1076	1020	1054	281			BM (032) CP (068)
3	Clearwater River lower mainstem	CRLMA-s	1690566/ 6841.51	642529		750	280	-482	2679	953	895	1735	233			BM (002) CP (035) IB (006) NR (057)
4	SF Clearwater River	CRSFC-s	556853/ 2253.51	551779		936	53	-1155	2347	483	1539	2199	704			IB (100)
5	Lolo Creek	CRLOL-s	155318/ 628.55	125444		1235	293	-695	2466	750	1073	1590	328			NR (100)
6	Selway River	CRSEL-s	1286987/ 5208.27	773822		1125	-80	-993	2290	591	1661	2315	461			IB (100)
7	Lochsa River	CRLOC-s	756499/ 3061.45	529284		1383	-120	-854	2236	641	1581	2127	449			IB (081) NR (019)
8	Grand Ronde River lower mainstem tributaries	GRLMT-s	767773/ 3107.08	481869		694	255	-582	2606	887	1086	1698	230			BM (085) CP (015)
9	Joseph Creek	GRJOS-s	351511/ 1422.52	376263		502	178	-664	2508	830	1274	1535	267			BM (100)

Id	Population Name	Code	Basin Area Acres / Km^2	Spawn / Rear Stream Length (M)		Population Basin Climate					Elevation (M)					Ecoregion Per Population Basin Level 3 (%)
						Mean Annual Precip. (mm)	Mean Temperature (°C × 100)				Basin Mean	Spawn/Rear Stream				
				Sum.	Wtr.		Jan. Max.	Jan. Min.	Jul. Max.	Jul. Min.		Sum. Max.	Sum. Min.	Wtr, Max.	Wtr. Min.	
10	Wallowa River	GRWAL-s	612202/ 2477.50	375364		818	40	-806	2287	569	1553	1738	718			BM (100)
11	Grande Ronde River upper mainstem	GRUMA-s	1046992/ 4237.04	957838		746	194	-606	2532	792	1267	1937	703			BM (100)
12	Little Salmon and Rapid River	SRLSR-s	1071930/ 4337.97	488946		754	148	-704	2544	849	1336	2468	261			BM (062) CP (006) IB (032)
13	South Fork Salmon River mainstem	SFMAI-s	1166768/ 4721.76	901259		938	-52	-1254	2211	399	1904	2569	542			IB (100)
14	Secesh River	SFSEC-s	156998/ 635.35	142416		1158	-107	-1165	2136	435	2046	2353	1104			IB (100)
15	Chamberlain Creek	SRCHA-s	522208/ 2113.31	294816		841	-55	-1324	2305	335	1824	2314	676			IB (100)
16	Big, Camas, and Loon Creek	MFBIG-s	1108196/ 4484.73	740112		705	-169	-1335	2323	327	2152	2739	942			IB (100)
17	Middle Fork Salmon River upper mainstem	MFUMA-s	733204/ 2967.19	752636		959	-114	-1302	2190	325	2170	2685	1224			IB (100)

Id	Population Name	Code	Basin Area Acres / Km^2	Spawn / Rear Stream Length (M)		Population Basin Climate					Elevation (M)					Ecoregion Per Population Basin Level 3 (%)
						Mean Annual Precip. (mm)	Mean Temperature (°C × 100)				Basin Mean	Spawn/Rear Stream				
				Sum.	Wtr.		Jan. Max.	Jan. Min.	Jul. Max.	Jul. Min.		Sum. Max.	Sum. Min.	Wtr, Max.	Wtr. Min.	
18	Panther Creek	SRPAN-s	636197/ 2574.61	152070		653	-170	-1281	2604	504	2033	2675	832			IB (100)
19	North Fork Salmon River	SRNFS-s	308053/ 1246.65	182253		600	-201	-1083	2536	745	1889	2566	1017			IB (090) MR (010)
20	Lemhi River	SRLEM-s	947967/ 3836.30	193422		461	-211	-1330	2309	672	2106	2899	1194			IB (004) MR (096)
21	Pahsimeroi River	SRPAH-s	840575/ 3401.70	139503		460	-181	-1283	2383	649	2156	2770	1328			IB (015) MR (085)
22	East Fork Salmon River	SREFS-s	815108/ 3298.64	290188		529	-188	-1114	2283	687	2251	2854	1457			IB (046) MR (054)
23	Salmon River upper mainstem	SRUMA-s	737164/ 2983.21	698280		723	-159	-1157	2113	484	2370	3153	1632			IB (099) MR (001)
24	Imnaha River	IRMAI-s	544356/ 2202.94	523822		679	87	-602	2287	900	1482	1999	352			BM (100)
25	Snake River Hells Canyon tributaries	SNHCT-s	346752/ 1403.26	72582		594	217	-480	2571	1065	1236	1304	288			BM (100)

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				Spawn / Rear Stream Length (M)		Population Basin Climate					Elevation (M)					
							Mean Temperature (°C × 100)					Spawn/Rear Stream				
Id	**Population Name**	**Code**	**Basin Area Acres / Km^2**	**Sum.**	**Wtr.**	**Mean Annual Precip. (mm)**	**Jan. Max.**	**Jan. Min.**	**Jul. Max.**	**Jul. Min.**	**Basin Mean**	**Sum. Max.**	**Sum. Min.**	**Wtr. Max.**	**Wtr. Min.**	**Ecoregion Per Population Basin Level 3 (%)**
1	Wenatchee River	UCWEN-s	851126/ 3444.40	212719		1522	-60	-664	2256	880	1198	1006	277			CP (004) NC (096)
2	Entiat River	UCENT-s	266012/ 1076.52	61492		1036	-1	-541	2140	964	1291	827	341			CP (003) NC (097)
3	Methow River	UCMET-s	1164315/ 4711.84	267870		860	-188	-788	2084	732	1416	1152	262			CP (015) NC (085)
4	Okanogan River	UCOKA-s	1465437/ 5930	95805		572	-18	-761	2497	1058	1037	1207	242			CP, NC

Ecoregion codes: BM = Blue Mountains, CM = Cascades, CP = Columbia Plateau, ECSF = Eastern Cascades Slopes and Foothills, IB = Idaho Batholith, MR = Middle Rockies, NC = North Cascades, NR = Northern Rockies

				Spawn / Rear Stream Length (M)		Population Basin Climate					Elevation (M)					
							Mean Temperature (°C × 100)					Spawn/Rear Stream				
Id	Population Name	Code	Basin Area Acres / Km²	Sum.	Wtr.	Mean Annual Precip. (mm)	Jan. Max.	Jan. Min.	Jul. Max.	Jul. Min.	Basin Mean	Sum. Max.	Sum. Min.	Wtr. Max.	Wtr. Min.	Ecoregion Per Population Basin Level 3 (%)
1	Klickitat River	MCKLI-s	892959/ 3613.69	158446	87677	921	306	-332	2570	863	900	876	23	513	23	CM (008) CP (012) ECSF (080)
2	Fifteenmile Creek (winters)	MCFIF-s	350423/ 1418.12		228819	667	501	-254	2831	1170	603			1162	22	CM (003) CP (046) ECSF (051)
3	Deschutes River - eastside	DREST-s	1244442/ 5036.10	485588		480	499	-378	2826	966	838	1370	87			BM (036) CM (006) CP (048) ECSF (010)
4	Deschutes River - westside	DRWST-s	466546/ 1888.05	200022		810	492	-292	2716	994	949	1294	376			BM (040) CM (022) ECSF (38)
5	John Day River lower mainstem tributaries	JDLMT-s	2380093/ 9631.93	1279288		383	463	-378	2784	950	915	1910	117			BM (056) CP (044)
6	NF John Day River	JDNFJ-s	1182522/ 4785.52	1247714		578	255	-654	2480	685	1366	2102	572			BM (100)
7	MF John Day River	JDMFJ-s	506870/ 2051.24	526443		545	271	-704	2558	672	1377	1955	695			BM (100)
8	South Fork John Day River	JDSFJ-s	387259/ 1567.19	246331		459	367	-547	2656	804	1454	1824	708			BM (100)

9	John Day River upper mainstem	JDUMA-s	620522/2511.17	587769	515	382	-508	2660	899	1411	2192	749	BM (100)
10	Rock Creek	MCROC-s	144567/585.04	52752	436	354	-401	2862	1029	698	718	92	CP (041) ECSF (059)
11	Umatilla River	MCUMA-s	1485336/6010.96	389538	534	478	-323	2826	1144	739	1333	161	BM (025) CP (075)
12	Walla Walla River	WWMAI-s	643046/2602.32	202141	704	412	-312	2915	1176	582	1267	182	BM (023) CP (077)
13	Touchet River	WWTOU-s	483204/1955.47	153234	652	432	-318	2853	1225	645	1283	369	BM (018) CP (082)
14	Toppenish and Satus Creek	YRTOS-s	713857/2888.89	155742	411	339	-391	2802	1057	726	1117	282	CP (069) ECSF (031)
15	Naches River	YRNAC-s	818595/3312.75	389993	1213	190	-405	2291	902	1217	1188	290	CM (028) CP (019) ECSF (053)
16	Yakima River upper mainstem	YRUMA-s	1368884/5539.70	219238	995	99	-522	2419	1008	966	989	330	CM (004) CP (044) ECSF (019) NC (033)

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					Population Basin Climate					Elevation (M)		Ecoregion
						Mean Temperature (°C × 100)						
Id	Population Name	Code	Basin Area Acres / Km^2	Length Lake Perimeter (M)	Mean Annual Precip. (mm)	Jan. Max.	Jan. Min.	Jul. Max.	Jul. Min.	Basin Mean	Lake Elevation	Per Population Basin Level 3 (%)
1	Redfish Lake	SRRED	27146 / 109.85	15080	833	-156	-1184	2093	434	2515	1997	IB (100)

Snake River Fall Chinook - Hatchery Releases Downloaded from the Fish Passage Center Database

Population	Code	% natural origin spawners 1998 - 2002*	% natural origin spawners 1980 - 1997*	Stock	Average annual releases 1979 - 1986	Average annual releases 1987 - 1994	Average annual releases 1995 - 2002	Total releases 1979 - 1986	Total releases 1987 - 1994	Total releases 1995 - 2002
Snake River	SNMAI	36	66	Lyons Ferry	432,652	1,694,568	344,489	3,461,212	13,556,546	2,755,909
				Snake River	79,303	75,458	1,444,303	634,420	603,661	11,554,427
				All Stocks	**511,954**	**1,770,026**	**1,788,792**	**4,095,632**	**14,160,207**	**14,310,336**

* Average among those years in the indicated period for which data was available

Snake River Sockeye - Hatchery Releases Downloaded from the Fish Passage Center Database

Population	Code	% natural origin spawners 1998 - 2002	% natural origin spawners 1980 - 1997	Stock	Average annual releases 1979 - 1986	Average annual releases 1987 - 1994	Average annual releases 1995 - 2002	Total releases 1979 - 1986	Total releases 1987 - 1994	Total releases 1995 - 2002
Redfish Lake	SRRED	0	0	Redfish Lake	-	12,304	86,557	-	98,428	692,452
*Alturas Lake**		0	0	Babine	7,875	-	-	63,000	-	-
				Redfish Lake	-	-	22,163	-	-	177,303
*Stanley Lake**		0	0	Babine	18,375	-	-	147,000	-	-
*Pettit Lake**		0	0	Redfish Lake	-	2,143	8,903	-	17,144	71,226
ESU total				**All Stocks**	**26,250**	**14,447**	**117,622**	**210,000**	**115,572**	**940,981**

*Not currently considered an independent population of Snake River Sockeye

Snake River Steelhead - Hatchery Releases Downloaded from the Fish passage Center Database

Population	Code	% natural origin spawners 1998 - 2002**	% natural origin spawners 1980 - 1997**	Stock	Average annual releases			Total releases		
					1979 - 1986	1987 - 1994	1995 - 2002	1979 - 1986	1987 - 1994	1995 - 2002
Tucannon River	SNTUC-s	26	39	Tucannon River	37,902	99,804	14,830	303,218	798,431	118,636
				Skamania	30,500	-	-	244,000	-	-
				Wallowa	58,952	-	-	471,618	-	-
				Wells	51,894	-	-	415,148	-	-
				Lyons Ferry	-	29,011	149,658	-	232,084	1,197,265
				Pahsimeroi A	-	14,908	-	-	119,264	-
				Mixed	-	16,255	-	-	130,040	-
				All Stocks	**179,248**	**159,977**	**164,488**	**1,433,984**	**1,279,819**	**1,315,901**
Asotin Creek	SNASO-s	unknown	unknown	Lyons Ferry	3,938	10,429	14,287	31,500	83,435	114,297
				Wallowa	4,126	3,625	-	33,005	29,000	-
				Wells	10,206	-	-	81,650	-	-
				Oxbow A	-	17,000	-	-	136,000	-
				Pahsimeroi A	-	17,231	-	-	137,847	-
				All Stocks	**18,269**	**48,285**	**14,287**	**146,155**	**386,282**	**114,297**
*Lower Mainstem Snake**		unknown	unknown	All Stocks	172,166	144,102	72,441	1,377,330	1,152,815	579,527
Lower Clearwater	CRLMA-s	unknown	unknown	Dworshak B	3,101,404	2,092,813	1,589,643	24,811,229	16,742,502	12,717,142
				Clearwater B	-	-	246,974	-	-	1,975,793
				All Stocks	**3,101,404**	**2,092,813**	**1,836,617**	**24,811,229**	**16,742,502**	**14,692,935**
South Fork Clearwater	CRSFC-s	unknown	unknown	Dworshak B	-	484,352	904,905	-	3,874,817	7,239,242
				Selway River	-	8,946	17,048	-	71,566	136,380
				Clearwater B	-	-	296,204	-	-	2,369,633
				All Stocks	**-**	**25,063**	**1,218,157**	**-**	**3,946,383**	**9,745,255**
Lolo Creek	CRLOL-s	unknown	unknown	Dworshak B	17,500	25,063	6,103	140,000	200,500	48,823
				Clearwater B	-	-	2,250	-	-	18,000
				All Stocks	**17,500**	**25,063**	**8,353**	**140,000**	**200,500**	**66,823**

Lochsa River	CRLOC-s	unknown	unknown	Dworshak B	555,063	-	-	4,440,500	-	-
Selway River	CRSEL-s	unknown	unknown		-	-	-	-	-	-
Low. Grande Ronde	GRLMT-s	unknown	unknown	Wallowa	141,719	563,134	358,119	1,133,750	4,505,073	2,864,951
				Wells	14,188	-	-	113,500	-	-
				All Stocks	**155,906**	**563,134**	**358,119**	**1,247,250**	**4,505,073**	**2,864,951**
Joseph Creek	GRJOS-s	100	100		-	-	-	-	-	-
Wallowa River	GRWAL-s	unknown	unknown	Wallowa	188,620	1,018,540	1,049,655	1,508,956	8,148,320	8,397,241
				Wells	14,688	-	-	117,500	-	-
				Snake River	12,063	-	-	96,500	-	-
				All Stocks	**215,370**	**1,018,540**	**1,049,655**	**1,722,956**	**8,148,320**	**8,397,241**
Up. Grande Ronde	GRUMA-s	76	89	Wallowa	-	59,268	31,249	-	474,144	249,989
Little Salmon	SRLSR-s	unknown	unknown	Salmon River A	147,671	632,672	423,977	1,181,364	5,061,374	3,391,815
				Pahsimeroi A	479,875	188,087	62,743	3,839,000	1,504,696	501,942
				Hagerman A	38,513	-	-	308,103	-	-
				Oxbow A	37,788	225,720	414,112	302,303	1,805,760	3,312,894
				Dworshak B	79,646	299,600	290,022	637,170	2,396,799	2,320,177
				Salmon River B	-	6,188	77,328	-	49,500	618,626
				Unknown	83,688	-	-	669,500	-	-
				All Stocks	**867,180**	**1,352,266**	**1,268,182**	**6,937,440**	**10,818,129**	**10,145,454**
South Fork Salmon	SFMAI-s	unknown	unknown	Salmon River A	31,625	12,500	-	253,000	100,000	-
Secesh River	SFSEC-s	unknown	unknown		-	-	-	-	-	-
Chamberlain Creek	SRCHA-s	unknown	unknown		-	-	-	-	-	-
Big, Camas, Loon	MFBIG-s	unknown	unknown		-	-	-	-	-	-

Upper Middle Fork	MFUMA-s	unknown	unknown		-	-	-	-	-	-
Panther Creek	SRPAN-s	unknown	unknown	Pahsimeroi A	30,790	-	-	246,320	-	-
				Salmon River A	17,500	70,688	-	140,000	565,500	-
				All Stocks	**48,290**	**70,688**	**-**	**386,320**	**565,500**	**-**
North Fork Salmon	SRNFS-s	unknown	unknown	Salmon River A	-	102,438	26,312	-	819,502	210,492
				Pahsimeroi A	-	23,813	38,063	-	190,500	304,500
				Oxbow A	-	16,872	-	-	134,979	-
				All Stocks	**-**	**143,123**	**64,374**	**-**	**1,144,981**	**514,992**
Lemhi River	SRLEM-s	unknown	unknown	Salmon River A	283,313	-	156,025	2,266,500	-	1,248,201
				Dworshak B	78,125	-	-	625,000	-	-
				Pahsimeroi A	-	54,286	116,149	-	434,288	929,188
				All Stocks	**361,438**	**54,286**	**272,174**	**2,891,500**	**434,288**	**2,177,389**
Pahsimeroi River	SRPAH-s	unknown	unknown	Pahsimeroi A	1,019,573	668,987	765,528	8,156,583	5,351,894	6,124,221
				Dworshak B	8,375	-	-	67,000	-	-
				Salmon River A	-	100,493	175,639	-	803,946	1,405,113
				All Stocks	**1,027,948**	**769,480**	**941,167**	**8,223,583**	**6,155,840**	**7,529,334**
East Fork Salmon	SREFS-s	unknown	unknown	East Fork Salmon B	193,585	205,644	29,998	1,548,676	1,645,150	239,981
				Hagerman B	33,776	-	-	270,208	-	-
				Pahsimeroi A	3,938	-	-	31,500	-	-
				Dworshak B	-	537,903	210,457	-	4,303,224	1,683,658
				Salmon River B	-	60,625	89,728	-	485,000	717,826
				All Stocks	**231,298**	**804,172**	**330,183**	**1,850,384**	**6,433,374**	**2,641,465**
Upper Mainstem Salmon	SRUMA-s	unknown	unknown	Salmon River A	196,423	887,034	635,937	1,571,385	7,096,275	5,087,492
				Hagerman A	98,273	-	-	786,186	-	-
				Pahsimeroi A	-	279,966	322,654	-	2,239,724	2,581,235
				Dworshak B	-	-	113,913	-	-	911,302
				Salmon River B	-	-	64,086	-	-	512,686
				Sawtooth A	-	-	28,304	-	-	226,435

				All Stocks	**294,696**	**1,167,000**	**1,164,894**	**2,357,571**	**9,335,999**	**9,319,150**
Imnaha River	IRMMT-s	79	88	Imnaha River	36,395	296,999	172,948	291,158	2,375,992	1,383,580
				Wallowa	5,022	-	-	40,179	-	-
				Little Sheep Creek	-	-	139,751	-	-	1,118,005
				All Stocks	**41,417**	**296,999**	**312,698**	**331,337**	**2,375,992**	**2,501,585**
Hell's Canyon	SNHCT-s	unknown	unknown	Oxbow A	591,669	743,227	385,874	4,733,348	5,945,815	3,086,990
				Salmon River A	6,311	43,000	147,431	50,487	344,000	1,179,444
				Imnaha River	-	4,202	-	-	33,613	-
				Wallowa	-	195,054	-		1,560,428	-
				Snake River A	-	-	83,141	-	-	665,125
				All Stocks	**597,979**	**985,482**	**616,445**	**4,783,835**	**7,883,856**	**4,931,559**
ESU Total		**15**	**23**	**All Stocks**	**7,916,797**	**10,260,475**	**9,723,481**	**63,334,374**	**82,083,797**	**77,787,847**

* Not currently considered an independent population

** Average among those years in the indicated period for which data was available.

Middle Columbia Steelhead - Hatchery Releases Downloaded from the Fish Passage Center Database

Population	Code	% natural origin spawners 1998 - 2002**	% natural origin spawners 1980 - 1997**	Stock	Average annual releases			Total releases		
					1979 - 1986	1987 - 1994	1995 - 2002	1979 - 1986	1987 - 1994	1995 - 2002
*White Salmon River**		unknown	unknown	All Stocks	21,710	36,256	40,974	173,676	290,049	327,791
*Little White Salmon River**		unknown	unknown	Skamania	-	-	13,471	-	-	107,765
Fifteenmile Cr	MCFIF-s	100	100		-	-	-	-	-	-
Klickitat River	MCKLI-s	unknown	unknown	Skamania	101,984	88,435	111,907	815,871	707,477	895,254
				Klickitat River	6,446	-	-	51,570	-	-
				All Stocks	**108,430**	**88,435**	**111,907**	**867,441**	**707,477**	**895,254**
Deschutes Westside	DRWST-s	unknown	unknown	Deschutes River	159,106	168,769	127,193	1,272,844	1,350,151	1,017,544
Deschutes Eastside	DREST-s	unknown	unknown	Deschutes River	89,377	-	40,355	715,015	-	322,838
				S Santiam River	46,250	-	-	370,000	-	-
				All Stocks	**135,627**	**-**	**40,355**	**1,085,015**	**-**	**322,838**
Rock Creek	MCROC-s	unknown	unknown		-	-	-	-	-	-
John Day Lower Mainstem	JDLMA-s	100	100		-	-	-	-	-	-
John Day Upper Mainstem	JDUMA-s	96	99		-	-	-	-	-	-
North Fork John Day	JDNFJ-s	100	100		-	-	-	-	-	-
Middle Fork John Day	JDMFJ-s	100	100		-	-	-	-	-	-
South Fork John Day	JDSFJ-s	100	100		-	-	-	-	-	-
Umatilla River	MCUMA-s	68	81	Umatilla River	51,127	106,547	144,206	409,014	852,375	1,153,648

Touchet River	WWTOU-s	84	91	Wells	52,909	-	-	423,270	-	-
				Lyons Ferry	-	100,716	125,092	-	805,728	1,000,732
				Ringold	-	14,543	-	-	116,345	-
				Touchet River	-	-	10,249	-	-	81,988
				Skamania	16,438	-	-	131,500	-	-
				All Stocks	**69,346**	**115,259**	**135,340**	**554,770**	**922,073**	**1,082,720**
Walla Walla River	WWMAI-s	99	92	Wells	55,990	32,713	-	447,920	261,700	-
				Lyons Ferry	30,183	119,406	159,664	241,465	955,244	1,277,312
				Skamania	19,688	-	-	157,500	-	-
				Ringold	-	20,302	-	-	162,417	
				Unknown	2,563	-	-	20,500	-	-
				All Stocks	**108,423**	**172,420**	**159,664**	**867,385**	**1,379,361**	**1,277,312**
Upper Mainstem Yakima	YRUMA-s	unknown	unknown	Yakima River	-	4,630	-	-	37,042	-
Naches River	YRNAC-s	unknown	unknown	Skamania	35,500	-	-	284,000	-	-
				Ringold	6,161	-	-	49,288	-	-
				Wells	11,246	-	-	89,970	-	-
				Yakima River	-	7,375	-	-	59,000	-
				All Stocks	**52,907**	**7,375**	**-**	**423,258**	**59,000**	**-**
Toppenish/Satus Cr	YRTOS-s	unknown	unknown		-	-	-	-	-	-
*Lower Mainstem Yakima**		unknown	unknown	All Stocks	18,922	26,121	-	151,375	208,967	-
*Lower Mainstem Columbia**		unknown	unknown	All Stocks	1,500	3,400	361	12,000	27,200	2,886
ESU Total		**49**	**66**	**All Stocks**	**727,097**	**729,212**	**773,470**	**5,816,778**	**5,833,695**	**6,187,758**

* Not currently considered an independent population

** Average among those years in the indicated span for which data was available

Upper Columbia Steelhead - Hatchery Releases Downloaded from the Fish Passage Center Database

Population	Code	% natural origin spawners 1998 - 2002+	% natural origin spawners 1980 - 1997+	Stock	Average annual releases			Total releases		
					1979 - 1986	1987 - 1994	1995 - 2002	1979 - 1986	1987 - 1994	1995 - 2002
Wenatchee River	UCWEN-s	32**	27**	Leavenworth	12,962	94,355	20,965	103,698	754,837	167,722
				Wenatchee River	50,670	-	135,227	405,360	-	1,081,815
				Ringold	19,905	70,766	-	159,240	566,125	-
				Skamania	17,875	-	-	143,000	-	-
				Wells	37,321	278,958	170,441	298,564	2,231,665	1,363,527
				Unknown	120,625	-	-	965,000	-	-
				All Stocks	**259,358**	**444,078**	**326,633**	**2,074,862**	**3,552,627**	**2,613,064**
Entiat River	UCENT-s	32**	27**	Wells	22,373	43,136	15,836	178,986	345,085	126,690
				Wenatchee River	-	-	10,908	-	-	87,260
				Unknown	17,000	-	-	136,000	-	-
				All Stocks	**39,373**	**43,136**	**26,744**	**314,986**	**345,085**	**213,950**
Methow River	UCMET-s	13	14	Wells	355,990	453,481	449,186	2,847,916	3,627,850	3,593,490
Okanogan River	UCOKA-s	unknown	unknown	Wells	35,262	157,307	127,104	282,098	1,258,458	1,016,835
*Upper Mainstem Columbia**		unknown	unknown	All Stocks	261,043	200,105	206,160	2,088,341	1,600,840	1,649,279
ESU Total		**unknown**	**30**	**All Stocks**	**951,025**	**1,298,108**	**1,135,827**	**7,608,203**	**10,384,860**	**9,086,618**

* Not currently considered and independent population

** Wenatchee and Entiat rivers combined

+ Average among those years in the indicated period for which data was available

Snake River Spring / Summer Chinook - Hatchery Releases Downloaded from the Fish Passage Center Database

					Average annual releases			**Total releases**		
Population	**Code**	**% natural origin spawners 1998 - 2002****	**% natural origin spawners 1980 - 1997****	**Stock**	**1979 - 1986**	**1987 - 1994**	**1995 - 2002**	**1979 - 1986**	**1987 - 1994**	**1995 - 2002**
Tucannon R	SNTUC	40	82	Tucannon River	-	107,931	100,373	-	863,448	802,983
Catherine Cr	GRCAT	unknown	57	Catherine Creek	4,720	-	44,395	37,760	-	355,156
				Rapid River		8,750	-	-	70,002	-
				Carson	50,288	13,000	-	402,306	104,000	-
				Lookingglass	52,563	43,325	-	420,500	346,600	-
				All Stocks	**107,571**	**65,075**	**44,395**	**860,566**	**520,602**	**355,156**
Wallowa/Lostine R	GRLOS	94	74	Wallowa	17,750	-	-	142,000	-	-
				Carson	33,955	10,125	-	271,643	81,000	-
				Lookingglass	-	34,450	-	-	275,602	-
				Rapid River	-	18,039	-	-	144,313	-
				Lostine River	**-**	**-**	36,826	**-**	**-**	294,605
				All Stocks	**51,705**	**62,614**	**36,826**	**413,643**	**500,915**	**294,605**
Minam R	GRMIN	96	77		-	-	-	-	-	-
Upper MS Grande Ronde R	GRUMA	unknown	64	Grande Ronde River	-	-	**29,057**	-	-	**232,453**
Wenaha R	GRWEN	unknown	65		-	-	**-**	-	-	-
*Lower MS Grande Ronde R**		unknown	unknown	All Stocks	66,283	10,005	4,683	530,260	80,043	37,460
*Lookingglass Creek**		10	45	All Stocks	813,252	798,947	218,505	6,506,017	6,391,576	1,748,036
Little Salmon R	SRLSR	unknown	unknown	Rapid River	2,611,946	2,618,051	1,729,918	20,895,566	20,944,407	13,839,341
Secesh R	SFSEC	95	98		-	-	-	-	-	-

South Fork Salmon R	SFUMA	92	96	South Fork Salmon	328,578	938,083	906,445	2,628,623	7,504,663	7,251,559
EF SF Salmon R/Johnson Cr	SFUEF	100	100	South Fork Salmon	-	88,663	17,043	-	709,300	136,342
Chamberlain Cr	SRCHA	unknown	unknown		-	-	-	-	-	-
MF Salmon R blw Indian Cr	MFLMA	100	100		-	-	-	-	-	-
Big Cr	MFBIG	100++	100++		-	-	-	-	-	-
Camas Cr	MFCAM	100	100		-	-	-	-	-	-
Loon Cr	SRLCR	100	100		-	-	-	-	-	-
MF Salmon R abv Indian Cr	MFUMA	100	100		-	-	-	-	-	-
Pistol Cr	MFPIS	100	100		-	-	-	-	-	-
Sulphur Cr	MFSUL	100	100		-	-	-	-	-	-
Marsh Cr	MFMAR	100	100		-	-	-	-	-	-
Bear Valley Cr/Elk Cr	MFBEA	100	100		-	-	-	-	-	-
NF Salmon R	SRNFS	unknown	unknown		-	-	-	-	-	-
Lemhi R	SRLEM	100	100	Lemhi River Salmon River **All Stocks**	22,063 77,875 **99,938**	- - **-**	- - **-**	176,500 623,000 **799,500**	- - **-**	- - **-**
Pahsimeroi R	SRPAH	unknown	unknown	Pahsimeroi River Rapid River	44,788 197,566	533,839 -	129,110 -	358,303 1,580,529	4,270,710 -	1,032,879 -

				Salmon River	34,880	-	35,389	279,043	-	283,110
				All Stocks	**277,234**	**533,839**	**164,499**	**2,217,875**	**4,270,710**	**1,315,989**
East Fork Salmon R	SRUEF	100+	100+	Salmon River	13,586	192,796	5,444	108,690	1,542,368	43,554
Yankee Fork	SRYFS	100+	100+	Pahsimeroi River	-	90,688	-	-	725,500	-
				Rapid River	-	18,763	-	-	150,100	-
				Salmon River	-	152,913	-	-	1,223,300	-
				All Stocks	**-**	**262,363**	**-**	**-**	**2,098,900**	**-**
Valley Cr	SRELK	100+	100+		-	-	-	-	-	-
Salmon R, above Redfish Lake	SRUMA	unknown	unknown	Salmon River	264,261	1,176,573	132,977	2,114,091	9,412,580	1,063,812
Salmon R, below Redfish Lake	SRLMA	unknown	unknown		-	-	-	-	-	-
Big Sheep Cr	IRBSH	unknown	unknown		-	-	-	-	-	-
Imnaha River mainstem	IRMAI	unknown	unknown	Imnaha River	22,498	325,882	203,355	179,987	2,607,054	1,626,843
*Snake Mainstem Total**		unknown	unknown	All Stocks	332,777	508,194	208,956	2,662,216	4,065,554	1,671,645
ESU Total		**55**	**46**	**All Stocks**	**4,989,629**	**7,689,015**	**3,802,472**	**39,917,034**	**61,512,120**	**30,419,778**

* Not currently considered an independent population

** Average among those years in the indicated period for which data was available

+ Percent natural origin for summer run chinook, spring run data not available

++ Percent natural origin for spring run chinook, summer run data not available

Upper Columbia Spring Chinook - Hatchery Releases Downloaded from the Fish Passage Center Database

Population	**Code**	**% natural origin spawners 1998 - 2002****	**% natural origin spawners 1980 - 1997****	**Stock**	**Average annual releases**			**Total releases**		
					1979 - 1986	**1987 - 1994**	**1995 - 2002**	**1979 - 1986**	**1987 - 1994**	**1995 - 2002**
Wenatchee River+	UCWER	68	88	Chiwawa River	-	30,428	81,896	-	243,420	655,170
				Leavenworth	1,908,710	2,838,332	1,567,655	15,269,678	22,706,656	12,541,243
				Carson	255,000	-	-	2,040,000	-	-
				Little White Salmon	50,750	-	-	406,000	-	-
				All Stocks	**2,214,460**	**2,868,760**	**1,649,552**	**17,715,678**	**22,950,076**	**13,196,413**
Entiat River+	UCENT	56	85	Entiat River	502,130	844,144	409,421	4,017,036	6,753,152	3,275,370
				Little White Salmon	160,000	-	-	1,280,000	-	-
				Leavenworth	17,000	-	-	136,000	-	-
				Carson	96,940	-	-	775,522	-	-
				All Stocks	**776,070**	**844,144**	**409,421**	**6,208,558**	**6,753,152**	**3,275,370**
Methow River	UCMET	43	86	Carson	97,875	10,625	-	783,000	85,000	-
				Chewuch River	-	5,110	65,056	-	40,882	520,450
				Twisp River	-	4,485	50,407	-	35,881	403,255
				Leavenworth	142,625	207,937	-	1,141,002	1,663,496	-
				Little White Salmon	150,875	-	-	1,207,000	-	-
				Methow River	53,375	-	361,905	427,000	-	2,895,238
				Winthrop	571,037	801,103	159,432	4,568,298	6,408,820	1,275,458
				All Stocks	**1,015,788**	**1,029,260**	**636,800**	**8,126,300**	**8,234,079**	**5,094,401**
*Okanogan River**		unknown	unknown	Carson	-	-	54,859	-	-	438,869
*Mainstem Columbia**		unknown	unknown	**All Stocks**	**492,387**	**690,018**	**556,575**	**3,939,092**	**5,520,142**	**4,452,597**
ESU Total				**All Stocks**	**4,498,704**	**5,432,181**	**3,307,206**	**35,989,628**	**43,457,449**	**26,457,650**

* Not currently considered an independent population

** Average among those years in the indicated period for which data was available

+ Includes Icicle Creek and Winthrop returns, which are not part of the Upper Columbia Spring Chinook ESU