MONITORING AND EVALUATION OF THE CHELAN COUNTY PUD HATCHERY PROGRAMS

2010 ANNUAL REPORT

June 1, 2011

Prepared by:

T. Hillman
M. Miller
BioAnalysts, Inc.

J. Miller
B. Keesee
Chelan PUD

T. Miller
M. Tonseth
M. Hughes
A. Murdoch
WA Dept of Fish and Wildlife

Prepared for:
HCP Hatchery Committee
Wenatchee, WA

Citation: Hillman, T., M. Miller, T. Miller, M. Tonseth, M. Hughes, A. Murdoch, J. Miller, and B. Kessee. 2011. Monitoring and evaluation of the Chelan County PUD hatchery programs: 2010 annual report. Report to the HCP Hatchery Committee, Wenatchee, WA.

TABLE OF CONTENTS

PREFACE

This annual report is the result of coordinated field efforts conducted by Washington Department of Fish and Wildlife (WDFW), the Confederated Tribes and Bands of the Yakama Nation (Yakama Nation), Chelan County Public Utility District (Chelan PUD), and BioAnalysts, Inc. An extensive amount of work was conducted in 2006 through 2010 to collect the data needed to monitor the effects of the Chelan County PUD Hatchery Programs. This work was directed and coordinated by the Habitat Conservation Plan (HCP) Hatchery Committee, consisting of the following members: Bill Gale, U.S. Fish and Wildlife Service (USFWS); Rob Jones, National Marine Fisheries Service (NMFS); Joe Miller, Chelan County PUD; Tom Scribner, the Yakama Nation; Mike Tonseth, WDFW; and Kirk Truscott, Confederated Tribes of the Colville Reservation (Colville Tribes).

The approach to monitoring the hatchery programs was guided by the "*Conceptual Approach to Monitoring and Evaluating the Chelan County Public Utility District Programs*" written by Andrew Murdoch and Chuck Peven. Technical aspects of the monitoring and evaluation program were developed by the Hatchery Evaluation Technical Team (HETT), which consists of the following scientists: Carmen Andonaegui, Anchor Environmental; Matt Cooper, USFWS; Steve Hays, Chelan PUD; Tracy Hillman, BioAnalysts; Tom Kahler, Douglas PUD; Russell Langshaw, Grant PUD; Greg Mackey, Douglas PUD; Joe Miller, Chelan PUD; Andrew Murdoch, WDFW; Keely Murdoch, Yakama Nation; Todd Pearsons, Grant PUD; and Ali Wick, Anchor Environmental. The HETT developed an "*Analytical Framework for Monitoring and Evaluating PUD Hatchery Programs*" (Hays et al. 2006), which directs the analyses of hypotheses developed under the conceptual approach. Most of the analyses outlined in the Analytical Framework paper will be conducted in 2011 after the fifth year of monitoring.

Most of the work reported in this paper was funded by Chelan PUD. Bonneville Power Administration purchased the Passive Integrated Transponder (PIT) tags that were used to mark juvenile Chinook and steelhead captured in tributaries. This is the fifth annual report written under the direction of the HCP.

"I often say that when you can measure something and express it in numbers, you know something about it. When you cannot measure it, when you cannot express it in numbers, your knowledge is of a meager and unsatisfactory kind. It may be the beginning of knowledge, but you have scarcely in your thoughts advanced to the stage of science, whatever it may be."

Lord Kelvin

SECTION 1: INTRODUCTION

Chelan PUD implements hatchery programs as part of two Habitat Conservation Plan (HCP) agreements related to the operation of Rocky Reach and Rock Island dams. The HCPs define the goal of achieving no net impact to spring Chinook, summer/fall Chinook, sockeye salmon, steelhead, and coho salmon affected by the operation of these dams. The two HCPs identify general program objectives as "*contributing to the rebuilding and recovery of naturally reproducing populations in their native habitats, while maintaining genetic and ecologic integrity, and supporting harvest*." The fish resource management agencies initially developed the following general goal statements for each hatchery program, which were adopted by the Hatchery Committee:

(1) Support the recovery of ESA listed species by increasing the abundance of natural adult population, while ensuring appropriate spatial distribution, genetic stock integrity, and adult spawner productivity.

Includes the Wenatchee spring Chinook, Wenatchee summer steelhead, and Methow spring Chinook programs.

(2) Increase the abundance of the natural adult population of unlisted plan species, while ensuring appropriate spatial distribution, genetic stock integrity, and adult spawner productivity. In addition, provide harvest opportunities in years when spawning escapement is sufficient to support harvest.

Includes the Wenatchee sockeye, Wenatchee summer/fall Chinook, Methow summer/fall Chinook, Okanogan summer/fall Chinook, and Okanogan sockeye programs.

(3) Provide salmon for harvest and increase harvest opportunities, while segregating returning adults from natural tributary spawning populations.

Includes the Turtle Rock summer/fall Chinook program.

Thus, there are two different types of artificial propagation strategies that address the different goals of the program: supplementation and harvest augmentation. The supplementation programs primarily focus on increasing the natural production of fish in tributaries. A fundamental assumption of this strategy is that hatchery fish returning to the spawning grounds are "reproductively similar" to naturally produced fish. The second program type, harvest augmentation, focuses on increasing harvest opportunities. This is accomplished by releasing hatchery fish directly into the Columbia River with the intent that returning adults remain segregated from the naturally spawning populations in tributaries.

Monitoring is needed to determine if the programs are performing properly. The HCP Hatchery Committee adopted a monitoring and evaluation (M&E) approach that will guide the assessment of the hatchery programs. The approach, developed by Murdoch and Peven (2005), identified the following objectives:

(1) Determine if supplementation programs have increased the number of naturally spawning and naturally produced adults of the target population relative to a non-supplemented population (i.e., reference stream) and the changes in the natural

replacement rate (NRR) of the supplemented population is similar to that of the non-supplemented population.

(2) Determine if the run timing, spawn timing, and spawning distribution of both the natural and hatchery components of the target population are similar.

(3) Determine if genetic diversity, population structure, and effective population size have changed in natural spawning populations as a result of the hatchery program. Additionally, determine if hatchery programs have caused changes in phenotypic characteristics of natural populations.

(4) Determine if the hatchery adult-to-adult survival (i.e., hatchery replacement rate or HRR) is greater than the natural adult-to-adult survival (i.e., natural replacement rate or NRR) and equal to or greater than the program-specific HRR expected value based on estimated survival rates listed in Appendix D in Murdoch and Peven(2005).

(5) Determine if the stray rate of hatchery fish is below the acceptable levels to maintain genetic variation between stocks.

(6) Determine if hatchery fish were released at the programmed size and number.

(7) Determine if the proportion of hatchery fish on the spawning grounds affects the freshwater productivity (i.e., number of juveniles per redd) of supplemented streams when compared to non-supplemented streams.

(8) Determine if harvest opportunities have been provided using hatchery returning adults where appropriate (e.g., Turtle Rock program).

Two additional objectives that were not explicit in the goals specified above but were included in the M&E approach because they relate to goals and concerns of all artificial production programs include:

(9) Determine whether bacterial kidney disease (BKD) management actions lower the prevalence of disease in hatchery fish and subsequently in the naturally spawning population. In addition, when feasible, assess the transfer of *Renibacterium salmoninarum* (Rs) infection at various life stages from hatchery fish to naturally produced fish.

(10) Determine if the release of hatchery fish impact non-target taxa of concern (NTTOC) within acceptable limits.

Attending each objective is one or more testable hypotheses (see Murdoch and Peven 2005). Each hypothesis will be tested statistically following the routines identified in Hays et al. (2006). Most of these analytical routines will be conducted at the end of five-year monitoring blocks, as outlined in the M&E plan (Murdoch and Peven 2005; Hays et al. 2006).

Throughout each five-year monitoring period, annual reports will be generated that describe the M&E data collected during a specific year. This is the fifth annual report developed under the direction of the M&E guidance approach (Murdoch and Peven 2005). The purpose of this report is to describe monitoring activities conducted in 2010. Activities included broodstock collection, collection of life-history information, within hatchery spawning and rearing activities, juvenile monitoring within streams, and redd and carcass surveys. Data from reference areas are not included in this annual report, because the process of selecting reference areas is still occurring. To the extent currently possible, we have included information collected before 2010.

This report is divided into several sections, each representing a different species or stock (i.e., steelhead, sockeye salmon, spring Chinook, and summer Chinook). For all species we provide broodstock information; hatchery rearing history, release data, and survival estimates; disease information; juvenile migration and productivity estimates; redd counts, distribution, and spawn timing; spawning escapements; and life-history characteristics. For salmon species, we also provide information on carcasses.

Finally, we end each section by addressing compliance issues with ESA/HCP mandates. For each Chelan PUD Hatchery Program, WDFW and the PUD are authorized annual take of ESA-listed spring Chinook and steelhead through Section 10 of the Endangered Species Act (ESA), including:

1. ESA Section 10(a)(1)(A) Permit No. 1395, which authorizes the annual take of adult and juvenile endangered upper Columbia River (UCR) spring Chinook and endangered UCR steelhead associated with implementing artificial propagation programs for the enhancement of UCR steelhead. The authorization includes takes associated with adult broodstock collection, hatchery operations, juvenile fish releases, monitoring and evaluation activities, and management of adult returns related to UCR steelhead artificial propagation programs in the UCR region (NMFS 2003a).
2. ESA Section 10(a)(1)(A) Permit No. 1196, which authorizes the annual take of adult and juvenile endangered UCR spring Chinook and endangered UCR steelhead associated with implementing artificial propagation programs for the enhancement of UCR spring Chinook. The authorization includes takes associated with adult broodstock collection, hatchery operations, juvenile fish releases, and monitoring and evaluation activities supporting UCR spring Chinook artificial propagation programs in the UCR region (NMFS 2004).
3. ESA Section 10(a)(1)(A) Permit No. 1347, which authorizes the annual incidental take of adult and juvenile endangered UCR spring Chinook and endangered UCR steelhead through actions associated with implementing artificial propagation programs for the enhancement of non-listed anadromous fish populations in the UCR. The authorization includes incidental takes associated with adult broodstock collection, hatchery operations, juvenile fish releases, and monitoring and evaluation activities associated with non-listed summer Chinook, fall Chinook, and sockeye salmon artificial propagation programs in the UCR region (NMFS 2003b).

SECTION 2: SUMMARY OF METHODS

Sampling in 2010 followed the methods and protocols described in Murdoch and Peven (2005). In this section we only briefly review the methods and protocols. More detailed information can be found in Murdoch and Peven (2005).

2.1 Broodstock Collection and Sampling

Methods for collecting broodstock during 2010 are described in Appendix A in WDFW (2008). Methods for sampling broodstock are described in Appendices A and B in Murdoch and Peven (2005). Generally, broodstock were collected over the migration period (to the extent allowed in ESA-permit provisions) in proportion to their temporal occurrence at collection sites, with in-season adjustments dictated by 2010 run timing and trapping success relative to achieving weekly and annual collection objectives. Pre-season weekly collection objectives are shown in Table 2.1 and assumptions associated with broodstock trapping are provided in Table 2.2.

Table 2.1. Weekly collection objectives for steelhead, sockeye, and Chinook in 2010.

Collection week beginning day	Chiwawa Spring Chinook[a]		Wild Wenatchee Summer Chinook	Wild ME/OK Summer Chinook	Wenatchee Steelhead		Wild Wenatchee Sockeye[b]	
	Hatchery	Wild			Hatchery	Wild	Male	Female
1-30 May	2							
31 May	3	2						
7 June	7	6						
14 June	10	8						
21 Jun	14	12						
28 Jun	18	14	126	91	1	1		
5 Jul	16	17	98	87	1	1		
12 Jul	11	14	82	84	1	1	20	20
19 Jul	7	6	63	73	1	1	40	40
26 Jul	5	4	44	61	1	1	25	25
2 Aug		2	29	44	4	4	20	20
9 Aug			21	41	7	7	16	16
16 Aug			16	26	8	8	9	9
23 Aug			13	24	7	7		
30 Aug				15	6	6		
6 Sep				8	6	6		
13 Sep				2	8	8		
20 Sep					9	9		
27 Sep					17	17		
4 Oct					15	15		
11 Oct					8	8		
18 Oct					4	4		
Total	**93**	**85**	**492**	**556**	**104**	**104**	**130**	**130**

[a] Collection quota based on 1999-2009 average cumulative Tumwater Dam spring Chinook passage (WDFW unpublished data) and pre-season broodstock collection objectives.

[b] Collection targeted equal numbers of males and females.

Table 2.2. Biological and trapping assumptions associated with collecting broodstock for the Chelan PUD Hatchery Programs (from Appendix A in Murdoch and Peven 2005).

Assumptions	Wenatchee Steelhead	Wenatchee Sockeye	Chiwawa Spring Chinook	Wenatchee Summer Chinook	ME/OK Summer Chinook
Production level	400,000 yearling smolts	200,000 subyearlings	672,000 yearling smolts	864,000 yearling smolts	976,000 yearling smolts
Broodstock required	208 adults (not to exceed 33% of population)	260 adults (not to exceed 33% of population)	379 adults (not to exceed 33% of population)	492 adults (not to exceed 33% of the population)	556 adults (not to exceed 33% of the population)
Trapping period	7 July – 12 Nov	7 July – 28 Aug	1 May – 12 Sep	7 Jul – 12 Sep	7 Jul – 15 Sep
# days/week	5	3	4	5	3
# hours/day	24	16	24	24	16
Broodstock composition	50% wild; 50% WxW and/or HxW	100% wild	Sliding scale; minimum 33% wild (depends on the number of wild fish)	100% wild	100% wild
Trapping site	Dryden Dam (Tumwater will be used if weekly quota not achieved at Dryden Dam)	Tumwater Dam	Tumwater Dam (hatchery fish only) and the Chiwawa Weir (both hatchery and wild fish)	Dryden Dam (Tumwater will be used if weekly quota not achieved at Dryden Dam)	Wells Dam east ladder

Several biological parameters were measured during broodstock collection at adult collection sites. Those parameters included the date and start and stop time of trapping; number of each species collected for broodstock; origin, size, and sex of trapped fish; age from scale analysis; and pre-spawn mortality. For each species, trap efficiency, extraction rate, and trap operation effectiveness were estimated following procedures in Appendix B in Murdoch and Peven (2006). In addition, a representative sample of most species trapped but not taken for broodstock were sampled for origin, sex, age, and size (stock assessment). All steelhead trapped were sampled.

2.2 Within Hatchery Monitoring

Methods for monitoring hatchery activities are described in Appendix C in Murdoch and Peven (2005). Biological information collected from all spawned adult fish included age at maturity, length at maturity, spawn timing, and fecundity of females. In addition, all fish were checked for tags and females were sampled for disease.

Throughout the rearing period in the hatchery, fish were sampled for growth, health, and survival. Each month, lengths and weights were collected from a sample of fish and rearing density indices were calculated. In addition, fish were examined monthly for health problems following standard fish health monitoring practices for hatcheries. Various life-stage survivals were estimated for each hatchery stock. These estimates were then compared to the "standard" survival rates identified in Table 2.3 to provide insight as to how well the hatchery operations were performing. Failure to achieve a survival standard could indicate a problem with some part of the hatchery program. However, failure to meet a standard may not be indicative of the overall success of the program to meet the goals identified in Section 1.

Table 2.3. Standard life-stage survival rates for fish reared within the Chelan PUD hatchery programs (from Appendix C in Murdoch and Peven 2005).

Life stage	Standard survival rate (%)
Collection-to-spawning (females)	90
Collection-to-spawning (males)	85
Unfertilized egg-to-eyed	92
Unfertilized egg-to-ponding	98
30 d after ponding	97
100 d after ponding	93
Ponding-to-release	90
Transport-to-release	95
Unfertilized egg-to-release	81

Nearly all hatchery fish from each stock were marked (adipose fin clip) or tagged (coded-wire tag or elastomer tag). Different combinations of marks and tags were used depending on the stock. In addition, Chelan PUD personnel PIT tagged about 10,100 juvenile hatchery spring Chinook in June and about 10,100 steelhead from each release site and production cross (HxW production and WxW production) during September through October. They also tagged about 15,100 juvenile sockeye in late June and early July. Several summer Chinook groups were PIT tagged in 2010. Personnel tagged about 10,100 summer Chinook at Ringold Hatchery in August (half of these were for Turtle Rock and the other half for Chelan Net Pens). In addition, about 10,100 summer Chinook from each of three treatment groups (circular pond R1, circular pond R2, and a standard raceway) were tagged in September. Finally, about 5,100 Okanogan summer Chinook and 5,100 Methow summer Chinook were PIT tagged for each respective program. PIT tags will be used to estimate migration timing and survival rates (e.g., smolt-to-adult) outside the hatchery.

Lastly, the size and number of fish released were assessed and compared to programmed production levels. The goal of the program is that numbers released and their sizes should fall within 10% of the programmed targets identified in Table 2.4. However, because of constraints due to run size and proportions of wild and hatchery adults, production levels may not be met every year.

Table 2.4. Targets for fish released from the Chelan PUD hatchery programs; CV = coefficient of variation (from Appendix C in Murdoch and Peven 2005).

Hatchery stock	Release targets	Size targets		
		Fork length (CV)	Weight (g)	Fish/pound
Wenatchee Summer Chinook	864,000	176 (9.0)	45.4	10
Okanogan Summer Chinook	576,000	176 (9.0)	45.4	10
Methow Summer Chinook	400,000	176 (9.0)	45.4	10
Turtle Rock Summer Chinook (yearlings)	200,000	176 (9.0)	45.4	10

Hatchery stock	Release targets	Size targets		
		Fork length (CV)	Weight (g)	Fish/pound
Turtle Rock Summer Chinook (subyearlings)	1,620,000	112 (9.0)	11.4	40
Chiwawa Spring Chinook	672,000	176 (9.0)	37.8	12
Wenatchee Sockeye	200,000	133 (9.0)	22.7	20
Wenatchee Steelhead	400,000	198 (9.0)	75.6	6

2.3 Juvenile Sampling

Juvenile sampling within streams included operation of rotary smolt traps, snorkel observations, and PIT tagging. Methods for sampling juvenile fish are described in Appendix E in Murdoch and Peven (2005).

Smolt traps were located on the Wenatchee River at river km 9.6 at the West Monitor Bridge (Lower Wenatchee Trap) and about 0.5 km downstream from the mouth of Lake Wenatchee (Upper Wenatchee Trap), and in the Chiwawa River about 1 km upstream from the mouth (Chiwawa Trap). All traps operated throughout the smolt migration period. The Chiwawa Trap operated throughout most of the year (March through November), but not during icing or extreme high flow conditions. The following data were collected at each trap site: water temperature, discharge, number and identification of all species captured, degree of smoltification for anadromous fish, presence of marks and tags, size (fork lengths and weights), and scales from steelhead and sockeye salmon smolts. Trap efficiencies at each trap site were estimated by using mark-recapture trials conducted over a wide range of discharges. Linear regression models relating discharge and trap efficiencies were developed to estimate daily trap efficiencies during periods when no mark-recapture trials were conducted. The total number of fish migrating past the trap each day was estimated as the quotient of the daily number of fish captured and the estimated daily trap efficiency. Summing the daily totals resulted in the total emigration estimate.

Snorkel observations were used to estimate the number of juvenile spring Chinook salmon, juvenile rainbow/steelhead, and bull trout within the Chiwawa River Basin. The focus of the study was on juvenile spring Chinook salmon. Sampling followed a stratified random design with proportional allocation of sites among strata. Strata were identified based on unique combinations of geology, land type, valley bottom type, stream state condition, and habitat types. A total of 189 randomly selected sites were surveyed during August (Table 2.5). Counts of fish within each sampling site were adjusted based on detection efficiencies, which were related to water temperature. That is, non-linear models that described relationships between water temperatures and detection efficiencies (Hillman et al. 1992) were used to estimate total numbers of fish within sampling sites. These numbers were then converted to densities by dividing total fish numbers by the wetted surface area and water volume of sample sites. Total numbers within a stratum were estimated as the product of fish densities times the total wetted surface or water volume for the stratum. The sum of fish numbers across strata resulted in the total number of fish within the basin. The calculation of total numbers, densities, and degrees of certainty are fully explained in Hillman and Miller (2004).

Working in collaboration with the Integrated Status and Effectiveness Monitoring Program (ISEMP) funded by NOAA Fisheries and Bonneville Power Administration (BPA), crews PIT tagged juvenile wild Chinook, wild and hatchery steelhead, and wild sockeye salmon throughout the Wenatchee basin. Tags were injected into juvenile fish collected at the Chiwawa Trap, Upper Wenatchee Trap, and the Lower Wenatchee Trap. In addition, fish were collected and tagged in the Chiwawa River upstream from the trap, in Nason Creek, and in the Wenatchee River. The proposed number of wild spring Chinook and steelhead to be tagged at each location is provided in Table 2.6. The goal of this work was to better understand the life-history characteristics of fish in the Wenatchee Basin and to estimate SARs. This in turn improves the ability to detect potential effects of the hatchery program on wild fish.

Table 2.5. Location of strata and numbers of randomly sampled sites within each strata that were sampled in the Chiwawa River Basin in 2010.

Reach/stratum	River kilometers (RKm)	Number of randomly selected sites
	Chiwawa River	
1	0.0-6.1	11
2	6.1-8.9	5
3	8.9-12.7	8
4	12.7-14.3	6
5	14.3-17.4	5
6	17.4-19.0	6
7	19.0-32.2	28
8	32.2-40.9	24
9	40.9-46.4	12
10	46.4-50.1	11
	Phelps Creek	
1	0.0-0.6	3
	Chikamin Creek (includes Minnow Creek)	
1	0.0-1.5	24
	Rock Creek	
1	0.0-1.2	10
	Peven Creek (unnamed stream on USGS map)	
1	0.0-0.1	1
	Big Meadow Creek	
1	0.0-1.6	7
	Alder Creek	
1	0.0-0.1	5
	Brush Creek	
1	0.0-0.1	2
	Clear Creek	
1	0.0-0.1	2

Table 2.6. Number of wild spring Chinook and steelhead proposed for tagging at different locations within the Wenatchee Basin, 2010.

Sampling location	Target sample size	
	Wild spring Chinook	Wild steelhead
Chiwawa Trap	2,500-8,000	500-2,000
Chiwawa River	500-2,000	500-2,000
Upper Wenatchee Trap	500-1,000	50-250
Wenatchee River	500-2,000	500-2,000
Nason Creek	500-2,000	500-2,000
Lower Wenatchee Trap	1,000-2,000	500-2,500
Total	**5,500-17,000**	**2,550-10,750**

Survival rates for various juvenile life-stages were calculated based on estimates of seeding levels (total egg deposition), numbers of parr, numbers of emigrants, and numbers of smolts. Total egg deposition was estimated as the product of the number of redds counted in the basin times the mean fecundity of female spawners. Fecundity was estimated from females collected for broodstock using an electronic egg counter. Numbers of emigrants and smolts were estimated at trapping sites and numbers of parr were estimated using snorkel observations only in the Chiwawa Basin. Survival estimates could not be calculated for some stocks (e.g., summer Chinook) because specific life-stage abundance estimates were lacking.

2.4 Spawning/Carcass Surveys

Methods for conducting carcass and spawning ground surveys are detailed in Appendix F in Murdoch and Peven (2005). Information collected during spawning surveys included spawn timing, redd distribution, and redd abundance. Data collected during carcass surveys included sex, size (fork length and postorbital-to-hypural length), scales for aging[1], degree of egg voidance, DNA samples, and identification of marks or tags. The sampling goal for carcasses was 20% of the spawning population. Crews also conducted snorkel surveys to assess the incidence of precocial fish spawning naturally in streams.

Both redd and carcass surveys were conducted in reaches that encompassed the spawning distribution of most populations. Steelhead surveys were the exception. These surveys were conducted within major spawning areas in the basin and therefore may not capture the entire spawning distribution of the population. Steelhead surveys were conducted during March through June in reaches and index areas described in Table 2.7. Total redd counts were estimated by expanding counts within non-index areas by expansion factors developed within index areas.

---

1 In this report we use two methods of describing age. One is termed the "European Method." This method has two digits, separated by a period. The first digit represents the number of winters the fish spent in freshwater before migrating to the sea. The second digit indicates the number of winters the fish spent in the ocean. For example, a fish designated as 1.2 spent one winter in freshwater and two in the ocean. A fish designated as 0.3 migrated to the ocean in its first year and spent three winters in the ocean. The other method describes the total age of the fish (egg-to-spawning adult, i.e., gravel-to-gravel), so fish demarcated as 0.3 or 1.2 are considered 4-year-olds, from the same brood.

Table 2.7. Description of reaches and index areas surveyed for steelhead redds in the Wenatchee Basin.

Stream	Code	Reach	Index/reference area
Wenatchee River	W2	Sleepy Hollow Br to L. Cashmere Br	Monitor Boat Rmp to Cashmere Boat Rmp
	W6	Leavenworth Br to Icicle Rd Br	Leavenworth Boat Ramp to Icicle Ck
	W8	Tumwater Dam to Tumwater Br	Swift Boat Ramp to Tumwater Br
	W9	Tumwater Br to Chiwawa R	Tumwater Br to Plain
	W10	Chiwawa R to Lk Wenatchee	Chiwawa Pump St. to Lk Wenatchee
Peshastin Creek	P1	Mouth to Camas Cr	Kings Br to Camas Cr
	P2A	Camas Cr to Mouth of Scotty Cr	Ingalls Cr to Ruby Cr
	P2	Camas Cr to Mouth of Scotty Cr	FR7620 to Shaser Cr
Ingalls Creek	D1	Mouth to Trailhead RM 1	Mouth to Trailhead RM 1
	D2	Trailhead to Wilderness Bd RM 1.5	Trailhead to Wilderness Bd RM 1.5
Chiwawa River	C1	Mouth to Grouse Cr	Mouth to Rd 62 Br RM 6.4
	C2	Grouse Cr to Rock Cr	Chikamin Cr to Log Jam
Clear Creek	V1	Mouth to Hwy 22	Mouth to Hwy 22
	V2	Hwy 22 to Lower Culvert RM 2	Hwy 22 to Lower Culvert
Nason Creek	N1	Mouth to Kahler Cr Br	Mouth to Swamp Cr
	N3	Hwy 2 Br to Lower RR Br	Hwy 2 Br to Merrit Br
	N4	Lower RR Br to Whitepine Cr	Rayrock to Church Camp
Icicle River	I1	Mouth to Hatchery	Mouth to Boulder Block
Little Wenatchee	L2	Mouth to Lost Cr	Old Fish Weir to Lost Cr
	L3	Lost Cr to Rainy Cr Br	Lost Cr to Rainy Cr Br
White River	H2	Sears Cr Br to Napeequa R	Riprap Bank to Napeequa R
	H3	Napeequa R to Mouth of Panther Cr	Napeequa R to Grasshopper Meadows
Napeequa River	Q1	Mouth to RM 1	Mouth to RM1

Spring Chinook redd and carcass surveys were conducted during August through September in the Chiwawa River (including Rock and Chikamin creeks), Nason Creek, Icicle Creek, Peshastin Creek (including Ingalls Creek), upper Wenatchee River, Little Wenatchee River, and the White River (including the Napeequa River and Panther Creek). Survey reaches for spring Chinook are described in Table 2.8.

Table 2.8. Description of reaches surveyed for spring Chinook redds and carcasses in the Wenatchee Basin.

Stream	Code	Reach	River mile (RM)
Chiwawa River	C1	Mouth to Grouse Creek	0.0-11.7
	C2	Grouse Creek to Rock Creek	11.7-19.3
	C3	Rock Creek to Schaefer Creek	19.3-22.4
	C4	Schaefer Creek to Atkinson Flats	22.4-25.6
	C5	Atkinson Flats to Maple Creek	25.6-27.0
	C6	Maple Creek to Trinity	27.0-30.3
Rock Creek	R1	Mouth to End	0.0-0.5
Chikamin Creek	K1	Mouth to End	0.0-0.5
Nason Creek	N1	Mouth to Kahler Creek Bridge	0.0-3.9
	N2	Kahler Creek Bridge to Hwy 2 Bridge	3.9-8.3
	N3	Hwy 2 Bridge to Lower RR Bridge	8.3-13.2
	N4	Lower RR Bridge to Whitepine Creek	13.2-15.4
Little Wenatchee River	L2	Old Fish Weir to Lost Creek	2.7-5.2
	L3	Lost Creek to Rainy Creek	5.2-9.2
	L4	Rainy Creek to Falls	9.2-Falls
White River	H2	Sears Creek Bridge to Napeequa River	6.4-11.0
	H3	Napeequa River to Grasshopper Meadows	11.0-12.9
Napeequa River	Q1	Mouth to End	0.0-1.0
Panther Creek	T1	Mouth to End	0.0-0.7
Wenatchee River	W8	Tumwater Dam to Tumwater Bridge	30.9-35.6
	W9	Tumwater Bridge to Chiwawa River	35.6-48.4
	W10	Chiwawa River to Lake Wenatchee	48.4-54.2
Icicle Creek	I1	Mouth to Boulder Block	0.0-4.0
Peshastin Creek	P1	Mouth to Camas Creek	0.0-5.9
	P2	Camas Creek to Mouth of Scotty Creek	5.9-16.3
Ingalls Creek	D1	Mouth to Trailhead	0.0-1.0

Surveys for live sockeye and carcass were conducted during August through October in the White, Napeequa, and Little Wenatchee rivers. No sockeye redds were counted in 2010. Live fish counts were used to estimate spawning escapements using the area-under-the-curve (AUC) method.

Table 2.9. Description of reaches surveyed for sockeye salmon carcasses and live fish in the Wenatchee Basin.

Stream	Code	Reach	River mile (RM)
Little Wenatchee River	L1	Mouth to Old Fish Weir	0.0-2.7
	L2	Old Fish Weir to Lost Creek	2.7-5.2
	L3	Lost Creek to Rainy Creek	5.2-9.2
White River	H1	Mouth to Sears Creek Bridge	0.0-6.4
	H2	Sears Creek Bridge to Napeequa River	6.4-11.0
	H3	Napeequa River to Grasshopper Meadows	11.0-12.9
Napeequa River	Q1	Mouth to End	0.0-1.0

Wenatchee summer Chinook redd and carcass surveys were conducted during September through November within ten reaches on the Wenatchee River (Table 2.10). Peak redd counts, map redd counts, and naïve counts were estimated in the Wenatchee River. Map redd counts and naïve counts were only conducted within index areas, not throughout the entire river. Two different methods were used to estimate total redd counts for the entire river. The first method used map counts to expand peak counts. The second relied on naïve counts to expand redd numbers in reaches that did not have map counts. These two approaches are described in Appendix F in Murdoch and Peven (2005).

Table 2.10. Description of reaches and index areas surveyed for summer Chinook redds in the Wenatchee Basin.

Code	Reach	River mile	Index/reference area (RM)
W1	Mouth to Sleepy Hollow Br	0.0-3.3	River Bend to Sleepy Hollow Br (1.7-3.3)
W2	Sleepy Hollow Br to L. Cashmere Br	3.3-9.5	L. Cashmere Br to Old Monitor Br (7.1-9.5)
W3	L. Cashmere Br to Dryden Dam	9.5-17.8	Williams Canyon to Dryden Dam (15.5-17.8)
W4	Dryden Dam to Peshastin Br	17.8-20.0	Dryden Dam to Peshastin Br (17.8-20.0)
W5	Peshastin Br to Leavenworth Br	20.0-23.9	Irrigation Flume to Leavenworth Br (22.8-23.9)
W6	Leavenworth Br to Icicle Rd Br	23.9-26.4	Icicle to Boat Takeout (24.5-25.6)
W7	Icicle Rd Br to Tumwater Dam	26.4-30.9	Icicle Br to Penstock Br (26.4-28.7)
W8	Tumwater Dam to Tumwater Br	30.9-35.6	Swiftwater Campgd to Tumwater Br (33.5-35.6)
W9	Tumwater Br to Chiwawa River	35.6-47.9	Swing Pool to Railroad Tunnel (36.7-39.3)
W10	Chiwawa River to Lake Wenatchee	47.9-54.2	Swamp to Bridge (52.7-53.6)

Summer Chinook redd and carcass surveys were also conducted in the Methow, Okanogan, Similkameen, and Chelan rivers during September through November. Total (map) redd counts were conducted in these rivers. Table 2.11 describes the survey reaches in these rivers.

Table 2.11. Description of reaches surveyed for summer Chinook redds and carcasses on the Methow, Okanogan, and Similkameen rivers.

Stream	Code	Reach	River mile (RM)
Methow River	M1	Mouth to Methow Bridge	0.0-14.8
	M2	Methow Bridge to Carlton Bridge	14.8-27.2
	M3	Carlton Bridge to Twisp Bridge	27.2-39.6
	M4	Twisp Bridge to MVID	39.6-44.9
	M5	MVID to Winthrop Bridge	44.9-49.8
	M6	Winthrop Bridge to Hatchery Dam	49.8-51.6
Okanogan River	O1	Mouth to Mallot Bridge	0.0-16.9
	O2	Mallot Bridge to Okanogan Bridge	16.9-26.1
	O3	Okanogan Bridge to Omak Bridge	26.1-30.7
	O4	Omak Bridge to Riverside Bridge	30.7-40.7
	O5	Riverside Bridge to Tonasket Bridge	40.7-56.8
	O6	Tonasket Bridge to Zosel Dam	56.8-77.4
Similkameen River	S1	Driscoll Channel to Oroville Bridge	0.0-1.8
	S2	Oroville Bridge to Enloe Dam	1.8-5.7

Except for sockeye, total spawning escapements for each population were estimated as the product of total number of redds times the ratio of fish per redd for a specific stock. Fish per redd ratios were estimated as the ratio of males to females sampled at broodstock collection sites and monitoring sites. Total spawning escapement for sockeye salmon was estimated using the AUC approach (where escapement = [AUC/redd residence time] x observer efficiency). This method relied on weekly counts of live sockeye and assumed a redd residence time of 11 days (from Hyatt et al. 2006) and an observer efficiency of 100%.[2] In addition, sockeye escapement was estimated using mark-recapture methods. Adult sockeye were PIT tagged at Tumwater Dam and Bonneville Dam[3] and detected in the Little Wenatchee and White rivers with stationary PIT-tag interrogators.

During carcass surveys for summer Chinook, crews collected tissue samples for genetic analysis. Tissue was collected from the operculum of wild and hatchery carcasses (target of 144 wild and 144 hatchery fish). Sampling within a population was proportional to the distribution of carcasses across survey reaches. That is, samples were collected in all reaches but the number collected within a given reach was proportional to the density of carcasses within that reach. In addition, tissue samples were collected from Wenatchee spring Chinook as part of the spring Chinook reproductive study. Methods for analyzing samples are described in Appendix H in Murdoch and Peven (2005).

Derived metrics calculated from carcass surveys, broodstock sampling, stock assessments, and harvest records included proportion of hatchery spawners, stray rates, age-at-maturity, length-at-age, smolt-to-adult survival (SAR), hatchery replacement rates (HRR), exploitation rates,

[2] It is very unlikely that observer efficiency is 100%, especially within the White River.

[3] Adult sockeye that were tagged at Bonneville Dam and detected at Tumwater Dam were included in the mark-recapture analyses.

harvest rates, and natural replacement rates (NRR). The expected SARs and HRRs for different stocks raised in the Chelan PUD hatchery programs are provided in Table 2.12. Methods for calculating these variables are described in Appendices D, F, and G in Murdoch and Peven (2005) and in "White Papers" developed by the Hatchery Evaluation Technical Team (HETT).

Table 2.12. Expected smolt-to-adult (SAR) and hatchery replacement rates (HRR) for stocks raised in the Chelan PUD Hatchery Programs (from Table 6 in Appendix D in Murdoch and Peven 2005).

Program	Number of broodstock	Smolts released	SAR	Adult equivalents	Number of smolts/adult	HRR
Chiwawa Spring Chinook	379	672,000	0.003	2,016	333	5.3
Wenatchee Summer Chinook	492	864,000	0.003	2,592	333	5.3
Similkameen Summer Chinook	328	576,000	0.003	1,728	333	5.3
Methow Summer Chinook	228	400,000	0.003	1,200	333	5.3
Wenatchee Sockeye	260	200,000	0.007	1,400	143	5.4
Wenatchee Steelhead	208	400,000	0.010	4,000	100	19.2

Derived data that rely on CWTs (e.g., HRR, SAR, stray rates, etc.) are five or more years behind release information because of the lag time for returning adult fish to enter the fishery and the processing of tags. Consequently, complete information on rates and ratios based on CWTs is generally only available for years prior to 2004. In addition, some methods for calculating derived variables are still being developed by the HETT. Therefore, estimates of derived data in this report are subject to change after the HETT and Hatchery Committee decide on standard methods for calculating derived data.

SECTION 3: WENATCHEE STEELHEAD

3.1 Broodstock Sampling

This section focuses on results from sampling 2009 and 2010 brood years of Wenatchee steelhead, which were collected at Dryden and Tumwater dams. The 2009 brood begins the tracking of the life cycle of steelhead released in 2010. The 2010 brood is included because juveniles from this brood are still maintained within the hatchery.

Origin of Broodstock

A total of 208 Wenatchee steelhead from the 2008 return (2009 brood) were collected at Dryden and Tumwater dams (Table 3.1). About 49% of these were natural-origin (adipose fin present, no CWT, and no elastomer tags) fish and the remaining 51% were hatchery-origin (elastomer tagged and/or adipose fin absent) adults. Origin was determined by analyzing scales and/or otoliths. The total number of steelhead spawned from the 2009 brood was 159 adults (54% natural-origin and 46% hatchery-origin).

A total of 211 steelhead were collected from the 2009 return (2010 brood) at Dryden and Tumwater dams; 106 (50%) natural-origin (adipose fin present, no CWT, and no elastomer tags) and 105 (50%) hatchery-origin (elastomer tagged and/or adipose fin absent) adults. A total of 171 steelhead were spawned; 56% were natural-origin fish and 44% were hatchery fish (Table 3.1). Origin was confirmed by sampling scales and/or otoliths.

Table 3.1. Numbers of wild and hatchery steelhead collected for broodstock, numbers that died before spawning, and numbers of steelhead spawned, 1998-2010. Unknown origin fish (i.e., undetermined by scale analysis, no elastomer, CWT, or fin clips, and no additional hatchery marks) were considered naturally produced. Mortality includes fish that died of natural causes typically near the end of spawning and were not needed for the program or were immature fish killed at spawning.

Brood year	Wild steelhead					Hatchery steelhead					Total number spawned
	Number collected	Prespawn loss	Mortality	Number spawned	Number released	Number collected	Prespawn loss	Mortality	Number spawned	Number released	
1998	35	0	0	35	0	43	4	2	37	0	72
1999	58	5	1	52	0	67	1	2	64	0	116
2000	39	2	1	36	0	101	9	12	60	20	96
2001	64	5	8	51	0	114	5	6	103	0	154
2002	99	0	1	96	2	113	1	0	64	48	160
2003	63	10	4	49	0	92	2	0	90	0	139
2004	85	3	0	75	7	132	1	0	61	70	136
2005	95	8	0	87	0	114	7	1	104	2	191
2006	101	5	0	93	3	98	0	0	69	29	162
2007	79	0	2	76	1	97	0	14	58	25	134
2008	104	0	3	77	22	107	0	28	54	25	131
2009	101	2	0	86	13	107	1	4	73	29	159
2010	106	1	1	96	8	105	2	23	75	5	171
Average	***79***	***3***	***2***	***70***	***4***	***99***	***3***	***7***	***70***	***19***	***140***

Age/Length Data

Broodstock ages were determined from examination of scales and/or otoliths. For the 2009 return, both natural-origin and hatchery steelhead consisted primarily of 2-salt adults (Table 3.2). A small proportion (2.4%) of the 2009 return, natural-origin steelhead were 3-salt adults. For the 2010 return, both hatchery and natural-origin steelhead consisted primarily of 1-salt adults (Table 3.2).

Table 3.2. Percent of hatchery and wild steelhead of different ages (saltwater ages) collected from broodstock, 1998-2010.

Return year	Origin	Saltwater age		
		1	2	3
1998	Wild	39.4	60.6	0.0
	Hatchery	20.9	79.1	0.0
1999	Wild	50.0	48.3	1.7
	Hatchery	81.8	18.2	0.0
2000	Wild	56.4	43.6	0.0
	Hatchery	67.9	32.1	0.0
2001	Wild	51.7	48.3	0.0
	Hatchery	14.9	85.1	0.0
2002	Wild	55.6	44.4	0.0
	Hatchery	94.6	5.4	0.0
2003	Wild	13.1	85.3	1.6
	Hatchery	29.4	70.6	0.0
2004	Wild	94.8	5.2	0.0
	Hatchery	95.2	4.8	0.0
2005	Wild	22.1	77.9	0.0
	Hatchery	20.5	79.5	0.0
2006	Wild	28.7	71.3	0.0
	Hatchery	60.3	39.7	0.0
2007	Wild	40.3	59.3	0.0
	Hatchery	62.1	37.9	0.0
2008	Wild	65.4	33.7	0.9
	Hatchery	88.8	11.2	0.0
2009	Wild	39.8	57.8	2.4
	Hatchery	23.4	76.6	0.0
2010	Wild	65.2	33.7	1.1
	Hatchery	76.5	23.5	0.0
Average	***Wild***	***47.9***	***51.5***	***0.6***
	Hatchery	***56.6***	***43.4***	***0.0***

There was little difference between mean lengths of hatchery and natural-origin steelhead for both the 2009 and 2010 return years (Table 3.3). Natural-origin fish were on average <1 to 3 cm larger than hatchery-origin fish of the same age.

Table 3.3. Mean fork length (cm) at age (saltwater ages) of hatchery and wild steelhead collected from broodstock, 1998-2010; N = sample size and SD = 1 standard deviation.

Return year	Origin	Steelhead fork length (cm)								
		1-Salt			2-Salt			3-Salt		
		Mean	N	SD	Mean	N	SD	Mean	N	SD
1998	Wild	63	15	4	79	20	5	-	0	-
	Hatchery	61	9	4	73	34	4	-	0	-
1999	Wild	65	29	5	74	28	5	77	1	-
	Hatchery	62	54	4	73	12	4	-	0	-
2000	Wild	64	22	3	74	17	5	-	0	-
	Hatchery	60	57	3	71	27	4	-	0	-
2001	Wild	61	33	6	77	31	5	-	0	-
	Hatchery	62	17	4	72	97	4	-	0	-
2002	Wild	64	55	4	77	44	4	-	0	-
	Hatchery	63	106	4	73	6	4	-	0	-
2003	Wild	69	8	6	77	52	5	91	1	-
	Hatchery	66	27	4	75	65	4	-	0	-
2004	Wild	63	73	6	78	4	2	-	0	-
	Hatchery	61	59	3	73	3	1	-	0	-
2005	Wild	59	21	4	74	74	5	-	0	-
	Hatchery	59	23	4	72	89	4	-	0	-
2006	Wild	63	27	5	75	67	6	-	0	-
	Hatchery	61	41	4	72	27	5	-	0	-
2007	Wild	64	31	6	76	46	5	-	0	-
	Hatchery	60	60	4	71	36	5	-	0	-
2008	Wild	64	68	4	77	35	4	80	1	-
	Hatchery	60	95	4	72	12	2	-	0	-
2009	Wild	65	33	5	76	48	6	81	2	0
	Hatchery	63	18	4	75	59	5	-	-	-
2010	Wild	64	60	5	74	31	5	76	1	-
	Hatchery	61	53	5	73	23	5	-	-	-

Sex Ratios

Male steelhead in the 2009 return made up about 47% of the adults collected, resulting in an overall male to female ratio of 0.89:1.00 (Table 3.4). For the 2010 return, males made up about 53% of the adults collected, resulting in an overall male to female ratio of 1.11:1.00. On average

(1998-2010), the sex ratio is slightly less than the 1:1 ratio assumed in the broodstock protocol (Table 3.4).

Table 3.4. Numbers of male and female wild and hatchery steelhead collected for broodstock, 1998-2010. Ratios of males to females are also provided.

Return year	Number of wild steelhead			Number of hatchery steelhead			Total M/F ratio
	Males (M)	Females (F)	M/F	Males (M)	Females (F)	M/F	
1998	13	22	0.59:1.00	15	28	0.54:1.00	0.56:1.00
1999	22	36	0.61:1.00	35	32	1.09:1.00	0.84:1.00
2000	18	21	0.86:1.00	60	41	1.46:1.00	1.26:1.00
2001	38	26	1.46:1.00	40	74	0.54:1.00	0.78:1.00
2002	32	67	0.48:1.00	81	32	2.53:1.00	1.14:1.00
2003	19	44	0.43:1.00	44	48	0.92:1.00	0.68:1.0
2004	43	42	1.02:1.00	90	42	2.14:1.00	1.58:1.00
2005	36	59	0.61:1.00	46	68	0.68:1.00	0.65:1.00
2006	38	63	0.60:1.00	47	51	0.92:1.00	0.75:1.00
2007	36	43	0.84:1.00	49	48	1.02:1.00	0.93:1.00
2008	61	43	1.42:1.00	68	39	1.74:1.00	1.57:1.00
2009	44	57	0.77:1.00	54	53	1.02:1.00	0.89:1.00
2010	49	57	0.86:1.00	62	43	1.44:1.00	1.11:1.00
Total	***449***	***580***	***0.77:1.00***	***691***	***599***	***1.15:1.00***	***0.97:1.00***

Fecundity

Fecundities for Wenatchee steelhead returning in 2009 and 2010 averaged 6,408 and 5,442 eggs per female, respectively, which were similar to the overall average (Table 3.5). Mean fecundities for the 2009 and 2010 returns were at or greater than the 5,400 eggs per female assumed in the broodstock protocol.

Table 3.5. Mean fecundity of wild, hatchery, and all female steelhead collected for broodstock, 1998-2010.

Return year	Mean fecundity		
	Wild	Hatchery	Total
1998	6,202	5,558	5,924
1999	5,691	5,186	5,424
2000	5,858	5,729	5,781
2001	5,951	6,359	6,270
2002	5,776	5,262	5,626
2003	6,561	6,666	6,621
2004	5,118	5,353	5,238
2005	5,545	6,061	5,832
2006	5,688	5,251	5,492
2007	5,840	5,485	5,660

Return year	Mean fecundity		
	Wild	Hatchery	Total
2008	5,693	5,153	5,433
2009	6,199	6,586	6,408
2010	5,458	5,423	5,442
Average	***5,814***	***5,698***	***5,781***

3.2 Hatchery Rearing

Rearing History

Number of eggs taken

Based on the unfertilized egg-to-release survival standard of 81%, a total of 493,827 eggs are required to meet the program release goal of 400,000 smolts. Between 1998 and 2010, the egg take goal was reached 54% of the time (Table 3.6).

Table 3.6. Numbers of eggs taken from steelhead broodstock, 1998-2010.

Brood year	Number of eggs taken
1998	224,315
1999	303,083
2000	280,872
2001	549,464
2002	503,030
2003	532,708
2004	408,538
2005	672,667
2006	546,382
2007	462,662
2008	439,980
2009	633,229
2010	499,499
Average	***465,879***

Number of acclimation days

Juvenile steelhead were transferred from Chelan FH to Turtle Rock FH in December 2009 and from Eastbank FH to Turtle Rock FH in January 2010. At Turtle Rock FH, juvenile steelhead were reared on Columbia River water (range, 114-153 d) before being trucked and released into the Wenatchee River and tributaries. In March 2010, a small group of early HxW steelhead were transferred to Black Bird Pond near Leavenworth for acclimation on Wenatchee River water. Fish were acclimated for 38 d before a volitional release was initiated on 24 April.

Acclimation of Wenatchee juvenile steelhead has occurred on occasion in the Chiwawa Ponds when space is available. At Chiwawa Ponds, steelhead were reared under the same water source as spring Chinook (Chiwawa and Wenatchee River water). Typically, Wenatchee steelhead are reared on Columbia River water from January through April before being trucked and released into the Wenatchee Basin (Table 3.7).

Table 3.7. Water source and mean acclimation period for Wenatchee steelhead, brood years 1998-2009.

Brood year	Release year	Parental origin	Water source	Number of Days
1998	1999	H x H	Wenatchee/Chiwawa	36
		H x W	Wenatchee/Chiwawa	36
		W x W	Wenatchee/Chiwawa	36
1999	2000	H x H	Wenatchee/Chiwawa	138
		H x W	Wenatchee/Chiwawa	138
		W x W	Wenatchee/Chiwawa	138
		H x W	Eastbank	0
		W x W	Eastbank	0
2000	2001	H x H	Wenatchee/Chiwawa	122
		H x W	Wenatchee/Chiwawa	122
		H x W	Wenatchee/Chiwawa	122
		W x W	Wenatchee/Chiwawa	122
2001	2002	H x H	Columbia	92
		H x H	Wenatchee/Chiwawa	63
		H x W	Columbia	92
		H x W	Wenatchee/Chiwawa	63
		W x W	Columbia	153
2002	2003	H x H	Columbia	98
		H x W	Columbia	98
		W x W	Columbia	117
2003	2004	H x H	Columbia	88
		H x W	Wenatchee/Chiwawa	84
		W x W	Columbia	148
2004	2005	H x H	Columbia	160
		H x W	Columbia	160
		W x W	Columbia	160
2005	2006	H x H	Columbia	116
		H x W	Columbia	113
		W x W	Columbia	141
2006	2007	Early H x W	Columbia	111
		Late H x W	Columbia	112

Brood year	Release year	Parental origin	Water source	Number of Days
		W x W	Columbia	148
2007	2008	Early H x W	Columbia	94-95
		Late H x W	Columbia	91-93
		W x W	Columbia	138
2008	2009	Early H x W	Columbia	120-121
		Early H x W	Columbia/Wenatchee	120-121/28-95
		Late H x W	Columbia	114-115
		W x W	Columbia	152-153
2009	2010	Early H x W	Columbia	93-94
		Early H x W	Columbia/Wenatchee	99-111
		Early H x W	Wenatchee	31-129
		Late H x W	Columbia	84-87
		W x W	Columbia/Nason	118-120/28

Release Information

Numbers released

The release of 2009 brood Wenatchee steelhead achieved 121% of the 400,000 target goal with about 484,772 fish released into the Wenatchee and Chiwawa rivers and Nason Creek (Table 3.8). Distribution of juvenile steelhead released in each of the three basins was determined by the mean proportion of steelhead redds in each basin. About 19.9% and 22.9% of the steelhead were released in Nason Creek and the Chiwawa River, respectively. The balance of the program was split between the Wenatchee River downstream from Tumwater Dam (10.4%) and the Wenatchee River upstream from the dam (36.8%).

Table 3.8. Numbers of steelhead smolts released from the hatchery, brood years 1998-2009. The release target for steelhead is 400,000 smolts.

Brood year	Release year	Number of smolts
1998	1999	172,078
1999	2000	175,701
2000	2001	184,639
2001	2002	335,933
2002	2003	302,060
2003	2004	374,867
2004	2005	294,114
2005	2006	452,184
2006	2007	299,937
2007	2008	306,690
2008	2009	327,143
2009	2010	484,772

Average	***309,177***

Numbers elastomer tagged

Wenatchee hatchery steelhead from the 2009 brood were marked with elastomer tags in the clear tissue posterior of the eye to denote parental origin. About 48% of the juveniles released were also adipose fin clipped (Table 9).

Table 3.9. Release location and marking scheme for the 1998-2009 brood Wenatchee steelhead.

Brood year	Release location	Parental origin	Proportion Ad-clip	VIE color/side	Tag rate	Number released
1998	Chiwawa River	H x H	0.000	Red Left	0.994	52,765
	Chiwawa River	H x W	0.000	Green Left	0.990	37,013
	Chiwawa River	W x W	0.000	Orange Left	0.827	82,300
1999	Wenatchee River	H x H	0.000	Green Left	0.911	45,347
	Wenatchee River	H x W	0.000	Orange Left	0.927	30,713
	Chiwawa River	H x H	0.000	Red Right	0.936	25,622
	Chiwawa River	H x W	0.000	Green Right	0.936	43,379
	Chiwawa River	W x W	0.000	Orange Right	0.936	30,600
2000	Chiwawa River	H x H	0.000	Red Left	0.963	33,417
	Chiwawa River	H x W	0.000	Green Left	0.963	57,716
	Chiwawa River	H x W	0.000	Green Right	0.949	48,029
	Chiwawa River	W x W	0.000	Orange Right	0.949	45,477
2001	Nason Creek	H x W	0.000	Green Right	0.934	75,276
	Nason Creek	W x W	0.000	Orange Right	0.934	48,115
	Chiwawa River	H x W	0.000	Green Left	0.895	92,487
	Chiwawa River	H x H	0.000	Red Left	0.895	120,055
2002	Chiwawa River	H x H	0.000	Red Left	0.920	156,145
	Chiwawa River	H x W	0.000	Green Left	0.928	33,528
	Nason Creek	W x W	0.000	Orange Right	0.928	112,387
2003	Wenatchee River	H x H	0.000	Red Left	0.968	117,663
	Chiwawa River	H x W	0.000	Green Left	0.927	191,796
	Nason Creek	W x W	0.000	Orange Right	0.962	65,408
2004	Wenatchee River	H x H	0.500	Red Left	0.804	39,636
	Chiwawa River	H x W	0.000	Green Left	0.977	153,959
	Nason Creek	W x W	0.000	Pink Right	0.940	100,519
2005	Wenatchee River	H x H	1.000	Red Left	0.983	104,552

Brood year	Release location	Parental origin	Proportion Ad-clip	VIE color/side	Tag rate	Number released
	Wenatchee River	H x W	0.616	Green Left	0.979	190,319
	Chiwawa River	H x W	0.616	Green Left	0.979	18,634
	Chiwawa River	W x W	0.000	Pink Right	0.969	14,124
	Nason Creek	W x W	0.000	Pink Right	0.969	124,555
2006	Wenatchee River	H x W (early)	1.000	Green Right	0.918	66,022
	Wenatchee River	H x W (late)	0.671	Green Left	0.935	92,176
	Chiwawa River	H x W (late)	0.671	Green Left	0.935	41,240
	Chiwawa River	W x W	0.000	Pink Right	0.945	7,500
	Nason Creek	W x W	0.000	Pink Right	0.945	92,999
2007	Wenatchee River	H x W (early)	0.967	Green Right	0.950	64,310
	Wenatchee River	H x W (late)	0.586	Green Left	0.951	97,549
	Chiwawa River	H x W (late)	0.586	Green Left	0.951	43,011
	Chiwawa River	W x W	0.000	Pink Right	0.952	7,026
	Nason Creek	W x W	0.000	Pink Right	0.952	94,794
2008	Blackbird Pond	HxW (early)	0.917	Green Right	0.910	49,878
	Wenatchee River	H x W (early)	0.917	Green Right	0.910	48,624
	Wenatchee River	H x W (late)	0.595	Green Left	0.908	74,848
	Chiwawa River	H x W (late)	0.595	Green Left	0.908	25,835
	Chiwawa River	W x W	0.000	Pink Right	0.904	25,778
	Nason Creek	W x W	0.000	Pink Right	0.904	102,170
2009	Blackbird Pond	H x W (early)	0.969	Green Right	0.934	50,248
	Wenatchee River	H x W (early)	0.969	Green Right	0.934	105,239
	Wenatchee River	H x W (late)	0.973	Green Left	0.975	27,612
	Wenatchee River	H x W (late)	0.000	Green Left	0.975	45,435
	Chiwawa River	H x W (early)	0.969	Green Right	0.934	23,835
	Chiwawa River	H x W (late)	0.973	Green Left	0.975	33,047
	Chiwawa River	H x W (late)	0.000	Green Left	0.975	54,381
	Nason	W x W	0.000	Pink Right	0.979	145,029

Numbers PIT tagged

Table 3.10 summarizes the number of hatchery steelhead of different parental origins that have been PIT-tagged and released into the Wenatchee Basin.

Table 3.10. Summary of PIT-tagging activities for Wenatchee hatchery steelhead, brood years 2006-2009.

Brood year	Release location	Parental origin	Number of fish tagged	Number of tagged fish that died	Number of tags shed	Number of tagged fish released
2006	Wenatchee River	H x W (early)	10,035	479	24	9,533
	Wenatchee/Chiwawa rivers	H x W (late)	10,031	922	20	9,089
	Chiwawa River/Nason Creek	W x W	10,019	152	352	9,515
2007	Wenatchee River	H x W (early)	10,052	22	10	9,820
	Wenatchee/Chiwawa rivers	H x W (late)	10,063	73	78	9,912
	Chiwawa River/Nason Creek	W x W	10,051	55	1	9,982
2008	Wenatchee River	H x W (early)	10,101	59	15	10,027
	Wenatchee/Chiwawa rivers	H x W (late)	10,104	106	17	9,981
	Chiwawa River/Nason Creek	W x W	10,101	159	80	9,862
2009	Wenatchee/Chiwawa rivers	H x W (early)	10,114	574	11	9,529
	Wenatchee (Blackbird)	H x W (early)	8,100	0	0	8,100
	Wenatchee/Chiwawa rivers	H x W (late)	10,115	271	11	9,833
	Chiwawa pilot	H x W (early)	10,107	532	103	9,472
	Chiwawa River/Nason Creek	W x W	10,101	38	3	10,060

2010 Brood Wenatchee (Turtle Rock) Summer Steelhead (H x H)—A total of 10,100 H x H steelhead were PIT tagged at the Eastbank Hatchery during 11-13 October 2010. These fish were not fed during tagging or for two-three days before or after tagging. These fish averaged 87 mm in length and 7.0 g at time of tagging.

At the end of January 2011, a total of 557 H x H steelhead had died (primarily because of Bacterial Cold Water Disease) and 21 others had shed their tags, leaving 9,522 tagged steelhead alive at the end of the month.

2010 Brood Wenatchee (Chelan Falls) Summer Steelhead (W x W)—A total of 10,100 W x W steelhead were PIT tagged at the Chelan Falls Hatchery during 1-3 January 2010. These fish were not fed during tagging or for two-three days before or after tagging. These fish averaged 124 mm in length and 21.0 g at time of tagging.

At the end of January 2011, a total of 202 W x W steelhead had died. None had shed their tags. This left 9,898 tagged steelhead alive at the end of the month.

2010 Brood Wenatchee (Blackbird Pond) Summer Steelhead—A total of 10,101 steelhead were PIT tagged at the Eastbank Hatchery during 4-6 October 2010. These fish were not fed during tagging or for two-three days before or after tagging. These fish averaged 82 mm in length and 6.2 g at time of tagging.

At the end of January 2011, a total of 214 steelhead had died (primarily because of Bacterial Cold Water Disease) and eight others had shed their tags, leaving 9,879 tagged steelhead alive at the end of the month.

2010 Brood Wenatchee (Chiwawa Pond) Summer Steelhead (H x H)—A total of 10,100 H x H steelhead were PIT tagged at the Eastbank Hatchery during 27-30 September 2010. These fish were not fed during tagging or for two-three days before or after tagging. These fish averaged 80 mm in length and 5.8 g at time of tagging.

At the end of January 2011, a total of 42 H x H steelhead had died and 28 others had shed their tags, leaving 10,030 tagged steelhead alive at the end of the month.

Fish size and condition at release

With the exception of the Blackbird Pond, Chiwawa Ponds, and Rolfhing Pond release, all 2009 brood steelhead were trucked and released as yearling smolts in May of 2010. The other three groups mentioned above were released volitionally beginning 24 April. All three parental groups did not meet the length target and only the early H x W group met or exceeded the weight target. All groups except for the early H x W group met the fish per pound release target. All three groups exceeded the target for coefficient of variation for fork length (Table 3.11).

Table 3.11. Mean lengths (FL, mm), weight (g and fish/pound), and coefficient of variation (CV) of steelhead smolts released from the hatchery, brood years 1998-2009. Size targets are provided in the last row of the table.

Brood year	Release year	Parental origin	Fork length (mm)		Mean weight	
			Mean	CV	Grams (g)	Fish/pound
1998	1999	H x H	201	11.1	92.3	5
		H x W	190	12.8	76.9	6
		W x W	173	12.0	55.3	8
1999	2000	H x H	181	8.9	70.6	6
		H x W	187	7.2	75.3	6
		W x W	184	11.3	71.5	6
2000	2001	H x H	218	15.2	122.4	4
		H x W	209	10.6	107.5	4
		W x W	205	10.7	100.9	5
2001	2002	H x H	179	17.4	67.0	7
		H x W	192	15.6	82.8	6
		W x W	206	11.6	102.6	4
2002	2003	H x H	194	13.1	83.0	6
		H x W	191	13.0	77.4	6
		W x W	180	19.1	70.3	7
2003	2004	H x H	191	14.4	73.1	6
		H x W	199	12.9	83.9	5
		W x W	200	11.1	90.1	5

Brood year	Release year	Parental origin	Fork length (mm)		Mean weight	
			Mean	CV	Grams (g)	Fish/pound
2004	2005	H x H	204	11.3	87.2	6
		H x W	202	13.5	71.9	5
		W x W	198	12.4	76.6	6
2005	2006	H x H	215	12.6	116.6	4
		H x W	198	11.8	86.3	5
		W x W	189	15.4	55.3	6
2006	2007	H x H (early)	213	12.1	109.6	4
		H x W (late)	186	11.8	68.3	7
		W x W	178	11.1	58.6	8
2007	2008	H x W (early)	192	17.4	77.1	6
		H x W (late)	179	19.3	63.8	7
		W x W	183	12.3	62.8	7
2008	2009	H x W (early)	184	11.6	68.0	7
		H x W (late)	186	11.6	73.5	6
		W x W	181	13.0	59.7	8
2009	2010	H x W (early)	197	11.3	84.2	5
		H x W (late)	192	11.1	72.7	6
		W x W	190	9.6	70.5	6
Targets			***198***	***9.0***	***75.6***	***6***

Survival Estimates

Overall survival of Wenatchee steelhead from green (unfertilized) egg to release was slightly below the standard set for the program. This is due in part because of poor green egg-to-eyed egg, eyed egg-to-ponding, and the 30 day after ponding survivals (Table 3.12). The Wenatchee steelhead program, from its inception, has experienced highly variable fertilization rates. It is unknown at this time what mechanisms may be influencing stock performance at these stages.

Table 3.12. Hatchery life-stage survival rates (%) for steelhead, brood years 1998-2009. Survival standards or targets are provided in the last row of the table.

Brood year	Collection to spawning		Unfertilized egg-eyed	Eyed egg-ponding	30 d after ponding	100 d after ponding	Ponding to release	Transport to release	Unfertilized egg-release
	Female	Male							
1998	92.0	100.0	85.5	91.7	99.2	98.8	97.8	99.9	76.7
1999	91.2	100.0	66.9	93.0	95.9	94.9	93.1	99.7	58.0
2000	83.9	96.2	77.6	86.7	99.3	98.9	97.7	99.5	65.7
2001	90.0	100.0	73.0	91.8	99.1	97.8	91.3	99.7	61.1
2002	99.0	100.0	69.2	93.1	95.9	94.4	89.6	89.6	60.0

Brood year	Collection to spawning		Unfertilized egg-eyed	Eyed egg-ponding	30 d after ponding	100 d after ponding	Ponding to release	Transport to release	Unfertilized egg-release
	Female	Male							
2003	87.0	96.8	86.3	83.8	97.2	94.8	97.6	85.3	70.4
2004	97.6	98.5	83.4	93.7	97.8	94.1	92.2	99.9	72.0
2005	91.3	95.1	81.3	92.1	95.6	91.8	89.7	99.6	67.2
2006	99.1	95.3	73.2	85.4	95.4	94.6	87.8	98.5	54.9
2007	100.0	100.0	80.3	92.0	95.7	92.7	89.8	99.1	66.3
2008	100.0	100.0	87.1	88.4	99.0	97.4	96.6	99.5	74.4
2009	97.3	100.0	89.0	97.2	96.0	95.2	88.6	96.6	76.6
Standard	***90.0***	***85.0***	***92.0***	***98.0***	***97.0***	***93.0***	***90.0***	***95.0***	***81.0***

3.3 Disease Monitoring

Rearing of the 2009 brood Wenatchee summer steelhead was typical to previous years with fish being held on Chelan spring water, Eastbank well water, and Columbia River water before being released directly into Nason Creek and the Chiwawa and Wenatchee rivers. No significant disease-related mortality events occurred in the 2009 brood steelhead.

3.4 Natural Juvenile Productivity

During 2010, juvenile steelhead were sampled at the Upper Wenatchee, Lower Wenatchee, and Chiwawa traps and counted during snorkel surveys within the Chiwawa Basin. Because the snorkel surveys targeted juvenile Chinook salmon, the entire distribution of juvenile steelhead in the Chiwawa Basin was not surveyed. Therefore, the parr numbers presented below represent a minimum estimate.

Parr Estimates

A total of 25,018 (±15.0%) age-0 (<100 mm) and 9,616 (±13.0%) age-1+ (100-200 mm)[4] steelhead/rainbow were estimated in the Chiwawa Basin in August 2010 (Table 3.13 and 3.14). During the survey period 1992-2010, numbers of age-0 and 1+ steelhead/rainbow have ranged from 1,410 to 45,727 and 2,533 to 22,128, respectively, in the Chiwawa Basin (Table 3.13 and 3.14; Figure 3.1). Numbers of all fish counted in the Chiwawa Basin are reported in Appendix A.

Juvenile steelhead/rainbow were distributed primarily throughout the lower seven reaches of the Chiwawa River (downstream from Rock Creek). Their densities were highest in the lower portions of the river and in tributaries. Age-0 steelhead/rainbow most often used riffle and multiple channel habitats in the Chiwawa River, although they also associated with woody debris in pool and glide habitat. In tributaries they were generally most abundant in small pools. Those that were observed in riffles selected stations in quiet water behind small and large boulders or occupied stations in quiet water along the stream margin. In pool and multiple-channel habitats, age-0 steelhead/rainbow used the same kinds of habitat as age-0 Chinook.

Age-1+ steelhead/rainbow most often used pool, riffle, and multiple-channel habitats. Those that used pools were usually in deeper water than subyearling steelhead/rainbow and Chinook. Like

[4] A steelhead/rainbow trout larger than 200 mm (8 in) was considered a resident trout.

age-0 steelhead/rainbow, age-1+ steelhead/rainbow selected stations in quiet water behind boulders in riffles, but the two age groups rarely occurred together. Age-1+ steelhead/rainbow appeared to use deeper and faster water than did subyearling steelhead/rainbow.

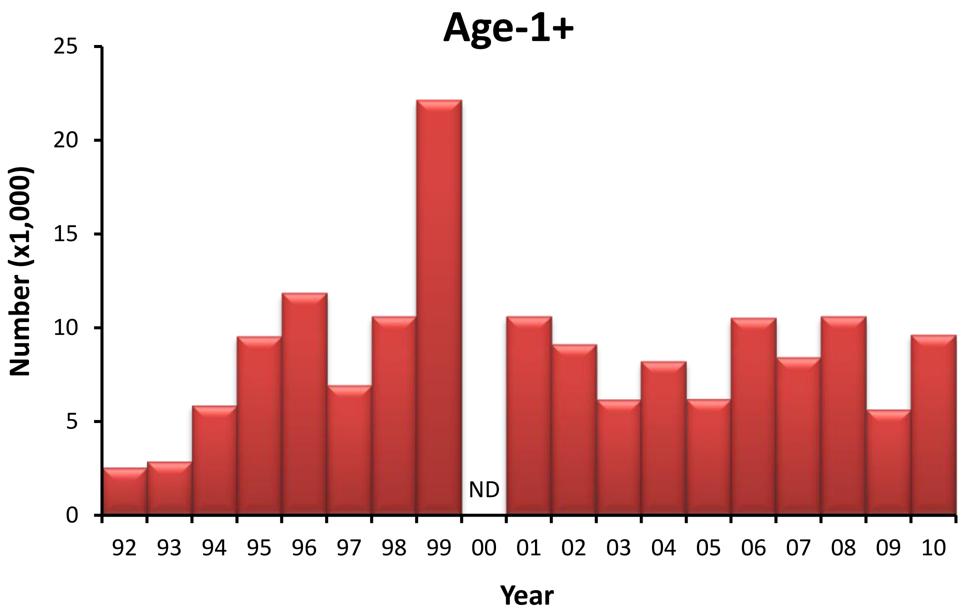
Table 3.13. Total numbers of age-0 steelhead/rainbow trout estimated in different steams in the Chiwawa Basin during snorkel surveys in August 1992-2010; NS = not sampled.

Sample Year	Chiwawa River	Phelps Creek	Chikamin Creek	Rock Creek	Unnamed Creek	Big Meadow Creek	Alder Creek	Brush Creek	Clear Creek	Total
1992	4,927	NS	NS	NS	NS	NS	NS	NS	NS	**4,927**
1993	3,463	0	356	185	NS	NS	NS	NS	NS	**4,004**
1994	953	0	256	24	0	177	0	0	0	**1,410**
1995	6,005	0	744	90	0	371	40	107	0	**7,357**
1996	3,244	0	71	40	0	763	127	0	0	**4,245**
1997	6,959	224	84	324	0	1,124	58	50	0	**8,823**
1998	2,972	22	280	96	113	397	18	22	0	**3,921**
1999	5,060	20	253	189	0	255	34	27	0	**5,838**
2000	NS	NS	NS	NS	NS	NS	NS	NS	NS	**NS**
2001	35,759	192	1,449	1,826	0	6,345	156	0	0	**45,727**
2002	12,137	0	2,252	889	0	4,948	277	18	0	**20,521**
2003	9,911	296	996	1,166	96	5,366	73	116	0	**18,020**
2004	8,464	110	583	113	40	957	35	78	0	**10,380**
2005	4,852	120	2,931	477	45	2,973	65	0	0	**11,463**
2006	10,669	21	858	872	34	3,647	73	71	0	**16,245**
2007	8,442	53	2,137	348	11	2,955	65	28	34	**14,073**
2008	9,863	0	2,260	859	0	1,987	57	168	36	**15,230**
2009	13,231	0	1,183	449	0	2,062	170	67	17	**17,179**
2010	17,572	0	2,870	1,478	5	2,843	182	35	33	**25,018**
Average	***9,386***	***62***	***1,151***	***554***	***22***	***2,323***	***89***	***49***	***8***	***13,021***

Table 3.14. Total numbers of age-1+ steelhead/rainbow trout estimated in different steams in the Chiwawa Basin during snorkel surveys in August 1992-2010; NS = not sampled.

Sample Year	Chiwawa River	Phelps Creek	Chikamin Creek	Rock Creek	Unnamed Creek	Big Meadow Creek	Alder Creek	Brush Creek	Clear Creek	Total
1992	2,533	NS	NS	NS	NS	NS	NS	NS	NS	**2,533**
1993	2,530	0	228	102	NS	NS	NS	NS	NS	**2,860**
1994	4,972	0	476	296	5	107	0	0	0	**5,856**
1995	8,769	0	494	71	0	183	0	0	0	**9,517**
1996	11,381	0	6	27	0	435	0	0	0	**11,849**
1997	6,574	160	0	105	0	66	0	0	0	**6,905**
1998	10,403	0	133	49	0	0	0	0	0	**10,585**
1999	21,779	0	68	201	0	82	0	0	0	**22,130**
2000	NS	NS	NS	NS	NS	NS	NS	NS	NS	**NS**
2001	9,368	16	186	407	0	646	0	0	0	**10,623**

Sample Year	Chiwawa River	Phelps Creek	Chikamin Creek	Rock Creek	Unnamed Creek	Big Meadow Creek	Alder Creek	Brush Creek	Clear Creek	Total
2002	7,200	0	199	165	0	1,526	0	0	0	**9,090**
2003	4,745	362	426	599	0	47	0	0	0	**6,179**
2004	7,700	107	209	0	0	174	0	0	0	**8,190**
2005	4,624	63	957	257	0	287	0	0	0	**6,188**
2006	7,538	76	748	1,186	0	985	0	0	0	**10,533**
2007	6,976	0	945	96	0	431	0	0	0	**8,448**
2008	8,317	0	1,168	298	0	793	0	0	0	**10,576**
2009	4,998	16	320	102	0	167	21	0	5	**5,629**
2010	8,324	32	366	393	0	780	21	0	0	**9,616**
Average	***7,707***	***49***	***408***	***256***	***0***	***419***	***3***	***0***	***0***	***8,739***



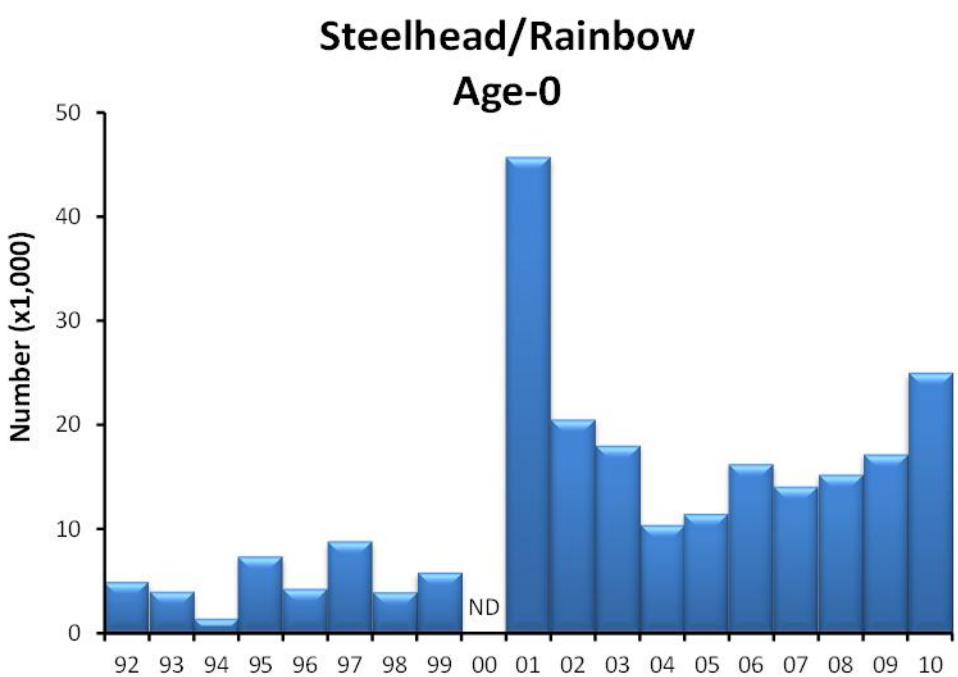


Figure 3.1. Numbers of subyearling and yearling steelhead/rainbow trout within the Chiwawa River Basin in August 1992-2010; ND = no data.

Emigrant and Smolt Estimates

Numbers of steelhead smolts and emigrants were estimated at the Upper Wenatchee, Chiwawa, and Lower Wenatchee traps in 2010.

Chiwawa Trap

The Chiwawa Trap operated between 5 March and 22 November 2010. During that time period the trap was inoperable for 20 days because of high river flows, debris, snow/ice, mechanical failure, or statewide furlough days. The trap operated in two different positions depending on stream flow; lower position at flows greater than 12 m^3/s and an upper position at flows less than 12 m^3/s. Monthly captures of all fish collected at the Chiwawa Trap are reported in Appendix B.

A total of 210 wild steelhead/rainbow smolts, 9,921 hatchery smolts, and 1,016 wild parr were captured at the Chiwawa Trap. Nearly all (99%) of the hatchery smolts were collected in May, while most (62%) of the wild steelhead smolts were captured during April and May (Figure 3.2). Although steelhead/rainbow parr emigrated throughout the sampling period, most emigrated during April through May and in September (Figure 3.2). No mark-recapture efficiency trials were conducted with steelhead/rainbow at the Chiwawa Trap to estimate total population sizes.

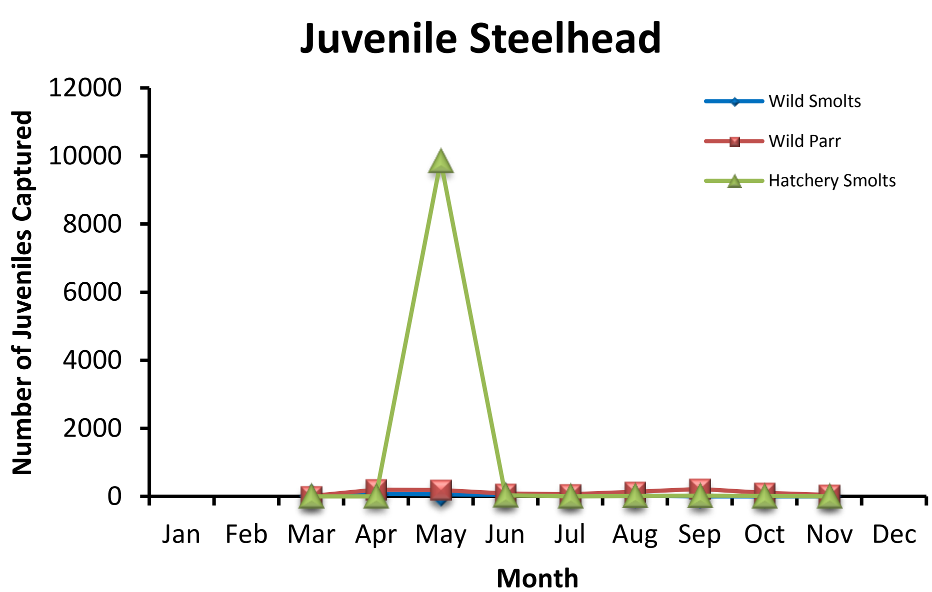


Figure 3.2. Monthly captures of wild smolts, wild parr, and hatchery smolt steelhead/rainbow at the Chiwawa Trap, 2010.

Upper Wenatchee Trap

The Upper Wenatchee Trap operated nightly between 12 March and 8 July 2010. During the five-month sampling period, a total of 43 wild steelhead/rainbow smolts, 357 hatchery smolts, and 52 wild parr were captured at the Upper Wenatchee Trap. Monthly captures of all fish collected at the Upper Wenatchee Trap are reported in Appendix B.

Lower Wenatchee Trap

The Lower Wenatchee Trap operated nightly between 4 February and 20 July 2010. During that time period, the trap was inoperable for 19 days because of high river flows, debris, snow/ice, or mechanical failure. During the six-month sampling period, a total of 407 wild steelhead/rainbow smolts, 2,735 hatchery smolts, and 77 wild parr were captured at the Lower Wenatchee Trap. Based on capture efficiencies estimated from the flow model, the total number of wild yearling steelhead/rainbow that emigrated past the Lower Wenatchee Trap was 36,826 (± 22,782). Most (91%) of the wild yearling steelhead/rainbow migrated during April and May. Nearly all (96%) the hatchery yearling steelhead/rainbow migrated during May. Monthly captures of all fish collected at the Lower Wenatchee Trap are reported in Appendix B.

PIT Tagging Activities

As part of the Integrated Status and Effectiveness Monitoring Program (ISEMP), a total of 3,899 juvenile steelhead/rainbow trout (3,735 wild and 164 hatchery) were PIT tagged and released in 2010 throughout the Wenatchee Basin (Table 3.15a). Most of these were tagged in the Chiwawa Basin and Tumwater Canyon. Few were tagged and released at the Upper Wenatchee trap and in the Upper Wenatchee River. A total of 465 juvenile steelhead/rainbow trout were tagged and released at the Lower Wenatchee trap. See Appendix C for a complete list of all fish captured, tagged, lost, and released.

Table 3.15a. Numbers of wild and hatchery steelhead/rainbow trout that were captured, tagged, and released at different locations within the Wenatchee Basin, 2010. Numbers of fish that died or shed tags are also given.

Sampling Location	Species and Life Stage	Number held	Number of recaptures	Number tagged	Number died	Shed Tags	Total released	Percent mortality
Chiwawa Trap	Wild Steelhead/Rainbow	988	7	931	1	0	930	0.10
	Hatchery Steelhead/Rainbow	3	0	2	0	0	2	0.00
	Total	**991**	**7**	**933**	**1**	**0**	**932**	**0.10**
Chiwawa Remote	Wild Steelhead/Rainbow	103	2	99	0	0	99	0.00
	Hatchery Steelhead/Rainbow	67	3	64	0	0	64	0.00
	Total	**170**	**5**	**163**	**0**	**0**	**163**	**0.00**
Upper Wenatchee Trap	Wild Steelhead/Rainbow	72	2	69	0	0	69	0.00
	Hatchery Steelhead/Rainbow	0	0	0	0	0	0	--
	Total	**72**	**2**	**69**	**0**	**0**	**69**	**0.00**
Nason Creek Remote	Wild Steelhead/Rainbow	328	8	318	0	0	318	0.00
	Hatchery Steelhead/Rainbow	37	5	32	0	0	32	0.00
	Total	**365**	**13**	**350**	**0**	**0**	**350**	**0.00**
Upper Wenatchee Remote	Wild Steelhead/Rainbow	30	0	30	0	0	30	0.00
	Hatchery Steelhead/Rainbow	9	0	9	0	0	9	0.00
	Total	**39**	**0**	**39**	**0**	**0**	**39**	**0.00**
Middle Wenatchee Remote	Wild Steelhead/Rainbow	1,608	84	1,518	1	0	1,517	0.06
	Hatchery Steelhead/Rainbow	67	10	57	0	0	57	0.00
	Total	**1,675**	**94**	**1,575**	**1**	**0**	**1,574**	**0.06**
Peshastin Creek Remote	Wild Steelhead/Rainbow	312	5	307	0	0	307	0.00
	Hatchery Steelhead/Rainbow	0	0	0	0	0	0	--
	Total	**312**	**5**	**307**	**0**	**0**	**307**	**0.00**
Lower Wenatchee Trap	Wild Steelhead/Rainbow	483	9	465	0	0	465	0.00
	Hatchery Steelhead/Rainbow	4	2	0	0	0	0	0.00

Sampling Location	Species and Life Stage	Number held	Number of recaptures	Number tagged	Number died	Shed Tags	Total released	Percent mortality
	Total	**487**	**11**	**465**	**0**	**0**	**465**	**0.00**
Total:	**Wild Steelhead/Rainbow**	**3,924**	**117**	**3,737**	**2**	**0**	**3,735**	**0.05**
	Hatchery Steelhead/Rainbow	**187**	**20**	**164**	**0**	**0**	**164**	**0.00**
Grand Total:		**4,111**	**137**	**3,901**	**2**	**0**	**3,899**	**0.04**

Numbers of steelhead/rainbow PIT-tagged and released as part of ISEMP during the period 2006-2010 are shown in Table 3.15b.

Table 3.15b. Summary of the numbers of wild and hatchery steelhead/rainbow trout that were tagged and released at different locations within the Wenatchee Basin, 2006-2010.

Sampling Location	Species and Life Stage	Numbers of PIT-tagged steelhead/rainbow released				
		2006	2007	2008	2009	2010
Chiwawa Trap	Wild Steelhead/Rainbow	1,366	832	1,431	1,127	930
	Hatchery Steelhead/Rainbow	0	3	2	1	2
	Total	**1,366**	**835**	**1,433**	**1,128**	**932**
Chiwawa Remote	Wild Steelhead/Rainbow	33	167	94	35	99
	Hatchery Steelhead/Rainbow	1	47	35	43	64
	Total	**34**	**214**	**129**	**78**	**163**
Upper Wenatchee Trap	Wild Steelhead/Rainbow	21	37	24	46	69
	Hatchery Steelhead/Rainbow	0	0	0	0	0
	Total	**21**	**37**	**24**	**46**	**69**
Nason Creek Remote	Wild Steelhead/Rainbow	174	452	255	459	318
	Hatchery Steelhead/Rainbow	26	75	87	197	32
	Total	**200**	**527**	**342**	**656**	**350**
Upper Wenatchee Remote	Wild Steelhead/Rainbow	413	1,001	21	7	30
	Hatchery Steelhead/Rainbow	2	64	26	23	9
	Total	**415**	**1,065**	**47**	**30**	**39**
Middle Wenatchee Remote	Wild Steelhead/Rainbow	0	0	981	867	1,517
	Hatchery Steelhead/Rainbow	0	0	11	5	57
	Total	**0**	**0**	**992**	**872**	**1,574**
Lower Wenatchee Remote	Wild Steelhead/Rainbow	0	0	102	69	0
	Hatchery Steelhead/Rainbow	0	0	10	9	0
	Total	**0**	**0**	**112**	**78**	**0**
Peshastin Creek Remote	Wild Steelhead/Rainbow	0	0	0	92	307
	Hatchery Steelhead/Rainbow	0	0	0	0	0
	Total	**0**	**0**	**0**	**92**	**307**
Lower Wenatchee Trap	Wild Steelhead/Rainbow	131	461	285	227	465
	Hatchery Steelhead/Rainbow	0	0	0	1	0

Sampling Location	Species and Life Stage	Numbers of PIT-tagged steelhead/rainbow released				
		2006	2007	2008	2009	2010
	Total	131	461	285	228	465
Total:	Wild Steelhead/Rainbow	2,138	2,950	3,193	2,928	3,735
	Hatchery Steelhead/Rainbow	29	189	171	278	164
Grand Total:		2,167	3,139	3,364	3,206	3,899

3.5 Spawning Surveys

Surveys for steelhead redds were conducted during March through May, 2010, in the Wenatchee River (including Beaver and Chiwaukum creeks), Chiwawa River (including Meadow, Alder, and Clear creeks), Nason Creek (including White Pine, Roaring, and an un-named stream), Icicle Creek, Peshastin Creek (including Mill, Ingalls, Tronsen, Scotty, Shaser, and Schafer creeks), and the White River (including the Napeequa River and Panther Creek). Surveys were conducted in both index and non-index areas throughout the Wenatchee Basin (see Appendix D for more details).

Redd Counts

A total of 969 steelhead redds were estimated in the Wenatchee Basin in 2010 (Table 3.16). This is about a 146% increase over the estimate in 2009 (the higher count is partly due to the larger run size in 2010; see Appendix D). Most spawning occurred in the Wenatchee River (39.2%), Nason Creek (27.9%), and Icicle Creek (12.4%) (Table 3.16; Figure 3.3). Peshastin Creek contained 12.2% of all redds in the Wenatchee Basin. The Little Wenatchee and White Rivers contained 0.4% and 0.3%, respectively, of the steelhead redds in the Wenatchee Basin. The number of redds estimated in the Chiwawa Basin was just above the average for that area.

Table 3.16. Numbers of steelhead redds estimated within different streams/watersheds within the Wenatchee Basin, 2001-2010; NS = not sampled. Redd counts beginning in 2004 have been conducted within the same areas and with the same methods. Therefore, comparing redd numbers before 2004 with estimates since may not be valid.

Survey year	Number of steelhead redds							
	Chiwawa	Nason	Little Wenatchee	White	Wenatchee River[a]	Icicle	Peshastin	Total
2001	25	27	NS	NS	116	19	NS	**187**
2002	80	80	1	0	315	27	NS	**503**
2003	64	121	5	3	248	16	15	**472**
2004	62	127	0	0	151	23	34	**397**
2005	162	412	0	2	459	8	97	**1,140**
2006	19	77	NS	0	191	41	67	**395**
2007	11	78	0	1	46	6	17	**159**
2008	11	88	NS	1	100	37	49	**286**
2009	75	126	0	0	327	102	32	**662**
2010	74	270	4	3	380	120	118	**969**

Survey year	Number of steelhead redds							
	Chiwawa	Nason	Little Wenatchee	White	Wenatchee River[a]	Icicle	Peshastin	Total
Average[b]	*59*	*168*	*1*	*1*	*236*	*48*	*59*	*573*

[a] Includes redds in Beaver and Chiwaukum creeks.
[b] The average is based on estimates from 2004 to present.

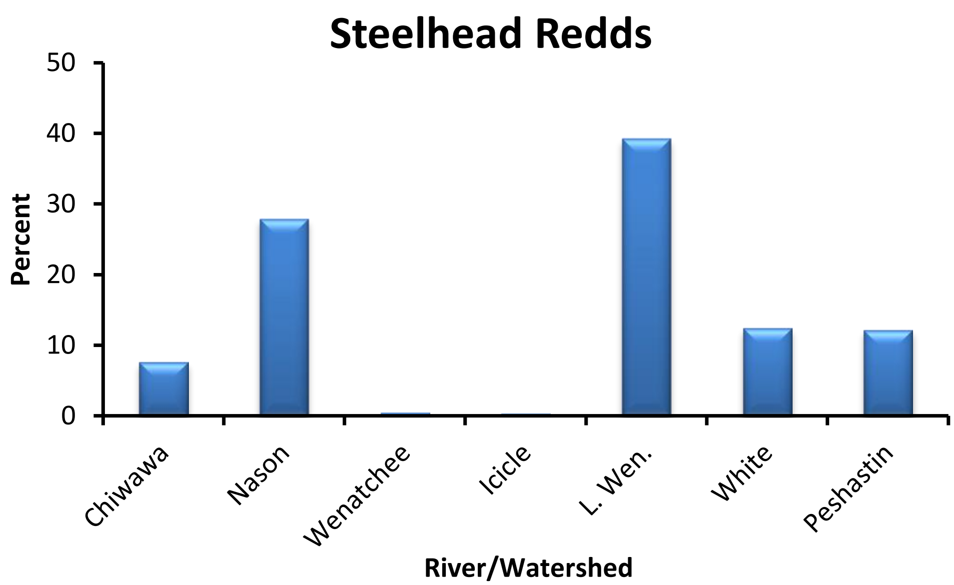


Figure 3.3. Percent of the total number of steelhead redds counted in different streams/watersheds within the Wenatchee Basin during March through May, 2010.

Redd Distribution

Steelhead redds were not evenly distributed among reaches within survey streams in 2010 (Table 3.17). Most of the spawning in the Chiwawa Basin occurred in Reach 1. The number of redds observed in Chikamin Creek and Clear Creek were 11 and 12, respectively. In addition, redds were observed in Alder Creek (N = 8) and Meadow Creek (N = 3). No redds were observed in Rock Creek.

Most of the spawning in the Nason Creek Basin occurred in Nason Creek, primarily in Reach 3. One redd was observed in Whitepine Creek and no spawning was observed in the remaining tributaries. Most spawning activity in the Peshastin Creek Basin was confined to Peshastin Creek proper, while three redds were observed in Tronsen Creek. About 73% of the spawning in the Wenatchee River occurred upstream from Tumwater Dam (Table 3.17).

Table 3.17. Numbers and percentages of steelhead redds counted within different streams/watersheds within the Wenatchee Basin during March through May, 2010.

Stream/watershed	Reach	Number of redds	Percent of redds within stream/watershed
Chiwawa	Chiwawa 1	40	54.1
	Rock Creek	0	0.0
	Chikamin Creek	11	14.9
	Meadow Creek	3	4.0
	Alder Creek	8	10.8
	Clear Creek	12	16.2
	Total	**74**	**100.0**
Nason	Nason 1	30	11.1
	Nason 2	53	19.6
	Nason 3	154	57.0
	Nason 4	32	11.9
	White Pine Creek	1	0.4
	Un-named Creek	0	0.0
	Roaring Creek	0	0.0
	Total	**270**	**100.0**
White	White 2	3	100.0
	White 3	0	0.0
	Panther Creek	0	0.0
	Naqeequa River	0	0.0
	Total	**3**	**100.0**
Icicle	Icicle	120	100.0
	Total	**120**	**100.0**
Peshastin	Peshastin 1	69	58.5
	Peshastin 2	46	39.0
	Mill Creek	0	0.0
	Ingalls Creek	0	0.0
	Tronsen Creek	3	2.5
	Scotty Creek	0	0.0
	Shaser Creek	0	0.0
	Schafer Creek	0	0.0
	Total	**118**	**100.0**
Wenatchee	Wenatchee 1	8	2.1
	Wenatchee 2	27	7.1
	Wenatchee 3	6	1.6
	Wenatchee 4	0	0.0
	Wenatchee 5	0	0.0
	Wenatchee 6	52	13.7

Stream/watershed	Reach	Number of redds	Percent of redds within stream/watershed
	Wenatchee 7	0	0
	Wenatchee 8	7	1.8
	Wenatchee 9	117	30.8
	Wenatchee 10	160	42.2
	Beaver Creek	2	0.5
	Chiwaukum Creek	1	0.2
	Total	**380**	**100.0**

Spawn Timing

Steelhead began spawning during the first week of March in Peshastin Creek, the second week of March in the Wenatchee River and Icicle Creek, and the third week of March in Nason Creek. Spawning progressed upstream as water temperature increased. Spawning activity appeared to begin once a mean daily stream temperature reached 4.4^{o}C and was observed in water temperatures ranging from 3.1 to 9.0^{o}C. Steelhead spawning peaked in Peshastin Creek the second week of April. Peak spawning occurred the third week in April and the fourth week in April for the Wenatchee River and Nason Creek, respectively (Figure 3.4).

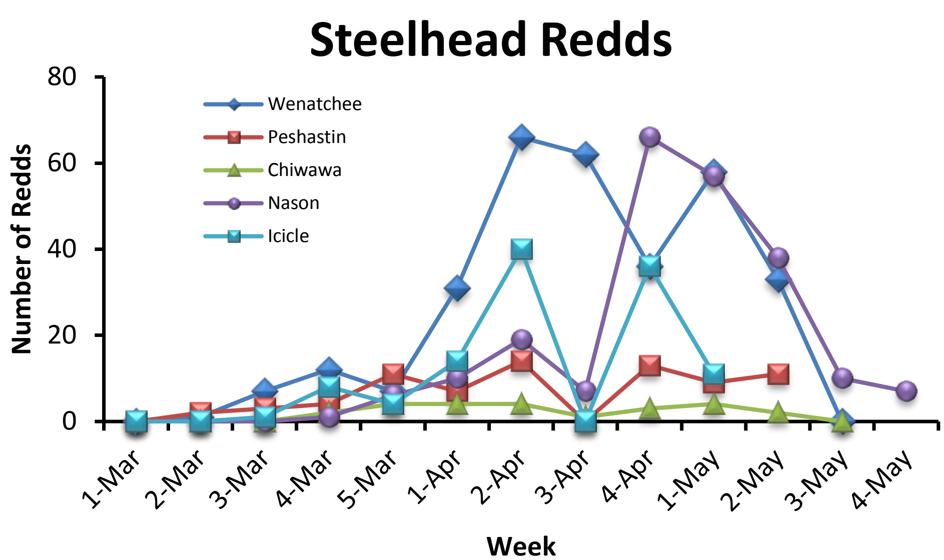


Figure 3.4. Numbers of steelhead redds counted during different weeks in different index areas within the Wenatchee Basin, March through May 2010.

Spawning Escapement

Spawning escapement for steelhead upstream from Tumwater Dam was calculated as the number of redds (upstream from the dam) times the fish per redd ratio (based on sex ratios estimated at Tumwater Dam using video surveillance). The estimated fish per redd ratio for steelhead in 2010 was 2.33 (Table 3.18). Multiplying this ratio by the total number of redds upstream from the dam resulted in a total spawning escapement of 1,494 steelhead (Table 3.18). This means that of the 2,270 steelhead counted at Tumwater, about 66% of them were estimated to have spawned upstream from the dam. This estimate was lower than the average of 48%.

The low estimated spawning escapement in 2010 may have resulted from the difficult survey conditions that biologists experienced in that year. That is, poor survey conditions may have obscured redds and high spring flows prevented post-peak surveys to be conducted in some areas. The effect of other factors, such as pre-spawning mortality, fallback, illegal harvest, etc. remain unknown.

Table 3.18. Numbers of steelhead counted at Tumwater Dam, fish/redd estimates (based on male-to-female ratios estimated at Tumwater Dam), numbers of steelhead redds counted upstream from Tumwater Dam, total spawning escapement upstream from Tumwater Dam (estimated as the total number of redds times the fish/redd ratio), and the proportion of the Tumwater Dam count that made up the spawning escapement.

Survey year	Total count at Tumwater Dam	Fish/redd	Number of redds			Spawning escapement	Proportion of Tumwater count that spawned
			Index area	Non-index area	Total redds		
2001	820	2.08	118	19	137	285	0.35
2002	1,720	2.68	296	179	475	1,273	0.74
2003	1,810	1.60	353	88	441	706	0.39
2004	1,869	2.21	277	92	369	815	0.44
2005	2,650	1.61	828	136	964	1,552	0.59
2006	1,053	2.05	192	34	226	463	0.44
2007	657	1.94	105	29	134	260	0.40
2008	1,328	2.81	124	35	159	447	0.34
2009	1,781	1.83	284	107	931	716	0.40
2010	2,270	2.33	517	95	641	1,494	0.66
Average[a]	***1,658***	***2.11***	***332***	***75***	***394***	***821***	***0.47***

[a] The average is based on estimates from 2004 to present.

3.6 Life History Monitoring

Life history characteristics of steelhead were assessed by examining fish collected at broodstock collection sites, examining videotape at Tumwater Dam, and by reviewing tagging data and fisheries statistics. Some statistics could not be calculated at this time because few fish have been tagged with CWTs. All steelhead released from the hatchery received elastomer tags and about 40,000 were PIT tagged. With the placement of remote PIT tag detectors in spawning streams in 2007 and 2008, statistics such as origin on spawning grounds, stray rates, and SARs can be estimated more accurately in the future.

Migration Timing

Sampling at Tumwater Dam indicates that steelhead migrate throughout the year; however, the migration distribution is bimodal, indicating that steelhead migrate past Tumwater Dam in two pulses: one pulse during summer-autumn the year before spawning and another during winter-spring the year of spawning (Figure 3.5). Most steelhead passed Tumwater Dam during July through October and April. The highest proportion of both wild and hatchery fish migrated during October.

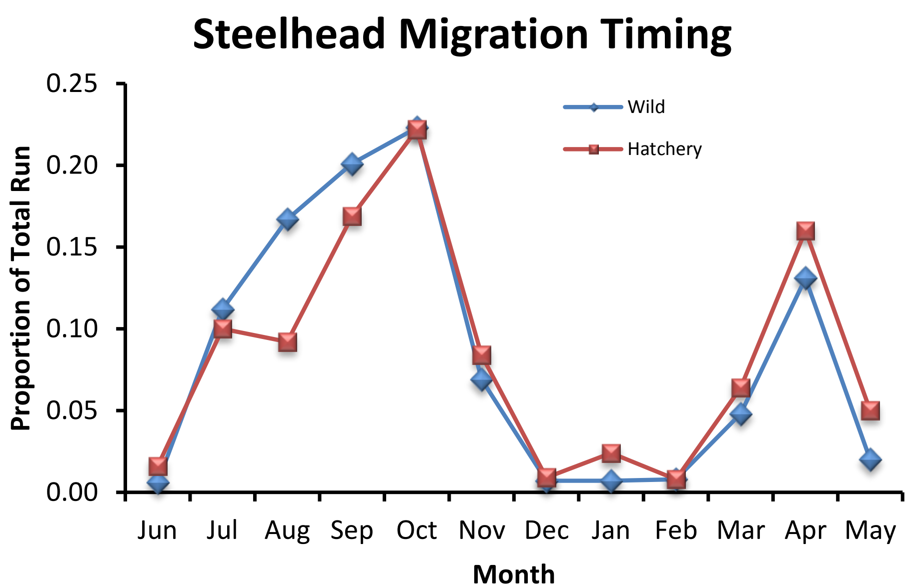


Figure 3.5. Proportion of wild and hatchery steelhead sampled at Tumwater Dam for the combined brood years of 1999-2010.

Because the migration of steelhead is bimodal, we estimated migration statistics separately for each migration pulse (i.e., summer-autumn migration and winter-spring migration). That is, we compared migration statistics for wild and hatchery steelhead passing Tumwater Dam during the summer-autumn period independent of those for the winter-spring migration period. We estimated the week and month that 10%, 50% (median), and 90% of the wild and hatchery steelhead passed Tumwater Dam during the two migration periods. We also estimated the mean weekly and monthly migration timing for wild and hatchery steelhead.

Overall, there was little difference in migration timing of wild and hatchery fish enumerated at Tumwater Dam (Table 3.19a and b; Figure 3.5). For both the summer-autumn and winter-spring migration periods, wild and hatchery steelhead arrived at the dam during the same week and month. The mean and median migration timing for wild and hatchery steelhead was also similar. However, at the tail end of both migration periods, on average, wild steelhead appeared to end their migration about one week earlier than hatchery steelhead.

Table 3.19a. The week that 10%, 50% (median), and 90% of the wild and hatchery steelhead passed Tumwater Dam during their summer-autumn migration (June through December) and during their winter-spring migration (January through May), 1999-2010. The average week is also provided for both migration periods. Migration timing is based on video sampling at Tumwater. The presence of eroded fins and/or missing adipose fins was used to distinguish hatchery fish from wild fish during video monitoring at Tumwater Dam. Estimates also include steelhead collected for broodstock.

Spawn year	Origin	Steelhead Migration Time (week)									
		Summer-Autumn Migration (Jun-Dec)					Winter-Spring Migration (Jan-May)				
		10%	50%	90%	Mean	Sample size	10%	50%	90%	Mean	Sample size
1999	Wild	27	32	47	35	81	12	16	17	15	29
	Hatchery	25	31	47	34	47	12	16	18	15	27
2000	Wild	31	36	41	36	238	11	14	18	14	40
	Hatchery	31	34	41	36	194	12	14	16	14	69
2001	Wild	29	34	41	35	391	13	15	17	15	84
	Hatchery	30	38	41	36	227	12	16	17	15	156
2002	Wild	29	39	46	38	810	13	14	17	14	181
	Hatchery	35	42	46	41	610	12	15	18	15	124
2003	Wild	30	33	40	35	731	3	9	16	9	193
	Hatchery	30	35	51	37	372	3	9	15	9	538
2004	Wild	30	40	45	39	644	13	16	18	16	222
	Hatchery	29	40	44	38	677	11	17	19	16	361
2005	Wild	30	39	43	38	986	10	15	17	15	206
	Hatchery	27	38	42	36	1,112	12	16	18	15	377
2006	Wild	29	40	43	39	428	12	15	17	15	191
	Hatchery	29	41	43	39	334	4	13	16	12	181
2007	Wild	30	36	41	35	277	11	17	17	15	108
	Hatchery	29	38	43	36	90	11	17	18	16	214
2008	Wild	30	38	43	38	397	13	15	18	16	123
	Hatchery	33	41	45	40	554	14	18	19	17	311
2009	Wild	30	37	46	37	338	13	15	19	15	87
	Hatchery	29	35	46	36	1,133	13	16	19	16	229
2010	Wild	31	37	45	38	648	11	15	18	15	171
	Hatchery	31	40	45	40	1,207	12	16	19	16	309
Average	***Wild***	***30***	***37***	***43***	***37***	***498***	***11***	***15***	***17***	***15***	***136***
	Hatchery	***30***	***38***	***45***	***37***	***546***	***11***	***15***	***18***	***15***	***241***

Table 3.19b. The month that 10%, 50% (median), and 90% of the wild and hatchery steelhead passed Tumwater Dam during their summer-autumn migration (June through December) and during their winter-spring migration (January through May), 1999-2010. The average month is also provided for both migration periods. Migration timing is based on video sampling at Tumwater. The presence of eroded fins and/or missing adipose fins was used to distinguish hatchery fish from wild fish during video monitoring at Tumwater Dam. Estimates also include steelhead collected for broodstock.

Spawn year	Origin	Steelhead Migration Time (month)									
		Summer-Autumn Migration (Jun-Dec)					Winter-Spring Migration (Jan-May)				
		10%	50%	90%	Mean	Sample size	10%	50%	90%	Mean	Sample size
1999	Wild	7	8	11	8	81	3	4	4	4	29
	Hatchery	6	8	11	8	47	3	4	4	4	27
2000	Wild	8	9	10	9	238	3	4	5	4	40
	Hatchery	8	8	10	9	194	3	4	4	4	69
2001	Wild	7	8	10	8	391	3	4	4	4	84
	Hatchery	7	9	10	9	227	3	4	4	4	156
2002	Wild	7	9	11	9	810	3	4	4	4	181
	Hatchery	9	10	11	10	610	3	4	5	4	124
2003	Wild	7	8	10	8	731	1	3	4	3	193
	Hatchery	7	8	12	9	372	1	3	4	2	538
2004	Wild	7	10	11	9	644	3	4	4	4	222
	Hatchery	7	10	10	9	677	3	4	5	4	361
2005	Wild	7	9	10	9	986	3	4	4	4	206
	Hatchery	7	9	10	9	1,112	3	4	5	4	377
2006	Wild	7	10	10	10	428	3	4	4	4	191
	Hatchery	7	10	10	9	334	1	3	4	3	181
2007	Wild	7	9	10	9	277	3	4	4	4	108
	Hatchery	7	9	10	9	90	3	4	5	4	214
2008	Wild	7	9	10	9	397	3	4	5	4	123
	Hatchery	8	10	11	10	554	4	4	5	4	311
2009	Wild	7	9	11	9	338	3	4	5	4	87
	Hatchery	7	8	11	9	1,133	3	4	5	4	229
2010	Wild	8	9	11	9	648	3	4	5	4	171
	Hatchery	8	10	11	10	1,207	3	4	5	4	309
Average	***Wild***	***7***	***9***	***10***	***9***	***497***	***3***	***4***	***4***	***4***	***136***
	Hatchery	***7***	***9***	***11***	***9***	***546***	***3***	***4***	***5***	***4***	***241***

Age at Maturity

Nearly all steelhead broodstock collected at Tumwater and Dryden dams lived in saltwater 1 to 2 years (saltwater age) (Table 3.20; Figure 3.6). Very few saltwater age-3 fish returned and those that did were wild fish. On average, there was a difference between the saltwater age at return of wild and hatchery fish. A greater number of wild fish returned as saltwater age-2 fish than did hatchery fish. In contrast, a greater number of hatchery fish returned as saltwater-1 fish than did wild fish.

Table 3.20. Proportions of wild and hatchery steelhead broodstock of different ages collected at Tumwater and Dryden dams, 1998-2010. Age represents the number of years the fish lived in salt water.

Sample year	Origin	Saltwater age			Sample size
		1	2	3	
1998	Wild	0.39	0.61	0.00	35
	Hatchery	0.21	0.79	0.00	43
1999	Wild	0.50	0.48	0.02	58
	Hatchery	0.82	0.18	0.00	67
2000	Wild	0.56	0.44	0.00	39
	Hatchery	0.68	0.32	0.00	101
2001	Wild	0.52	0.48	0.00	64
	Hatchery	0.15	0.85	0.00	114
2002	Wild	0.56	0.44	0.00	99
	Hatchery	0.95	0.05	0.00	113
2003	Wild	0.13	0.85	0.02	63
	Hatchery	0.29	0.71	0.00	92
2004	Wild	0.95	0.05	0.00	85
	Hatchery	0.95	0.05	0.00	132
2005	Wild	0.22	0.78	0.00	95
	Hatchery	0.21	0.79	0.00	114
2006	Wild	0.29	0.71	0.00	101
	Hatchery	0.60	0.40	0.00	98
2007	Wild	0.40	0.59	0.00	79
	Hatchery	0.62	0.38	0.00	97
2008	Wild	0.65	0.34	0.01	104
	Hatchery	0.89	0.11	0.00	107
2009	Wild	0.40	0.58	0.20	83
	Hatchery	0.23	0.77	0.0	77
2010	Wild	0.65	0.34	0.01	92
	Hatchery	0.77	0.23	0.0	98
Average	***Wild***	***0.48***	***0.51***	***0.02***	***77***
	Hatchery	***0.57***	***0.43***	***0.00***	***96***

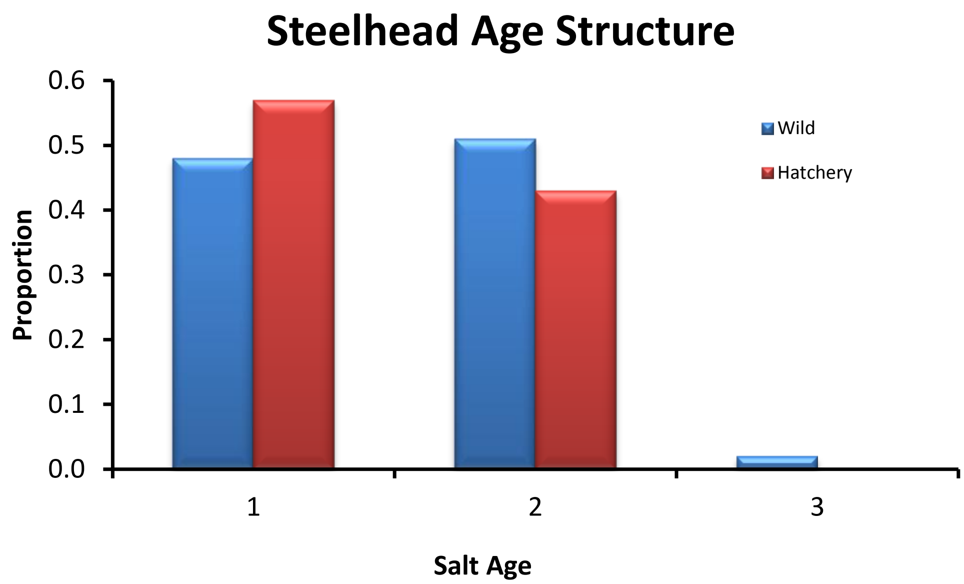


Figure 3.6. Proportions of wild and hatchery steelhead of different saltwater ages sampled at Tumwater Dam for the combined years 1998-2010.

Size at Maturity

On average, hatchery steelhead collected at Tumwater and Dryden dams were about 2-3 cm smaller than wild steelhead (Table 3.21). This may be related to the fact that more wild steelhead return as saltwater age-2 fish than hatchery steelhead.

Table 3.21. Mean fork length (cm) at age (saltwater ages) of hatchery and wild steelhead collected from broodstock, 1998-2010; N = sample size and SD = 1 standard deviation.

Return year	Origin	Steelhead fork length (cm)								
		1-Salt			2-Salt			3-Salt		
		Mean	N	SD	Mean	N	SD	Mean	N	SD
1998	Wild	63	15	4	79	20	5	-	0	-
	Hatchery	61	9	4	73	34	4	-	0	-
1999	Wild	65	29	5	74	28	5	77	1	-
	Hatchery	62	54	4	73	12	4	-	0	-
2000	Wild	64	22	3	74	17	5	-	0	-
	Hatchery	60	57	3	71	27	4	-	0	-
2001	Wild	61	33	6	77	31	5	-	0	-
	Hatchery	62	17	4	72	97	4	-	0	-
2002	Wild	64	55	4	77	44	4	-	0	-
	Hatchery	63	106	4	73	6	4	-	0	-
2003	Wild	69	8	6	77	52	5	91	1	-
	Hatchery	66	27	4	75	65	4	-	0	-
2004	Wild	63	73	6	78	4	2	-	0	-
	Hatchery	61	59	3	73	3	1	-	0	-

Return year	Origin	Steelhead fork length (cm)								
		1-Salt			2-Salt			3-Salt		
		Mean	N	SD	Mean	N	SD	Mean	N	SD
2005	Wild	59	21	4	74	74	5	-	0	-
	Hatchery	59	23	4	72	89	4	-	0	-
2006	Wild	63	27	5	75	67	6	-	0	-
	Hatchery	61	41	4	72	27	5	-	0	-
2007	Wild	64	31	6	76	46	5	-	0	-
	Hatchery	60	60	4	71	36	5	-	0	-
2008	Wild	64	68	4	77	35	4	80	2	-
	Hatchery	60	95	4	72	12	2	-	0	-
2009	Wild	65	33	5	76	48	6	81	2	0
	Hatchery	63	18	4	75	59	5	-	0	-
2010	Wild	64	60	5	74	31	5	76	1	-
	Hatchery	62	75	4	73	23	5	-	0	-
Average	Wild	64	37	5	76	38	5	81	1	0
	Hatchery	62	49	4	73	38	4	-	0	-

Contribution to Fisheries

Nearly all harvest on Wenatchee steelhead occurs within the Columbia basin. Harvest rates on steelhead in the Lower Columbia River fisheries (both tribal and non-tribal) are generally less than 5-10% (NMFS 2004). WDFW regulates steelhead harvest in the Upper Columbia. Under certain conditions, WDFW may allow a harvest on hatchery steelhead (adipose fin clipped fish). The intent is to reduce the number of hatchery steelhead that exceed habitat seeding levels in spawning areas and to increase the proportion of wild steelhead in spawning populations.

Origin on Spawning Grounds

At this time, origin of steelhead (wild or hatchery) on spawning grounds cannot be determined precisely. However, based on scales collected during steelhead run composition sampling at Dryden Dam in 2008 (2009 spawners), naturally produced steelhead made up about 23% of the escapement. More precise estimates of wild and hatchery spawners within tributaries can be generated after remote PIT tag detectors are installed within spawning tributaries.

Straying

Stray rates are currently difficult to estimate because fish are not handled on spawning grounds. As remote PIT-tag detectors are installed in spawning streams, we will be able to more accurately determine steelhead stray rates.

Genetics

A report on the genetic analysis of Wenatchee steelhead will be completed in the future.

Proportion of Natural Influence

Another method for assessing the genetic risk of a supplementation program is to determine the influence of the hatchery and natural environments on the adaptation of the composite population. This is estimated by the proportion of natural-origin fish in the hatchery broodstock (pNOB) and the proportion of hatchery-origin fish in the natural spawning escapement (pHOS). The ratio pNOB/(pHOS+pNOB) is the Proportion of Natural Influence (PNI). The larger the ratio (PNI), the greater the strength of selection in the natural environment relative to that of the hatchery environment. In order for the natural environment to dominate selection, PNI should be greater than 0.5 (HSRG/WDFW/NWIFC 2004).

For brood years 2001-2010, the PNI was generally equal to or greater than 0.4 (Table 3.22). This indicates that the hatchery environment has an equal or greater influence on adaptation of Wenatchee steelhead than does the natural environment.

Table 3.22. Proportionate natural influence (PNI) of the Wenatchee steelhead supplementation program for brood years 2001-2010. PNI was calculated as the proportion of naturally produced steelhead in the hatchery broodstock (pNOB) divided by the proportion of hatchery steelhead on the spawning grounds (pHOS) plus pNOB. NOS = number of natural-origin steelhead on the spawning grounds; HOS = number of hatchery-origin steelhead on the spawning grounds; NOB = number of natural-origin steelhead collected for broodstock; and HOB = number of hatchery-origin steelhead included in hatchery broodstock.

Brood year	Spawners[a]			Broodstock			PNI
	NOS	HOS	pHOS	NOB	HOB	pNOB	
2001	158	127	0.45	51	103	0.33	0.43
2002	731	542	0.43	96	64	0.60	0.59
2003	356	350	0.50	49	90	0.35	0.42
2004	371	444	0.55	75	61	0.55	0.50
2005	690	862	0.56	87	104	0.46	0.45
2006	253	210	0.45	93	69	0.57	0.56
2007	145	115	0.44	76	58	0.57	0.56
2008	168	279	0.62	77	54	0.59	0.48
2009	171	545	0.76	86	73	0.57	0.24
2010	524	970	0.65	96	75	0.56	0.46
Average	***357***	***444***	***0.54***	***79***	***75***	***0.51***	***0.49***

[a] Proportions of natural-origin and hatchery-origin spawners were determined from video tape at Tumwater Dam. Therefore, these PNI estimates are appropriate for steelhead spawning upstream from Tumwater Dam. They may not represent PNI for steelhead spawning downstream from Tumwater Dam.

Natural Replacement Rates

Natural replacement rates (NRR) were calculated as the ratio of natural-origin recruits (NOR) to the parent spawning population. For brood years 1989-2001, NRR in the Wenatchee averaged 0.83 (range, 0.07-3.13) (Table 3.23). NRRs for more recent brood years will be calculated as soon as the data are available.

Table 3.23. Spawning escapements, natural-origin recruits (NOR), and natural replacement rates (NRR) for Wenatchee steelhead, 1989-2004. Numbers of hatchery and wild steelhead were based on radio telemetry results, numbers of steelhead passing Priest and Wells dams, and the number of steelhead harvested or removed for broodstock. *(The numbers in this table may change as the HETT and HC refine the methods for estimating steelhead escapement, NORs, and NRRs.)*

Brood year	Spawning escapement			NOR	NRR
	Hatchery	Wild	Total		
1989	1,849	1,001	2,851	348	0.122
1990	1,487	936	2,423	342	0.141
1991	990	481	1,471	321	0.218
1992	1,333	888	2,221	262	0.118
1993	2,951	566	3,516	241	0.068
1994	985	309	1,294	342	0.265
1995	1,637	303	1,940	427	0.220
1996	1,036	409	1,445	1,037	0.717
1997	245	269	514	1,609	3.129
1998	391	278	668	1,225	1.832
1999	114	268	382	796	2.085
2000	738	406	1,144	1,260	1.101
2001	1,065	773	1,838	1,301	0.707
2002	NA	NA	NA	NA	NA
Average	***1,140***	***530***	***1,670***	***731***	***0.825***

Hatchery Replacement Rates

Hatchery replacement rates were estimated as hatchery adult-to-adult returns. These rates should be greater than the NRRs and greater than or equal to 19.2 (the calculated target value in Murdoch and Peven 2005). In years with data, HRRs and adjusted HRRs were consistently greater than NRRs (Table 3.24). In contrast, HRRs exceeded the estimated target value of 19.2 in only one year and adjusted HRRs exceeded the estimated target in two of the six years (Table 3.24).

Table 3.24. Hatchery replacement rates (HRR), adjusted HRR (for estimated tag loss), and NRR for Wenatchee steelhead, 1998-2006. *(The numbers in this table may change as the HETT and HC refine the methods for estimating steelhead HRRs and NRRs.)*

Brood year	HRR	Adjusted HRR	NRR
1998	1.89	3.49	1.83
1999	15.47	23.16	2.09
2000	2.60	3.33	1.10
2001	57.97	63.37	0.71
2002	11.76	12.18	NA
2003	6.56	6.56	NA
2004	NA	NA	NA

Brood year	HRR	Adjusted HRR	NRR
Average	***16.04***	***18.68***	***1.43***

Smolt-to-Adult Survivals

Smolt-to-adult ratios (SARs) are calculated as the number of returning hatchery adults divided by the number of tagged hatchery smolts released. SARs are generally based on CWT returns. However, Wenatchee steelhead have not been extensively tagged with CWTs. Therefore, elastomer-tagged fish were used to estimate SARs from release to capture at Priest Rapids Dam. Two different estimates are provided. One (unadjusted) is based on elastomer tag recaptures at Priest Rapids Dam; the other (adjusted) is corrected for tag loss after release (based on the number of unmarked hatchery adults that could not be accounted for). SARs for steelhead may change once a more accurate methodology for estimating adult survival has been developed.

Unadjusted SARs for Wenatchee steelhead ranged from 0.0017 to 0.0307 (mean = 0.0076) for brood years 1996-2006 (Table 3.25). Accounting for post-release tag loss, SARs ranged from 0.0016 to 0.0336 (mean = 0.0105) for brood years 1998-2005.

Table 3.25. Smolt-to-adult ratios (SARs) for Wenatchee hatchery steelhead, 1996-2006; NA = not available. Unadjusted estimates were based on elastomer tags recaptured at Priest Rapids Dam. Adjusted estimates were corrected for tag loss after release.

Brood year	Number of tagged smolts released	SAR (unadjusted)	SAR (adjusted)
1996	348,693	0.0034	NA
1997	429,422	0.0041	NA
1998	172,078	0.0009	0.0016
1999	175,661	0.0110	0.0165
2000	184,639	0.0017	0.0022
2001	335,933	0.0307	0.0336
2002	302,060	0.0063	0.0065
2003	374,867	0.0027	0.0027
2004	276,773	NA	NA
2005	NA	NA	NA
Average	***278,355***	***0.0076***	***0.0105***

3.7 ESA/HCP Compliance

Broodstock Collection

Collection of BY 2009 broodstock for Wenatchee steelhead at Tumwater and Dryden dams began on 1 July and ended on 25 October 2008 and represented a slightly shortened collection duration from the 1 July – 12 November collection period detailed in the 2008 broodstock collection protocol. The broodstock collection protocols specified a total collection of 208 steelhead, including 104 natural-origin steelhead. Actual broodstock collection totaled 208 steelhead collected at Tumwater and Dryden dams, including 102 natural-origin fish (49% of the total collection). The total number and proportion of natural-origin steelhead in the broodstock were less than the 104 and slightly below the 50% values identified in the 2008 protocol and ESA Permit 1395, respectively.

About 233 and 1,033 steelhead were handled and released at Dryden Dam and Tumwater Dam, respectively, during BY 2009 Wenatchee steelhead broodstock collection. These fish were released because the weekly quota for hatchery or wild steelhead had been attained, but not both, or because they were non-target (red VIE), or they were unidentifiable hatchery-origin steelhead. All steelhead released were allowed to fully recover from the anesthesia and released immediately upstream from the trap sites.

In addition to steelhead encountered at Dryden Dam during steelhead broodstock collection, 59 spring Chinook salmon were captured and released unharmed immediately upstream from the trap facility. Consistent with ESA Section 10 Permit 1395 impact minimization measures, all ESA species handled at this site were subject of water-to-water transfers.

Hatchery Rearing and Release

The 2009 brood Wenatchee steelhead reared throughout all life-stages without significant mortality (defined as >10% population mortality associated with a single event). However, the 2009 brood had poor fertilization to eyed-egg and eyed-egg to ponding survival resulting in an unfertilized-to-release survival of 76.6%, which was less than the program target of 81% (see Section 3.2).

Juvenile rearing occurred at three separate facilities including Eastbank Fish Hatchery, Chelan Falls Fish Hatchery, and Turtle Rock Fish Hatchery. Multiple facilities were used to take advantage of variable water temperatures to manipulate growth of juveniles from different parental crosses. Typically, wild steelhead spawn later than their hatchery cohort and are therefore reared at Chelan Falls Fish Hatchery on warmer water to accelerate their growth so they achieve a size at release similar to HxH and HxW parental cross progeny reared on cooler water at Eastbank Fish Hatchery. All parental cross groups received final rearing at Turtle Rock Fish Hatchery on Columbia River surface water before direct release (scatter planting) in the Wenatchee River basin.

The 2009 brood steelhead smolt release in the Wenatchee Basin totaled 484,772 smolts, representing about 121% of the program target of 400,000 smolts identified in the Rocky Reach and Rock Island Dam HCPs and in ESA Section 10 Permit 1395. As specified in ESA Section 10 Permit 1395, all steelhead smolts released were externally marked or tagged and a representative number were PIT tagged (see Section 3.2)

Hatchery Effluent Monitoring

Per ESA Permits 1196, 1347, and 1395, permit holders shall monitor and report hatchery effluents in compliance with applicable National Pollution Discharge Elimination Systems (NPDES) (EPA 1999) permit limitations. There were no NPDES violations reported at Chelan PUD Hatchery facilities during the period 1 January 2010 through 31 December 2010. NPDES monitoring and reporting for Chelan PUD Hatchery Programs during 2010 are provided in Appendix E.

Smolt and Emigrant Trapping

Per ESA Section 10 Permit No. 1395, the permit holders are authorized a direct take of 20% of the emigrating steelhead population and a lethal take not to exceed 2% of the fish captured (NMFS 2003). Based on the estimated wild steelhead population (smolt trap expansion) and hatchery juvenile steelhead population estimate (hatchery release data) for the Wenatchee Basin, the reported steelhead encounters during the 2010 emigration complied with take provisions in the Section 10 permit and are detailed in Table 3.26. Additionally, juvenile fish captured at the trap locations were handled consistent with provisions in ESA Section 10 Permit 1395 Section B.

Table 3.26. Estimated take of Upper Columbia River steelhead resulting from juvenile emigration monitoring in the Wenatchee Basin, 2010. NA = not available.

Trap location	Population estimate				Number trapped				Total	Take allowed by Permit
	Wild[a]	Hatchery[b]	Parr[c]	Fry	Wild	Hatchery	Parr	Fry		
Chiwawa Trap										
Population	NA	111,263	NA	NA	210	9,921	1,016	302	11,449	
Encounter rate	NA	NA	NA	NA	NA	0.0892	NA	NA	NA	0.20
Mortality [d]	NA	NA	NA	NA	0	28	8	5	41	
Mortality rate	NA	NA	NA	NA	0.0000	0.0028	0.0079	0.0166	0.0036	0.02
Upper Wenatchee Trap										
Population	NA	145,029	NA	NA	43	357	52	0	452	
Encounter rate	NA	NA	NA	NA	NA	0.0025	NA	NA		0.20
Mortality [d]	NA	NA	NA	NA	2	3	3	0	8	
Mortality rate	NA	NA	NA	NA	0.0465	0.0084	0.0577	NA	0.0177	0.02
Lower Wenatchee Trap										
Population	36,826	484,772	NA	NA	407	2,735	77	215	3,434	
Encounter rate	NA	NA	NA	NA	0.0111	0.0056	NA	NA	0.0066	0.20
Mortality [d]	NA	NA	NA	NA	0	4	0	1	5	
Mortality rate	NA	NA	NA	NA	0.0000	0.0015	0.0000	0.0047	0.0015	0.02
Wenatchee Basin Total										
Population	36,826	484,772	NA	NA	660	13,013	1,145	517	15,335	
Encounter rate	NA	NA	NA	NA	0.0248	0.0148	NA	NA	0.0294	0.20
Mortality [d]	NA	NA	NA	NA	2	35	11	6	54	
Mortality rate	NA	NA	NA	NA	0.0030	0.0027	0.0096	0.0116	0.0035	0.02

[a] Smolt production estimates based on juvenile emigration monitoring (Miller 2009).

[b] 2010 smolt release data for the Wenatchee basin.

[c] Estimated parr emigrating past juvenile trap sites (Miller et al. 2009)

[d] Mortality includes trapping and PIT tag mortalities.

Spawning Surveys

Steelhead spawning ground surveys were conducted in the Wenatchee Basin during 2010, as authorized by ESA Section 10 Permit No. 1395. Because of the difficulty of quantifying the level of take associated with spawning ground surveys, the Permit does not specify a take level associated with these activities, even though it does authorize implementation of spawning ground surveys. Therefore, no take levels are reported. However, to minimize potential impacts to established redds, wading was restricted to the extent practical, and extreme caution was used to avoid established redds when wading was required.

Stock Assessment at Priest Rapids Dam

Upper Columbia River steelhead stock assessment sampling at Priest Rapids Dam (PRD) is authorized through ESA Section 10 Permit No. 1395 (NMFS 2003). Permit authorizations include interception and biological sampling of up to 10% of the UCR steelhead passing PRD to determine upriver adult population size, estimate hatchery to wild ratios, determine age-class contribution, and evaluate the need for managing hatchery steelhead consistent with ESA recovery objectives, which include fully seeding spawning habitat with naturally produced Upper Columbia River steelhead supplemented with artificially propagated enhancement steelhead (NMFS 2003). The 2009-10 run-cycle report (BY 2009) for stock assessment sampling at Priest Rapids Dam was compiled under provisions of ESA Section 10 Permit 1395. Data and reporting information are included in Appendix F.

SECTION 4: WENATCHEE SOCKEYE SALMON

4.1 Broodstock Sampling

This section focuses on results from sampling 2008 and 2009 Wenatchee sockeye broodstock, which were collected at Tumwater Dam. The 2008 brood begins the tracking of the life cycle of sockeye that were released as parr into Lake Wenatchee in 2009 and some of which began smolt migrations in 2010. The 2009 brood is included because juveniles from this brood were released as parr in the lake in 2010. Complete information is not currently available for the 2010 brood (this information will be provided in the 2011 annual report). Collection of sockeye broodstock targets naturally produced fish and equal numbers of male and female fish.

Origin of Broodstock

The 2008 broodstock consisted of naturally produced sockeye collected at Tumwater Dam between 21 July and 6 August 2008 (Table 4.1). A total of 245 naturally produced sockeye were spawned. The 2009 broodstock consisted of naturally produced Wenatchee sockeye salmon collected at Tumwater Dam between 11 July and 21 August 2009 (Table 4.1). A total of 214 naturally produced sockeye were spawned.

Table 4.1. Numbers of wild and hatchery sockeye salmon collected for broodstock, numbers that died before spawning, and numbers of sockeye spawned, 1989-2009. Unknown origin fish (i.e., undetermined by scale analysis, no CWT or fin clips, and no additional hatchery marks) were considered naturally produced. Mortality includes sockeye that died of natural causes typically near the end of spawning and were not needed for the program, surplus sockeye killed at spawning, sockeye that died but were not recovered from the net pens, and sockeye that may have jumped out of the net pens.

Brood year	Wild sockeye					Hatchery sockeye					Total number spawned
	Number collected	Prespawn loss	Mortality	Number spawne d	Number released	Number collected	Prespawn loss	Mortality	Number spawned	Number released	
1989	299	93	47	115	44	0	0	0	0	0	115
1990	333	7	7	302	17	0	0	0	0	0	302
1991	357	18	16	199	124	0	0	0	0	0	199
1992	362	18	5	320	19	0	0	0	0	0	320
1993	307	79	21	207	0	0	0	0	0	0	207
1994	329	15	9	236	69	5	0	0	5	0	241
1995	218	5	7	194	12	3	0	0	3	0	197
1996	291	2	0	225	64	20	0	0	0	20	225
1997	283	12	3	192	76	19	0	0	19	0	211
1998	225	37	25	122	41	6	0	0	6	0	128
1999	90	7	1	79	3	60	0	0	60	0	139
2000	256	19	1	170	66	5	0	0	5	0	175
2001	252	27	10	200	15	8	1	0	7	0	207
2002	257	0	1	256	0	0	0	0	0	0	256
2003	261	12	9	198	42	0	0	0	0	0	198
2004	211	13	12	177	9	0	0	0	0	0	177
2005	243	29	12	166	36	0	0	0	0	0	166
2006	260	2	4	214	40	0	0	0	0	0	214

Brood year	Wild sockeye					Hatchery sockeye					Total number spawned
	Number collected	Prespawn loss	Mortality	Number spawned	Number released	Number collected	Prespawn loss	Mortality	Number spawned	Number released	
2007	248	15	3	210	20	0	0	0	0	0	210
2008	258	4	11	243	0	2	0	0	2	0	245
2009	258	5	14	239	0	3	0	3	0	0	239
Average	***267***	***20***	***10***	***203***	***33***	***6***	***0***	***0***	***5***	***1***	***208***

Age/Length Data

Ages of sockeye were determined from scales and otoliths collected from broodstock. The 2008 return was comprised primarily of age-4 returning adults (95.0%; Table 4.2). Age-5 and 6 sockeye made up 4.0% and 1.0% of the 2008 return, respectively. The 2009 return consisted primarily of age-4 adults (78.5%; Table 4.2). Age-5 sockeye made up 21.5% of the 2009 return, respectively.

Table 4.2. Percent of hatchery and wild sockeye salmon of different ages (total age) collected from broodstock, 1994-2009.

Return year	Origin	Total age		
		4	5	6
1994	Wild	57.3	41.7	1.0
	Hatchery	40.0	60.0	0.0
1995	Wild	77.3	20.7	2.0
	Hatchery	66.7	33.3	0.0
1996	Wild	65.8	34.2	0.0
	Hatchery	0.0	0.0	0.0
1997	Wild	86.5	13.5	0.0
	Hatchery	57.9	42.1	0.0
1998	Wild	9.9	88.6	1.5
	Hatchery	66.7	33.3	0.0
1999	Wild	21.8	74.7	3.5
	Hatchery	90.0	8.3	1.7
2000	Wild	97.7	2.3	0.0
	Hatchery	100.0	0.0	0.0
2001	Wild	69.9	29.6	0.5
	Hatchery	71.4	28.6	0.0
2002	Wild	31.6	67.6	0.8
	Hatchery	0.0	0.0	0.0
2003	Wild	2.6	90.5	6.9
	Hatchery	0.0	0.0	0.0
2004	Wild	97.5	2.0	0.5
	Hatchery	0.0	0.0	0.0

Return year	Origin	Total age		
		4	5	6
2005	Wild	74.2	25.8	0.0
	Hatchery	0.0	0.0	0.0
2006	Wild	34.0	65.5	0.5
	Hatchery	0.0	0.0	0.0
2007	Wild	1.9	88.4	9.7
	Hatchery	0.0	0.0	0.0
2008	Wild	95.0	4.0	1.0
	Hatchery	100.0	0.0	0.0
2009	Wild	78.5	21.5	0.0
	Hatchery	100.0	0.0	0.0
Average	***Wild***	***56.3***	***21.5***	***0.0***
	Hatchery	***43.3***	***0.0***	***0.0***

Lengths of sockeye for the 2008 and 2009 return years are provided in Table 4.3. Lengths of age-4 and 5 sockeye sampled in 2009 averaged 54 and 59 cm, respectively.

Table 4.3. Mean fork length (cm) at age (total age) of hatchery and wild sockeye salmon collected for broodstock, 1994-2009; SD = 1 standard deviation.

Return year	Origin	Sockeye fork length (cm)								
		Age-4			Age-5			Age-6		
		Mean	N	SD	Mean	N	SD	Mean	N	SD
1994	Wild	56	125	3	55	91	3	54	2	3
	Hatchery	57	2	1	56	3	1	-	0	-
1995	Wild	51	153	2	55	41	4	54	4	5
	Hatchery	53	2	4	59	1	-	-	0	-
1996	Wild	52	146	4	53	76	3	-	0	-
	Hatchery	-	0	-	-	0	-	-	0	-
1997	Wild	50	166	3	53	26	5	-	0	-
	Hatchery	54	11	4	59	8	2	-	0	-
1998	Wild	51	13	4	55	117	3	53	2	3
	Hatchery	52	4	2	55	2	8	-	0	-
1999	Wild	52	19	4	50	65	4	56	3	1
	Hatchery	50	54	3	56	5	4	56	1	-
2000	Wild	52	167	2	54	4	3	-	0	-
	Hatchery	54	5	1	-	0	-	-	0	-
2001	Wild	54	151	3	56	65	4	58	1	-
	Hatchery	51	5	5	55	2	4	-	0	-
2002	Wild	54	77	2	56	165	4	57	2	0
	Hatchery	-	0	-	-	0	-	-	0	-

Return year	Origin	Sockeye fork length (cm)								
		Age-4			Age-5			Age-6		
		Mean	N	SD	Mean	N	SD	Mean	N	SD
2003	Wild	54	5	4	60	172	2	60	13	4
	Hatchery	-	0	-	-	0	-	-	0	-
2004	Wild	53	192	3	56	4	3	63	1	-
	Hatchery	-	0	-	-	0	-	-	0	-
2005	Wild	51	132	3	57	46	4	-	0	-
	Hatchery	-	0	-	-	0	-	-	0	-
2006	Wild	52	70	3	56	135	4	54	2	3
	Hatchery	-	0	-	-	0	-	-	0	-
2007	Wild	57	4	2	58	182	5	58	20	5
	Hatchery	-	0	-	-	0	-	-	0	-
2008	Wild	52	245	3	52	11	3	62	2	6
	Hatchery	53	2	3	-	-	-	-	-	-
2009	Wild	54	197	3	59	54	4	-	-	-
	Hatchery	54	2	1	-	-	-	-	-	-

Sex Ratios

Male sockeye in the 2008 return made up about 49% of the adults collected, resulting in an overall male to female ratio of 0.97:1.00 (Table 4.4). In 2009, males made up about 51% of the adults collected, resulting in an overall male to female ratio of 1.04:1.00. Ratios for both years were near the 1:1 ratio target in the broodstock protocol.

Table 4.4. Numbers of male and female wild and hatchery sockeye collected for broodstock, 1989-2009. Ratios of males to females are also provided.

Return year	Number of wild sockeye			Number of hatchery sockeye			Total M/F ratio
	Males (M)	Females (F)	M/F	Males (M)	Females (F)	M/F	
1989	162	137	1.18:1.00	0	0	-	1.18:1.00
1990	177	156	1.13:1.00	0	0	-	1.13:1.00
1991	260	97	2.68:1.00	0	0	-	2.68:1.00
1992	180	182	0.99:1.00	0	0	-	0.99:1.00
1993	130	177	0.73:1.00	0	0	-	0.73:1.00
1994	162	167	0.97:1.00	1	4	0.25:1.00	0.95:1.00
1995	102	116	0.88:1.00	1	2	0.50:1.00	0.87:1.00
1996	150	161	0.93:1.00	0	0	-	0.93:1.00
1997	139	144	0.97:1.00	10	9	1.11:1.00	0.97:1.00
1998	115	110	1.05:1.00	2	4	0.50:1.00	1.03:1.00
1999	22	68	0.32:1.00	37	23	1.61:1.00	0.65:1.00
2000	155	101	1.53:1.00	3	2	1.50:1.00	1.53:1.00
2001	114	138	0.83:1.00	4	4	1.00:1.00	0.83:1.00

Return year	Number of wild sockeye			Number of hatchery sockeye			Total M/F ratio
	Males (M)	Females (F)	M/F	Males (M)	Females (F)	M/F	
2002	128	129	0.99:1.00	0	0	-	0.99:1.00
2003	161	100	1.61:1.00	0	0	-	1.61:1.00
2004	108	103	1.05:1.00	0	0	-	1.05:1.00
2005	130	113	1.15:1.00	0	0	-	1.15:1.00
2006	130	130	1.00:1.00	0	0	-	1.00:1.00
2007	127	121	1.05:1.00	0	0	-	1.05:1.00
2008	127	131	0.97:1.00	1	1	1.00:1.00	0.97:1.00
2009	133	125	1.06:1.00	0	3	0.00:1.00	1.04:1.00
Total	***2,912***	***2,706***	***1.08:1.00***	***59***	***52***	***1.13:1.00***	***1.08:1.00***

Fecundity

Fecundities for the 2008 and 2009 returns of sockeye salmon averaged 2,555 and 2,459 eggs per female, respectively (Table 4.5). The lower mean fecundity for the 2009 return was likely because of the strong age-4 component in the return. Fecundities for this program between 1989 and 2006 are based upon the total (pooled) number of eyed eggs divided by the number of females spawned. For brood years 2007 to present, mean fecundities were derived from individual fecundities.

Table 4.5. Mean fecundity of female sockeye salmon collected for broodstock, 1989-2009. Fecundities were determined from pooled egg lots and were not identified for individual females.

Return year	Mean fecundity
1989	2,344
1990	2,225
1991	2,598
1992	2,341
1993	2,340
1994	2,798
1995	2,295
1996	2,664
1997	2,447
1998	2,813
1999	2,319
2000	2,673
2001	2,960
2002	2,856
2003	3,511
2004	2,505
2005	2,718
2006	2,656

Return year	Mean fecundity
2007	3,115
2008	2,555
2009	2,459
Average	***2,628***

4.2 Hatchery Rearing

Rearing History

Number of eggs taken

Based on the unfertilized egg-to-release survival standard of 81%, a total of 246,914 eggs are required to meet the program release goal of 200,000 smolts. From 1989 to 2009, the egg take goal was reached in 59% of the years (Table 4.6). The number of eggs taken in 2010 was above the egg take target by 13%.

Table 4.6. Numbers of eggs taken from sockeye broodstock, 1989-2010.

Return year	Number of eggs taken
1989	133,600
1990	326,267
1991	231,254
1992	381,561
1993	231,700
1994	338,562
1995	247,900
1996	314,390
1997	254,459
1998	163,278
1999	190,732
2000	227,234
2001	301,925
2002	356,982
2003	319,470
2004	225,499
2005	211,985
2006	292,136
2007	302,363
2008	316,476
2009	304,963
2010	278,171
Average	***270,496***

Number of acclimation days

Wenatchee sockeye have only been acclimated on Lake Wenatchee water. For brood years 1989 through 1998, unfed fry were transferred from Eastbank FH to Lake Wenatchee Net Pens until release (Table 4.7). For brood years 1999 to present, juvenile sockeye were reared at Eastbank Fish Hatchery until July in an effort to increase growth before release.

Table 4.7. Water source and mean acclimation period for Wenatchee sockeye, brood years 1989-2008.

Brood year	Release year	Transfer date	Release date	Number of Days	Water source
1989	1990	5-Apr	24-Oct	202	Lake Wenatchee
1990	1991	10-Apr	19-Oct	192	Lake Wenatchee
1991	1992	1-Apr	20-Oct	202	Lake Wenatchee
1992	1993	5-Apr	7-Sep	155	Lake Wenatchee
		5-Apr	26-Oct	204	Lake Wenatchee
1993	1994	5-Apr	1-Sep	149	Lake Wenatchee
		5-Apr	17-Oct	195	Lake Wenatchee
1994	1995	4-Apr	15-Sep	164	Lake Wenatchee
		4-Apr	23-Oct	202	Lake Wenatchee
1995	1996	4-Apr	25-Oct	204	Lake Wenatchee
1996	1997	4-Apr	22-Oct	201	Lake Wenatchee
1997	1998	1-Apr	9-Nov	222	Lake Wenatchee
1998	1999	1-Apr	29-Oct	211	Lake Wenatchee
1999	2000	25-Jul	28-Aug	34	Lake Wenatchee
		26-Jul	1-Nov	98	Lake Wenatchee
2000	2001	2-Jul	27-Aug	56	Lake Wenatchee
		3-Jul	27-Sep	86	Lake Wenatchee
2001	2002	15-Jul	28-Aug	44	Lake Wenatchee
		16-Jul	22-Sep	68	Lake Wenatchee
2002	2003	30-Jun	25-Aug	56	Lake Wenatchee
		1-Jul	22-Oct	113	Lake Wenatchee
2003	2004	6-Jul	25-Aug	50	Lake Wenatchee
		7-Jul	3-Nov	119	Lake Wenatchee
2004	2005	5-Jul	29-Aug	55	Lake Wenatchee
		6-Jul	2-Nov	120	Lake Wenatchee
2005	2006	11-Jul	30-Oct	111	Lake Wenatchee
2006	2007	9-10 Jul	31-Oct	113-114	Lake Wenatchee

Brood year	Release year	Transfer date	Release date	Number of Days	Water source
2007	2008	7-8 Jul	29-Oct	113-114	Lake Wenatchee
2008	2009	21-Jul	28-Oct	100	Lake Wenatchee

Release Information

Numbers released

The 2008 Wenatchee sockeye program achieved 113.9% of the 200,000 target goal with about 227,743 fish being released (Table 4.8).

Table 4.8. Total number of sockeye parr released and numbers of released fish with CWTs and PIT tags for brood years 1989-2008. The release target for sockeye is 200,000 fish.

Brood year	Release year	CWT mark rate	Number of released fish with PIT tags	Number released
1989	1990	Not marked	0	108,400
1990	1991	0.9308	0	270,802
1991	1992	0.8940	0	167,523
1992	1993	0.9240	0	340,597
1993	1994	0.7278	0	190,443
1994	1995	0.8869	0	252,859
1995[a]	1996	1.0000	0	150,808
1996[a]	1997	0.9680	0	284,630
1997[a]	1998	0.9642	0	197,195
1998[a]	1999	0.8713	0	121,344
1999	2000	0.9527	0	167,955
2000	2001	0.9558	0	190,174
2001	2002	0.9911	0	200,938
2002	2003	0.9306	0	315,783
2003	2004	0.9291	0	240,459
2004	2005	0.8995	0	172,923
2005	2006	0.9811	14,791	140,542
2006	2007	0.9735	14,764	225,670
2007	2008	0.9863	14,947	252,133
2008	2009	0.9576	14,858	154,772
2009	2010	0.9847	14,486	227,743
Average		***0.9355***	***14,769***[b]	***208,271***

[a] These groups were only adipose fin clipped.
[b] Average is based on brood years 2005 to present.

Numbers tagged

About 98% of the hatchery sockeye released in 2010 were CWT and adipose fin clipped (Table 4.8). In addition, a total of 15,102 juvenile sockeye were PIT tagged at the Eastbank Hatchery during 28 June to 1 July 2010. These fish were transported to the Lake Wenatchee net pens in July and released into the lake on 28 October 2010. At the time of release, a total of 609 fish had died and seven others had shed their tags. Thus, the total number of PIT-tagged sockeye released into the lake was 14,486 (Table 4.8).

Fish size and condition at release

The 2008 brood sockeye were released as parr in 2009 and emigrated as yearling smolts in spring of 2010. Size at release was 3.8% and 52.4% of the fork length and weight goals, respectively. The 2008 brood year was also above the CV goal for length by 6.7% (Table 4.9).

Table 4.9. Mean lengths (FL, mm), weight (g and fish/pound), and coefficient of variation (CV) of sockeye released, brood years 1989-2008. Size targets are provided in the last row of the table.

Brood year	Release year	Fork length (mm)		Mean weight	
		Mean	CV	Grams (g)	Fish/pound
1989	1990	128	-	18.2	25
1990	1991	131	-	18.9	24
1991	1992	117	3.0	20.6	22
1992	1993	73	6.8	4.2	44
1993	1994	103	-	13.6	40
1994	1995	75	6.1	4.5	38
1995	1996	137	8.2	14.7	30
1996	1997	107	5.6	15.1	30
1997	1998	122	6.1	21.3	21
1998	1999	112	5.4	17.0	27
1999	2000	94	9.5	9.5	48
		134	11.5	31.3	15
2000	2001	123	6.5	22.3	20
		146	8.4	26.0	12
2001	2002	118	7.4	20.7	22
		135	7.3	30.5	15
2002	2003	73	5.6	4.4	104
		118	7.7	13.7	23
		145	9.4	38.6	13
2003	2004	79	4.6	4.8	96
		118	5.9	17.0	26
		158	8.1	44.3	10

Brood year	Release year	Fork length (mm)		Mean weight	
		Mean	CV	Grams (g)	Fish/pound
2004	2005	116	4.5	17.2	18
		151	7.0	39.3	12
2005	2006	149	7.5	43.7	10
2006	2007	138	10.6	32.4	14
2007	2008	137	9.3	33.0	14
2008	2009	138	9.6	34.6	13
Targets		***133***	***9.0***	***22.7***	***20***

Survival Estimates

Overall survival of Wenatchee sockeye from green (unfertilized) egg to release was above the standard set for the program. Survivals for unfertilized-to-eyed egg were well below the standard for the program. Because of the highly variable unfertilized-to-eyed egg survivals, studies should be considered that assess the effects of holding adults on warm surface water at Lake Wenatchee on gamete maturation/viability in addition to reducing negative phototactic behavior at swim up (potential influences on survival at the fertilization to ponding stages) (Table 4.10).

Table 4.10. Hatchery life-stage survival rates (%) for sockeye salmon, brood years 1989-2008. Survival standards or targets are provided in the last row of the table.

Brood year	Collection to spawning		Unfertilized egg-eyed	Eyed egg-ponding	30 d after ponding	100 d after ponding	Ponding to release	Transport to release	Unfertilized egg-release
	Female	Male							
1989	41.6	100.0	88.1	63.9	99.2	98.9	98.1	65.2	83.0
1990	96.2	99.4	90.8	96.3	99.9	99.2	98.4	98.4	81.1
1991	91.8	94.1	79.2	94.8	99.8	99.3	96.4	96.4	72.4
1992	91.1	98.8	92.3	98.0	99.9	99.8	98.6	98.8	89.2
1993	57.1	99.2	89.2	98.3	99.6	99.1	93.7	93.8	82.2
1994	89.8	99.2	79.2	96.0	99.5	98.6	98.3	98.2	74.7
1995	97.5	99.1	87.5	95.0	99.0	93.3	73.2	73.2	60.8
1996	99.2	100.0	95.1	98.7	99.7	99.3	96.4	96.5	90.5
1997	92.8	99.3	84.8	97.9	97.9	97.6	95.5	94.9	77.5
1998	75.4	95.5	77.7	98.4	98.6	98.2	97.1	97.2	74.3
1999	92.3	100.0	92.2	97.3	99.6	99.3	98.2	99.7	88.1
2000	84.5	98.1	93.8	97.7	96.7	96.1	91.4	96.8	83.7
2001	75.4	99.2	78.5	97.6	98.0	97.6	86.9	95.1	66.6
2002	100.0	100.0	95.7	97.8	99.6	99.2	94.6	99.8	88.5
2003	91.0	98.1	87.2	96.9	99.0	98.2	94.8	95.5	74.6
2004	88.7	92.6	88.0	93.1	97.9	97.4	93.7	96.1	76.7
2005	98.5	98.5	85.3	94.9	97.8	96.6	95.5	99.2	66.3

Brood year	Collection to spawning		Unfertilized egg-eyed	Eyed egg-ponding	30 d after ponding	100 d after ponding	Ponding to release	Transport to release	Unfertilized egg-release
	Female	Male							
2006	95.3	99.1	73.2	85.4	95.4	94.6	87.8	98.5	54.9
2007	88.4	99.2	89.1	98.6	97.0	95.9	94.9	99.0	83.4
2008	97.0	100.0	59.0	88.3	99.1	97.2	93.8	97.4	48.9
Standard	***90.0***	***85.0***	***92.0***	***98.0***	***97.0***	***93.0***	***90.0***	***95.0***	***81.0***

4.3 Disease Monitoring

Rearing of the 2008 brood sockeye was typical to previous years with fish being held on Lake Wenatchee water in net pens for 100 days before being released directly into the lake. No significant disease-related mortality occurred during the rearing of the 2008 brood sockeye.

4.4 Natural Juvenile Productivity

During 2010, juvenile sockeye salmon were sampled at the Upper Wenatchee and Lower Wenatchee traps.

Emigrant and Smolt Estimates

Upper Wenatchee Trap

The Upper Wenatchee Trap operated nightly between 12 March and 8 July 2010. During the five-month sampling period, a total of 60,792 wild sockeye and 1,909 hatchery sockeye smolts were captured at the Upper Wenatchee Trap. Based on a pooled daily trap efficiency of 0.53% for both wild and hatchery sockeye (based on eight mark-recapture trials), the total number of smolts that emigrated past the trap in 2010 was 11,551,430 (±805,182) wild and 368,600 (±30,120) hatchery sockeye (Table 4.11). This was the fourth brood year since 1999 that all hatchery sockeye parr were released at a similar size and time. Monthly captures of all fish and results of capture efficiency tests at the Upper Wenatchee Trap are reported in Appendix B.

Because the estimated hatchery smolt number (368,600) was greater than the actual number of hatchery parr released (154,772), we adjusted our emigrant estimate and assumed that survival was 100% (Tables 4.11 and 4.14). Overestimation of the smolt migration is likely due to an underestimate of actual trap efficiency and probability of trap avoidance.

Table 4.11. Estimated numbers of wild and hatchery sockeye smolts that emigrated from Lake Wenatchee during run years 1997-2010.

Run year	Numbers of sockeye smolts	
	Wild smolts	Hatchery smolts
1997	55,359	28,828
1998	1,447,259	55,985
1999	1,944,966	112,524
2000	985,490	24,684
2001	39,353	94,046
2002	729,716	121,511

Run year	Numbers of sockeye smolts	
	Wild smolts	Hatchery smolts
2003	5,439,032	140,322
2004	5,771,187	216,023
2005	723,413	122,399
2006	1,266,971	159,500
2007	2,797,313	140,542
2008	549,682	102,907
2009	732,686	247,098
2010	11,551,430	154,772
Average	***2,430,990***	***122,939***

Age classes of wild sockeye smolts were determined from a length frequency analysis based on scales collected randomly each year since 1997 (Table 4.12). For the available run years, most wild sockeye smolts migrated as age 1+ fish. Only in two years (1997 and 2005) did more smolts migrate as age 2+ fish. Relatively few smolts migrated at age 3+.

Table 4.12. Age structure and estimated number of wild sockeye smolts that emigrated from Lake Wenatchee, 1997-2010.

Run year	Proportion of wild smolts			Total wild emigrants
	Age 1+	Age 2+	Age 3+	
1997	0.075	0.906	0.019	55,359
1998	0.955	0.037	0.008	1,447,259
1999	0.619	0.381	0.000	1,944,966
2000	0.599	0.400	0.001	985,490
2001	0.943	0.051	0.006	39,353
2002	0.961	0.039	0.000	729,716
2003	0.740	0.026	0.000	5,439,032
2004	0.929	0.071	0.000	5,771,187
2005	0.230	0.748	0.022	723,413
2006	0.994	0.006	0.000	1,266,971
2007	0.996	0.004	0.000	2,797,313
2008	0.804	0.195	0.001	549,682
2009	0.930	0.055	0.051	732,686
2010*	0.975	0.024	0.001	11,551,430
Average	***0.768***	***0.210***	***0.008***	***2,430,990***

* Ages have not been confirmed with scale analysis.

Lower Wenatchee Trap

The Lower Wenatchee Trap operated nightly between 4 February and 20 July 2010. Because of high river flows, debris, snow/ice, or mechanical failure, traps 1 and 2 were inoperable for 19 and 68 days, respectively. During the six-month sampling period, a total of 3,153 wild sockeye smolts and 440 hatchery sockeye smolts were captured at the Lower Wenatchee Trap. Most of the smolts migrated during April and May. Monthly captures and mortalities of all fish collected at the Lower Wenatchee Trap are reported in Appendix B.

Freshwater Productivity

Egg-smolt survival estimates for wild sockeye salmon are provided in Table 4.13. Estimates of egg deposition were calculated based on the spawner escapement at Tumwater Dam and the sex ratio and fecundity of the broodstock. Egg-smolt survival rates for brood years 1995-2007 have ranged from 0.012 to 0.212 (mean = 0.114).

Table 4.13. Estimated egg deposition (estimated as mean fecundity times estimated number of females), numbers of smolts, and survival rates for wild Wenatchee sockeye salmon, 1995-2009; NA = not available.

Brood year	Number of females	Mean fecundity	Total eggs	Numbers of wild smolts				Egg-smolt survival
				Age 1+	Age 2+	Age 3+	Total	
1995	2,136	2,295	4,902,120	4,174	53,549	0	57,723	0.012
1996	3,767	2,664	10,035,288	1,382,133	741,032	985	2,124,150	0.212
1997	5,404	2,447	13,223,588	1,203,934	394,196	236	1,598,366	0.121
1998	2,024	2,813	5,693,512	590,309	2,007	0	592,316	0.104
1999	513	2,319	1,189,647	37,110	28,459	0	65,569	0.055
2000	11,413	2,673	30,506,949	701,257	1,378,795	0	2,080,052	0.068
2001	21,685	2,960	64,187,600	4,024,884	409,754	15,915	4,450,553	0.069
2002	17,226	2,856	49,197,456	5,361,433	541,113	0	5,902,546	0.120
2003	2,158	3,511	7,576,738	166,385	7,602	8,392	182,379	0.024
2004	15,469	2,534	39,198,446	1,259,369	106,298	550	1,366,216	0.035
2005	5,867	2,718	15,946,506	2,786,123	107,243	37,367	2,930,733	0.184
2006	2,747	2,656	7,296,032	442,164	53,413	4,621	500,197	0.069
2007	2,001	3,115	6,232,804	679,273	280,469	NA	NA	NA
2008	11,775	2,555	30,084,691	11,266,110	NA	NA	NA	NA
2009	7,526	2,459	18,507,000	NA	NA	NA	NA	NA
Average	***7,447***	***2,703***	***20,288,281***	***2,136,047***	***308,371***	***1,836***	***1,809,138***	***0.114***

Juvenile survival rates for hatchery sockeye salmon are provided in Table 4.14. Release-smolt survival rates for brood years 1995-2008 have ranged from 0.000 to 1.000 (mean = 0.593). Egg-smolt survival rates for the same brood years ranged from 0.000 to 0.817 (mean = 0.305). On average, egg-smolt survival of hatchery sockeye is about three times greater than egg-smolt survival of wild sockeye. On four separate occasions, however, the estimated number of hatchery smolts equaled or exceeded the number of hatchery parr released in the lake. This is probably because the pooled trap efficiencies are biased high.

Table 4.14. Juvenile survival rates for hatchery Wenatchee sockeye, brood years 1995-2008.

<table>
<tr><th>Brood year</th><th>Number of eggs</th><th>Number of parr released</th><th>Date of release</th><th>Estimated number of smolts</th><th>Egg-smolt survival</th><th>Release-smolt survival</th></tr>
<tr><td>1995</td><td>247,900</td><td>150,808</td><td>10/25/96</td><td>28,828</td><td>0.116</td><td>0.191</td></tr>
<tr><td>1996</td><td>314,390</td><td>284,630</td><td>10/22/97</td><td>55,985</td><td>0.178</td><td>0.197</td></tr>
<tr><td>1997</td><td>254,459</td><td>197,195</td><td>11/9/98</td><td>112,524</td><td>0.442</td><td>0.571</td></tr>
<tr><td>1998</td><td>163,278</td><td>121,344</td><td>10/27/99</td><td>24,684</td><td>0.151</td><td>0.203</td></tr>
<tr><td rowspan="2">1999</td><td rowspan="2">190,732</td><td>84,466</td><td>8/28/00</td><td>30,326</td><td>0.159</td><td>0.359</td></tr>
<tr><td>83,489</td><td>11/1/00</td><td>63,720</td><td>0.334</td><td>0.763</td></tr>
<tr><td rowspan="2">2000</td><td rowspan="2">227,234</td><td>92,055</td><td>8/27/01</td><td>30,918</td><td>0.136</td><td>0.336</td></tr>
<tr><td>98,119</td><td>9/27/01</td><td>90,593</td><td>0.399</td><td>0.923</td></tr>
<tr><td rowspan="2">2001</td><td rowspan="2">301,925</td><td>96,486</td><td>8/28/02</td><td>36,484</td><td>0.121</td><td>0.378</td></tr>
<tr><td>104,452</td><td>9/23/02</td><td>103,838</td><td>0.344</td><td>0.994</td></tr>
<tr><td rowspan="3">2002</td><td rowspan="3">356,982</td><td>98,509</td><td>6/16/03</td><td>5,192</td><td>0.015</td><td>0.053</td></tr>
<tr><td>104,855</td><td>8/25/03</td><td>98,412</td><td>0.276</td><td>0.939</td></tr>
<tr><td>112,419</td><td>10/22/03</td><td>112,419</td><td>0.315</td><td>1.000</td></tr>
<tr><td rowspan="3">2003</td><td rowspan="3">319,470</td><td>32,755</td><td>6/15/04</td><td>0</td><td>0.000</td><td>0.000</td></tr>
<tr><td>104,879</td><td>8/25/04</td><td>19,574</td><td>0.061</td><td>0.187</td></tr>
<tr><td>102,825</td><td>11/3/04</td><td>102,825</td><td>0.322</td><td>1.000</td></tr>
<tr><td rowspan="2">2004</td><td rowspan="2">225,499</td><td>81,428</td><td>8/29/05</td><td rowspan="2">159,500</td><td rowspan="2">0.707</td><td rowspan="2">0.922</td></tr>
<tr><td>91,495</td><td>11/2/05</td></tr>
<tr><td rowspan="2">2005</td><td rowspan="2">211,985</td><td>70,386</td><td>10/30/06</td><td rowspan="2">140,542</td><td rowspan="2">0.663</td><td rowspan="2">1.000</td></tr>
<tr><td>70,156</td><td>10/30/06</td></tr>
<tr><td>2006</td><td>292,136</td><td>225,670</td><td>10/31/07</td><td>102,907</td><td>0.352</td><td>0.456</td></tr>
<tr><td>2007</td><td>302,363</td><td>252,133</td><td>10/29/08</td><td>247,098</td><td>0.817</td><td>0.980</td></tr>
<tr><td>2008</td><td>316,476</td><td>154,772</td><td>10/28/09</td><td>154,772</td><td>0.489</td><td>1.000</td></tr>
</table>

PIT Tagging Activities

As part of the Integrated Status and Effectiveness Monitoring Program (ISEMP), a total of 10,006 juvenile sockeye salmon were PIT tagged and released in 2010 (Table 4.15a). All of these were tagged at the Upper Wenatchee Trap. No sockeye were tagged and released at the Lower Wenatchee trap. See Appendix C for a complete list of all fish captured, tagged, lost, and released.

Table 4.15a. Numbers of wild sockeye salmon that were captured, tagged, and released at different locations within the Wenatchee Basin, 2010. Numbers of fish that died or shed tags are also given.

Sampling Location	Number held	Number of recaptures	Number tagged	Number died	Shed Tags	Total released	Percent mortality
Upper Wenatchee Trap	11,103	7	10,082	76	0	10,006	0.68
Lower Wenatchee Trap	0	0	0	0	0	0	--
Total:	**11,103**	**7**	**10,082**	**76**	**0**	**10,006**	**068**

Numbers of wild sockeye salmon PIT-tagged and released as part of ISEMP during the period 2006-2010 are shown in Table 4.15b.

Table 4.15b. Summary of the numbers of wild sockeye salmon that were tagged and released at different locations within the Wenatchee Basin, 2006-2010.

Sampling Location	Numbers of PIT-tagged sockeye salmon released				
	2006	2007	2008	2009	2010
Upper Wenatchee Trap	0	0	3,165	3,683	10,006
Lower Wenatchee Trap	0	0	0	0	0
Total:	**0**	**0**	**3,165**	**3,683**	**10,006**

4.5 Spawning Surveys

Spawning surveys were conducted in the Little Wenatchee and White (including the Napeequa River) rivers from 24 August to 19 October 2010. Surveys in 2010 only included counting numbers of live sockeye spawners. No redd counts have been conducted since 2007 (see Appendix G for more details).

Spawn Timing

Sockeye began spawning during the first week of September and peaked around the third week of September (Figure 4.1). Peak spawning was determined using the total number of spawners observed on the spawning grounds.

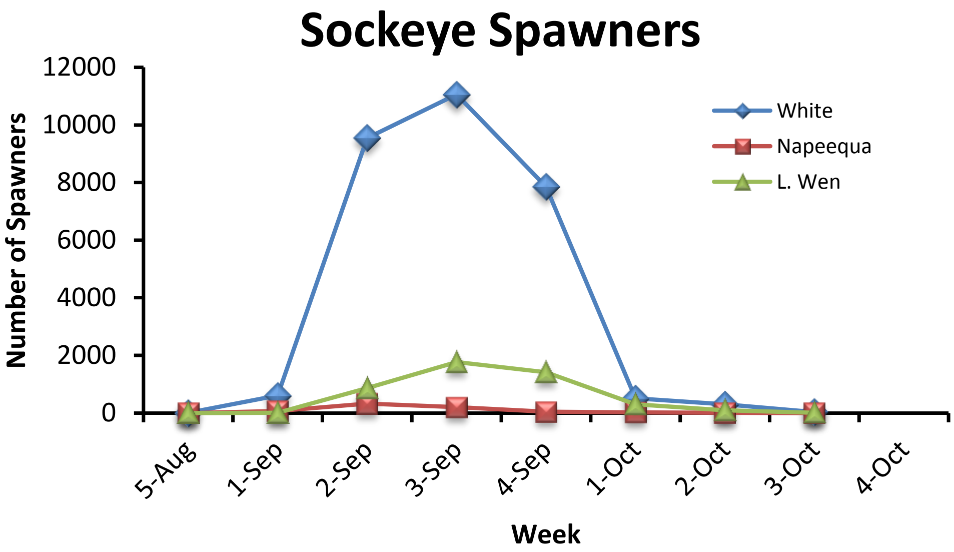


Figure 4.1. Numbers of sockeye spawners counted during different weeks in different sampling streams within the Wenatchee Basin, August through October 2010.

Spawning Escapement

Spawning escapement of sockeye salmon in 2010 was estimated using the area-under-the-curve (AUC) method (i.e., escapement = (AUC/redd residence time) x observer efficiency) and mark-recapture methods. AUC relied on weekly counts of live sockeye and assumed a redd residence time of 11 days and an observer efficiency of 100%. The mark-recapture method used PIT tags to estimate sockeye spawning escapement (see Appendix G for more details).

Area-under-the-curve

Based on the AUC approach, the estimated total spawning escapement of sockeye in the Wenatchee Basin in 2010 was 21,700 (Table 4.16). About 88% of the escapement spawned in the White River Basin (including the Napeequa River).

Table 4.16. Peak numbers of live spawners and total spawning escapement estimates for sockeye salmon in the Wenatchee Basin, August through October 2010.

Sampling basin	Peak number of live fish	Spawning escapement
Little Wenatchee	1,762	2,543
White River	11,380	19,157
Total	***13,142***	***21,700***

The spawning escapement of 7,767 Wenatchee sockeye is less than the overall average of 14,857 (Table 4.17).

Table 4.17. Spawning escapements for sockeye salmon in the Wenatchee Basin for return years 1989-2010; NA = not available. Total escapements before 2003 were based on counts at Tumwater Dam.

Return year	Spawning escapement		
	Little Wenatchee	White	Total
1989	NA	NA	**21,802**
1990	NA	NA	**27,325**
1991	NA	NA	**26,689**
1992	NA	NA	**16,461**
1993	NA	NA	**27,726**
1994	NA	NA	**7,330**
1995	NA	NA	**3,448**
1996	NA	NA	**6,573**
1997	NA	NA	**9,693**
1998	NA	NA	**4,014**
1999	NA	NA	**1,025**
2000	NA	NA	**20,735**
2001	NA	NA	**29,103**
2002	NA	NA	**27,565**
2003	NA	NA	**4,855**
2004	NA	NA	**27,556**
2005	NA	NA	**14,011**
2006	574	5,634	**6,208**
2007	150	1,720	**1,870**
2008	3,491	16,757	**20,248**
2009	763	7,004	**7,767**
2010	2,543	19,157	**21,700**
Average	***1,504***	***10,054***	***15,168***

Mark-recapture method

Using mark-recapture methods, the estimated total escapement of sockeye in the Upper Wenatchee Basin in 2010 was 21,604 (Table 4.18). About 90% of the escapement entered the White River Basin (including the Napeequa River).

Table 4.18. Estimated escapement of adult sockeye into the Little Wenatchee and White River basins for return years 2009-2010. Escapement is based on recapture of PIT tagged fish.

Return year	Tumwater Dam count	Recreational harvest	Little Wenatchee escapement	White River escapement	Total spawning escapement
2009	16,034	2,229	576	13,876	14,452
2010	35,824	4,129	2,062	19,542	21,604
Average	***25,929***	***3,179***	***1,319***	***16,709***	***13,528***

4.6 Carcass Surveys

Carcass surveys were conducted in the Little Wenatchee and White (including the Napeequa River) rivers from 15 September to 25 October 2010.

Number sampled

A total of 8,119 sockeye carcasses were sampled during September through October, 2010, in the Wenatchee Basin (Table 4.19). This is considerably higher than the 1993-2010 average of 2,832 carcasses. Most of the carcasses sampled in 2010 were collected in the White River basin (97% or 7,902 carcasses) (Figure 4.2). The remaining 3% were sampled in the Little Wenatchee River (217 carcasses).

Table 4.19. Numbers of sockeye carcasses sampled within different streams/watersheds within the Wenatchee Basin, 1989-2010.

Survey year	Numbers of sockeye carcasses			
	Little Wenatchee	White	Napeequa	Total
1993	90	195	0	**285**
1994	121	165	0	**286**
1995	0	56	0	**56**
1996	43	1,387	3	**1,433**
1997	69	1,425	41	**1,535**
1998	61	524	4	**589**
1999	40	186	0	**226**
2000	821	5,494	0	**6,315**
2001	650	3,127	0	**3,777**
2002	506	7,258	55	**7,819**
2003	86	1,002	14	**1,102**
2004	625	6,960	138	**7,723**
2005	1	7	0	**8**
2006	101	2,158	38	**2,297**
2007	17	363	3	**383**
2008	476	5,132	125	**5,733**
2009	84	3,103	103	**3,290**
2010	217	7,832	70	**8,119**
Average	***223***	***2,576***	***33***	***2,832***

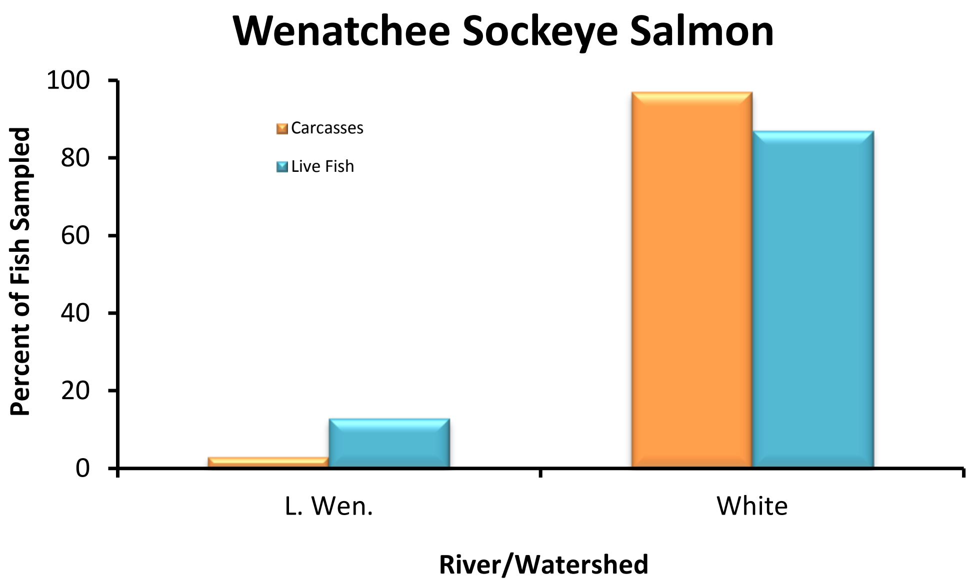


Figure 4.2. Percent of the peak number of live sockeye observed and the total number of sockeye carcasses sampled in different streams/watersheds within the Wenatchee Basin during August through October, 2010.

Carcass Distribution and Origin

Sockeye carcasses were not evenly distributed among reaches within survey streams in 2010 (Table 4.20). Carcasses were only found in Reaches 2 (Lost Creek to Rainy Creek) on the Little Wenatchee. Most (99%) of the carcasses sampled in the White River Basin were in Reach 2 (Sears Creek Bridge to Napeequa River). About 1% of the carcasses sampled in the White River Basin were in the Napeequa River.

Table 4.20. Numbers of carcasses sampled within different streams/watersheds within the Wenatchee Basin during August through September, 2010.

Stream/watershed	Reach	Total carcasses
Little Wenatchee	Little Wen 1	0
	Little Wen 2	217
	Little Wen 3	0
	Total	**217**
White	White 1	0
	White 2	7,832
	White 3	0
	Napeequa 1	70
	Total	**7,902**
Grand Total		***8,119***

Numbers of wild and hatchery-origin sockeye carcasses sampled in 2010 will be available after analysis of marks/tags and scales. Based on the available data (1993-2009), the largest percentage of both wild and hatchery sockeye spawned in Reach 2 on the White River (Table 4.21 and Figure 4.3). However, a greater percentage of wild fish were found in Reach 2 than hatchery fish. The opposite occurred in Reach 2 on the Little Wenatchee. There, a larger percentage of hatchery fish were found compared to wild fish.

Table 4.21. Numbers of wild and hatchery sockeye carcasses sampled within different reaches in the Wenatchee Basin, 1993-2010. Reach codes are described in Table 2.9.

Survey year	Origin	Numbers of sockeye carcasses					
		Little Wenatchee		White River			Total
		L2	L3	H1	H2	Q1	
1993	Wild	86	0	0	183	0	**269**
	Hatchery	4	0	0	12	0	**16**
1994	Wild	112	0	0	155	0	**267**
	Hatchery	9	0	0	9	0	**18**
1995	Wild	0	0	0	55	0	**55**
	Hatchery	0	0	0	1	0	**1**
1996	Wild	41	0	0	1,299	3	**1,343**
	Hatchery	2	0	0	88	0	**90**
1997	Wild	65	0	0	1,411	40	**1,516**
	Hatchery	4	0	0	11	1	**16**
1998	Wild	61	0	0	515	4	**580**
	Hatchery	0	0	0	9	0	**9**
1999	Wild	30	0	0	164	0	**194**
	Hatchery	10	0	0	22	0	**32**
2000	Wild	694	0	3	5,239	0	**5,936**
	Hatchery	127	0	0	252	0	**379**
2001	Wild	625	0	0	3,063	0	**3,688**
	Hatchery	25	0	0	64	0	**89**
2002	Wild	504	0	0	7,207	55	**7,766**
	Hatchery	2	0	0	51	0	**53**
2003	Wild	81	0	0	993	14	**1,088**
	Hatchery	5	0	0	9	0	**14**
2004	Wild	606	0	0	6,755	166	**7,527**
	Hatchery	19	0	0	205	22	**246**
2005	Wild	201	0	5	2,966	21	**3,193**
	Hatchery	1	0	0	8	0	**9**
2006	Wild	80	0	0	2,112	36	**2,228**
	Hatchery	21	0	0	46	2	**69**
2007	Wild	17	0	0	346	3	**366**
	Hatchery	0	0	0	17	0	**17**
2008	Wild	472	0	0	5,118	124	**5,714**
	Hatchery	4	0	0	14	1	**19**
2009	Wild	80	0	0	3,084	103	**3,267**
	Hatchery	4	0	0	19	0	**23**

Survey year	Origin	Numbers of sockeye carcasses					
		Little Wenatchee		White River			Total
		L2	L3	H1	H2	Q1	
2010	Wild	210	0	0	7,711	69	**7,990**
	Hatchery	7	0	0	121	1	**129**
Average	***Wild***	***220***	***0***	***0***	***2,688***	***35***	***2,944***
	Hatchery	***14***	***0***	***0***	***53***	***2***	***68***

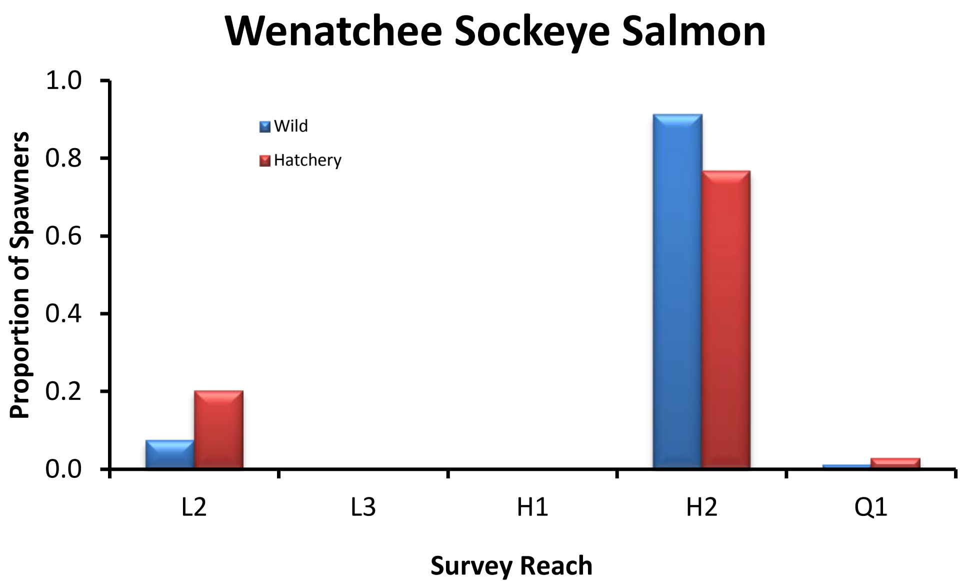


Figure 4.3. Distribution of wild and hatchery produced carcasses in different reaches in the Wenatchee Basin, pooled data from 1993-2010. Reach codes are described in Table 2.9; L = Little Wenatchee, H = White River, and Q = Napeequa River.

Sampling Rate

The sampling rate of sockeye carcasses differed among basins, with a higher sampling rate in the White than in the Little Wenatchee (Table 4.22). Nevertheless, the overall sampling rate for both basins combined exceeded the target of 20%.

Table 4.22. Numbers of carcasses, estimated spawning escapements (based on AUC), and sampling rates for sockeye salmon in the Wenatchee Basin, 2010.

Sampling basin	Total number of carcasses	Total spawning escapement	Sampling rate
Little Wenatchee	217	2,543	0.09
White	7,902	19,157	0.41
Total	***8,119***	***21,700***	***0.37***

Length Data

Mean lengths (POH, cm) of male and female hatchery sockeye carcasses sampled during surveys in the Wenatchee Basin in 2010 are provided in Table 4.23. Wild sockeye are sampled at Tumwater Dam, not on the spawning grounds. On average, males were slightly larger than females.

Table 4.23. Mean lengths (postorbital-to-hypural length; cm) and standard deviations (in parentheses) of male and female hatchery sockeye carcasses sampled in different streams/watersheds in the Wenatchee Basin, 2010; N = number of fish sampled. Wild sockeye were sampled at Tumwater Dam.

Stream/watershed	Male		Female	
	N	Length (cm)	N	Length (cm)
Little Wenatchee River	0	NA	7	41 (1)
White River	43	42 (2)	79	41 (2)
Napeequa River	0	NA	1	40 (NA)
Wenatchee River	0	NA	0	NA
Total	***43***	***41.7 (2.1)***	***87***	***40.6 (1.8)***

4.7 Life History Monitoring

Life history characteristics of Wenatchee sockeye were assessed by examining carcasses on spawning grounds and fish sampled at broodstock collection sites, and by reviewing tagging data and fisheries statistics.

Migration Timing

There was little difference in migration timing of hatchery and wild sockeye past Tumwater Dam (Table 4.24a and b; Figure 4.4). On average, early in the run, hatchery and wild sockeye arrived at the dam at about the same time. Toward the end of the migration period, hatchery sockeye tended to arrive at the dam slightly later than did wild sockeye. Most hatchery and wild sockeye migrated upstream past Tumwater Dam during July through early August. The peak migration time for both hatchery and wild sockeye was the last week of July (Figure 4.4).

Table 4.24a. The Julian day and date that 10%, 50% (median), and 90% of the wild and hatchery sockeye salmon passed Tumwater Dam, 1998-2010. The average Julian day and date are also provided. Migration timing is based on video sampling at Tumwater. Data for 1998 through 2003 were based on videotapes and broodstock trapping and may not reflect the actual number of hatchery sockeye salmon. All sockeye were visually examined during trapping from 2004 to present.

Survey year	Origin	Sockeye Migration Time (days)								Sample size
		10 Percentile		50 Percentile		90 Percentile		Mean		
		Julian	Date	Julian	Date	Julian	Date	Julian	Date	
1998	Wild	195	14-Jul	201	20-Jul	208	27-Jul	202	21-Jul	4,173
	Hatchery	196	15-Jul	204	23-Jul	220	8-Aug	206	25-Jul	31
1999	Wild	226	14-Aug	233	21-Aug	241	29-Aug	234	22-Aug	908
	Hatchery	228	16-Aug	234	22-Aug	242	30-Aug	235	23-Aug	264
2000	Wild	200	18-Jul	206	24-Jul	213	31-Jul	207	25-Jul	18,390

Survey year	Origin	Sockeye Migration Time (days)								Sample size
		10 Percentile		50 Percentile		90 Percentile		Mean		
		Julian	Date	Julian	Date	Julian	Date	Julian	Date	
	Hatchery	199	17-Jul	206	24-Jul	213	31-Jul	206	24-Jul	2,589
2001	Wild	189	8-Jul	194	13-Jul	214	2-Aug	198	17-Jul	32,554
	Hatchery	199	18-Jul	212	31-Jul	240	28-Aug	214	2-Aug	79
2002	Wild	204	23-Jul	208	27-Jul	219	7-Aug	210	29-Jul	27,241
	Hatchery	204	23-Jul	209	28-Jul	222	10-Aug	211	30-Jul	580
2003	Wild	194	13-Jul	200	19-Jul	208	27-Jul	201	20-Jul	4,699
	Hatchery	194	13-Jul	201	20-Jul	211	30-Jul	203	22-Jul	375
2004	Wild	191	9-Jul	196	14-Jul	207	25-Jul	198	16-Jul	31,408
	Hatchery	189	7-Jul	194	12-Jul	203	21-Jul	196	14-Jul	1,758
2005	Wild	192	11-Jul	199	18-Jul	227	15-Aug	204	23-Jul	14,176
	Hatchery	187	6-Jul	200	19-Jul	251	8-Sep	212	31-Jul	42
2006	Wild	201	20-Jul	204	23-Jul	214	2-Aug	206	25-Jul	9,151
	Hatchery	202	21-Jul	219	7-Aug	228	16-Aug	215	3-Aug	507
2007	Wild	201	20-Jul	210	29-Jul	227	15-Aug	213	1-Aug	2,542
	Hatchery	205	24-Jul	213	1-Aug	231	19-Aug	216	4-Aug	65
2008	Wild	200	18-Jul	207	25-Jul	219	6-Aug	208	26-Jul	29,229
	Hatchery	201	19-Jul	206	24-Jul	215	2-Aug	208	26-Jul	103
2009	Wild	198	17-Jul	204	23-Jul	213	1-Aug	206	25-Jul	15,552
	Hatchery	199	18-Jul	205	24-Jul	215	3-Aug	207	26-Jul	534
2010	Wild	199	18-Jul	205	24-Jul	220	8-Aug	208	27-Jul	34,519
	Hatchery	200	19-Jul	215	3-Aug	244	1-Sep	218	6-Aug	1,302
Average	Wild	***199***	-	***205***	-	***218***	-	***207***	-	***17,272***
	Hatchery	***200***	-	***209***	-	***226***	-	***211***	-	***633***

Table 4.24b. The week that 10%, 50% (median), and 90% of the wild and hatchery sockeye salmon passed Tumwater Dam, 1998-2010. The average week is also provided. Migration timing is based on video sampling at Tumwater. Data for 1998 through 2003 were based on videotapes and broodstock trapping and may not reflect the actual number of hatchery sockeye salmon. All sockeye were visually examined during trapping from 2004 to present.

Survey year	Origin	Sockeye Migration Time (week)				Sample size
		10 Percentile	50 Percentile	90 Percentile	Mean	
1998	Wild	28	29	30	29	4,173
	Hatchery	28	30	32	30	31
1999	Wild	33	34	35	34	908
	Hatchery	33	34	35	34	264
2000	Wild	29	30	31	30	18,390
	Hatchery	29	30	31	30	2,589

Survey year	Origin	Sockeye Migration Time (week)				Sample size
		10 Percentile	50 Percentile	90 Percentile	Mean	
2001	Wild	27	28	31	29	32,554
	Hatchery	29	31	35	31	79
2002	Wild	30	30	32	30	27,241
	Hatchery	30	30	32	31	580
2003	Wild	28	29	30	29	4,699
	Hatchery	28	29	31	29	375
2004	Wild	28	28	28	29	31,408
	Hatchery	27	28	29	28	1,758
2005	Wild	28	29	33	30	14,176
	Hatchery	27	29	36	31	42
2006	Wild	29	29	31	30	9,151
	Hatchery	29	32	33	31	507
2007	Wild	29	30	33	31	2,542
	Hatchery	30	31	33	31	65
2008	Wild	29	30	32	30	29,229
	Hatchery	29	30	31	30	103
2009	Wild	29	30	31	30	15,552
	Hatchery	29	29	31	30	534
2010	Wild	29	30	32	30	34,519
	Hatchery	29	31	35	32	1,302
Average	Wild	***29***	***30***	***31***	***30***	***17,272***
	Hatchery	***29***	***30***	***33***	***31***	***633***

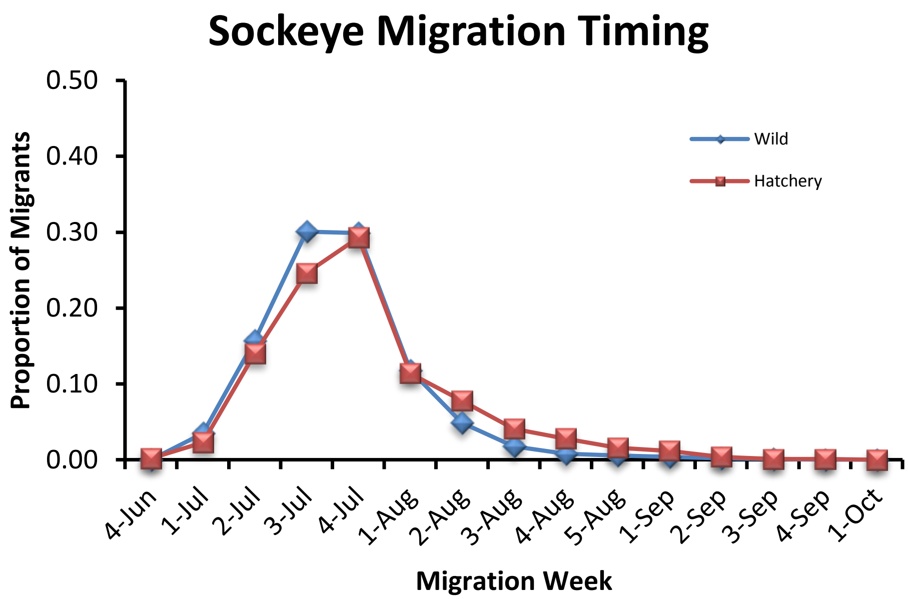


Figure 4.4. Proportion of wild and hatchery sockeye observed (using video) passing Tumwater Dam each week during their migration period late-June through early-October; data were pooled over survey years 1998-2010.

Age at Maturity

Although sample sizes are small, it appears that most wild sockeye returned as age-5 fish, while most hatchery sockeye returned as age-4 fish (Table 4.25; Figure 4.5). Only wild fish have returned at age-6.

Table 4.25. Proportions of wild and hatchery sockeye of different ages (total age) sampled in broodstock and on spawning grounds, 1994-2009.

Survey year	Origin	Total age						Sample size
		2	3	4	5	6	7	
1994	Wild	-	-	-	-	-	-	0
	Hatchery	0.00	0.00	0.88	0.13	0.00	0.00	16
1995	Wild	-	-	-	-	-	-	0
	Hatchery	0.00	0.00	0.00	1.00	0.00	0.00	1
1996	Wild	-	-	-	-	-	-	0
	Hatchery	0.00	0.00	1.00	0.00	0.00	0.00	82
1997	Wild	-	-	-	-	-	-	0
	Hatchery	0.00	0.00	0.77	0.23	0.00	0.00	13
1998	Wild	0.00	0.08	0.85	0.08	0.00	0.00	26
	Hatchery	0.00	0.00	0.64	0.36	0.00	0.00	11
1999	Wild	0.00	0.00	0.18	0.73	0.10	0.00	113
	Hatchery	0.00	0.00	0.65	0.35	0.00	0.00	31
2000	Wild	0.00	0.00	0.00	1.00	0.00	0.00	1
	Hatchery	0.00	0.00	0.98	0.02	0.00	0.00	359

Survey year	Origin	Total age						Sample size
		2	3	4	5	6	7	
2001	Wild	0.00	0.00	0.76	0.24	0.00	0.00	29
	Hatchery	0.00	0.00	0.75	0.25	0.00	0.00	171
2002	Wild	0.00	0.00	0.20	0.80	0.00	0.00	5
	Hatchery	0.00	0.00	0.29	0.71	0.00	0.00	63
2003	Wild	0.00	0.00	0.00	1.00	0.00	0.00	5
	Hatchery	0.00	0.33	0.67	0.00	0.00	0.00	6
2004	Wild	-	-	-	-	-	-	0
	Hatchery	0.00	0.02	0.93	0.05	0.00	0.00	244
2005	Wild	-	-	-	-	-	-	0
	Hatchery	0.00	0.13	0.75	0.13	0.00	0.00	8
2006	Wild	0.00	0.00	0.34	0.65	0.01	0.00	207
	Hatchery	0.00	0.00	1.00	0.00	0.00	0.00	65
2007	Wild	0.00	0.00	0.02	0.88	0.10	0.00	206
	Hatchery	0.00	0.00	0.35	0.65	0.00	0.00	17
2008	Wild	0.00	0.00	0.95	0.04	0.01	0.00	258
	Hatchery	0.00	0.08	0.92	0.00	0.00	0.00	12
2009	Wild	0.00	0.00	0.79	0.21	0.00	0.00	251
	Hatchery	0.00	0.00	1.00	0.00	0.00	0.00	2
Average	***Wild***	***0.00***	***0.01***	***0.41***	***0.56***	***0.02***	***0.00***	***1,101***
	Hatchery	***0.00***	***0.04***	***0.72***	***0.24***	***0.00***	***0.00***	***1,101***

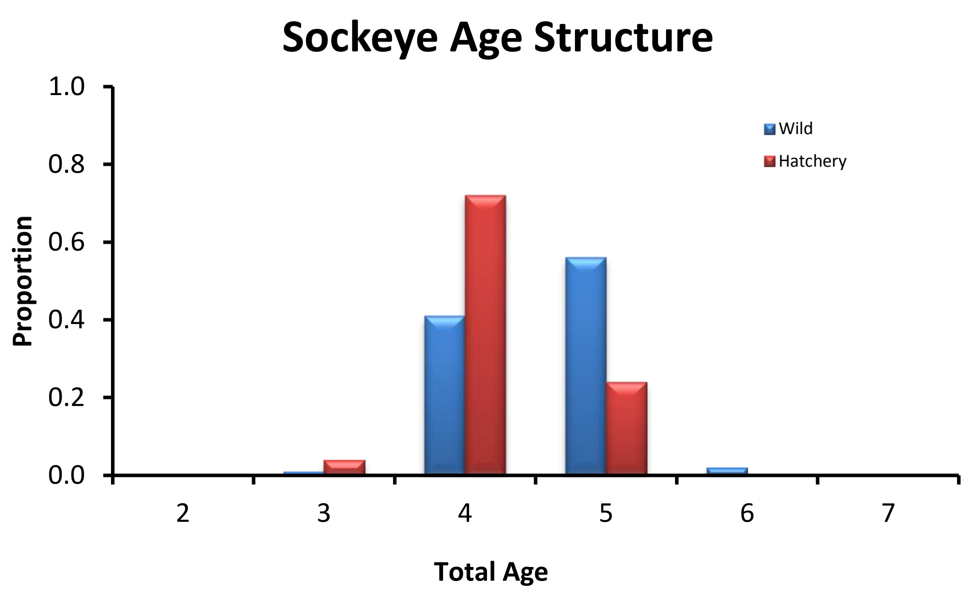


Figure 4.5. Proportions of wild and hatchery sockeye salmon of different total ages sampled at Tumwater Dam and on spawning grounds in the Wenatchee Basin for the combined years 1994-2009.

Size at Maturity

Although sample sizes are small, wild sockeye were larger than hatchery sockeye in 2009 (Table 4.26). This is because more wild fish return at age 5, while more hatchery fish return at age 4. However, the pooled data indicate that there is virtually no difference in mean sizes of hatchery and wild sockeye salmon sampled in the Wenatchee Basin (Table 4.26). Future analyses will compare sizes of hatchery and wild fish of the same age groups and gender.

Table 4.26. Mean lengths (POH; cm) and variability statistics for wild and hatchery sockeye salmon sampled at Tumwater Dam (broodstock) and on spawning grounds in the Wenatchee Basin, 1994-2009; SD = 1 standard deviation.

Survey year	Origin	Sample size	Sockeye length (POH; cm)			
			Mean	SD	Minimum	Maximum
1994	Wild	0	-	-	-	-
	Hatchery	14	42	3	37	47
1995	Wild	0	-	-	-	-
	Hatchery	1	53	-	53	53
1996	Wild	0	-	-	-	-
	Hatchery	5	51	3	49	55
1997	Wild	6	40	3	38	45
	Hatchery	17	41	3	37	50
1998	Wild	585	43	3	34	50
	Hatchery	20	43	3	40	51
1999	Wild	99	42	3	36	50
	Hatchery	31	41	3	36	47
2000	Wild	1	48	-	48	48
	Hatchery	377	40	2	30	49
2001	Wild	29	42	2	38	47
	Hatchery	184	43	3	35	51
2002	Wild	5	42	1	40	43
	Hatchery	52	44	3	37	49
2003	Wild	5	44	4	38	47
	Hatchery	13	42	5	30	48
2004	Wild	0	-	-	-	-
	Hatchery	230	40	3	33	49
2005	Wild	0	-	-	-	-
	Hatchery	8	43	9	35	64
2006	Wild	248	45	4	34	52
	Hatchery	17	41	5	31	48
2007	Wild	248	45	3	32	52
	Hatchery	16	41	5	31	48
2008	Wild	261	52	3	44	66
	Hatchery	20	39	3	30	41

Survey year	Origin	Sample size	Sockeye length (POH; cm)			
			Mean	SD	Minimum	Maximum
2009	Wild	260	43	3	33	53
	Hatchery	22	41	2	36	46
Pooled	***Wild***	***109***	***44***	***3***	***32***	***66***
	Hatchery	***64***	***43***	***4***	***30***	***64***

Contribution to Fisheries

The total number of hatchery and wild sockeye captured in different fisheries is provided in Tables 4.27 and 4.28. Harvest on hatchery-origin sockeye has been less than the harvest on wild sockeye.

Table 4.27. Estimated number and percent (in parentheses) of hatchery-origin Wenatchee sockeye captured in different fisheries, 1989-2004.

Brood year	Ocean fisheries	Columbia River Fisheries			Total
		Tribal	Commercial (Zones 1-5)	Recreational[a] (sport)	
1989	0 (0)	333 (34)	4 (0)	639 (65)	976
1990	0 (0)	23 (100)	0 (0)	0 (0)	23
1991	0 (0)	6 (100)	0 (0)	0 (0)	6
1992	0 (0)	37 (97)	1 (3)	0 (0)	38
1993	0 (0)	5 (100)	0 (0)	0 (0)	5
1994	0 (0)	3 (100)	0 (0)	0 (0)	3
1995	0 (0)	10 (100)	0 (0)	0 (0)	10
1996	0 (0)	80 (83)	11 (11)	5 (5)	96
1997	0 (0)	80 (73)	14 (13)	15 (14)	109
1998	0 (0)	7 (100)	0 (0)	0 (0)	7
1999	0 (0)	3 (20)	0 (0)	12 (80)	15
2000	0 (0)	80 (16)	13 (3)	414 (82)	507
2001	0 (0)	1 (25)	0 (0)	3 (75)	4
2002	0 (0)	16 (100)	0 (0)	0 (0)	16
2003	0 (0)	3 (100)	0 (0)	0 (0)	3
2004	0 (0)	7 (26)	1 (4)	19 (70)	27

[a] Includes the Lake Wenatchee fishery.

Table 4.28. Estimated number and percent (in parentheses) of wild Wenatchee sockeye captured in different fisheries, 1989-2004.

Brood year	Ocean fisheries	Columbia River Fisheries			Total
		Tribal	Commercial (Zones 1-5)	Recreational[a] (sport)	
1989	0 (0)	2,572 (35)	30 (0)	4,838 (65)	7,440
1990	0 (0)	193 (100)	0 (0)	0 (0)	193
1991	0 (0)	289 (99)	2 (1)	0 (0)	291
1992	0 (0)	360 (98)	6 (2)	0 (0)	366
1993	0 (0)	850 (100)	4 (0)	0 (0)	854
1994	0 (0)	149 (100)	0 (0)	0 (0)	149
1995	0 (0)	71 (87)	4 (5)	7 (9)	82
1996	0 (0)	1,953 (60)	306 (9)	993 (31)	3,252
1997	0 (0)	3,455 (56)	438 (7)	2,266 (37)	6,159
1998	0 (0)	980 (98)	5 (1)	10 (1)	995
1999	0 (0)	29 (24)	4 (3)	90 (73)	123
2000	0 (0)	1,608 (24)	224 (3)	4,881 (73)	6,713
2001	0 (0)	890 (100)	0 (0)	0 (0)	890
2002	0 (0)	383 (84)	2 (0)	72 (16)	457
2003	0 (0)	149 (27)	12 (2)	382 (70)	543
2004	0 (0)	1,785 (26)	171 (3)	4,786 (71)	6,742

[a] Includes the Lake Wenatchee fishery.

Straying

Stray rates were determined by examining CWTs recovered on spawning grounds within and outside the Wenatchee Basin. Targets for strays based on return year (recovery year) outside the Wenatchee Basin should be less than 5%. The target for brood year strays should also be less than 5%.

There is no record that hatchery-origin Wenatchee sockeye have strayed into other spawning areas outside the Wenatchee Basin. This may be related to the lack of carcass surveys in other locations. Nevertheless, the existing data indicate that hatchery-origin sockeye stray at a rates less than the target of 5%.

Based on brood year analysis, virtually no hatchery-origin Wenatchee sockeye have strayed into non-target spawning areas or hatchery programs (Table 4.29). These data indicate that hatchery-origin Wenatchee sockeye stray at rates less than the target of 5%.

Table 4.29. Number and percent of hatchery-origin Wenatchee sockeye that homed to target spawning areas and the target hatchery program, and number and percent that strayed to non-target spawning areas and hatchery programs, by brood years 1990-2004. Hatchery-origin sockeye from brood years 1995-1998 were not tagged because of columnaris disease. Percent stays should be less than 5%.

Brood year	Homing				Straying			
	Target streams		Target hatchery		Non-target streams		Non-target hatcheries	
	Number	%	Number	%	Number	%	Number	%
1990	402	99.5	2	0.5	0	0.0	0	0.0
1991	1	100.0	0	0.0	0	0.0	0	0.0
1992	92	98.9	0	0.0	0	0.0	1	1.1
1993	29	96.7	1	3.3	0	0.0	0	0.0
1994	66	94.3	4	5.7	0	0.0	0	0.0
1995	-	-	-	-	-	-	-	-
1996	-	-	-	-	-	-	-	-
1997	-	-	-	-	-	-	-	-
1998	-	-	-	-	-	-	-	-
1999	65	100.0	0	0.0	0	0.0	0	0.0
2000	571	100.0	0	0.0	0	0.0	0	0.0
2001	17	100.0	0	0.0	0	0.0	0	0.0
2002	3	100.0	0	0.0	0	0.0	0	0.0
2003	0	0.0	0	0.0	0	0.0	0	0.0
2004	0	0.0	0	0.0	0	0.0	0	0.0
Total	***1,246***	***99.4***	***7***	***0.6***	***0***	***0.0***	***1***	***0.1***

Genetics

Genetic studies were conducted to determine the potential impacts of the Wenatchee sockeye supplementation program on natural-origin sockeye in the upper Wenatchee Basin (Blankenship et al. 2008; the entire report is appended as Appendix H). Specifically, the objective of the study was to determine if the genetic composition of the Lake Wenatchee sockeye population had been altered by the supplementation program, which was based on the artificial propagation of a small subset of the Wenatchee population. Microsatellite DNA allele frequencies were used to differentiate between temporally replicated collections of natural and hatchery-origin sockeye in the Wenatchee Basin. A total of 13 collections of Wenatchee sockeye were analyzed; eight temporally replicated collections of natural-origin sockeye and five temporally replicated collections of hatchery-origin sockeye. Paired natural-hatchery collections were available from return years 2000, 2001, 2004, 2006, and 2007.

Overall, the study showed that allele frequency distributions were consistent over time, regardless of origin, resulting in small, insignificant measures of genetic differentiation among collections. This indicates that there was no year-to-year differences in allele frequencies between natural and hatchery-origin sockeye. In addition, the analyses found no differences between pre- and post-supplementation collections. Thus, it was concluded that the allele frequencies of the broodstock collections equaled the allele frequency of the natural collections.

Proportion of Natural Influence

Another method for assessing the genetic risk of a supplementation program is to determine the influence of the hatchery and natural environments on the adaptation of the composite population. This is estimated by the proportion of natural-origin fish in the hatchery broodstock (pNOB) and the proportion of hatchery-origin fish in the natural spawning escapement (pHOS). The ratio pNOB/(pHOS+pNOB) is the Proportion of Natural Influence (PNI). The larger the ratio (PNI), the greater the strength of selection in the natural environment relative to that of the hatchery environment. In order for the natural environment to dominate selection, PNI should be greater than 0.5 (HSRG/WDFW/NWIFC 2004).

For brood years 1989-2008, the PNI was consistently been greater than 0.5 (Table 4.30). This indicates that the natural environment has a greater influence on adaptation of Wenatchee sockeye than does the hatchery environment.

Table 4.30. Proportionate natural influence (PNI) of the Wenatchee sockeye supplementation program for brood years 1989-2008. PNI was calculated as the proportion of naturally produced sockeye in the hatchery broodstock (pNOB) divided by the proportion of hatchery sockeye counted at Tumwater Dam (pHOS) plus pNOB. NOS = number of natural-origin sockeye counted at Tumwater Dam; HOS = number of hatchery-origin sockeye counted at Tumwater Dam; NOB = number of natural-origin sockeye collected for broodstock; and HOB = number of hatchery-origin sockeye included in hatchery broodstock.

Brood year	Spawners[a]			Broodstock			PNI
	NOS	HOS	pHOS	NOB	HOB	pNOB	
1989	21,802	0	0.00	115	0	1.00	1.00
1990	27,325	0	0.00	302	0	1.00	1.00
1991	26,689	0	0.00	199	0	1.00	1.00
1992	16,461	0	0.00	320	0	1.00	1.00
1993	25,064	2,662	0.10	207	0	1.00	0.91
1994	6,929	396	0.05	236	5	0.98	0.95
1995	3,259	186	0.05	194	3	0.98	0.95
1996	6,009	546	0.08	225	0	1.00	0.93
1997	9,597	77	0.01	192	19	0.91	0.99
1998	3,976	32	0.01	122	6	0.95	0.99
1999	905	60	0.06	79	60	0.57	0.90
2000	19,569	1,161	0.06	170	5	0.97	0.94
2001	28,280	815	0.03	200	7	0.97	0.97
2002	27,372	193	0.01	256	0	1.00	0.99
2003	4,797	58	0.01	198	0	1.00	0.99
2004	26,095	1,460	0.05	177	0	1.00	0.95
2005	13,983	28	0.00	166	0	1.00	1.00
2006	9,183	255	0.03	214	0	1.00	0.97
2007	2,320	59	0.02	210	0	1.00	0.98

Brood year	Spawners[a]			Broodstock			PNI
	NOS	HOS	pHOS	NOB	HOB	pNOB	
2008	23,136	93	0.00	243	2	0.99	1.00
2009	13,144	449	0.03	239	0	1.00	0.97
Average	***15,043***	***406***	***0.03***	***203***	***5***	***0.97***	***0.97***

[a] Proportions of natural-origin and hatchery-origin spawners were determined from video tape at Tumwater Dam.

Natural Replacement Rates

Natural replacement rates (NRR) were calculated as the ratio of natural-origin recruits (NOR) to the parent spawning population. For brood years 1989-2004, NRR in the Wenatchee averaged 1.17 (range, 0.13-4.28) if harvested fish were not included in the estimate and 1.34 (range, 0.14-4.78) if harvested fish were included in the estimate (Table 4.31).

Hatchery replacement rates (HRR) were estimated as hatchery adult-to-adult returns. These rates should be greater than the NRRs and greater than or equal to 5.40 (the calculated target value in Murdoch and Peven 2005). HRRs exceeded NRRs in nine of the 16 years of data, regardless if harvest was or was not included in the estimates (Table 4.31). Hatchery replacement rates for Wenatchee sockeye have equaled or exceeded the estimated target value of 5.40 in only three years regardless if harvest was or was not included in the estimate (Table 4.31).

Table 4.31. Broodstock collected, spawning escapements, natural and hatchery-origin recruits (NOR and HOR), and natural and hatchery replacement rates (NRR and HRR; with and without harvest) for sockeye salmon in the Wenatchee Basin, 1989-2004.

Brood year	Broodstock Collected	Spawning Escapement	Harvest not included				Harvest included			
			HOR	NOR	HRR	NRR	HOR	NOR	HRR	NRR
1989	255	21,802	2,757	23,616	10.81	1.08	3,734	31,057	14.64	1.42
1990	316	27,325	401	3,509	1.27	0.13	423	3,703	1.34	0.14
1991	233	26,689	95	4,814	0.41	0.18	101	5,105	0.43	0.19
1992	343	16,461	599	5,491	1.75	0.33	637	5,858	1.86	0.36
1993	307	27,726	78	12,224	0.25	0.44	83	13,078	0.27	0.47
1994	265	7,325	47	1,194	0.18	0.16	50	1,344	0.19	0.18
1995	209	3,445	121	839	0.58	0.24	131	922	0.63	0.27
1996	227	6,553	1,348	28,049	5.94	4.28	1,444	31,300	6.36	4.78
1997	226	9,674	739	36,097	3.27	3.73	848	42,258	3.75	4.37
1998	190	4,008	104	16,166	0.55	4.03	111	17,161	0.58	4.28
1999	147	965	68	566	0.46	0.59	84	692	0.57	0.72
2000	195	20,730	1,425	29,082	7.31	1.40	1,933	35,795	9.91	1.73
2001	245	29,095	23	17,242	0.09	0.59	27	18,132	0.11	0.62
2002	257	27,565	281	5,755	1.09	0.21	297	6,214	1.16	0.23
2003	219	4,855	28	2,070	0.13	0.43	31	2,626	0.14	0.54
2004	202	27,555	95	23,798	0.47	0.86	121	30,539	0.60	1.11
Average	***240***	***16,361***	***513***	***13,157***	***2.16***	***1.17***	***628***	***15,362***	***2.66***	***1.34***

Juvenile-to-Adult Survivals

When possible, both parr-to-adult ratios (PAR) and smolt-to-adult ratios (SAR) were calculated for hatchery sockeye salmon. Ratios were calculated as the number of hatchery adult recaptures divided by the number of tagged hatchery parr released or the estimated number of smolts emigrating from Lake Wenatchee. Survival ratios were based on CWT returns, when available, or on the estimated number of hatchery adults recovered on the spawning grounds, in broodstock, and harvested. For the available brood years, PARs have ranged from 0.0001 to 0.0143 for hatchery sockeye salmon and SARs have ranged from 0.0002 to 0.0258 (Table 4.32).

Table 4.32. Parr-to-adult ratios (PAR) and smolt-to-adult ratios (SAR) for Wenatchee hatchery sockeye salmon, brood years 1990-2003; NA = not available.

Brood year	Number of parr released	Number of smolts	Estimated adult recaptures	PAR	SAR
1989	260,400	NA	3,734	0.0143	NA
1990	372,102	NA	423	0.0011	NA
1991	167,523	NA	101	0.0006	NA
1992	340,557	NA	637	0.0019	NA
1993	190,443	NA	83	0.0004	NA
1994	252,859	NA	50	0.0002	NA
1995	150,808	28,828	131	0.0009	0.0045
1996	284,630	55,985	1,444	0.0051	0.0258
1997	197,195	112,524	848	0.0043	0.0075
1998	121,344	24,684	111	0.0009	0.0045
1999	167,955	94,046	84	0.0005	0.0009
2000	190,174	121,511	1,933	0.0102	0.0159
2001	200,938	140,322	27	0.0001	0.0002
2002	315,783	216,023	297	0.0009	0.0014
2003	240,459	122,399	31	0.0001	0.0003
Average	***230,211***	***101,814***	***662***	***0.0029***	***0.0054***

4.8 ESA/HCP Compliance

Broodstock Collection

The 2008 sockeye broodstock collections at Tumwater Dam occurred concurrently with the spring Chinook reproductive success monitoring and evaluation activities (BPA Project No. 2003-039-00) and Wenatchee steelhead broodstock collection activities authorized under ESA permits 1196 and 1395, respectively. No ESA-listed spring Chinook or steelhead take occurred during sockeye broodstock collections at Tumwater Dam that were outside those authorized through ESA Section 10 permits 1196 and 1395.

Hatchery Rearing and Release

The 2008 Wenatchee sockeye program released 154,772 juveniles, representing 77% of the program production objective production overage allowance in ESA Section 10 Permit 1347.

Hatchery Effluent Monitoring

Per ESA Permits 1196, 1347, and 1395, permit holders shall monitor and report hatchery effluents in compliance with applicable National Pollution Discharge Elimination Systems (NPDES) (EPA 1999) permit limitations. NPDES monitoring and reporting for Chelan PUD Hatchery Programs during 2010 are provided in Appendix E.

Smolt and Emigrant Trapping

ESA-listed spring Chinook and steelhead were encountered during operation of the upper and lower Wenatchee traps. ESA takes are reported in the steelhead (Section 3.8) and spring Chinook (Section 5.8) sections and will not be repeated here.

Spawning Surveys

Sockeye spawning ground surveys conducted in the Wenatchee Basin during 2010 were consistent with ESA Section 10 Permit No. 1347. Because of the difficulty of quantifying the level of take associated with spawning ground surveys, the Permit does not specify a take level associated with these activities, even though it does authorize implementation of spawning ground surveys. Therefore, no take levels are reported. However, to minimize potential impacts to established redds, wading was restricted to the extent practical and extreme caution was used to avoid established redds when wading was required.

SECTION 5: WENATCHEE (CHIWAWA) SPRING CHINOOK

Although this section of the report focuses on results from monitoring the Chiwawa spring Chinook program, information on spring Chinook collected throughout the Wenatchee Basin is also provided.

5.1 Broodstock Sampling

This section focuses on results from sampling 2008-2010 Chiwawa spring Chinook broodstock, which were collected at the Chiwawa weir and at Tumwater Dam. Some information for the 2010 return is not available at this time (e.g., age structure and final origin determination). This information will be provided in the 2011 annual report.

Origin of Broodstock

Hatchery-origin adults made up between 55-73% of the Chiwawa spring Chinook broodstock for return years 2008-2010 (Table 5.1). Hatchery-origin adults were collected at both Tumwater Dam and the Chiwawa weir. In an effort to partially address straying of Chiwawa spring Chinook to other tributaries in the basin, and secondarily to ensure meeting adult collection quotas, hatchery-origin adults were collected to the greatest extent possible at Tumwater Dam. Natural-origin fish were collected only at the Chiwawa weir. Broodstock were trapped at Tumwater Dam and Chiwawa weir from mid-June through August.

Table 5.1. Numbers of wild and hatchery Chiwawa spring Chinook collected for broodstock, numbers that died before spawning, and numbers of Chinook spawned, 1989-2010. Unknown origin fish (i.e., undetermined by scale analysis, no CWT or fin clips, and no additional hatchery marks) were considered naturally produced. Mortality includes fish that died of natural causes typically near the end of spawning and were not needed for the program or were surplus fish killed at spawning.

Brood year	Wild spring Chinook					Hatchery spring Chinook					Total number spawned
	Number collected	Prespawn loss	Mortality	Number spawned	Number released	Number collected	Prespawn loss	Mortality	Number spawned	Number released	
1989	28	0	0	28	0	0	0	0	0	0	28
1990	19	1	0	18	0	0	0	0	0	0	18
1991	32	0	5	27	0	0	0	0	0	0	27
1992	113	0	0	78	35	0	0	0	0	0	78
1993	100	3	3	94	0	0	0	0	0	0	94
1994	9	0	1	8	0	4	0	0	4	0	12
1995	No Program										
1996	8	0	0	8	0	10	0	0	10	0	18
1997	37	0	5	32	0	83	1	3	79	0	111
1998	13	0	0	13	0	35	1	0	34	0	47
1999	No Program										
2000	10	0	1	9	0	38	1	16	21	0	30
2001	115	2	0	113	0	267	8	0	259	0	372
2002	21	0	1	20	0	63	1	11	51	0	71
2003	44	1	2	41	0	75	2	20	53	0	94
2004	100	1	16	83	0	196	30	34	132	0	215

Brood year	Wild spring Chinook					Hatchery spring Chinook					Total number spawned
	Number collected	Prespawn loss	Mortality	Number spawned	Number released	Number collected	Prespawn loss	Mortality	Number spawned	Number released	
2005	98	1	6	91	0	185	3	1	181	0	279
2006	95	0	4	91	0	303	0	29	224	50	315
2007	45	1	1	43	0	124	2	18	104	0	147
2008	88	2	3	83	0	241	5	16	220	0	303
2009	113	6	11	96	0	151	3	37	111	0	207
2010	83	0	6	77	0	103	0	5	98	0	175
Average[a]	***59***	***1***	***3***	***53***	***2***	***94***	***3***	***10***	***79***	***3***	***132***

[a] Origin determinations should be considered preliminary pending scale analyses.

Age/Length Data

Ages were determined from scales and/or coded wire tags (CWT) collected from broodstock. For both the 2008 and 2009 returns, most adults, regardless of origin, were age-4 Chinook (Table 5.2). A larger percentage of the age-5 Chinook were natural-origin fish, whereas a larger percentage of the age-3 fish were hatchery-origin fish.

Table 5.2. Percent of hatchery and wild spring Chinook of different ages (total age) collected from broodstock, 1991-2009.

Return year	Origin	Total age			
		2	3	4	5
1991	Wild	0.0	15.6	59.4	25.0
	Hatchery	0.0	0.0	0.0	0.0
1992	Wild	0.0	0.0	0.0	0.0
	Hatchery	0.0	0.0	0.0	0.0
1993	Wild	0.0	0.0	22.0	78.0
	Hatchery	0.0	0.0	0.0	0.0
1994	Wild	0.0	0.0	28.6	71.4
	Hatchery	0.0	0.0	50.0	50.0
1995	Wild	No program			
	Hatchery				
1996	Wild	0.0	28.6	71.4	0.0
	Hatchery	0.0	50.0	50.0	0.0
1997	Wild	0.0	0.0	87.5	12.5
	Hatchery	0.0	1.2	98.8	0.0
1998	Wild	0.0	0.0	63.6	36.4
	Hatchery	0.0	0.0	62.9	37.1
1999	Wild	No program			
	Hatchery				
2000	Wild	0.0	20.0	70.0	10.0
	Hatchery	0.0	76.3	23.7	0.0
2001	Wild	0.0	2.8	94.4	2.8

Return year	Origin	Total age			
		2	3	4	5
	Hatchery	0.0	1.5	98.5	0.0
2002	Wild	0.0	0.0	66.7	33.3
	Hatchery	0.0	0.0	93.4	6.6
2003	Wild	0.0	27.0	2.7	70.3
	Hatchery	0.0	21.3	5.3	73.3
2004	Wild	1.1	4.3	89.4	5.3
	Hatchery	0.0	36.9	63.1	0.0
2005	Wild	0.0	1.1	84.5	14.4
	Hatchery	0.0	4.3	94.6	1.1
2006	Wild	0.0	1.1	71.1	27.8
	Hatchery	0.0	1.4	81.3	17.3
2007	Wild	2.3	16.3	48.8	32.6
	Hatchery	0.0	27.4	61.5	11.1
2008	Wild	0.0	9.1	75.3	15.6
	Hatchery	0.0	7.9	86.5	5.6
2009	Wild	0.0	8.4	80.0	11.6
	Hatchery	0.0	18.9	77.8	3.3
Average	***Wild***	***0.7***	***12.1***	***55.7***	***25.6***
	Hatchery	***1.1***	***18.0***	***51.3***	***11.9***

There was little difference in mean lengths between hatchery and natural-origin broodstock of age-4 and 5 Chinook in 2008 and 2009 (Table 5.3). Additionally, for the 2008 and 2009 returns, there was relatively little difference in mean lengths within or among years for age-3 hatchery and natural-origin fish.

Table 5.3. Mean fork length (cm) at age (total age) of hatchery and wild spring Chinook collected from broodstock, 1991-2009; N = sample size and SD = 1 standard deviation.

Return year	Origin	Spring Chinook fork length (cm)											
		Age-2			Age-3			Age-4			Age-5		
		Mean	N	SD	Mean	N	SD	Mean	N	SD	Mean	N	SD
1991	Wild	-	0	-	-	5	-	-	19	-	-	8	-
	Hatchery	-	0	-	-	0	-	-	0	-	-	0	-
1992	Wild	-	0	-	-	0	-	-	0	-	-	0	-
	Hatchery	-	0	-	-	0	-	-	0	-	-	0	-
1993	Wild	-	0	-	-	0	-	79	22	3	92	78	4
	Hatchery	-	0	-	-	0	-	-	0	-	-	0	-
1994	Wild	-	0	-	-	0	-	79	2	3	96	5	6
	Hatchery	-	0	-	-	0	-	82	2	11	91	2	3
1995	Wild	No program											

Return year	Origin	Spring Chinook fork length (cm)											
		Age-2			Age-3			Age-4			Age-5		
		Mean	N	SD	Mean	N	SD	Mean	N	SD	Mean	N	SD
	Hatchery												
1996	Wild	-	0	-	51	2	1	79	5	7	-	0	-
	Hatchery	-	0	-	56	5	4	74	5	6	-	0	-
1997	Wild	-	0	-	-	0	-	80	28	5	99	4	8
	Hatchery	-	0	-	56	1	-	82	82	4	-	0	-
1998	Wild	-	0	-	-	0	-	78	7	13	83	4	18
	Hatchery	-	0	-	-	0	-	77	22	8	93	13	7
1999	Wild	No program											
	Hatchery												
2000	Wild	-	0	-	51	2	3	82	7	4	98	1	-
	Hatchery	-	0	-	58	29	7	79	9	8	-	0	-
2001	Wild	-	0	-	49	3	6	82	101	6	95	3	3
	Hatchery	-	0	-	56	4	7	83	261	5	-	0	-
2002	Wild	-	0	-	-	0	-	79	12	4	96	6	10
	Hatchery	-	0	-	-	0	-	81	57	6	94	4	9
2003	Wild	-	0	-	55	10	5	83	1	-	99	26	6
	Hatchery	-	0	-	59	16	5	86	4	18	96	55	6
2004	Wild	47	1	-	57	4	4	80	84	5	95	5	9
	Hatchery	-	0	-	49	72	6	79	123	6	-	0	-
2005	Wild	-	0	-	49	1	-	80	82	6	96	14	8
	Hatchery	-	0	-	56	8	5	82	175	6	93	2	2
2006	Wild	-	0	-	48	1	-	80	64	7	96	25	5
	Hatchery	-	0	-	49	4	4	80	240	6	95	51	7
2007	Wild	54	1	-	57	7	10	79	21	6	93	14	7
	Hatchery	-	0	-	59	32	8	81	72	6	93	13	6
2008	Wild	-	0	-	54	7	8	82	58	5	93	12	7
	Hatchery	-	0	-	56	20	10	82	218	6	95	14	6
2009	Wild	-	-	-	53	8	6	81	76	4	95	11	5
	Hatchery	-	-	-	56	29	5	82	119	5	94	5	7

Sex Ratios

Male spring Chinook in 2008-2010 return years made up 46%, 50%, and 51%, respectively, of the adults collected. This resulted in overall male to female ratios of 0.84:1.00, 1.00:1.00, and 1.02:1.00, respectively (Table 5.4). Only returns in 2009 and 2010 were ratios at or above the 1:1 target in the broodstock protocol. For the 2010 return year, natural-origin fish consisted of a slightly lower proportion of males than females, whereas hatchery-origin fish consisted of a slightly higher proportion of males than females (Table 5.4.).

Table 5.4. Numbers of male and female wild and hatchery spring Chinook collected for broodstock, 1989-2010. Ratios of males to females are also provided.

Return year	Number of wild spring Chinook			Number of hatchery spring Chinook			Total M/F ratio
	Males (M)	Females (F)	M/F	Males (M)	Females (F)	M/F	
1989	11	17	0.65:1.00	-	-	-	0.65:1.00
1990	7	12	0.58:1.00	-	-	-	0.58:1.00
1991	13	19	0.68:1.00	-	-	-	0.68:1.00
1992	39	39	1.00:1.00	-	-	-	1.00:1.00
1993	50	50	1.00:1.00	-	-	-	1.00:1.00
1994	5	4	1.25:1.00	2	2	1.00:1.00	1.17:1.00
1995	No program						
1996	6	2	3.00:1.00	8	2	4.00:1.00	3.50:1.00
1997	14	23	0.61:1.00	34	49	0.69:1.00	0.67:1.00
1998	9	4	2.25:1.00	18	17	1.06:1.00	1.29:1.00
1999	No program						
2000	5	5	1.00:1.00	32	6	5.33:1.00	3.36:1.00
2001	45	70	0.64:1.00	90	177	0.51:1.00	0.55:1.00
2002	9	12	0.75:1.00	30	33	0.91:1.00	0.87:1.00
2003	28	16	1.75:1.00	42	33	1.27:1.00	1.43:1.00
2004	58	42	1.38:1.00	102	94	1.09:1.00	1.18:1.00
2005	58	40	1.45:1.00	89	96	0.93:1.00	1.08:1.00
2006	49	46	1.07:1.00	123	179	0.69:1.00	0.77:1.00
2007	20	25	0.80:1.00	66	58	1.14:1.00	1.04:1.00
2008	41	47	0.87:1.00	109	132	0.83:1.00	0.84:1.00
2009	53	60	0.88:1.00	79	72	1.10:1.00	1.00:1.00
2010	41	42	0.98:1.00	53	50	1.06:1.00	1.02:1.00
Total	***561***	***575***	***0.98:1.00***	***877***	***1,000***	***0.88:1.00***	***0.91:1.00***

Fecundity

Mean fecundities for the 2008-2010 returns of spring Chinook ranged from 4,314-4,592 eggs per female (Table 5.5). These fecundities were less than the overall average of 4,825 eggs per female, but were close to the expected fecundity of 4,400 eggs per female assumed in the broodstock protocol. For the three return years, natural-origin Chinook produced more eggs per female than did hatchery-origin fish (Table 5.5). This could be attributed to differences in size and age of hatchery and natural-origin fish described above.

Table 5.5. Mean fecundity of wild, hatchery, and all female spring Chinook collected for broodstock, 1989-2010; NA = not available.

Return year	Mean fecundity		
	Wild	Hatchery	Total
1989*	NA	NA	2,832
1990*	NA	NA	5,024
1991*	NA	NA	4,600
1992*	NA	NA	5,199[a]
1993*	NA	NA	5,249
1994*	NA	NA	5,923
1995	No program		
1996*	NA	NA	4,645
1997	4,752	4,479	4,570
1998	5,157	5,376	5,325
1999	No program		
2000	5,028	5,019	5,023
2001	4,530	4,663	4,624
2002	5,024	4,506	4,654
2003	6,191	5,651	5,844
2004	4,846	4,775	4,799
2005	4,365	4,312	4,327
2006	4,773	4,151	4,324
2007	4,656	4,351	4,441
2008	4,691	4,560	4,592
2009	4,691	4,487	4,573
2010	4,548	4,114	4,314
Average	***4,866***	***4,630***	***4,825***

* Individual fecundities were not tracked with females until 1997.
[a] Estimated as the mean of fecundities two years before and two years after 1992.

5.2 Hatchery Rearing

Rearing History

Number of eggs taken

Based on the unfertilized egg-to-release survival standard of 81%, a total of 829,630 eggs are required to meet the program release goal of 672,000 smolts. Between 1989 and 2010, the egg take goal was reached in one of those years (Table 5.6). The green egg takes for 2008-2010 brood years were 92%, 68%, and 46% of program goals, respectively.

ESA Permit 1196 sets limits on the percentage of the total run, natural-origin run, and a minimum contribution of natural-origin fish that must be in the broodstock. Applying these criteria to the low total abundance of spring Chinook salmon to the Chiwawa Basin and the low abundance of natural-origin fish returning to the basin has resulted in the program not meeting production goals.

Table 5.6. Numbers of eggs taken from spring Chinook broodstock, 1989-2010.

Return year	Number of eggs taken
1989	45,311
1990	60,287
1991	73,601
1992	111,624
1993	257,208
1994	35,539
1995	No program
1996	18,579
1997	312,182
1998	90,521
1999	No program
2000	55,256
2001	1,099,630
2002	196,186
2003	247,501
2004	538,176
2005	536,490
2006	744,344
2007	359,739
2008	761,821
2009	564,912
2010	383,941
Average	***324,642***

Number of acclimation days

Early rearing of the 2008 brood Chiwawa spring Chinook was similar to previous years with fish being held on well water before being transferred to Chiwawa Ponds for final acclimation. Beginning in 2006 (2005 brood acclimation), modifications were made to the Chiwawa Fish Hatchery intakes so that Wenatchee River water could be applied to the Chiwawa River intakes during severe cold periods to prevent the formation of frazzle ice. During acclimation of the 2008 brood, fish were acclimated for 212 to 241 days on Chiwawa River water, with 129 of those days containing a small percentage of Wenatchee River water to prevent freezing of hatchery intakes (Table 5.7).

Table 5.7. Number of days spring Chinook broods were acclimated and water source, brood years 1989-2008; NA = not available.

Brood year	Release year	Transfer date	Release date	Number of days and water source		
				Total	Chiwawa	Wenatchee
1989	1991	19-Oct	11-May	204	NA	NA
1990	1992	13-Sep	27-Apr	227	NA	NA
1991	1993	24-Sep	24-Apr	212	NA	NA
1992	1994	30-Sep	20-Apr	202	NA	NA
1993	1995	28-Sep	20-Apr	204	NA	NA
1994	1996	1-Oct	25-Apr	207	NA	NA
1995	1997	No Program				
1996	1998	25-Sep	29-Apr	216	NA	NA
1997	1999	28-Sep	22-Apr	206	NA	NA
1998	2000	27-Sep	24-Apr	210	NA	NA
1999	2001	No Program				
2000	2002	26-Sep	25-Apr	211	NA	NA
2001	2003	22-Oct	1-May	191	NA	NA
2002	2004	25-Sep	2-May	220	NA	NA
2003	2005	30-Sep	3-May	215	NA	NA
		30-Sep	18-Apr-18-May	200	NA	NA
2004	2006	3-Sep	1-May	240	88-104	124
		3-Sep	17-Apr-17-May	226	NA	NA
2005	2007	25-Sep	1-May	217	217	98[a]
		26-Sep	16-Apr-15-May	202-232	202-232	98[a]
2006	2008	24-27-Sep	14-Apr-13-May	231	231	95[a]
2007	2009	1-Oct	15-Apr-13-May	223	223	103[a]
2008	2010	14-15-Sep	14-Apr-12-May	212-241	212-241	129

[a] Represents the number of days Wenatchee River water was applied to the Chiwawa River intake screen to prevent the formation of frazzle ice.

Release Information

Numbers released

The 2008 brood Chiwawa spring Chinook program achieved 90.7% of the 672,000 target goal with about 609,789 smolts being released volitionally into the Chiwawa River (Table 5.8).

Table 5.8. Numbers of spring Chinook smolts tagged and released from the hatchery, brood years 1989-2008. The release target for Chiwawa spring Chinook is 672,000 smolts.

Brood year	Release year	Type of release	CWT mark rate	Number released that were PIT tagged	Number of smolts released	Total number of smolts released
1989	1991	Volitional	0.9932	0	43,000	43,000
1990	1992	Volitional	0.9931	0	53,170	53,170
1991	1993	Volitional	0.9831	0	62,138	62,138
1992	1994	Volitional	0.9747	0	85,113	85,113
1993	1995	Volitional	0.9892	0	223,610	223,610
1994	1996	Volitional	0.9967	0	27,226	27,226
1995	1997	No program				
1996	1998	Forced	0.8413	0	15,176	15,176
1997	1999	Volitional	0.9753	0	266,148	266,148
1998	2000	Volitional	0.9429	0	75,906	75,906
1999	2001	No program				
2000	2002	Volitional	0.9920	0	47,104	47,104
2001	2003	Forced	0.9961	0	192,490[a]	377,544
		Volitional	0.9856	0	185,054[a]	
2002	2004	Volitional	0.9693	0	149,668	149,668
2003	2005	Forced	0.9783	0	69,907	222,131
		Volitional	0.9743	0	152,224	
2004	2006	Forced	0.9533	0	243,505	494,517
		Volitional	0.9493	0	251,012	
2005	2007	Forced	0.9882	4,993	245,406	494,012
		Volitional	0.9864	4,988	248,606	
2006	2007	Direct	0.0000	0	12,977[b]	612,482
	2008	Volitional	0.9795	9,894	612,482	
2007	2008	Direct	0.0000	0	9,494	305,542
	2009	Volitional	0.9948	10,035	296,048	
2008	2010	Volitional	0.9835	10,006	609,789	609,789

[a] This does not include the 226,456 eyed eggs that were planted in the Chiwawa River.
[b] This high ELISA group was only adipose fin clipped and directly planted into Big Meadow Creek in May.

Numbers tagged

The 2008 brood Chiwawa spring Chinook were 98.4% CWT and adipose fin clipped (Table 5.8).

In 2010, a total of 10,101 spring Chinook from the 2009 brood were PIT tagged at the Eastbank Hatchery during 8-10 June. These fish were transferred to the Chiwawa raceway in September. As of the end of January 2011, a total of 442 tagged fish have died and four others have shed their tags, leaving 9,655 tagged spring Chinook alive. These fish will be released in the Chiwawa River in spring of 2011. Table 5.9 summarizes the number of hatchery spring Chinook that have been PIT-tagged and released into the Chiwawa River.

Table 5.9. Summary of PIT-tagging activities for Chiwawa hatchery spring Chinook, brood years 2005-2008.

Brood year	Release year	Number of fish tagged	Number of tagged fish that died	Number of tags shed	Number of tagged fish released
2005	2007	10,063	74	8	9,981[a]
2006	2008	10,055	134	27	9,894
2007	2009	10,112	61	16	10,035
2008	2010	10,101	81	14	10,006

[a] This release consisted of 4,988 tagged Chinook that were released volitionally and 4,993 that were forced released.

Fish size and condition at release

Spring Chinook from the 2008 brood were released as yearling smolts between 14 April and 15 May 2010. Size at release was below the targets established for the program. The coefficient of variation for fork length was 19% above the target (Table 5.10).

Table 5.10. Mean lengths (FL, mm), weight (g and fish/pound), and coefficient of variation (CV) of spring Chinook smolts released from the hatchery, brood years 1989-2008. Size targets are provided in the last row of the table.

Brood year	Release year	Fork length (mm)		Mean weight	
		Mean	CV	Grams (g)	Fish/pound
1989	1991	147	4.4	37.8	12
1990	1992	137	5.0	32.4	14
1991	1993	135	4.2	30.3	15
1992	1994	133	5.0	28.4	16
1993	1995	136	4.5	30.2	15
1994	1996	139	7.1	34.4	13
1995	1997	No Program			
1996	1998	157	5.3	52.1	9
1997	1999	146	7.2	38.7	12
1998	2000	143	9.1	39.5	12
1999	2001	No Program			
2000	2002	150	6.8	46.7	10
2001	2003	142	7.1	37.6	12
2002	2004	146	8.5	40.3	11
2003	2005	167[a]	5.9	59.4	8
		151[b]	7.4	44.2	10

Brood year	Release year	Fork length (mm)		Mean weight	
		Mean	CV	Grams (g)	Fish/pound
2004	2006	146[a]	6.4	39.1	12
		139[b]	5.7	34.3	13
2005	2007	136[a]	4.6	30.8	15
		129[b]	5.8	26.6	17
2006	2008	124	8.8	23.5	19
2007	2008	70[a]	4.0	3.7	122
	2009	140[b]	11.0	33.6	14
2008	2010	141	107	36.0	13
Targets		***176***	***9.0***	***37.8***	***12***

[a] Forced release group.
[b] Volitional release group.

Survival Estimates

Overall survival of Chiwawa spring Chinook from green (unfertilized) egg to release was slightly below the standard set for the program (Table 5.11). Survival from the eyed egg-to-ponding stage was slightly below program objectives. Pre-spawn survival of adults was above the standard set for the program.

Table 5.11. Hatchery life-stage survival rates (%) for spring Chinook, brood years 1989-2008. Survival standards or targets are provided in the last row of the table.

Brood year	Collection to spawning		Unfertilized egg-eyed	Eyed egg-ponding	30 d after ponding	100 d after ponding	Ponding to release	Transport to release	Unfertilized egg-release
	Female	Male							
1989	100.0	100.0	98.0	99.1	99.1	99.0	96.4	99.3	94.8
1990	100.0	85.7	91.8	98.1	99.5	98.9	97.9	99.2	88.2
1991	100.0	100.0	94.4	96.1	99.6	97.9	93.2	95.0	84.4
1992	100.0	100.0	98.4	96.7	99.9	99.9	80.0	80.6	76.2
1993	96.0	98.0	89.7	98.0	99.7	99.3	98.9	99.7	86.9
1994	100.0	100.0	98.6	100.0	99.8	99.4	77.0	78.9	76.6
1995	No program								
1996	100.0	100.0	88.3	100.0	93.8	93.0	89.9	97.7	81.7
1997	98.6	100.0	93.2	95.7	98.3	99.6	95.6	99.3	85.3
1998	95.2	100.0	94.5	99.0	98.5	98.3	89.6	99.1	83.9
1999	No program								
2000	100.0	100.0	91.0	98.1	97.2	96.6	95.4	99.3	85.2
2001	97.6	97.0	88.9	98.1	99.7	99.6	51.3	51.8	34.3
2002	97.8	100.0	82.1	98.0	97.4	96.7	94.8	99.1	76.3
2003	93.9	100.0	93.2	97.7	99.5	99.3	98.5	98.1	89.7
2004	97.8	82.5	93.3	98.4	98.8	94.3	93.9	97.2	91.9
2005	97.1	100.0	95.9	98.0	99.2	99.0	97.9	99.1	92.1
2006	100.0	100.0	90.1	98.1	99.2	99.0	95.3	97.7	84.2

Brood year	Collection to spawning		Unfertilized egg-eyed	Eyed egg-ponding	30 d after ponding	100 d after ponding	Ponding to release	Transport to release	Unfertilized egg-release
	Female	Male							
2007	98.8	97.7	92.9	97.2	99.4	99.0	98.0	99.4	88.5
2008	96.6	99.3	90.8	93.2	97.4	97.1	95.6	97.6	80.0
Standard	***90.0***	***85.0***	***92.0***	***98.0***	***97.0***	***93.0***	***90.0***	***95.0***	***81.0***

5.3 Disease Monitoring

Results of 2010 adult broodstock bacterial kidney disease (BKD) monitoring indicated that most females (95.6%) had ELISA values less than 0.199. About 95% of females had ELISA values less than 0.120, which would have required about 5% of the progeny to be reared at densities not to exceed 0.06 fish per pound (Table 5.12). As per the HCP Hatchery Committee Agreement, progeny from the four high ELISA females were culled to minimize possible negative effects to the balance of the program. These progeny represented about 7% of the estimated production for the 2010 brood.

Mortalities resulting from external fungal infections began increasing shortly after transfer to the Chiwawa Ponds. The first formalin drip treatment failed to control the infection. The failure precipitated a second treatment, which was successful. No significant health issues were encountered for the remainder of juvenile rearing.

Table 5.12. Proportion of bacterial kidney disease (BKD) titer groups for the Chiwawa spring Chinook broodstock, brood years 1996-2010. Also included are the proportions to be reared at either 0.125 fish per pound or 0.060 fish per pound.

Brood year[a]	Optical density values by titer group				Proportion at rearing densities (fish per pound, fpp)	
	Very Low (≤ 0.099)	Low (0.1-0.199)	Moderate (0.2-0.449)	High (≥ 0.450)	≤ 0.125 fpp (<0.119)	≤ 0.060 fpp (>0.120)
1996	0.0000	0.2500	0.2500	0.5000	0.0000	1.0000
1997	0.1176	0.7353	0.0588	0.0882	0.3529	0.6471
1998	0.1176	0.8235	0.0588	0.0000	0.4706	0.5294
1999	No Program					
2000	0.0000	0.9091	0.0909	0.0000	0.1818	0.8182
2001	0.4066	0.5436	0.0373	0.0124	0.6515	0.3485
2002	0.2195	0.6585	0.0732	0.0488	0.5610	0.4390
2003	0.6957	0.1087	0.0652	0.1304	0.7174	0.2826
2004	0.8182	0.1515	0.0227	0.0076	0.8939	0.1061
2005	0.9084	0.0916	0.0000	0.0000	0.9695	0.0305
2006	0.7222	0.2556	0.0000	0.0222	0.8444	0.1556
2007	0.5854	0.3415	0.0244	0.0488	0.7073	0.2927
2008	0.8304	0.1520	0.0058	0.0117	0.9357	0.0643
2009	0.7600	0.1840	0.0080	0.0480	0.8480	0.1520

Brood year[a]	Optical density values by titer group				Proportion at rearing densities (fish per pound, fpp)	
	Very Low (≤ 0.099)	Low (0.1-0.199)	Moderate (0.2-0.449)	High (≥ 0.450)	≤ 0.125 fpp (<0.119)	≤ 0.060 fpp (>0.120)
2010	0.8791	0.0769	0.0000	0.0439	0.9451	0.0549
Average	*0.5786*	*0.3580*	*0.0322*	*0.0311*	*0.7272*	*0.2728*

[a] Individual ELISA samples were not collected before the 1996 brood.

5.4 Natural Juvenile Productivity

During 2010, juvenile spring Chinook were sampled at the Upper Wenatchee, Lower Wenatchee, and Chiwawa traps and counted during snorkel surveys within the Chiwawa Basin.

Parr Estimates

A total of 128,220 (±14%) subyearling and 291 (±31%) yearling spring Chinook were estimated in the Chiwawa River Basin in August 2010 (Table 5.13 and 5.14). During the survey period 1992-2010, numbers of subyearling and yearling Chinook have ranged from 5,815 to 134,872 and 5 to 563, respectively, in the Chiwawa Basin (Table 5.13 and 5.14; Figure 5.1). Numbers of all fish counted in the Chiwawa Basin are reported in Appendix A.

Table 5.13. Total numbers of subyearling spring Chinook estimated in different steams in the Chiwawa Basin during snorkel surveys in August 1992-2010; NS = not sampled.

Sample Year	Number of subyearling spring Chinook									
	Chiwawa River	Phelps Creek	Chikamin Creek	Rock Creek	Peven Creek	Big Meadow Creek	Alder Creek	Brush Creek	Clear Creek	Total
1992	45,483	NS	NS	NS	NS	NS	NS	NS	NS	**45,483**
1993	77,269	0	1,258	586	NS	NS	NS	NS	NS	**79,113**
1994	53,492	0	398	474	68	624	0	0	0	**55,056**
1995	52,775	0	1,346	210	0	683	67	160	0	**55,241**
1996	5,500	0	29	10	0	248	28	0	0	**5,815**
1997	15,438	0	56	92	0	480	0	0	0	**16,066**
1998	65,875	0	1,468	496	57	506	0	13	0	**68,415**
1999	40,051	0	366	592	0	598	22	0	0	**41,629**
2000	NS	NS	NS	NS	NS	NS	NS	NS	NS	**NS**
2001	106,753	168	2,077	2,855	354	2,332	78	0	0	**114,617**
2002	117,230	75	8,233	2,953	636	5,021	429	0	297	**134,874**
2003	80,250	4,508	1,570	3,255	118	1,510	22	45	0	**91,278**
2004	43,360	102	717	215	54	637	21	71	0	**45,177**
2005	45,999	71	2,092	660	17	792	0	0	0	**49,631**
2006	73,478	113	2,500	1,681	51	1,890	62	127	0	**79,902**
2007	53,863	125	5,235	870	51	538	20	28	22	**60,752**
2008	72,431	214	3,287	4,730	163	1,221	28	255	22	**82,351**
2009	101,085	125	2,486	1,849	14	1,082	29	18	17	**106,705**
2010	117,499	526	4,571	4,052	0	1,449	56	42	25	**128,220**
Average	***64,880***	***355***	***2,217***	***1,505***	***99***	***1,226***	***54***	***47***	***24***	***70,018***

Table 5.14. Total numbers of yearling spring Chinook estimated in different steams in the Chiwawa Basin during snorkel surveys in August 1992-2010; NS = not sampled.

Sample Year	Number of yearling spring Chinook									
	Chiwawa River	Phelps Creek	Chikamin Creek	Rock Creek	Peven Creek	Big Meadow Creek	Alder Creek	Brush Creek	Y Creek	Total
1992	563	NS	NS	NS	NS	NS	NS	NS	NS	**563**
1993	174	0	0	0	NS	NS	NS	NS	NS	**174**
1994	14	0	0	4	0	0	0	0	0	**18**
1995	13	0	0	0	0	0	0	0	0	**13**
1996	22	0	0	0	0	0	0	0	0	**22**
1997	5	0	0	0	0	0	0	0	0	**5**
1998	63	0	0	0	0	0	0	0	0	**63**
1999	41	0	0	0	0	0	0	0	0	**41**
2000	NS	NS	NS	NS	NS	NS	NS	NS	NS	**NS**
2001	66	0	3	0	0	0	0	0	0	**69**
2002	32	0	0	0	0	0	0	0	0	**32**
2003	134	0	0	0	0	0	0	0	0	**134**
2004	14	0	0	0	0	7	0	0	0	**21**
2005	62	0	17	0	0	0	0	0	0	**79**
2006	345	0	0	43	0	0	0	0	0	**388**
2007	41	0	0	0	0	0	0	0	0	**41**
2008	144	0	45	0	0	0	0	0	0	**189**
2009	49	0	0	5	0	0	0	0	0	**54**
2010	207	27	19	38	0	0	0	0	0	**291**
Average	***111***	***2***	***5***	***5***	***0***	***0***	***0***	***0***	***0***	***122***

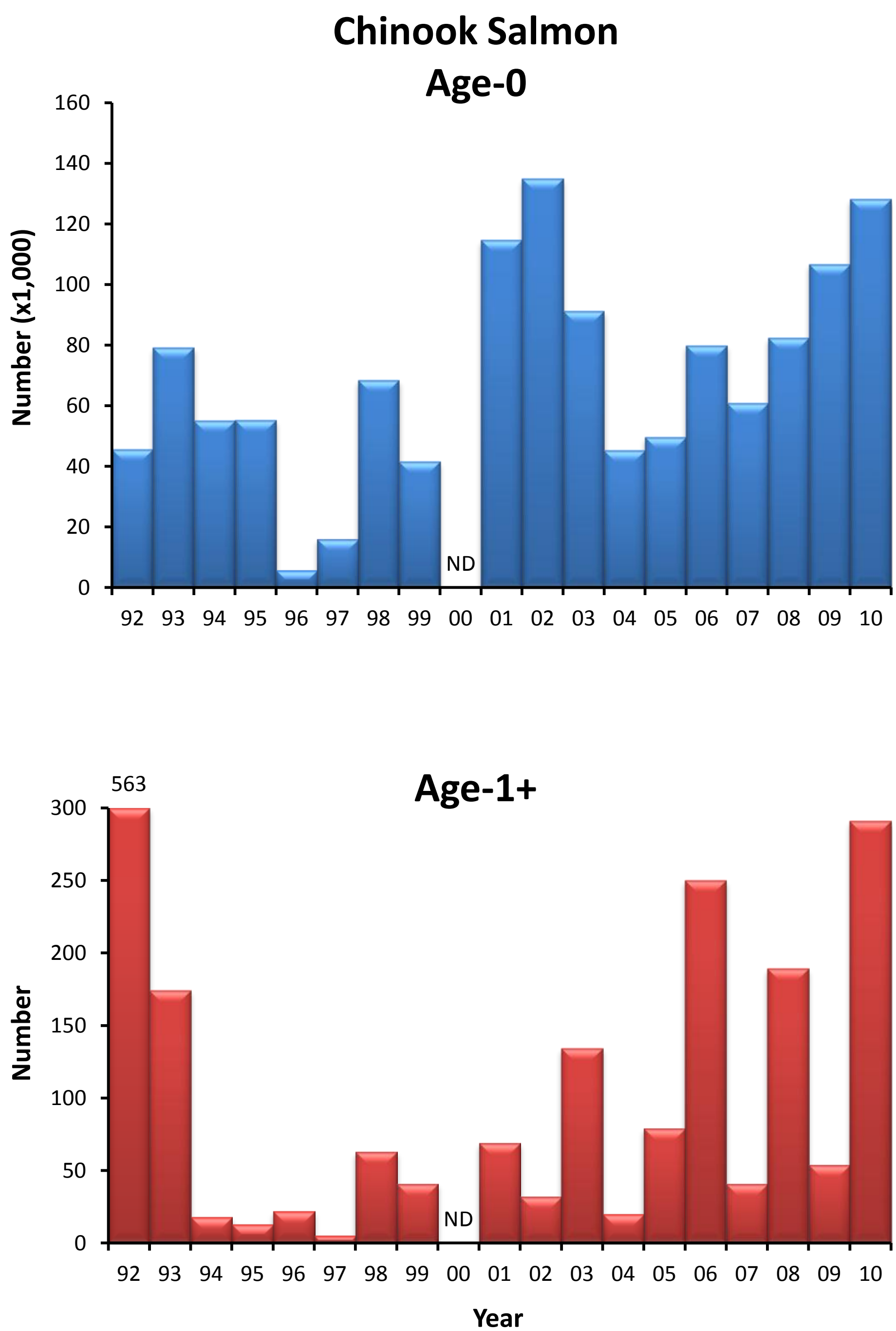


Figure 5.1. Numbers of subyearling and yearling Chinook salmon within the Chiwawa River Basin in August 1992-2010; ND = no data.

Juvenile Chinook were distributed contagiously among reaches in the Chiwawa River. Their densities were highest in the upper portions of the basin, with the highest densities within tributaries. Juvenile Chinook were most abundant in multiple channels and least abundant in glides. Most Chinook associated closely with woody debris in multiple channels. These sites (multiple channels) made up 16% of the total area of the Chiwawa Basin, but they provided habitat for 53% of all the subyearling Chinook in the basin in 2010. In contrast, riffles made up 53% of the total area, but provided habitat for only 11% of all juvenile Chinook in the Chiwawa Basin. Pools made up 23% of the total area and provided habitat for 34% of all juvenile Chinook in the basin. Virtually no Chinook used glides that lacked woody debris.

Mean densities of juvenile Chinook in two reaches of the Chiwawa River were generally less than those in corresponding reference areas (Nason Creek and the Little Wenatchee River) (Figure 5.2). Within both the Chiwawa River and its reference areas, pools and multiple channels consistently had the highest densities of juvenile Chinook.

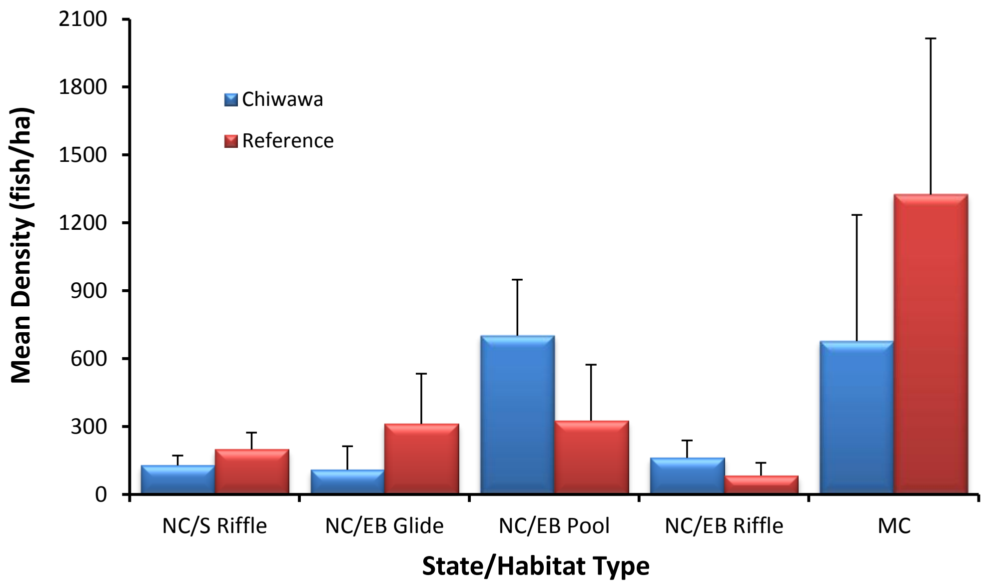


Figure 5.2. Comparison of the 17-year means of subyearling spring Chinook densities within state/habitat types in reaches 3 and 8 of the Chiwawa River and their matched reference areas on Nason Creek and the Little Wenatchee River. NC = natural channel; S = straight channel; EB = eroded banks; MC = multiple channel. There was no sampling in 2000 and no sampling within reference areas in 1992.

Smolt and Emigrant Estimates

Numbers of spring Chinook smolts and emigrants were estimated at the Upper Wenatchee, Chiwawa, and Lower Wenatchee traps in 2010.

Chiwawa Trap

The Chiwawa Trap operated between 5 March and 22 November 2010. During that time period the trap was inoperable for 20 days because of high river flows, debris, snow/ice, mechanical failure, or furlough days. The trap operated in two different positions depending on stream flow; lower position at flows greater than 12 m^3/s and an upper position at flows less than 12 m^3/s. Daily trap efficiencies were estimated from two regression models depending on trap position and age class of fish (e.g., subyearling and yearling). The daily number of fish captured was expanded by the estimated trap efficiency to estimate daily total emigration. Monthly captures of all fish and results of mark-recapture efficiency tests at the Chiwawa Trap are reported in Appendix B.

Wild yearling spring Chinook (2008 brood year) were primarily captured from March through June 2010 (Figure 5.3). Based on capture efficiencies estimated from the flow model, the total number of wild yearling Chinook emigrating from the Chiwawa River was 35,023 (±9,438). Combining the total number of subyearling spring Chinook (85,161) that emigrated during the fall of 2009 with the total number of yearling Chinook (35,023) that emigrated during 2010 resulted in a total emigrant estimate of 120,184 spring Chinook for the 2008 brood year (Table 5.15).

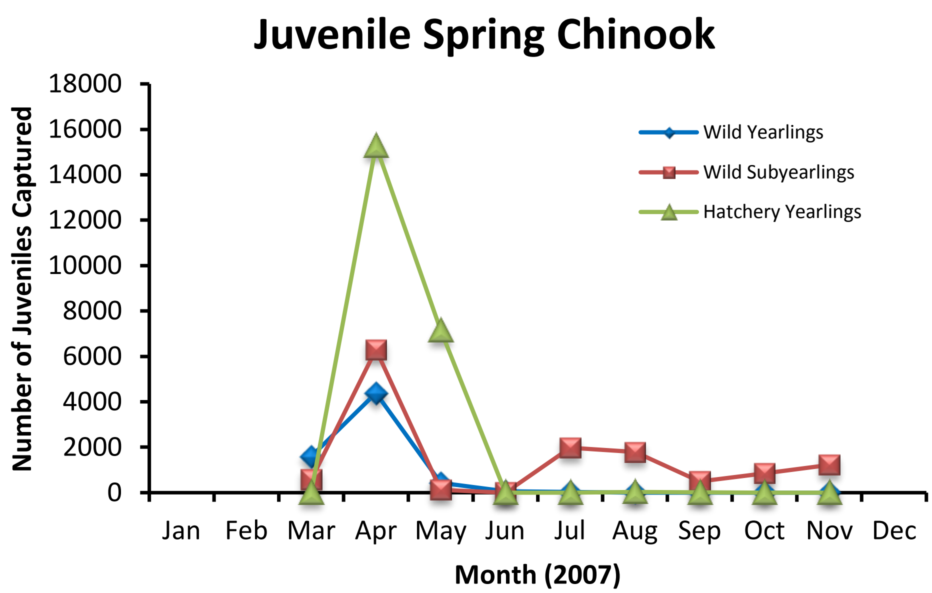


Figure 5.3. Monthly captures of wild subyearling, wild yearling, and hatchery yearling spring Chinook at the Chiwawa Trap, 2010.

Table 5.15. Numbers of redds and juvenile spring Chinook at different life stages in the Chiwawa Basin for brood years 1991-2010; NS = not sampled.

Brood year	Number of redds	Egg deposition	Number of parr	Number of smolts produced within Chiwawa Basin[a]	Total number of smolts[b]	Number of emigrants
1991	104	478,400	45,483[c]	42,525	42,525	NS
1992	302	1,570,098	79,113	39,723	56,763	65,541
1993	106	556,394	55,056	8,662	17,926	22,698
1994	82	485,686	55,240	16,472	22,145	25,067
1995	13	66,248	5,815	3,830	5,230	5,951
1996	23	106,835	16,066	15,475	17,922	19,183
1997	82	374,740	68,415	28,334	39,044	44,562
1998	41	218,325	41,629	23,068	24,953	25,923

Brood year	Number of redds	Egg deposition	Number of parr	Number of smolts produced within Chiwawa Basin[a]	Total number of smolts[b]	Number of emigrants
1999	34	166,090	NS	10,661	13,953	15,649
2000	128	642,944	114,617	40,831	50,634	55,685
2001	1,078	4,984,672	134,874	86,482	389,940	546,266
2002	345	1,605,630	91,278	90,948	152,547	184,279
2003	111	648,684	45,177	16,755	27,897	33,637
2004	241	1,156,559	49,631	72,080	101,172	116,158
2005	332	1,436,564	79,902	69,064	140,737	177,659
2006	297	1,284,228	60,752	45,050	86,579	107,972
2007	283	1,256,803	82,351	25,809	65,539	86,006
2008	689	3,163,888	106,705	35,023	91,229	120,184
2009	421	1,925,233	128,220	-	-	-
2010	502	2,165,628	-	-	-	-
Average	***261***	***1,215,140***	***71,461***	***37,266***	***74,819***	***97,201***

[a] The estimated number of smolts (yearlings) that are produced entirely within the Chiwawa Basin. Smolt estimates for brood years 1992-1996 were calculated with a mark-recapture model; brood years 1997-present were calculated with a flow model.
[b] These numbers represent Chiwawa smolts produced within the entire Wenatchee Basin. This assumes that 66% of the subyearling migrants from the Chiwawa Basin survive to smolt in the Wenatchee Basin, regardless of the number of subyearling migrants (i.e., no density dependence). Smolt estimates for brood years 1992-1996 were calculated with a mark-recapture model; brood years 1997-present were calculated with a flow model.
[c] Estimate only includes numbers of Chinook in the Chiwawa River. Tributaries were not sampled at that time.

Wild subyearling spring Chinook (2009 brood year) were captured between 5 March and 22 November 2010. Based on capture efficiencies estimated from the flow model for both the upper trap position and lower position, the total number of wild subyearling (fry and parr) Chinook from the Chiwawa Basin was 103,185 (±15,166). Removing fry from the estimate, a total of 31,913 (±5,779) parr emigrated from the Chiwawa Basin in 2010. Although subyearlings migrated during most months of sampling, the majority (91%) migrated during April, July, August, October, and November (Figure 5.3).

Yearling spring Chinook sampled in 2010 averaged 91 mm in length, 8.9 g in weight, and had a mean condition of 1.15 (Table 5.16). These size estimates were less than the overall mean of yearling spring Chinook sampled in previous years (overall means: 94 mm, 9.3 g, and condition of 1.08). Subyearling spring Chinook sampled in 2010 at the Chiwawa Trap averaged 77 mm in length, averaged 5.4 g, and had a mean condition of 1.11 (Table 5.16). These sizes were similar to the overall mean of subyearling spring Chinook sampled in previous years (overall means, 77 mm, 5.6 g, and condition of 1.09).

Table 5.16. Mean fork length (mm), weight (g), and condition factor of subyearling and yearling spring Chinook collected in the Chiwawa Trap, 1996-2010. Numbers in parentheses indicate 1 standard deviation.

Sample year	Life stage	Sample size[a]	Mean size		
			Length (mm)	Weight (g)	Condition (K)
1996	Subyearling	514	78 (25)	6.9 (4.2)	1.11 (0.11)
	Yearling	1,589	94 (9)	9.5 (3.0)	1.11 (0.08)
1997	Subyearling	840	86 (8)	7.5 (2.1)	1.16 (0.08)
	Yearling	1,114	100 (7)	10.2 (2.6)	1.02 (0.10)
1998	Subyearling	3,743	82 (11)	6.2 (2.2)	1.08 (0.09)
	Yearling	2,663	97 (7)	10.3 (2.8)	1.12 (0.23)
1999	Subyearling	569	89 (9)	8.5 (2.4)	1.15 (0.07)
	Yearling	3,664	95 (8)	9.6 (3.4)	1.09 (0.19)
2000	Subyearling	1,810	85 (10)	7.4 (2.4)	1.15 (0.10)
	Yearling	1,891	97 (8)	10.5 (5.2)	1.13 (0.07)
2001	Subyearling	4,657	82 (11)	6.6 (3.4)	1.14 (0.09)
	Yearling	2,935	97 (7)	10.5 (2.4)	1.15 (0.08)
2002	Subyearling	6,130	64 (12)	3.0 (1.6)	1.06 (0.10)
	Yearling	1,735	94 (8)	9.0 (2.3)	1.09 (0.08)
2003	Subyearling	3,679	64 (12)	3.2 (1.7)	1.08 (0.10)
	Yearling	2,657	87 (9)	7.2 (3.5)	1.07 (0.10)
2004	Subyearling	2,278	75 (16)	4.3 (2.1)	0.92 (0.16)
	Yearling	1,032	91 (9)	8.5 (2.7)	1.09 (0.10)
2005	Subyearling	2,702	73 (12)	4.6 (2.2)	1.08 (0.09)
	Yearling	803	96 (9)	9.9 (2.8)	1.08 (0.08)
2006	Subyearling	3,462	76 (11)	5.1 (2.0)	1.12 (0.21)
	Yearling	4,645	95 (7)	9.4 (2.3)	1.10 (0.13)
2007	Subyearling	1,718	72 (12)	4.5 (2.1)	1.13 (0.16)
	Yearling	2,245	91 (8)	8.6 (2.5)	1.10 (0.09)
2008	Subyearling	10,443	79 (12)	5.9 (2.3)	1.15 (0.15)
	Yearling	8,792	93 (7)	8.8 (2.1)	1.08 (0.10)
2009	Subyearling	10,536	75 (10)	5.0 (2)	0.91 (0.11)
	Yearling	3,630	92 (7)	8.8 (2)	0.89 (0.07)
2010	Subyearling	3,888	77 (12)	5.4 (2)	1.11 (0.16)
	Yearling	5,799	91 (8)	8.9 (2)	1.15 (0.14)
Average	***Subyearling***	***3,798***	***77 (7)***	***5.6 (1.6)***	***1.09 (0.08)***
	Yearling	***3,013***	***94 (3)***	***9.3 (0.9)***	***1.08 (0.06)***

[a] Sample size represents the number of fish that were measured for both length and weight.

Upper Wenatchee Trap

The Upper Wenatchee Trap operated nightly between 12 March and 8 July 2010. During the five-month sampling period, a total of 569 wild yearling Chinook, 254 wild subyearling Chinook, and 245 hatchery yearling Chinook were captured at the Upper Wenatchee Trap. Monthly captures of all fish collected at the Upper Wenatchee Trap are reported in Appendix B.

Lower Wenatchee Trap

The Lower Wenatchee Trap operated nightly between 4 February and 20 July 2010. During that time period the trap was inoperable for 19 days because of high river flows, debris, snow/ice, or mechanical failure. During the seven-month sampling period, a total of 1,079 wild yearling Chinook, 50,685 wild subyearling Chinook (mostly summer Chinook), and 43,613 hatchery yearling Chinook were captured at the Lower Wenatchee Trap. Based on capture efficiencies estimated from the flow model, the total number of wild yearling Chinook that emigrated past the Lower Wenatchee Trap was 82,137 (±87,931). The majority (59%) of these fish emigrated during April. Monthly captures of all fish collected at the Lower Wenatchee Trap are reported in Appendix B.

PIT Tagging Activities

As part of the Integrated Status and Effectiveness Monitoring Program (ISEMP), a total of 12,380 wild juvenile Chinook (4,689 subyearling and 7,691 yearlings) were PIT tagged and released in 2010 throughout the Wenatchee Basin (Table 5.17a). Most of these (82%) were tagged in the Chiwawa Basin (9,605 at the trap plus 535 others upstream from the trap). Few were tagged and released in the Wenatchee River. A total of 917 Chinook were tagged and released at the Lower Wenatchee trap. See Appendix C for a complete list of all fish captured, tagged, lost, and released.

Table 5.17a. Numbers of wild Chinook that were captured, tagged, and released at different locations within the Wenatchee Basin, 2010. Numbers of fish that died or shed tags are also given.

Sampling Location	Species and Life Stage	Number held	Number of recaptures	Number tagged	Number died	Shed Tags	Total released	Percent mortality
Chiwawa Trap	Wild Subyearling Chinook	3,637	127	3,326	2	0	3,324	0.05
	Wild Yearling Chinook	6,741	292	6,285	4	0	6,281	0.06
	Total	**10,378**	**419**	**9,611**	**6**	**0**	**9,605**	**0.06**
Chiwawa Remote	Wild Subyearling Chinook	574	12	532	0	1	531	0.00
	Wild Yearling Chinook	4	0	4	0	0	4	0.00
	Total	**578**	**12**	**536**	**0**	**1**	**535**	**0.00**
Upper Wenatchee Trap	Wild Subyearling Chinook	3	0	3	0	0	3	0.00
	Wild Yearling Chinook	524	13	491	5	0	486	0.95
	Total	**527**	**13**	**494**	**5**	**0**	**489**	**0.95**
Nason Creek Remote	Wild Subyearling Chinook	600	2	595	0	0	595	0.00
	Wild Yearling Chinook	3	0	3	0	0	3	0.00
	Total	**603**	**2**	**598**	**0**	**0**	**598**	**0.00**
Upper Wenatchee Remote	Wild Subyearling Chinook	2	0	2	0	0	2	0.00
	Wild Yearling Chinook	0	0	0	0	0	0	--

Sampling Location	Species and Life Stage	Number held	Number of recaptures	Number tagged	Number died	Shed Tags	Total released	Percent mortality
	Total	**2**	**0**	**2**	**0**	**0**	**2**	**0.00**
Middle Wenatchee Remote	Wild Subyearling Chinook	245	4	234	1	0	233	0.41
	Wild Yearling Chinook	0	0	0	0	0	0	--
	Total	**245**	**4**	**234**	**1**	**0**	**233**	**0.41**
Peshastin Creek Remote	Wild Subyearling Chinook	1	0	1	0	0	1	0.00
	Wild Yearling Chinook	0	0	0	0	0	0	--
	Total	**1**	**0**	**1**	**0**	**0**	**1**	**0.00**
Lower Wenatchee Trap	Wild Subyearling Chinook	0	0	0	0	0	0	--
	Wild Yearling Chinook	1,051	81	928	11	0	917	1.05
	Total	**1,051**	**81**	**928**	**11**	**0**	**917**	**1.05**
Total:	**Wild Subyearling Chinook**	**5,062**	**145**	**4,693**	**3**	**1**	**4,689**	**0.06**
	Wild Yearling Chinook	**8,323**	**386**	**7,711**	**20**	**0**	**7,691**	**0.24**
Grand Total:		**13,385**	**531**	**12,404**	**23**	**1**	**12,380**	**0.17**

Numbers of wild Chinook salmon PIT-tagged and released as part of ISEMP during the period 2006-2010 are shown in Table 5.17b.

Table 5.17b. Summary of the numbers of wild Chinook that were tagged and released at different locations within the Wenatchee Basin, 2006-2010.

Sampling Location	Species and Life Stage	Numbers of PIT-tagged Chinook salmon released				
		2006	**2007**	**2008**	**2009**	**2010**
Chiwawa Trap	Wild Subyearling Chinook	5,130	6,137	8,755	8,765	3,324
	Wild Yearling Chinook	2,793	4,659	8,397	3,694	6,281
	Total	**7,923**	**10,796**	**17,152**	**12,459**	**9,605**
Chiwawa Remote	Wild Subyearling Chinook	111	20	43	128	531
	Wild Yearling Chinook	0	0	0	3	4
	Total	**111**	**20**	**43**	**131**	**535**
Upper Wenatchee Trap	Wild Subyearling Chinook	0	15	0	37	3
	Wild Yearling Chinook	81	1,434	159	296	486
	Total	**81**	**1,449**	**159**	**333**	**489**
Nason Creek Remote[a]	Wild Subyearling Chinook	68	6	4	701	595
	Wild Yearling Chinook	1	7	0	13	3
	Total	**69**	**13**	**4**	**714**	**598**
Upper Wenatchee Remote	Wild Subyearling Chinook	0	61	1	0	2
	Wild Yearling Chinook	27	0	0	0	0
	Total	**27**	**61**	**1**	**0**	**2**
Middle Wenatchee Remote	Wild Subyearling Chinook	0	0	65	284	233
	Wild Yearling Chinook	0	0	0	0	0

Sampling Location	Species and Life Stage	Numbers of PIT-tagged Chinook salmon released				
		2006	2007	2008	2009	2010
	Total	**0**	**0**	**65**	**284**	**233**
Lower Wenatchee Remote	Wild Subyearling Chinook	0	0	0	0	0
	Wild Yearling Chinook	0	0	0	0	0
	Total	**0**	**0**	**0**	**0**	**0**
Peshastin Creek Remote	Wild Subyearling Chinook	0	0	0	0	1
	Wild Yearling Chinook	0	0	0	0	0
	Total	**0**	**0**	**0**	**0**	**1**
Lower Wenatchee Trap	Wild Subyearling Chinook	0	0	2	0	0
	Wild Yearling Chinook	522	1,641	506	468	917
	Total	**522**	**1,641**	**508**	**468**	**917**
Total:	**Wild Subyearling Chinook**	**5,309**	**6,239**	**8,870**	**9,915**	**4,689**
	Wild Yearling Chinook	**3,424**	**7,741**	**9,062**	**4,474**	**7,691**
Grand Total:		**8,733**	**13,980**	**17,932**	**14,389**	**12,380**

Freshwater Productivity

Both productivity and survival estimates for different life stages of spring Chinook in the Chiwawa Basin are provided in Table 5.18. Estimates for brood year 2008 fall within the ranges estimated over the period of brood years 1991-2007. During that period, freshwater productivities ranged from 125-1,015 parr/redd, 132-779 smolts/redd, and 174-834 emigrants/redd. Survivals during the same period ranged from 2.7-19.1% for egg-parr, 2.9-16.8% for egg-smolt, and 3.8-18.0% for egg-emigrants. Overwinter survival rates for juvenile spring Chinook within the Chiwawa Basin have ranged from 15.7-100.0%.

Table 5.18. Productivity (fish/redd) and survival (%) estimates for different juvenile life stages of spring Chinook in the Chiwawa Basin for brood years 1991-2009; ND = no data. These estimates were derived from data in Table 5.14.

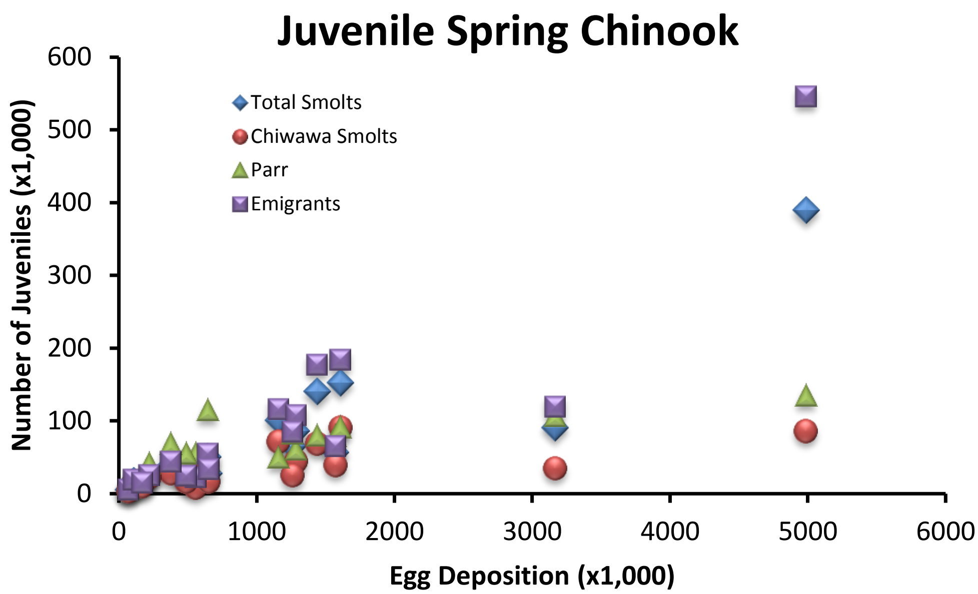
Brood year	Parr/Redd	Smolts/Redd[a]	Emigrants/ Redd	Egg-Parr (%)	Parr-Smolt[b] (%)	Egg-Smolt[a] (%)	Egg-Emigrant (%)
1991	437	409	ND	9.5	93.5	8.9	ND
1992	262	188	217	5.0	50.2	3.6	4.2
1993	519	169	214	9.9	15.7	3.2	4.1
1994	674	270	306	11.4	29.8	4.6	5.2
1995	447	402	458	8.8	65.9	7.9	9.0
1996	699	779	834	15.0	96.3	16.8	18.0
1997	834	476	543	18.3	41.4	10.4	11.9
1998	1,015	609	632	19.1	55.4	11.4	11.9
1999	ND	410	460	ND	ND	8.4	9.4
2000	895	396	435	17.8	35.6	7.9	8.7

Brood year	Parr/Redd	Smolts/Redd[a]	Emigrants/ Redd	Egg-Parr (%)	Parr-Smolt[b] (%)	Egg-Smolt[a] (%)	Egg-Emigrant (%)
2001	125	362	507	2.7	64.1	7.8	11.0
2002	265	442	534	5.7	99.6	9.5	11.5
2003	407	251	303	7.0	37.1	4.3	5.2
2004	206	420	482	4.3	100.0	8.7	10.0
2005	241	424	535	5.6	86.4	9.8	12.4
2006	205	292	364	4.7	74.2	6.7	8.4
2007	291	232	304	6.6	31.3	5.2	6.8
2008	155	132	174	3.4	32.8	2.9	3.8
2009	305	-	-	6.7	-	-	-
Average	***443***	***370***	***430***	***9.0***	***59.4***	***7.7***	***8.9***

[a] These estimates include Chiwawa smolts produced within the Wenatchee Basin. This assumes that 66% of the subyearling migrants survive to smolt, regardless of the number of subyearling migrants (i.e., no density dependence). Smolt estimates for brood years 1992-1996 were calculated with a mark-recapture model; brood years 1997-present were calculated with a flow model.

[b] These estimates represent overwinter survival within the Chiwawa Basin. It does not include Chiwawa smolts produced outside the Chiwawa Basin. As noted in footnote *a*, smolts/redd and egg-smolt survival include Chiwawa smolts produced in the Wenatchee Basin.

Seeding level (egg deposition) explained most of the variability in productivity and survival of juvenile spring Chinook in the Chiwawa Basin. That is, for estimates based on "within-Chiwawa-Basin" life stages (e.g., parr and within-Chiwawa-Basin smolts), survival and productivity decreased as seeding levels increased (Figure 5.4). This suggests that density dependence regulates juvenile productivity and survival within the Chiwawa Basin. This form of population regulation is less apparent with total smolts (i.e., Chiwawa smolts produced within the Wenatchee Basin) and total emigrants. However, one would expect the number of emigrants to increases as seeding levels exceed the capacity of the Chiwawa Basin.



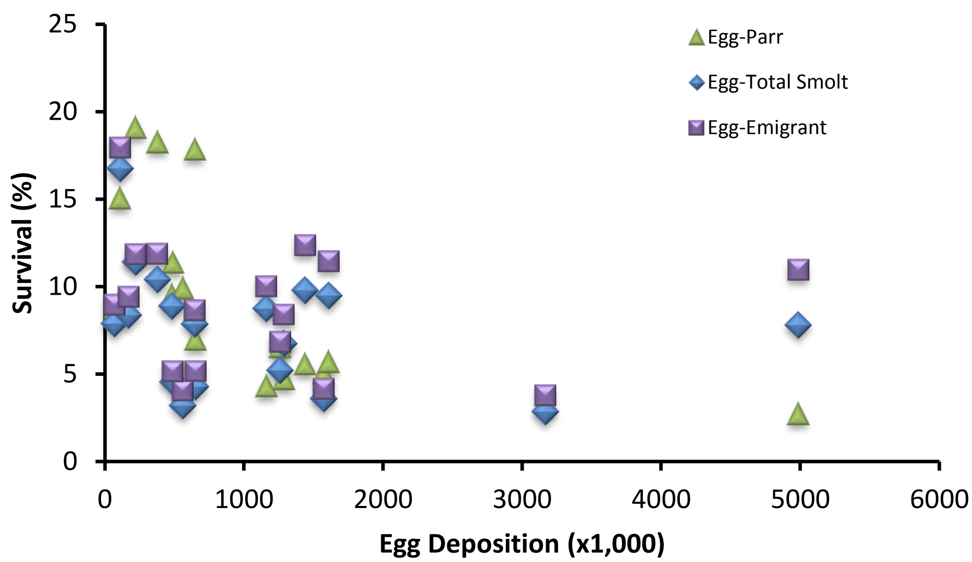


Figure 5.4. Relationships between seeding levels (egg deposition) and juvenile life-stage survivals and productivities for Chiwawa spring Chinook, brood years 1991-2008. Total smolts are Chiwawa smolts produced within and outside the Chiwawa Basin (assumes a 66% survival on subyearling emigrants). Chiwawa smolts are smolts produced only in the Chiwawa Basin.

5.5 Spawning Surveys

Surveys for spring Chinook carcasses were conducted during August through September, 2010, in the Chiwawa River (including Rock, Phelps, Big Meadow, and Chikamin creeks), Nason Creek, Icicle Creek, Peshastin Creek (including Ingalls Creek), Upper Wenatchee River (including Chiwaukum Creek), Little Wenatchee River, and White River (including the Napeequa River and Panther Creek).

Redd Counts

A total of 968 spring Chinook redds were counted in the Wenatchee Basin in 2010 (Table 5.19). This is higher than the average of 576 redds counted during the period 1989-2009 in the Wenatchee Basin. Most spawning occurred in the Chiwawa River (52% or 502 redds) (Table 5.19; Figure 5.5). Nason Creek contained 19% (188 redds), White River contained 3% (33 redds), Little Wenatchee contained 4% (38 redds), Icicle contained 16% (155 redds), Peshastin Creek contained 1% (5 redds), and the Upper Wenatchee River 5% (47 redds).

Table 5.19. Numbers of spring Chinook redds counted within different streams/watersheds within the Wenatchee Basin, 1989-2010. Redd counts in Peshastin Creek in 2001 and 2002 (*) were elevated because the U.S. Fish and Wildlife Service planted 487 and 350 spring Chinook adults, respectively, into the stream. These counts were not included in the total or average calculations.

Sample year	Number of spring Chinook redds							
	Chiwawa	Nason	Little Wenatchee	White	Wenatchee River	Icicle	Peshastin	Total
1989	314	98	45	64	94	24	NS	**639**
1990	255	103	30	22	36	50	4	**500**
1991	104	67	18	21	41	40	1	**292**
1992	302	81	35	35	38	37	0	**528**
1993	106	223	61	66	86	53	5	**600**
1994	82	27	7	3	6	15	0	**140**
1995	13	7	0	2	1	9	0	**32**
1996	23	33	3	12	1	12	1	**85**
1997	82	55	8	15	15	33	1	**209**
1998	41	29	8	5	0	11	0	**94**
1999	34	8	3	1	2	6	0	**54**
2000	128	100	9	8	37	68	0	**350**
2001	1,078	374	74	104	218	88	173*	**2,109**
2002	345	294	42	42	64	245	107*	**1,139**
2003	111	83	12	15	24	18	60	**323**
2004	241	169	13	22	46	30	55	**576**
2005	332	193	64	86	143	8	3	**829**
2006	297	152	21	31	27	50	10	**588**
2007	283	101	22	20	12	17	11	**466**
2008	689	336	38	31	180	116	21	**1,411**
2009	421	167	39	54	5	32	15	**733**
2010	502	188	38	33	47	155	5	**968**
Average	***261***	***131***	***27***	***31***	***51***	***51***	***10***	***576***

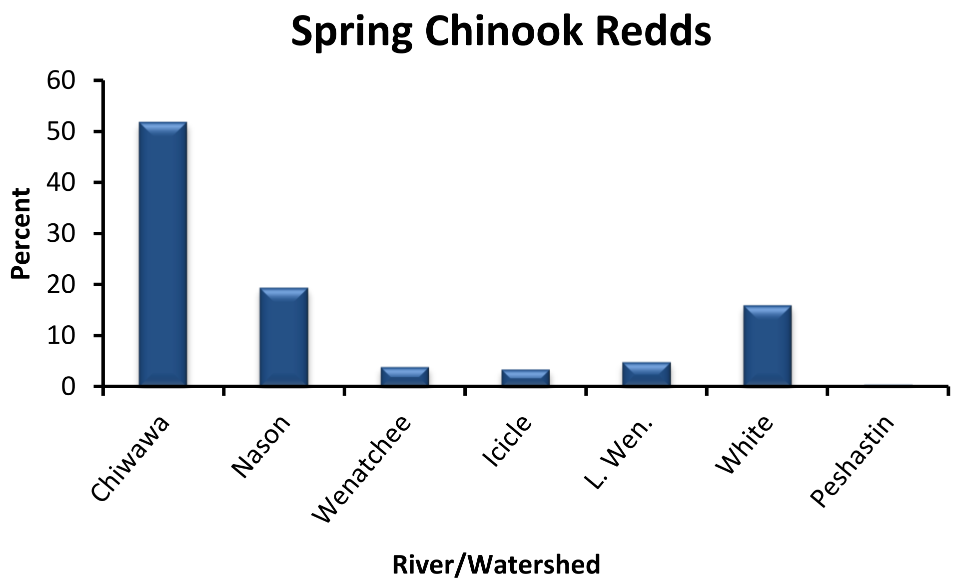


Figure 5.5. Percent of the total number of spring Chinook redds counted in different streams/watersheds within the Wenatchee Basin during August through September, 2010.

Redd Distribution

Spring Chinook redds were not evenly distributed among reaches within survey streams in 2010 (Table 5.20). Most of the spawning in the Chiwawa Basin occurred in Reaches 1 and 2. Over half of all the spawning in the Chiwawa Basin occurred in the lower two reaches (RM 0.0-19.3; from the mouth to Rock Creek). Relatively few fish spawned in Rock and Chikamin creeks. The spatial distribution of redds in Nason Creek was weighted towards Reach 3, having 33% of the Nason Creek redds. In the Little Wenatchee River, 92% of all spawning occurred in Reach 3 (RM 5.2-9.2; Lost Creek to Rainy Creek). On the White River, 85% occurred in Reach 3 (RM 11.0-12.9; Napeequa River to Grasshopper Meadows). Seventy five percent of all the spawning in the Wenatchee River occurred upstream from the mouth of the Chiwawa River.

Table 5.20. Numbers and proportions of spring Chinook redds counted within different streams/watersheds within the Wenatchee Basin during August through September, 2010.

Stream/watershed	Reach	Number of redds	Proportion of redds within stream/watershed
Chiwawa	Chiwawa 1	106	0.21
	Chiwawa 2	196	0.39
	Chiwawa 3	18	0.03
	Chiwawa 4	44	0.09
	Chiwawa 5	51	0.10
	Chiwawa 6	65	0.13
	Phelps 1	0	0.00
	Rock 1	13	0.03
	Chikamin 1	9	0.02
	Big Meadow 1	0	0.00

Stream/watershed	Reach	Number of redds	Proportion of redds within stream/watershed
	Total	**502**	**1.00**
Nason	Nason 1	49	0.26
	Nason 2	44	0.23
	Nason 3	61	0.33
	Nason 4	34	0.18
	Total	**188**	**1.00**
Little Wenatchee	Little Wen 2	3	0.08
	Little Wen 3	35	0.92
	Total	**38**	**1.00**
White	White 2	1	0.03
	White 3	28	0.85
	White 4	3	0.09
	Napeequa 1	1	0.03
	Panther 1	0	0.00
	Total	**33**	**1.00**
Wenatchee River	Wen 8	0	0.00
	Wen 9	9	0.19
	Wen 10	35	0.75
	Chiwaukum 1	3	0.06
	Total	**47**	**1.00**
Icicle	Icicle 1	155	1.00
	Total	**155**	**1.00**
Peshastin	Peshastin 1	5	1.00
	Peshastin 2	0	0.00
	Ingalls	0	0.00
	Total	**5**	**1.00**
Grand Total		***968***	**1.00**

Spawn Timing

Spring Chinook began spawning during the second week of August in the Chiwawa River, White River, Little Wenatchee, and Nason Creek, and the fourth week in the Upper Wenatchee River (Figure 5.6). Spawning generally peaked the fourth and fifth weeks of August. All spawning was completed by the end of September.

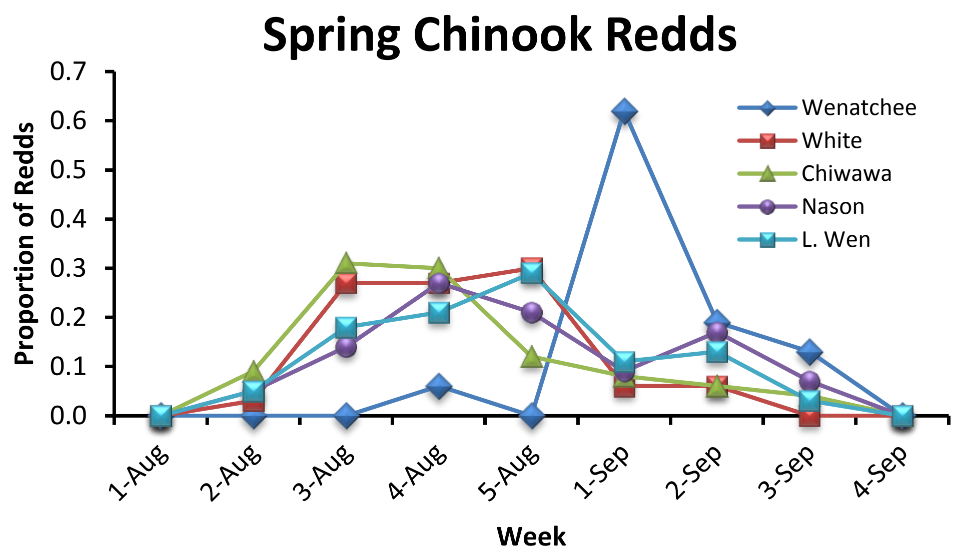


Figure 5.6. Proportion of spring Chinook redds counted during different weeks in different sampling streams within the Wenatchee Basin, August through September 2010.

The temporal distribution of spawning activity in the Chiwawa River in 2010 occurred earlier than the mean 1991-2009 spawning distribution for the Chiwawa (Figure 5.7). The greatest difference in distributions was noted in early August.

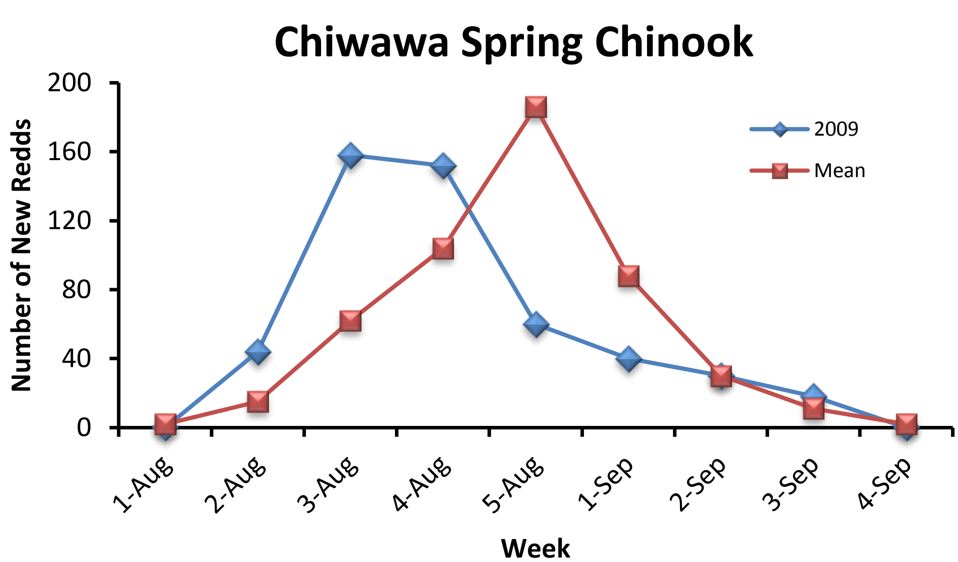


Figure 5.7. Comparison of the number of new spring Chinook redds counted during different weeks in the Chiwawa Basin, August through September, 2010, to the overall average.

Spawning Escapement

Spawning escapement for spring Chinook was calculated as the number of redds times the male-to-female ratio (i.e., fish per redd expansion factor) estimated from broodstock and fish sampled at adult trapping sites. The estimated fish per redd ratio for spring Chinook upstream from Tumwater in 2010 was 2.14 (based on sex ratios estimated at Tumwater Dam). The estimated fish per redd ratio for spring Chinook downstream from Tumwater (Icicle and Peshastin creeks) was 2.72 (derived from broodstock collected at the Leavenworth National Fish Hatchery). Multiplying these ratios by the number of redds counted in the Wenatchee Basin resulted in a total spawning escapement of 2,165 spring Chinook (Table 5.21). The Chiwawa Basin had the highest spawning escapement (1,074 Chinook), while Peshastin Creek had the lowest.

Table 5.21. Number of redds, fish per redd ratios, and total spawning escapement for spring Chinook in the Wenatchee Basin, 2010. Spawning escapement was estimated as the product of redds times fish per redd.

Sampling area	Total number of redds	Fish/redd	Total spawning escapement*
Chiwawa	502	2.14	1,074
Nason	188	2.14	402
Upper Wenatchee River	47	2.14	101
Icicle	155	2.72	422
Little Wenatchee	38	2.14	81
White	33	2.14	71
Peshastin	5	2.72	14
Total	***968***	-	***2,165***

* Spawning escapement estimate is based on total number of redds by stream. If escapement is calculated at the reach scale, then the total escapement may vary from what is shown here because of rounding errors.

The estimated total spawning escapement of 2,197 spring Chinook in 2010 was greater than the overall average of 1,267 spring Chinook (Table 5.22). The escapement in the Chiwawa Basin in 2010 was over twice the escapement in Icicle Creek, the second most abundant stream in the Wenatchee Basin (Table 5.22).

Table 5.22. Spawning escapements for spring Chinook in the Wenatchee Basin for return years 1989-2010; NA = not available.

Return year	Upper basin spawning escapement						Lower basin spawning escapement			Total
	Fish/redd	Chiwawa	Nason	Little Wenatchee	White	Wenatchee River	Fish/redd	Icicle	Peshastin	
1989	2.27	713	222	102	145	213	2.27	54	NA	**1,449**
1990	2.24	571	231	67	49	81	2.24	112	9	**1,120**
1991	2.33	242	156	42	49	96	2.33	93	2	**680**
1992	2.24	676	181	78	78	85	2.24	83	0	**1,181**
1993	2.20	233	491	134	145	189	2.20	117	11	**1,320**
1994	2.24	184	60	16	7	13	2.24	34	0	**314**
1995	2.51	33	18	0	5	3	2.51	23	0	**82**
1996	2.53	58	83	8	30	3	2.53	30	3	**215**
1997	2.22	182	122	18	33	33	2.22	73	2	**463**
1998	2.21	91	64	18	11	0	2.21	24	0	**208**

Return year	Upper basin spawning escapement						Lower basin spawning escapement			Total
	Fish/redd	Chiwawa	Nason	Little Wenatchee	White	Wenatchee River	Fish/redd	Icicle	Peshastin	
1999	2.77	94	22	8	3	6	2.77	17	0	**150**
2000	2.70	346	270	24	22	100	2.70	184	0	**946**
2001	1.60	1,725	598	118	166	349	1.60	141	277	**3,874**
2002	2.05	707	603	86	86	131	2.05	502	219	**2,334**
2003	2.43	270	202	29	36	58	2.43	44	146	**785**
2004[a]	3.56/3.00	858	507	39	66	138	1.79	54	98	**1,759**
2005	1.80	598	347	115	155	257	1.75	14	5	**1,491**
2006	1.78	529	271	37	55	48	1.80	90	18	**1,048**
2007	4.58	1,296	463	101	92	55	1.86	32	20	**2,059**
2008	1.68	1,158	565	64	52	302	1.77	205	37	**2,383**
2009	3.20	1,347	534	125	173	16	2.72	87	41	**2,323**
2010	2.18	1,094	410	83	72	102	2.72	422	14	**2,197**
Average	***2.45***	***591***	***292***	***60***	***70***	***104***	***2.23***	***111***	***43***	***1,267***

[a] In 2004 the fish/redd expansion estimate of 3.56 was applied to the Chiwawa River only and 3.00 fish/redd for the rest of the upper basin.

5.6 Carcass Surveys

Surveys for spring Chinook carcasses were conducted during August through September, 2010, in the Chiwawa River (including Rock, Phelps, Big Meadow, and Chikamin creeks), Nason Creek, Icicle Creek, Peshastin Creek (including Ingalls Creek), Upper Wenatchee River (including Chiwaukum Creek), Little Wenatchee River, and White River (including the Napeequa River and Panther Creek).

Number sampled

A total of 423 spring Chinook carcasses were sampled during August through September in the Wenatchee Basin (Table 5.23). Most were sampled in the Chiwawa Basin (46% or 193 carcasses) and Nason Creek (33% or 141 carcasses) (Figure 5.8). A total of 39 carcasses were sampled in Icicle Creek, seven in the Little Wenatchee, 11 in the White River, 30 in the upper Wenatchee River, and two in Peshastin Creek.

Table 5.23. Numbers of spring Chinook carcasses sampled within different streams/watersheds within the Wenatchee Basin, 1996-2010.

Survey year	Number of spring Chinook carcasses							
	Chiwawa	Nason	Little Wenatchee	White	Wenatchee River	Icicle	Peshastin	Total
1996	22	3	0	2	0	1	0	**28**
1997	13	42	3	8	1	28	1	**96**
1998	24	25	3	2	1	6	0	**61**
1999	15	5	0	0	2	1	0	**23**
2000	122	110	8	1	37	52	0	**330**
2001	751	388	68	74	213	163	63	**1,720**

Survey year	Number of spring Chinook carcasses							
	Chiwawa	Nason	Little Wenatchee	White	Wenatchee River	Icicle	Peshastin	Total
2002	190	292	30	24	34	91	49	**710**
2003	70	100	8	8	12	37	42	**277**
2004	178	186	1	13	29	16	40	**463**
2005	391	217	48	52	120	2	0	**830**
2006	241	190	13	25	15	7	0	**491**
2007	250	201	16	13	25	15	6	**526**
2008	386	243	15	13	108	68	5	**838**
2009	240	128	20	19	2	67	2	**478**
2010	193	141	7	11	30	39	2	**423**
Average	***206***	***151***	***16***	***18***	***42***	***40***	***14***	***486***

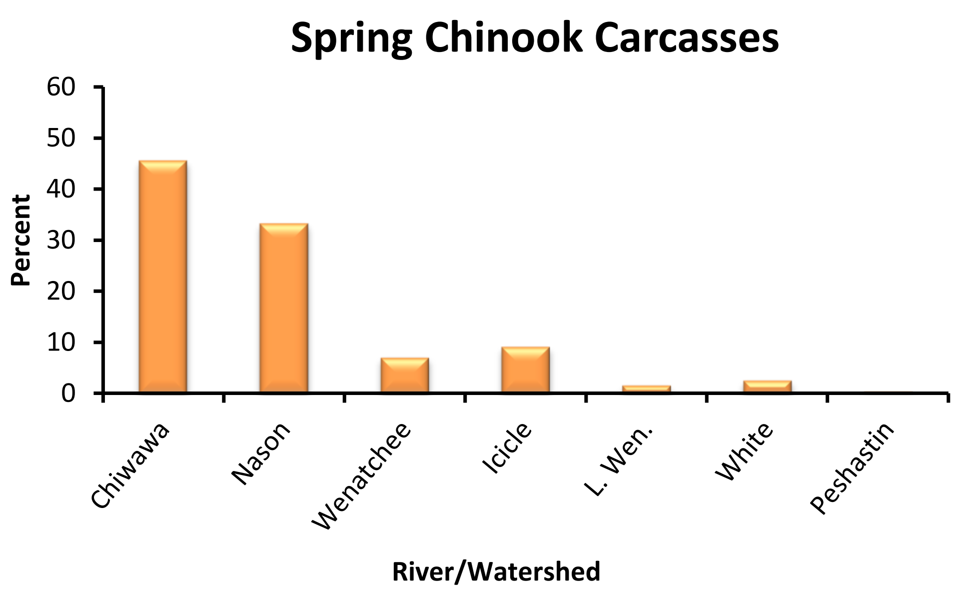


Figure 5.8. Percent of the total number of spring Chinook carcasses sampled in different streams/watersheds within the Wenatchee Basin during August through September, 2010.

Carcass Distribution and Origin

Spring Chinook carcasses were not evenly distributed among reaches within survey streams in 2010 (Table 5.24). Most of the carcasses in the Chiwawa Basin occurred in Reaches 1 and 2 (downstream from Rock Creek). In Nason Creek, most carcasses (35%) were collected in Reach 1 and the fewest (14%) in Reach 4. Most of the carcasses in the Little Wenatchee River (71%) were sampled in Reach 3 (Lost Creek to Rainy Creek). On the White River, 100% occurred in Reach 3 (Napeequa River to Grasshopper Meadows). On the Wenatchee River, 20 carcasses were found upstream from the confluence of the Chiwawa River and ten were found below the confluence.

Table 5.24. Numbers and proportions of carcasses sampled within different streams/watersheds within the Wenatchee Basin during August through September, 2010.

Stream/watershed	Reach	Number of carcasses	Proportion of redds within stream/watershed
Chiwawa	Chiwawa 1	69	0.36
	Chiwawa 2	67	0.35
	Chiwawa 3	9	0.05
	Chiwawa 4	18	0.09
	Chiwawa 5	17	0.09
	Chiwawa 6	8	0.04
	Phelps 1	0	0.00
	Rock 1	5	0.02
	Chikamin 1	0	0.00
	Big Meadow 1	0	0.00
	Total	**193**	**1.00**
Nason	Nason 1	49	0.35
	Nason 2	35	0.25
	Nason 3	36	0.26
	Nason 4	21	0.14
	Total	**141**	**1.00**
Little Wenatchee	Little Wen 2	2	0.29
	Little Wen 3	5	0.71
	Total	**7**	**1.00**
White	White 2	0	0.00
	White 3	11	1.00
	White 4	0	0.00
	Napeequa 1	0	0.00
	Panther 1	0	0.00
	Total	**11**	**1.00**
Wenatchee River	Wen 8	0	0.00
	Wen 9	10	0.33
	Wen 10	20	0.67
	Chiwaukum 1	0	0.00
	Total	**30**	**1.00**
Icicle	Icicle 1	39	1.00
	Total	**39**	**1.00**
Peshastin	Peshastin 1	2	1.00
	Ingalls	0	0.00
	Total	**2**	**1.00**
Grand Total		***423***	***1.00***

Of the 423 carcasses sampled in 2010, 30% were hatchery fish recovered in the Chiwawa River Basin (Table 5.25; these numbers may change after analysis of CWTs). Within the Chiwawa Basin, the spatial distribution of hatchery and wild fish was not equal (Table 5.25). A larger percentage of hatchery fish were found in the lower reaches (C1 and C2; Mouth to Rock Creek) than were wild fish. This general trend was also apparent in the pooled data (Figure 5.9).

Table 5.25. Numbers of wild and hatchery spring Chinook carcasses sampled within different reaches in the Chiwawa Basin, 1993-2010. See Table 2.8 for description of survey reaches.

Survey year	Origin	Survey Reach								Total
		C-1	C-2	C-3	C-4	C-5	C-6	Chikamin	Rock	
1993	Wild	0	0	0	0	0	0	0	0	**0**
	Hatchery	1	0	0	0	0	0	0	0	**1**
1994	Wild	0	6	0	2	0	1	0	0	**9**
	Hatchery	1	1	0	2	0	0	0	0	**4**
1995	Wild	0	0	0	0	0	0	0	0	**0**
	Hatchery	2	3	0	1	0	0	0	0	**6**
1996	Wild	11	1	1	1	0	0	0	0	**14**
	Hatchery	6	0	0	0	0	0	0	0	**6**
1997	Wild	5	2	0	1	0	0	0	0	**8**
	Hatchery	3	1	0	0	0	1	1	3	**9**
1998	Wild	0	3	5	1	2	4	0	0	**15**
	Hatchery	1	3	2	0	1	1	0	0	**8**
1999	Wild	1	8	0	5	0	0	0	0	**14**
	Hatchery	0	0	0	0	1	0	0	0	**1**
2000	Wild	25	27	1	1	1	1	0	0	**56**
	Hatchery	42	12	0	0	0	2	0	0	**56**
2001	Wild	24	57	15	40	16	20	1	3	**176**
	Hatchery	164	284	19	58	14	21	8	0	**568**
2002	Wild	15	11	9	6	7	5	2	0	**55**
	Hatchery	46	40	12	5	1	15	14	4	**137**
2003	Wild	7	13	0	11	3	2	0	0	**36**
	Hatchery	14	14	0	3	1	0	0	0	**32**
2004	Wild	23	48	2	11	7	3	0	1	**95**
	Hatchery	46	21	1	1	1	3	0	2	**75**
2005	Wild	16	36	3	4	3	2	0	0	**64**
	Hatchery	170	132	7	7	4	3	0	1	**324**
2006	Wild	10	17	2	8	4	3	1	0	**45**
	Hatchery	84	75	5	7	6	13	3	3	**196**
2007	Wild	3	20	3	4	4	2	0	0	**36**
	Hatchery	42	113	15	14	16	12	2	0	**214**
2008	Wild	4	24	0	5	4	8	0	0	**45**
	Hatchery	174	121	2	8	15	15	4	1	**340**
2009	Wild	4	22	4	8	4	1	0	3	**46**
	Hatchery	88	69	6	14	7	5	0	5	**194**

Survey year	Origin	Survey Reach								Total
		C-1	C-2	C-3	C-4	C-5	C-6	Chikamin	Rock	
2010	Wild	6	32	7	9	10	3	0	0	**67**
	Hatchery	63	35	2	9	7	5	0	5	**126**
Average	***Wild***	***9***	***18***	***3***	***7***	***4***	***3***	***0***	***0***	***43***
	Hatchery	***53***	***51***	***4***	***7***	***4***	***5***	***2***	***1***	***128***

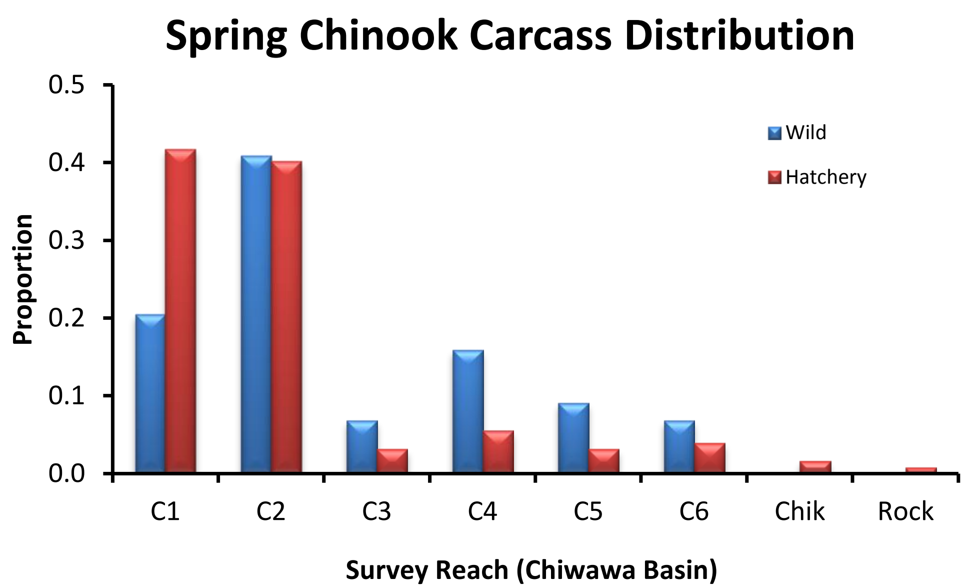


Figure 5.9. Distribution of wild and hatchery produced carcasses in different reaches in the Chiwawa Basin, 1993-2010; Chik = Chikamin Creek and Rock = Rock Creek. Reach codes are described in Table 2.8.

Sampling Rate

Overall, 19% of the estimated total spawning escapement of spring Chinook in the Wenatchee Basin was sampled in 2010 (Table 5.26). Sampling rates among streams/watershed varied from 8 to 34%.

Table 5.26. Number of redds and carcasses, total spawning escapement, and sampling rates for spring Chinook salmon in the Wenatchee Basin, 2010.

Sampling area	Total number of redds	Total number of carcasses	Total spawning escapement	Sampling rate
Chiwawa	502	193	1,094	0.18
Nason	188	141	410	0.34
Upper Wenatchee	47	30	102	0.29
Icicle	155	39	422	0.09
Little Wenatchee	38	7	83	0.08
White	33	11	72	0.15
Peshastin	5	2	14	0.14

Sampling area	Total number of redds	Total number of carcasses	Total spawning escapement	Sampling rate
Total	***968***	***423***	***2,197***	***0.19***

Length Data

Mean lengths (POH, cm) of male and female spring Chinook carcasses sampled during surveys in the Wenatchee Basin in 2010 are provided in Table 5.27. The average sizes of males and females sampled in the Wenatchee Basin were 62 and 63 cm, respectively.

Table 5.27. Mean lengths (postorbital-to-hypural length; cm) and standard deviations (in parentheses) of male and female spring Chinook carcasses sampled in different streams/watersheds in the Wenatchee Basin, 2010.

Stream/watershed	Mean lengths (cm)	
	Male	Female
Chiwawa	63 (9.5)	64 (4.2)
Nason	61(7.3)	62 (3.8)
Upper Wenatchee	65 (5.0)	65 (4.7)
Icicle	66 (4.2)	62 (4.8)
Little Wenatchee	--	65 (4.2)
White	41(37.5)	61 (4.6)
Peshastin	67 (0.0)	55 (0.0)
Total	***62 (9.1)***	***63 (4.4)***

5.7 Life History Monitoring

Life history characteristics of spring Chinook were assessed by examining carcasses on spawning grounds and fish collected at broodstock collection sites, and by reviewing tagging data and fisheries statistics.

Migration Timing

There was little difference in migration timing of hatchery and wild spring Chinook past Tumwater Dam (Table 5.28a and b; Figure 5.10). On average, early in the migration, wild Chinook arrived at Tumwater Dam slightly earlier than hatchery fish, but by the end of the migration, both were arriving at about the same time. Most hatchery and wild spring Chinook migrated upstream past Tumwater Dam during June and July (Figure 5.10).

Table 5.28a. The Julian day and date that 10%, 50% (median), and 90% of the wild and hatchery spring Chinook salmon passed Tumwater Dam, 1998-2010. The average Julian day and date are also provided. Migration timing is based on video sampling at Tumwater. Data for 1998 through 2003 were based on videotapes and broodstock trapping and may not reflect the actual number of hatchery spring Chinook. All spring Chinook were visually examined during trapping from 2004 to present.

Survey year	Origin	Spring Chinook Migration Time (days)								Sample size
		10 Percentile		50 Percentile		90 Percentile		Mean		
		Julian	Date	Julian	Date	Julian	Date	Julian	Date	
1998	Wild	156	5-Jun	156	5-Jun	156	5-Jun	156	5-Jun	49
	Hatchery	156	5-Jun	156	5-Jun	156	5-Jun	156	5-Jun	25
1999	Wild	192	11-Jul	207	26-Jul	224	12-Aug	207	26-Jul	173
	Hatchery	200	19-Jul	211	30-Jul	229	18-Aug	213	1-Aug	25
2000	Wild	171	19-Jun	186	4-Jul	194	12-Jul	184	2-Jul	651
	Hatchery	179	27-Jun	189	7-Jul	201	19-Jul	190	8-Jul	357
2001	Wild	154	3-Jun	166	15-Jun	185	4-Jul	167	16-Jun	2,073
	Hatchery	157	6-Jun	169	18-Jun	185	4-Jul	170	19-Jun	4,244
2002	Wild	174	23-Jun	189	8-Jul	204	23-Jul	189	8-Jul	1,033
	Hatchery	178	27-Jun	189	8-Jul	199	18-Jul	189	8-Jul	1,363
2003	Wild	162	11-Jun	181	30-Jun	200	19-Jul	181	30-Jun	919
	Hatchery	157	6-Jun	179	28-Jun	192	11-Jul	178	27-Jun	423
2004	Wild	156	4-Jun	172	20-Jun	189	7-Jul	172	20-Jun	969
	Hatchery	161	9-Jun	177	25-Jun	189	7-Jul	177	25-Jun	1,295
2005	Wild	153	2-Jun	172	21-Jun	193	12-Jul	173	22-Jun	1,038
	Hatchery	153	2-Jun	173	22-Jun	187	6-Jul	172	21-Jun	2,808
2006	Wild	177	26-Jun	184	3-Jul	193	12-Jul	185	7-Jul	577
	Hatchery	178	27-Jun	185	4-Jul	194	13-Jul	186	5-Jul	1,601
2007	Wild	169	18-Jun	185	4-Jul	203	22-Jul	185	4-Jul	351
	Hatchery	174	23-Jun	192	11-Jul	209	28-Jul	192	11-Jul	3,232
2008	Wild	173	21-Jun	188	6-Jul	209	27-Jul	189	7-Jul	634
	Hatchery	177	25-Jun	193	11-Jul	210	28-Jul	193	11-Jul	5,368
2009	Wild	174	23-Jun	186	5-Jul	201	20-Jul	187	6-Jul	1,008
	Hatchery	175	24-Jun	187	6-Jul	202	21-Jul	188	7-Jul	4,106
2010	Wild	173	22-Jun	190	9-Jul	214	2-Aug	191	10-Jul	977
	Hatchery	180	29-Jun	194	13-Jul	213	1-Aug	195	14-Jul	4,450
Average	Wild	***168***	-	***182***	-	***197***	-	***182***	-	***804***
	Hatchery	***171***	-	***184***	-	***197***	-	***185***	-	***2,254***

Table 5.28b. The week that 10%, 50% (median), and 90% of the wild and hatchery spring Chinook salmon passed Tumwater Dam, 1998-2010. The average week is also provided. Migration timing is based on video sampling at Tumwater. Data for 1998 through 2003 were based on videotapes and broodstock trapping and may not reflect the actual number of hatchery spring Chinook. All spring Chinook were visually examined during trapping from 2004 to present.

Survey year	Origin	Spring Chinook Migration Time (week)				Sample size
		10 Percentile	50 Percentile	90 Percentile	Mean	
1998	Wild	23	23	23	23	49
	Hatchery	23	23	23	23	25
1999	Wild	28	30	32	30	173
	Hatchery	29	31	34	31	25
2000	Wild	24	27	27	27	651
	Hatchery	26	27	29	28	357
2001	Wild	22	24	27	24	2,073
	Hatchery	23	25	27	25	4,244
2002	Wild	25	27	30	27	1,033
	Hatchery	26	27	29	27	1,363
2003	Wild	24	26	29	26	919
	Hatchery	23	26	28	26	423
2004	Wild	23	25	27	25	969
	Hatchery	23	26	27	26	1,295
2005	Wild	22	25	28	25	1,038
	Hatchery	22	25	27	25	2,808
2006	Wild	26	27	28	27	577
	Hatchery	26	27	28	27	1,601
2007	Wild	25	27	29	27	351
	Hatchery	25	28	30	28	3,232
2008	Wild	25	27	30	27	634
	Hatchery	26	28	30	28	5,368
2009	Wild	25	27	29	27	1,008
	Hatchery	25	27	29	27	4,106
2010	Wild	25	28	31	28	977
	Hatchery	26	28	31	28	4,450
Average	Wild	***24***	***26***	***28***	***26***	***790***
	Hatchery	***25***	***27***	***28***	***27***	***2,071***

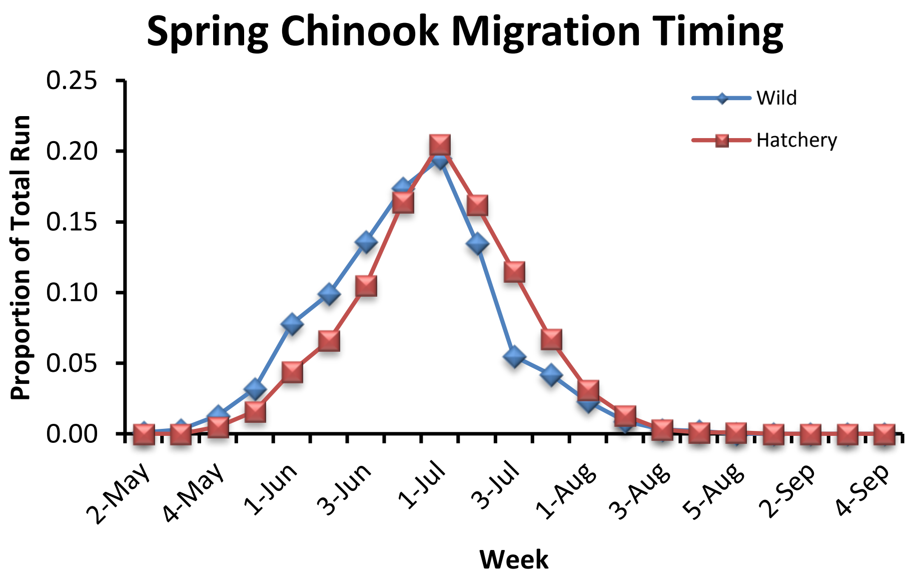


Figure 5.10. Proportion of wild and hatchery spring Chinook observed (using video) passing Tumwater Dam each week during their migration period May through September; data were pooled over survey years 1998-2010.

Age at Maturity

Most of the wild and hatchery spring Chinook sampled during the period 1994-2010 in the Chiwawa Basin were age-4 fish (total age) (Table 5.29; Figure 5.11). On average, hatchery fish made up a higher percentage of age-3 and 4 Chinook than did wild fish. In contrast, a higher proportion of age-5 wild fish returned than did age-5 hatchery fish. Thus, wild fish tended to return at an older age than hatchery fish.

Table 5.29. Proportions of wild and hatchery spring Chinook of different ages (total age) sampled on spawning grounds in the Chiwawa Basin, 1994-2010.

Sample year	Origin	Total age					Sample size
		2	3	4	5	6	
1994	Wild	0.00	0.00	0.33	0.67	0.00	9
	Hatchery	0.00	0.20	0.00	0.80	0.00	5
1995	Wild	0.00	0.00	0.00	0.00	0.00	0
	Hatchery	0.00	0.00	1.00	0.00	0.00	2
1996	Wild	0.00	0.36	0.64	0.00	0.00	14
	Hatchery	0.00	0.83	0.17	0.00	0.00	6
1997	Wild	0.00	0.00	0.75	0.25	0.00	8
	Hatchery	0.00	0.00	1.00	0.00	0.00	9
1998	Wild	0.00	0.00	0.00	1.00	0.00	15
	Hatchery	0.00	0.00	0.13	0.88	0.00	8
1999	Wild	0.00	0.07	0.50	0.43	0.00	14
	Hatchery	0.00	0.00	0.00	1.00	0.00	1

Sample year	Origin	Total age					Sample size
		2	3	4	5	6	
2000	Wild	0.00	0.02	0.95	0.03	0.00	56
	Hatchery	0.00	0.50	0.50	0.00	0.00	52
2001	Wild	0.00	0.01	0.95	0.04	0.00	176
	Hatchery	0.00	0.02	0.98	0.00	0.00	571
2002	Wild	0.00	0.00	0.56	0.44	0.00	55
	Hatchery	0.00	0.00	0.91	0.09	0.00	128
2003	Wild	0.00	0.09	0.00	0.91	0.00	36
	Hatchery	0.00	0.19	0.03	0.78	0.00	32
2004[a]	Wild	0.00	0.02	0.97	0.01	0.00	124
	Hatchery	0.00	0.43	0.57	0.00	0.00	80
2005 [a]	Wild	0.00	0.00	0.85	0.15	0.00	111
	Hatchery	0.00	0.07	0.93	0.00	0.00	656
2006 [a]	Wild	0.01	0.03	0.56	0.40	0.00	86
	Hatchery	0.00	0.16	0.72	0.12	0.00	451
2007 [a]	Wild	0.00	0.09	0.26	0.65	0.00	54
	Hatchery	0.00	0.32	0.61	0.07	0.00	304
2008 [a]	Wild	0.02	0.02	0.80	0.16	0.00	44
	Hatchery	0.00	0.07	0.89	0.04	0.00	339
2009 [a]	Wild	0.00	0.07	0.89	0.04	0.00	118
	Hatchery	0.00	0.17	0.81	0.02	0.00	417
2010 [a]	Wild	0.00	0.00	0.88	0.12	0.00	128
	Hatchery	0.00	0.05	0.94	0.01	0.00	288
Average	***Wild***	***0.00***	***0.05***	***0.58***	***0.31***	***0.00***	***62***
	Hatchery	***0.00***	***0.18***	***0.60***	***0.22***	***0.00***	***197***

[a] These years include carcass and live fish PIT-tag detection data (fish that were sampled both as carcasses and detected as live fish on the spawning grounds were not counted twice). Also origin assignments have been made to fish that were previously identified as fish of unknown origin.

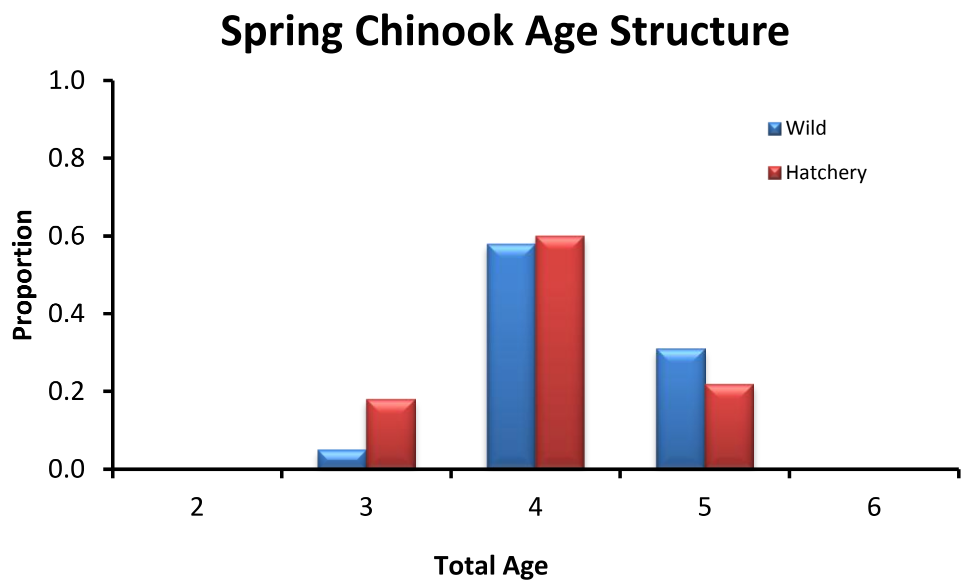


Figure 5.11. Proportions of wild and hatchery spring Chinook of different total ages sampled at the Chiwawa Weir and on spawning grounds in the Chiwawa Basin for the combined years 1994-2010.

Size at Maturity

On average, hatchery and wild spring Chinook of a given age differed slightly in length (Table 5.30). For example, wild age-5 fish were larger on average than the age-5 hatchery fish. In contrast, hatchery age-3 and 4 Chinook were generally larger than age-3 and 4 wild fish.

Table 5.30. Mean lengths (POH in cm; ±1SD) and sample sizes (in parentheses) of different ages (total age) of male and female spring Chinook of wild and hatchery-origin sampled in the Chiwawa Basin, 1994-2010. Brood years 2004-2010 include carcasses and live fish PIT-tag detections. In addition, 2005 and 2006 include fish released at the weir.

Brood year	Total age	Mean length (cm)			
		Male		Female	
		Wild	Hatchery	Wild	Hatchery
1994	3				43 ±0 (1)
	4			62 ±3 (3)	
	5	76 ±0 (1)		73 ±2 (5)	
	6				
1995	3				
	4		61 ±5 (5)		
	5				
	6				
1996	3	45 ±3 (5)	49 ±7 (10)		
	4	69 ±4 (6)	69 ±0 (1)	67 ±8 (2)	
	5				
	6				
1997	3				

Brood year	Total age	Mean length (cm)			
		Male		Female	
		Wild	Hatchery	Wild	Hatchery
	4	61 ±1 (2)	68 ±0 (1)	67 ±5 (3)	63 ±3 (8)
	5	67 ±5 (2)			
	6				
1998	3				
	4				54 ±0 (1)
	5	77 ±7 (8)	75 ±4 (4)	74 ±4 (7)	76 ±4 (3)
	6				
1999	3	44 ±0 (1)			
	4	61 ±0 (1)		64 ±3 (6)	
	5	76 ±5 (3)		72 ±5 (3)	66 ±0 (1)
	6				
2000	3		46 ±3 (17)		50 ±7 (3)
	4	60 ±8 (23)	62 ±5 (5)	61 ±5 (26)	62 ±3 (20)
	5	77 ±1 (2)			
	6				
2001	3	37 ±0 (1)	42 ±4 (11)	41 ±0 (1)	60 ±0 (1)
	4	63 ±5 (57)	65 ±5 (151)	62 ±4 (110)	63 ±4 (407)
	5	75 ±5 (2)	83 ±0 (1)	76 ±1 (5)	
	6				
2002	3				
	4	64 ±4 (14)	66 ±5 (46)	60 ±4 (15)	63 ±4 (71)
	5	80 ±6 (13)	75 ±5 (4)	72 ±3 (12)	73 ±6 (6)
	6				
2003	3	45 ±2 (3)	45 ±1 (6)		
	4		63 ±0 (1)		
	5	78 ±5 (12)	74 ±8 (11)	75 ±3 (19)	72 ±5 (14)
	6				
2004	3	42 ±3 (3)	44 ±5 (33)		
	4	63 ±7 (60)	66 ±5 (9)	63 ±4 (59)	63 ±6 (36)
	5			74 ±0 (1)	
	6				
2005	3		43 ±5 (48)		
	4	61 ±5 (32)	65 ±5 (224)	62 ±4 (61)	62 ±4 (382)
	5	74 ±5 (6)	54±0 (1)	71 ±3 (11)	
	6				
2006	3	45 ±3 (3)	43 ±3 (73)		
	4	64 ±3 (7)	62 ±6 (91)	63 ±5 (41)	60 ±4 (227)
	5	74 ±6 (8)	75 ±6 (17)	71 ±4 (26)	71± 4 (37)
	6				
2007	3	39 ±3 (5)	45 ±6 (90)		50 ±3 (7)
	4	60 ±4 (4)	66 ±5 (45)	61 ±4 (10)	63 ±3 (142)

Brood year	Total age	Mean length (cm)			
		Male		Female	
		Wild	Hatchery	Wild	Hatchery
	5	78 ±6 (15)	76 ±5 (8)	74 ±3 (20)	73 ±5 (12)
	6				
2008	3	43 ±0 (1)	44 ±5 (22)		
	4	65 ±4 (9)	64 ±6 (73)	62 ±4 (26)	64 ±4 (229)
	5	65 ±5 (3)	79 ±5 (10)	73 ±3 (4)	72 ±3 (5)
	6				
2009	3	45 ±3 (8)	46 ±6 (68)		65 ±0 (1)
	4	64 ±4 (38)	65 ±5 (136)	63 ±3 (67)	64 ±4 (202)
	5	79 ±0 (1)		72 ±2 (4)	71 ±4 (10)
	6				
2010	3		46 ±4 (11)		65 ±3 (3)
	4	64 ±5 (31)	66 ±5 (74)	64 ±4 (82)	65 ±3 (196)
	5	77 ±4 (6)		73 ±5 (9)	73 ±6 (4)
	6				

Contribution to Fisheries

Nearly all the harvest on hatchery-origin Chiwawa spring Chinook occurs within the Columbia Basin. Ocean catch records (Pacific Fishery Management Council) indicate that virtually no Upper Columbia spring Chinook are taken in ocean fisheries. Most of the harvest on hatchery-origin Chiwawa spring Chinook occurs in the Lower Columbia River fisheries, which are managed by the states and tribes pursuant to management plans developed in *U.S. v Oregon*. The Lower Columbia River fisheries occur during what is referred to in *U.S. v Oregon* as the winter, spring, and summer seasons, which begin in February and ends July 31 of each year. The Tribal fishery occurs upstream from Bonneville Dam, but primarily in Zone 6, the area between Bonneville and McNary dams; the non-treaty commercial fisheries occur in Zones 1-5, which are downstream from Bonneville Dam. The non-treaty recreational (sport) fishery occurs in the lower mainstem.

The total number of hatchery-origin spring Chinook captured in different fisheries has been relatively low (Table 5.31). The largest harvests occurred on the 1997, 1998, and 2004 brood years.

Table 5.31. Estimated number and percent (in parentheses) of hatchery-origin Chiwawa spring Chinook captured in different fisheries, brood years 1989-2004; NP = no hatchery program.

Brood year	Ocean fisheries	Columbia River Fisheries			Total
		Tribal	Commercial (Zones 1-5)	Recreational[a] (sport)	
1989	3 (13)	5 (21)	0 (0)	16 (67)	24
1990	0 (0)	0 (0)	0 (0)	18 (100)	18
1991	0 (0)	3 (100)	0 (0)	0 (0)	3
1992	0 (0)	1 (100)	0 (0)	0 (0)	1

Brood year	Ocean fisheries	Columbia River Fisheries			Total
		Tribal	Commercial (Zones 1-5)	Recreational[a] (sport)	
1993	3 (75)	1 (25)	0 (0)	0 (0)	4
1994	0 (0)	0 (0)	0 (0)	0 (0)	0
1995	NP	NP	NP	NP	NP
1996	0 (0)	2 (100)	0 (0)	0 (0)	2
1997	1 (0)	193 (51)	68 (18)	115 (31)	377
1998	9 (5)	47 (24)	12 (6)	126 (65)	194
1999	NP	NP	NP	NP	NP
2000	0 (0)	17 (74)	0 (0)	6 (26)	23
2001	17 (46)	8 (22)	1 (3)	11 (30)	37
2002	12 (17)	11 (15)	22 (31)	26 (37)	71
2003	18 (21)	29 (35)	11 (13)	26 (31)	84
2004	3 (1)	188 (40)	31 (7)	250 (53)	472

[a] Includes the Wanapum fishery.

Straying

Stray rates were determined by examining CWTs recovered on spawning grounds within and outside the Wenatchee Basin. Targets for strays based on return year (recovery year) within the Wenatchee Basin should be less than 10% and targets for strays outside the Wenatchee Basin should be less than 5%. The target for brood year stray rates should be less than 5%.

Rates of hatchery-origin Chiwawa spring Chinook straying into non-target spawning areas within the Wenatchee Basin have been high in some years and exceeded the target of 10% (Table 5.32). They have strayed into spawning areas on Nason Creek, the White River, the Little Wenatchee River, and the Upper Wenatchee River. On average, stray rates are typically highest in Nason Creek and the Upper Wenatchee River. Stray rates of hatchery-origin Chiwawa spring Chinook should decrease with the change in source water that was implemented in 2006 for the Chiwawa rearing ponds.

Table 5.32. Number (No.) and percent (%) of the spawning escapement in other non-target spawning streams within the Wenatchee Basin that consisted of hatchery-origin Chiwawa spring Chinook, return years 1992-2009. For example, for return year 2001, 35.3% of the spring Chinook spawning escapement in Nason Creek consisted of hatchery-origin Chiwawa spring Chinook. Percent strays should be less than 10%.

Return year	Nason Creek		Icicle Creek		Peshastin Creek		Upper Wenatchee		White River		Little Wenatchee	
	No.	%	No.	%	No.	%	No.	%	No.	%	No.	%
1992	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
1993	61	12.4	0	0.0	0	0.0	34	18.0	7	4.8	0	0.0
1994	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
1995	0	0.0	0	0.0	0	0.0	2	66.7	0	0.0	0	0.0
1996	25	30.1	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
1997	55	45.1	8	11.0	0	0.0	0	0.0	0	0.0	0	0.0
1998	3	4.7	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0

Return year	Nason Creek		Icicle Creek		Peshastin Creek		Upper Wenatchee		White River		Little Wenatchee	
	No.	%	No.	%	No.	%	No.	%	No.	%	No.	%
1999	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
2000	45	16.7	0	0.0	0	0.0	31	31.0	0	0.0	6	27.3
2001	211	35.3	0	0.0	0	0.0	271	77.7	46	39.0	52	31.3
2002	188	31.2	10	2.0	0	0.0	60	45.8	14	16.3	21	24.4
2003	14	6.9	0	0.0	0	0.0	30	51.7	0	0.0	0	0.0
2004	139	27.4	0	0.0	0	0.0	54	39.1	6	9.1	0	0.0
2005	252	72.6	7	50.0	0	0.0	256	99.6	106	68.4	65	56.5
2006	131	48.3	13	14.4	0	0.0	28	58.3	9	16.4	12	32.4
2007	303	65.4	0	0.0	0	0.0	37	67.3	7	7.6	6	5.9
2008	381	67.4	48	23.4	29	78.4	259	85.8	30	57.7	52	81.3
2009	289	54.1	8	9.2	0	0.0	16	100.0	73	42.2	56	44.8
Total	***2,097***	***38.8***	***94***	***5.4***	***29***	***3.3***	***1,078***	***60.4***	***298***	***25.5***	***270***	***25.4***

Rates of hatchery-origin Chiwawa spring Chinook straying into basins outside the Wenatchee have been low (Table 5.33). Hatchery-origin Chiwawa spring Chinook have strayed into the Methow and Entiat basins. During return years 2002, 2006, 2008, and 2009, their stray rates exceeded the target of 0.05 in the Entiat Basin. Stray rates of Chiwawa spring Chinook should decrease with the change in source water that was implemented in 2006 for the Chiwawa rearing ponds.

Table 5.33. Number and percent of spawning escapements within other non-target basins that consisted of hatchery-origin Chiwawa spring Chinook, return years 1992-2009. For example, for return year 2002, 9.2% of the spring Chinook spawning escapement in the Entiat Basin consisted of hatchery-origin Chiwawa spring Chinook. Percent strays should be less than 5%. NS = not sampled.

Return year	Methow Basin		Entiat Basin	
	Number	%	Number	%
1992	0	0.0	0	0.0
1993	0	0.0	0	0.0
1994	0	0.0	0	0.0
1995	0	0.0	0	0.0
1996	NS	NS	0	0.0
1997	0	0.0	0	0.0
1998	NS	NS	0	0.0
1999	0	0.0	0	0.0
2000	0	0.0	1	0.6
2001	0	0.0	1	0.2
2002	0	0.0	34	9.2
2003	0	0.0	6	2.3
2004	0	0.0	0	0.0
2005	10	0.7	15	4.2
2006	8	0.5	27	10.5

Return year	Methow Basin		Entiat Basin	
	Number	%	Number	%
2007	9	0.8	4	1.6
2008	12	1.2	61	21.9
2009	9	0.3	15	5.4
Total	***48***	***0.2***	***164***	***4.1***

On average, about 36% of the hatchery returns have strayed into non-target spawning areas, exceeding the target of 5% (Table 5.34). Depending on brood year, percent strays into non-target spawning areas have ranged from 0-81%. Few (<1%) have strayed into non-target hatchery programs. Stray rates of hatchery-origin Chiwawa spring Chinook should decrease with the change in source water that was implemented in 2006 for the Chiwawa rearing ponds.

Table 5.34. Number and percent of hatchery-origin Chiwawa spring Chinook that homed to target spawning areas and the target hatchery program, and number and percent that strayed to non-target spawning areas and non-target hatchery programs, by brood years 1989-2004. Percent stays should be less than 5%.

Brood year	Homing				Straying			
	Target stream		Target hatchery		Non-target streams		Non-target hatcheries	
	Number	%	Number	%	Number	%	Number	%
1989	74	41.1	1	0.6	102	56.7	3	1.7
1990	0	0.0	1	100.0	0	0.0	0	0.0
1991	29	87.9	0	0.0	2	6.1	2	6.1
1992	2	6.5	4	12.9	25	80.6	0	0.0
1993	134	47.5	82	29.1	63	22.3	3	1.1
1994	4	19.0	14	66.7	3	14.3	0	0.0
1995	No program							
1996	58	75.3	7	9.1	12	15.6	0	0.0
1997	1,242	55.6	298	13.4	687	30.8	5	0.2
1998	553	55.8	109	11.0	329	33.2	0	0.0
1999	No program							
2000	149	42.1	115	32.5	90	25.4	0	0.0
2001	647	35.8	276	15.3	881	48.7	4	0.2
2002	314	44.3	238	33.6	156	22.0	1	0.2
2003	556	80.0	11	1.6	123	17.7	5	0.7
2004	1,198	47.7	203	8.1	1,092	43.5	19	0.8
Total	***4,960***	***50.0***	***1,359***	***13.7***	***3,565***	***35.9***	***42***	***0.4***

Genetics

Genetic studies were conducted to determine the potential impacts of the Chiwawa Supplementation Program on natural-origin spring Chinook in the upper Wenatchee Basin (Blankenship et al. 2007; the entire report is appended as Appendix I). Microsatellite DNA allele frequencies collected from temporally replicated natural and hatchery-origin spring Chinook were used to statistically assign individual fish to specific demes (locations) within the Wenatchee population. In addition, genetic effects of the hatchery program were assessed by examining relationships between census and effective population sizes (N_e) from samples collected before and after supplementation.

Overall, this work showed that although allele frequencies within and between natural and hatchery-origin spring Chinook were significantly different, there was no evidence (i.e., robust signal) that the difference was the result of the hatchery program. Rather, the differences were more likely the result of life history characteristics. However, there was an increasing trend toward homogenization of the allele frequencies of the natural and hatchery-origin fish that comprised the broodstock, even though there was consistent year-to-year variation in allele frequencies among hatchery and natural-origin fish. In addition, there were no robust signals indicating that hatchery-origin hatchery broodstock, hatchery-origin natural spawners, natural-origin hatchery broodstock, and natural-origin natural spawners were substantially different from each other. Finally, the N_e estimate of 387 was only slightly larger than the pre-hatchery N_e (based on demographic data from 1989-1992), which means that the Chiwawa hatchery program has not reduced the N_e of the Wenatchee spring Chinook population.

Significant differences in allele frequencies were observed within and among major spawning areas in the Upper Wenatchee Basin. However, these differences made up only a very small portion of the overall variation, indicating genetic similarity among the major spawning areas. There was no evidence that the Chiwawa program has changed the genetic structure (allele frequency) of spring Chinook in Nason Creek and the White River, despite the presence of hatchery-origin spawners in both systems.

Proportion of Natural Influence

Another method for assessing the genetic risk of a supplementation program is to determine the influence of the hatchery and natural environments on the adaptation of the composite population. This is estimated by the proportion of natural-origin fish in the hatchery broodstock (pNOB) and the proportion of hatchery-origin fish in the natural spawning escapement (pHOS). The ratio pNOB/(pHOS+pNOB) is the Proportion of Natural Influence (PNI). The larger the ratio (PNI), the greater the strength of selection in the natural environment relative to that of the hatchery environment. In order for the natural environment to dominate selection, PNI should be greater than 0.5 (HSRG/WDFW/NWIFC 2004).

For brood years 1989-1996, the PNI was greater than 0.50, indicating that the natural environment had a greater influence on adaptation of Chiwawa spring Chinook than did the hatchery environment (Table 5.35). For brood years 1997-2009, however, the PNI was generally less than 0.50, indicating that the hatchery environment had a greater influence on adaptation than did the natural environment.

Table 5.35. Proportionate natural influence (PNI) of the Chiwawa spring Chinook supplementation program for brood years 1989-2009. PNI was calculated as the proportion of naturally produced Chinook in the hatchery broodstock (pNOB) divided by the proportion of hatchery Chinook on the spawning grounds (pHOS) plus pNOB. NOS = number of natural-origin Chinook on the spawning grounds; HOS = number of hatchery-origin Chinook on the spawning grounds; NOB = number of natural-origin Chinook collected for broodstock; and HOB = number of hatchery-origin Chinook included in hatchery broodstock.

Brood year	Spawners			Broodstock			PNI
	NOS	HOS	pHOS	NOB	HOB	pNOB	
1989	713	0	0.00	28	0	1.00	1.00
1990	571	0	0.00	18	0	1.00	1.00
1991	242	0	0.00	27	0	1.00	1.00
1992	676	0	0.00	78	0	1.00	1.00
1993	221	12	0.05	94	0	1.00	0.95
1994	123	61	0.33	8	4	0.67	0.67
1995	0	33	1.00	No Program			
1996	41	17	0.29	8	10	0.44	0.60
1997	60	122	0.67	32	79	0.29	0.30
1998	59	32	0.35	13	34	0.28	0.44
1999	87	7	0.07	No Program			
2000	173	173	0.50	9	21	0.30	0.38
2001	414	1,311	0.76	113	259	0.30	0.28
2002	205	502	0.71	20	51	0.28	0.28
2003	143	127	0.47	41	53	0.44	0.48
2004	582	276	0.32	83	132	0.39	0.55
2005	134	464	0.78	91	181	0.33	0.30
2006	116	413	0.78	91	224	0.29	0.27
2007	192	1,104	0.85	43	104	0.29	0.25
2008	205	953	0.82	83	220	0.27	0.25
2009	308	1,039	0.77	96	111	0.46	0.37
Average	***251***	***316***	***0.45***	***46***	***71***	***0.48***	***0.52***

Natural and Hatchery Replacement Rates

Natural replacement rates (NRR) were calculated as the ratio of natural-origin recruits (NOR) to the parent spawning population (spawning escapement). For brood years 1989-2004, NRR for spring Chinook in the Chiwawa averaged 1.06 (range, 0.00-4.27) if harvested fish were not include in the estimate and 1.15 (range, 0.00-4.73) if harvested fish were included in the estimate (Table 5.36). NRRs for more recent brood years will be calculated as soon as all tag recoveries and sampling rates have been loaded into the database.

Hatchery replacement rates (HRR) are the hatchery adult-to-adult returns and were calculated as the ratio of hatchery-origin recruits (HOR) to the parent broodstock collected. These rates should be greater than the NRRs and greater than or equal to 5.30 (the calculated target value in Murdoch and Peven 2005). In nearly all years, HRRs were greater than NRRs, regardless if harvest was or was not included (Table 5.36). HRRs exceeded the estimated target value of 5.3 in seven of the 16 years.

Table 5.36. Broodstock collected, spawning escapements, natural and hatchery-origin recruits (NOR and HOR), and natural and hatchery replacement rates (NRR and HRR; with and without harvest) for spring Chinook in the Chiwawa Basin, brood years 1989-2003; NP = no hatchery program.

Brood year	Broodstock Collected	Spawning Escapement	Harvest not included				Harvest included			
			HOR	NOR	HRR	NRR	HOR	NOR	HRR	NRR
1989	28	713	180	167	6.43	0.23	204	189	7.29	0.27
1990	19	571	1	44	0.05	0.08	19	52	1.00	0.09
1991	32	242	33	0	1.03	0.00	36	0	1.13	0.00
1992	113	676	31	52	0.27	0.08	32	55	0.28	0.08
1993	100	233	282	158	2.82	0.68	286	160	2.86	0.69
1994	13	184	21	45	1.62	0.24	21	46	1.62	0.25
1995	NP	33	NP	51	NP	1.55	NP	53	NP	1.61
1996	18	58	77	180	4.28	3.10	79	197	4.39	3.40
1997	120	182	2,232	777	18.60	4.27	2,609	861	21.74	4.73
1998	48	91	991	300	20.65	3.30	1,185	325	24.69	3.57
1999	NP	94	NP	10	NP	0.11	NP	11	NP	0.12
2000	48	346	354	714	7.38	2.06	377	749	7.85	2.16
2001	382	1,725	1,808	287	4.73	0.17	1,845	293	4.83	0.17
2002	84	707	709	267	8.44	0.38	780	278	9.29	0.39
2003	119	270	695	126	5.84	0.47	779	135	6.55	0.50
2004	296	858	2,512	279	8.49	0.33	2,984	301	10.08	0.35
Average	***101***	***436***	***709***	***216***	***6.47***	***1.06***	***803***	***232***	***7.40***	***1.15***

Smolt-to-Adult Survivals

Smolt-to-adult survival ratios (SARs) were calculated as the number of hatchery adult recaptures divided by the number of tagged hatchery smolts released. SARs were based on CWT returns. For the available brood years, SARs have ranged from 0.00036 to 0.01562 for hatchery spring Chinook (Table 5.37).

Table 5.37. Smolt-to-adult ratios (SARs) for Chiwawa hatchery spring Chinook, brood years 1989-2004.

Brood year	Number of tagged smolts released[a]	Estimated adult captures[b]	SAR
1989	42,707	204	0.00478
1990	52,798	19	0.00036
1991	61,088	36	0.00059
1992	82,976	31	0.00037
1993	221,316	284	0.00128

Brood year	Number of tagged smolts released[a]	Estimated adult captures[b]	SAR
1994	27,135	21	0.00077
1995	No hatchery program		
1996	12,767	67	0.00525
1997	259,585	2,549	0.00982
1998	71,571	1,118	0.01562
1999	No hatchery program		
2000	46,726	375	0.00803
2001	374,129	1,830	0.00489
2002	145,074	760	0.00524
2003	216,702	763	0.00352
2004	491,987	2,973	0.00604
Average	***150,469***	***788***	***0.00524***

[a] Includes all tag codes and CWT released fish (CWT + Ad Clip fish and CWT-only fish).

[b] Includes estimated recoveries (spawning ground, hatcheries, harvest, etc.) and observed recoveries if estimated recoveries were unavailable.

5.8 ESA/HCP Compliance

Broodstock Collection

The collection of 2008 Brood Chiwawa River spring Chinook broodstock was consistent with the 2008 Upper Columbia River salmon and steelhead broodstock objectives and site-based broodstock collection protocols. Specifically, broodstock collection targeted hatchery-origin fish at Tumwater Dam and the Chiwawa Weir, while only natural-origin spring Chinook were collected at the Chiwawa Weir. In-season adjustments were made to the number of hatchery and natural-origin spring Chinook collected for bloodstock and were based on in-season escapement monitoring at Tumwater Dam and estimated Chiwawa run-escapement.

Broodstock collection at Tumwater Dam began 10 June 2008, concluded on 29 July 2008, and targeted hatchery-origin, coded-wire tagged spring Chinook. Collection was implemented concurrent with trapping, sampling, and tagging associated with the spring Chinook reproductive success study (BPA project No. 2003-039-00). Trapping at the Chiwawa Weir began on 8 July 2008 and concluded on 26 August 2008. Broodstock collection targeted natural-origin spring Chinook and hatchery-origin spring Chinook as needed to attain a minimum 33% natural-origin broodstock and a maximum 33% extraction of the estimated natural-origin return to the Chiwawa River.

The BY 2008 brood collection retained a total of 329 spring Chinook, including 88 natural-origin fish, representing a 27% natural-origin broodstock. The brood collection failed to meet the targeted 33% natural-origin composition primarily because of false negative wire detection at Chiwawa weir that underestimated the number of hatchery-origin Chinook retained.

Both passive (low abundance periods) and active (high abundance periods) trapping were used to collect spring Chinook at Tumwater Dam. During passive trapping, the trap was checked and fish were processed several times per day. At the Chiwawa Weir, the trap was operated passively, checked several times per day, and fish were processed once daily. Trapping at the Chiwawa Weir generally followed a four-up and three-down schedule, and operated only as needed to meet weekly collection objectives consistent with the 2008 collection protocol or as adjusted based on in-season run escapement monitoring and ESA Section 10 Permit 1196 requirements. All spring Chinook, steelhead, and bull trout that were captured were anesthetized with tricaine methanesulfonate (MS-222) and subject to water-to-water transfers during handling. All fish were allowed to fully recover before release.

The estimated escapement of 2008 spring Chinook past Tumwater Dam totaled 5,514 adult and jack spring Chinook (Murdoch et al. 2008). Based on 2008 spawning ground data (redd and carcass surveys), an estimated 208 natural-origin spring Chinook spawned in the Chiwawa River Basin (Table 5.34). Assuming the pre-spawn survival of Chiwawa River natural-origin spring Chinook was similar to the at-large population upstream from Tumwater Dam (73%), combined with the 88 natural-origin Chinook extracted for broodstock, the natural-origin escapement to the Chiwawa Basin totaled 373 spring Chinook (i.e., (208/0.73) + 88 = 373). The 2008 broodstock retention of 329 spring Chinook (88 natural-origin and 241 hatchery-origin) represents 6.2% of the estimated 2008 Chiwawa spring Chinook escapement (24% of the wild Chiwawa escapement) to Tumwater Dam and 6.0% of the run escapement of spring Chinook upstream from Tumwater Dam. The estimated broodstock extraction rate of natural-origin Chiwawa spring Chinook and overall extraction of spring Chinook upstream from Tumwater Dam comply with provisions of ESA Permit 1196.

No additional spring Chinook were handled and released as a function of maintaining, at minimum, 33% natural-origin spring Chinook in the broodstock. About 400 bull trout were captured and released. To minimize fallback or impingement on the weir, all spring Chinook and bull trout were released unharmed about 10 km upstream from the weir.

Hatchery Rearing and Release

The rearing and release of 2008 Chiwawa spring Chinook was completed without incident. No mortality events occurred that exceeded 10% of the population. Fish were acclimated on Wenatchee River water and to the extent possible on Chiwawa River water (see Section 5.2).

The release of 2008 brood Chiwawa spring Chinook smolts totaled 609,789 spring Chinook, representing 90.7% of program objectives and complied with ESA Section 10 Permit 1196 production level of 672,000 smolts.

Hatchery Effluent Monitoring

Per ESA Permits 1196, 1347, and 1395, permit holders shall monitor and report hatchery effluents in compliance with applicable National Pollution Discharge Elimination Systems (NPDES) (EPA 1999) permit limitations. There were no NPDES violations reported at Chelan PUD Hatchery facilities during the period 1 January 2010 through 31 December 2010. NPDES monitoring and reporting for Chelan PUD Hatchery Programs during 2010 are provided in Appendix E.

Smolt and Emigrant Trapping

Per ESA Section 10 Permit No. 1196, the permit holders are authorized a direct take of 20% of the emigrating spring Chinook population during juvenile emigration monitoring and a lethal take not to exceed 2% of the fish captured (NMFS 2003). Based on the estimated wild spring Chinook population (smolt trap expansion) and hatchery juvenile spring Chinook population estimate (hatchery release data) for the Wenatchee Basin, the reported spring Chinook encounters during 2010 emigration monitoring complied with take provisions in the Section 10 permit. Spring Chinook encounter and mortality rates for each trap site (including PIT tag mortalities) are detailed in Table 5.38. Additionally, juvenile fish captured at the trap locations were handled consistent with provisions in ESA Section 10 Permit 1196, Section B.

Table 5.38. Estimated take of Upper Columbia River spring Chinook resulting from juvenile emigration monitoring in the Wenatchee Basin, 2010.

Trap location	Population estimate			Number trapped			Total	Take allowed under Permit
	Wild[a]	Hatchery[b]	Sub-yearling[c]	Wild	Hatchery	Sub-yearling		
Chiwawa Trap								
Population	35,023	609,789	31,913	6,482	22,481	13,344	42,307	
Encounter rate	NA	NA	NA	0.1851	0.0369	0.4181	0.0625	0.20
Mortality[e]	NA	NA	NA	23	121	64	208	
Mortality rate	NA	NA	NA	0.0035	0.0054	0.0048	0.0049	0.02
Upper Wenatchee Trap								
Population	NA[f]	38,329	NA[f]	569	245	254	1,068	
Encounter rate	NA	NA	NA	NA	0.0064	NA	NA	0.20
Mortality[e]	NA	NA	NA	4	4	12	20	
Mortality rate	NA	NA	NA	0.0070	0.0163	0.0472	0.0187	0.02
Lower Wenatchee Trap								
Population	82,137	648,118	NA	1,079	43,613	NA	44,692	
Encounter rate	NA	NA	NA	0.0089	0.0153	NA	0.0145	0.20
Mortality[e]	NA	NA	NA	5	257	NA	262	
Mortality rate	NA	NA	NA	0.0046	0.0059	NA	0.0059	0.02
Wenatchee Basin Total								
Population	117,160	648,118	NA	8,130	66,339	13,598	88,067	
Encounter rate	NA	NA	NA	0.0694	0.1024	NA	0.1151	0.20
Mortality[e]	NA	NA	NA	32	382	76	490	
Mortality rate	NA	NA	NA	0.0039	0.0057	0.0056	0.0056	0.02

[a] Smolt population estimate derived from juvenile emigration trap data.

[b] 2008 smolt release data for the Wenatchee Basin.

[c] Based on size, date of capture, and location of capture, subyearling Chinook encountered at the Lower Wenatchee Trap are categorized as summer Chinook.

[d] Combined trapping and PIT tagging mortality.

[e] Expanded total Wenatchee Basin natural-origin spring Chinook smolt estimates based on the estimated Chiwawa smolt production and proportion of total redds in the Chiwawa Basin.

[f] Insufficient numbers of natural-origin spring Chinook were encountered to derive a population estimate

Spawning Surveys

Spring Chinook spawning ground surveys were conducted in the Wenatchee Basin during 2010, as authorized by ESA Section 10 Permit 1196. Because of the difficulty of quantifying the level of take associated with spawning ground surveys, the Permit does not specify a take level associated with these activities, even though it does authorize implementation of spawning ground surveys. Therefore, no take levels are reported. However, to minimize potential impacts to established redds, wading was restricted to the extent practical, and extreme caution was used to avoid established redds when wading was required.

Spring Chinook Reproductive Success Study

ESA Section 10 Permit 1196 specifically provides authorization to capture, anesthetize, biologically sample, PIT tag, and release adult spring Chinook at Tumwater Dam for reproductive success studies and general program monitoring. During 2008 through 2009, all spring Chinook passing Tumwater Dam were enumerated, anesthetize, biologically sampled, PIT tagged, and released (not including hatchery-origin Chinook retained for broodstock) as a component of the reproductive success study (BPA Project No. 2003-039-00). Please refer to Murdoch et al. (2008) and Murdoch et al. (2009) for complete details on the methods and results of the spring Chinook reproductive success study for 2008 and 2009.

SECTION 6: WENATCHEE SUMMER CHINOOK

6.1 Broodstock Sampling

This section focuses on results from sampling 2008-2009 Wenatchee summer Chinook broodstock, which were collected at Dryden and Tumwater dams. Complete information is not currently available for the 2010 brood (this information will be provided in the 2011 annual report).

Origin of Broodstock

Both the 2008 and 2009 broodstock consisted primarily of natural-origin (adipose fin present) summer Chinook (Table 6.1). In order to meet production goals, hatchery-origin adults were collected in concert with natural-origin fish. About 2% of the 2009 broodstock was comprised of hatchery-origin fish (hatchery-origin was determined by examination of scales and/or CWTs).

Table 6.1. Numbers of wild and hatchery summer Chinook collected for broodstock, numbers that died before spawning, and numbers of Chinook spawned in the Wenatchee Basin, 1989-2009. Unknown origin fish (i.e., undetermined by scale analysis, no CWT or fin clips, and no additional hatchery marks) were considered naturally produced. Mortality includes fish that died of natural causes typically near the end of spawning and were not needed for the program and surplus fish killed at spawning.

Brood year	Wild summer Chinook					Hatchery summer Chinook					Total number spawned
	Number collected	Prespawn loss	Mortality	Number spawned	Number released	Number collected	Prespawn loss	Mortality	Number spawned	Number released	
1989	346	29	27	290	0	0	0	0	0	0	290
1990	87	6	24	57	0	0	0	0	0	0	57
1991	128	9	14	105	0	0	0	0	0	0	105
1992	341	48	19	274	0	0	0	0	0	0	274
1993	480	28	46	406	0	44	0	0	44	0	450
1994	363	29	1	333	0	55	1	0	54	0	387
1995	382	15	4	363	0	16	0	0	16	0	378
1996	331	34	34	263	0	3	0	0	3	0	266
1997	225	14	6	205	0	15	1	1	13	0	218
1998	378	40	39	299	0	94	4	12	78	0	377
1999	250	7	1	242	0	238	1	1	236	0	478
2000	298	18	5	275	0	194	7	7	180	0	455
2001	311	41	60	210	0	182	8	38	136	0	346
2002	469	28	32	409	0	13	1	2	10	0	419
2003	488	90	61	337	0	8	1	0	7	0	344
2004	494	24	46	424	0	2	0	0	2	0	426
2005	491	29	19	397	46	3	0	0	3	0	400
2006	483	29	21	433	0	5	1	0	4	0	437
2007	415	53	99	263	0	4	0	1	3	0	266
2008	400	11	11	378	0	72	2	1	69	0	447
2009	482	22	8	452	0	9	1	0	8	0	460
Average	***364***	***24***	***27***	***305***	***2***	***46***	***1***	***3***	***41***	***0***	***347***

Age/Length Data

Ages of summer Chinook broodstock were determined from analysis of scales and/or CWTs. Broodstock collected from the 2008 return consisted primarily of age-4 natural-origin Chinook (65%). Age-3, 5, and 6 natural-origin fish collectively made up 34% of the broodstock, while age-2, fish made up about 1% (Table 6.2). Of the 72 hatchery Chinook included in the broodstock, 69% were age-5 fish with age-4 and 6 comprising 13% and 15%, respectively. About 3% of the hatchery broodstock were age-3 fish.

Broodstock collected from the 2009 return consisted primarily of age-4 and age-5 natural-origin Chinook (93%). Age-2 and age-3 natural-origin fish collectively made up 7% of the broodstock. No age-6 fish were included in the broodstock (Table 6.2). Of the hatchery Chinook included in the broodstock, 53% were age-5 fish, with age-3 and 4 comprising 13% and 34%, respectively. About 3% of the hatchery broodstock were age-3 fish.

Table 6.2. Percent of hatchery and wild Wenatchee summer Chinook of different ages (total age) collected from broodstock in the Wenatchee Basin, 1991-2009.

Return Year	Origin	Total age				
		2	3	4	5	6
1991	Wild	0.0	4.6	36.8	57.5	1.1
	Hatchery	0.0	0.0	0.0	0.0	0.0
1992	Wild	0.0	2.6	40.4	50.9	6.1
	Hatchery	0.0	0.0	0.0	0.0	0.0
1993	Wild	0.0	1.5	36.0	60.3	2.2
	Hatchery	0.0	0.0	93.0	7.0	0.0
1994	Wild	0.0	1.0	33.7	64.3	1.0
	Hatchery	0.0	0.0	1.9	98.1	0.0
1995	Wild	0.0	3.3	18.9	76.6	1.2
	Hatchery	0.0	0.0	0.0	0.0	100.0
1996	Wild	0.0	4.6	40.1	53.3	2.0
	Hatchery	0.0	0.0	33.3	66.7	0.0
1997	Wild	0.0	2.3	42.6	53.2	1.9
	Hatchery	0.0	26.7	66.7	6.6	0.0
1998	Wild	0.0	5.5	34.8	58.6	1.1
	Hatchery	0.0	5.4	68.5	19.6	6.5
1999	Wild	0.5	1.9	39.0	56.3	2.4
	Hatchery	0.0	1.3	23.2	72.1	2.4
2000	Wild	2.6	6.3	24.6	66.5	0.0
	Hatchery	0.0	23.6	15.2	42.9	18.3
2001	Wild	0.3	16.4	53.9	27.7	1.7
	Hatchery	0.0	6.3	80.6	10.0	3.1
2002	Wild	1.6	8.4	61.1	28.3	0.6

Return Year	Origin	Total age				
		2	3	4	5	6
	Hatchery	0.0	0.0	41.7	58.3	0.0
2003	Wild	0.9	2.8	31.4	64.9	0.0
	Hatchery	0.0	12.5	25.0	62.5	0.0
2004	Wild	0.2	3.6	10.1	84.0	2.1
	Hatchery	0.0	0.0	50.0	50.0	0.0
2005	Wild	0.0	4.3	53.5	35.1	7.1
	Hatchery	0.0	0.0	0.0	100.0	0.0
2006	Wild	1.4	0.9	14.9	81.8	1.0
	Hatchery	0.0	0.0	0.0	80.0	20.0
2007	Wild	3.6	14.9	18.6	46.4	16.5
	Hatchery	0.0	0.0	0.0	100.0	0.0
2008	Wild	0.5	6.3	65.4	26.2	1.6
	Hatchery	0.0	3.0	13.2	69.1	14.7
2009	Wild	1.1	6.3	46.3	46.3	0.0
	Hatchery	0.0	12.5	34.4	53.1	0.0
Average	***Wild***	***0.7***	***5.1***	***37.0***	***54.6***	***2.6***
	Hatchery	***0.0***	***4.8***	***28.8***	***47.2***	***8.7***

Mean lengths of natural-origin summer Chinook of a given age differed little between return years 2008 and 2009 (Table 6.3). Mean lengths of age-2 and 5 Chinook differed between years by about 2 cm and 3 cm, respectively. The few hatchery fish that were included in broodstock were about 3-9 cm smaller than their natural counterparts in the 2009 brood (Table 6.3).

Table 6.3. Mean fork length (cm) at age (total age) of hatchery and wild Wenatchee summer Chinook collected from broodstock in the Wenatchee Basin, 1991-2009; N = sample size and SD = 1 standard deviation.

Return year	Origin	Summer Chinook fork length (cm)														
		Age-2			Age-3			Age-4			Age-5			Age-6		
		Mean	N	SD	Mean	N	SD	Mean	N	SD	Mean	N	SD	Mean	N	SD
1991	Wild	-	0	-	-	4	-	-	32	-	-	50	-	-	1	-
	Hatchery	-	0	-	-	0	-	-	0	-	-	0	-	-	0	-
1992	Wild	-	0	-	66	3	10	69	46	5	81	58	3	87	7	1
	Hatchery	-	0	-	-	0	-	-	0	-	-	0	-	-	0	-
1993	Wild	-	0	-	68	6	10	84	142	9	98	238	6	100	9	6
	Hatchery	-	0	-	-	0	-	79	41	8	101	3	8	-	0	-
1994	Wild	-	0	-	74	3	5	86	101	8	96	193	7	106	3	7
	Hatchery	-	0	-	-	0	-	75	1	-	90	53	8	-	0	-
1995	Wild	-	0	-	66	11	8	85	64	7	97	255	6	106	4	7
	Hatchery	-	0	-	-	0	-	-	0	-	-	0	-	91	16	8
1996	Wild	-	0	-	69	14	5	86	121	6	97	161	6	104	6	5

Return year	Origin	Summer Chinook fork length (cm)														
		Age-2			Age-3			Age-4			Age-5			Age-6		
		Mean	N	SD	Mean	N	SD	Mean	N	SD	Mean	N	SD	Mean	N	SD
	Hatchery	-	0	-	-	0	-	63	1	-	96	2	4	-	0	-
1997	Wild	-	0	-	54	5	10	85	92	7	98	115	7	97	4	9
	Hatchery	-	0	-	46	4	2	74	10	4	98	1	-	-	0	-
1998	Wild	-	0	-	66	19	9	85	120	7	99	201	7	106	4	7
	Hatchery	-	0	-	53	5	2	77	63	8	95	19	8	98	6	8
1999	Wild	42	1	-	65	4	6	86	83	6	97	120	7	103	5	8
	Hatchery	-	0	-	52	3	6	79	55	7	90	171	6	100	8	6
2000	Wild	43	7	4	60	17	7	84	67	5	98	181	6	-	0	-
	Hatchery	-	0	-	53	47	7	76	29	8	94	83	7	102	35	9
2001	Wild	48	1	-	66	48	7	88	155	7	97	80	6	102	5	3
	Hatchery	-	0	-	51	10	3	75	132	8	91	17	8	100	5	8
2002	Wild	48	7	4	64	37	8	89	270	7	100	125	7	99	3	13
	Hatchery	-	0	-	-	0	-	78	5	8	95	7	5	-	0	-
2003	Wild	41	4	2	58	13	4	87	144	8	100	297	7	-	0	-
	Hatchery	-	0	-	40	1	-	78	2	4	101	5	8	-	0	-
2004	Wild	51	1	-	69	17	5	84	47	8	99	392	6	109	10	7
	Hatchery	-	0	-	-	0	-	84	1	-	108	1	-	-	0	-
2005	Wild	-	0	-	68	20	7	86	247	8	95	162	6	101	33	6
	Hatchery	-	0	-	-	0	-	-	0	-	90	3	9	-	0	-
2006	Wild	44	6	6	63	4	11	88	66	7	99	363	6	96	5	7
	Hatchery	-	0	-	-	0	-	-	0	-	99	4	7	100	1	-
2007	Wild	44	14	5	65	58	7	89	72	8	99	180	7	102	64	6
	Hatchery	-	0	-	-	0	-	-	0	-	90	4	5	-	0	-
2008	Wild	46	2	3	69	24	7	90	247	6	98	99	7	105	6	9
	Hatchery	-	0	-	63	2	14	81	9	7	93	47	6	99	10	5
2009	Wild	48	7	6	70	25	6	89	199	7	101	199	6	-	0	-
	Hatchery	-	0	-	61	4	7	80	11	9	98	17	10	-	0	-

Sex Ratios

Male summer Chinook in the 2008 broodstock made up about 50% of the adults collected, resulting in an overall male to female ratio of 1.01:1.00 (Table 6.4.). In 2009, males made up about 50% of the adults collected, resulting in an overall male to female ratio of 1.02:1.00 (Table 6.4). The ratios in 2009 were nearly equal to the 1:1 ratio goal in the broodstock protocol.

Table 6.4. Numbers of male and female wild and hatchery summer Chinook collected for broodstock in the Wenatchee Basin, 1989-2009. Ratios of males to females are also provided.

Return year	Number of wild summer Chinook			Number of hatchery summer Chinook			Total M/F ratio
	Males (M)	Females (F)	M/F	Males (M)	Females (F)	M/F	
1989	166	180	0.92:1.00	0	0	-	0.92:1.00
1990	45	39	1.15:1.00	0	0	-	1.15:1.00

Return year	Number of wild summer Chinook			Number of hatchery summer Chinook			Total M/F ratio
	Males (M)	Females (F)	M/F	Males (M)	Females (F)	M/F	
1991	60	68	0.88:1.00	0	0	-	0.88:1.00
1992	154	187	0.82:1.00	0	0	-	0.82:1.00
1993	208	228	0.91:1.00	35	9	3.89:1.00	1.03:1.00
1994	158	179	0.88:1.00	24	31	0.77:1.00	0.87:1.00
1995	169	213	0.79:1.00	1	15	0.07:1.00	0.75:1.00
1996	150	181	0.83:1.00	2	1	2.00:1.00	0.84:1.00
1997	104	121	0.86:1.00	15	0	-	0.98:1.00
1998	211	167	1.26:1.00	64	30	2.13:1.00	1.40:1.00
1999	130	120	1.08:1.00	108	130	0.83:1.00	0.95:1.00
2000	153	145	1.06:1.00	112	82	1.37:1.00	1.17:1.00
2001	187	124	1.51:1.00	132	50	2.64:1.00	1.83:1.00
2002	266	203	1.31:1.00	5	8	0.63:1.00	1.28:1.00
2003	270	218	1.24:1.00	5	3	1.67:1.00	1.24:1.00
2004	230	264	0.87:1.00	1	1	1.00:1.00	0.87:1.00
2005	291	200	1.46:1.00	2	1	2.00:1.00	1.46:1.00
2006	237	246	0.96:1.00	1	4	0.25:1.00	0.95:1.00
2007	239	176	1.36:1.00	2	2	1.00:1.00	1.35:1.00
2008	208	192	1.08:1.00	29	43	0.67:1.00	1.01:1.00
2009	223	236	0.94:1.00	25	7	3.57:1.00	1.02:1.00
Total	***3,859***	***3,687***	***1.04:1.00***	***563***	***417***	***1.35:1.00***	***1.08:1.00***

Fecundity

Fecundities for the 2008 and 2009 returns of summer Chinook averaged 5,108 and 5,291 eggs per female, respectively (Table 6.5). These values are close to the overall average of 5,186 eggs per female. Mean observed fecundities for the 2008 and 2009 returns were above the expected fecundity of 5,000 eggs per female assumed in the broodstock protocol.

Table 6.5. Mean fecundity of wild, hatchery, and all female summer Chinook collected for broodstock in the Wenatchee Basin, 1989-2008; NA = not available.

Return year	Mean fecundity		
	Wild	Hatchery	Total
1989*	NA	NA	5,280
1990*	NA	NA	5,436
1991*	NA	NA	4,333
1992*	NA	NA	5,307
1993*	NA	NA	5,177
1994*	NA	NA	5,899
1995*	NA	NA	4,402
1996*	NA	NA	4,941

Return year	Mean fecundity		
	Wild	Hatchery	Total
1997	5,385	5,272	5,390
1998	5,393	4,825	5,297
1999	5,036	4,942	4,987
2000	5,464	5,403	5,441
2001	5,280	4,647	5,097
2002	5,502	5,027	5,484
2003	5,357	5,696	5,361
2004	5,372	6,681	5,377
2005	5,045	6,391	5,053
2006	5,126	5,633	5,133
2007	5,124	4,510	5,115
2008	5,147	4,919	5,108
2009	5,308	4,765	5,291
Average	***5,272***	***5,285***	***5,186***

* Individual fecundities were not tracked with females until 1997.

6.2 Hatchery Rearing

Rearing History

Number of eggs taken

Based on the unfertilized egg-to-release survival standard of 81%, a total of 1,066,667 eggs are required to meet the program release goal of 864,000 smolts. Between 1989 and 2009, the egg take goal was reached in seven of those years (Table 6.6).

Table 6.6. Numbers of eggs taken from Wenatchee summer Chinook broodstock, 1989-2009.

Return year	Number of eggs taken
1989	829,012
1990	163,109
1991	247,000
1992	827,911
1993	1,133,852
1994	999,364
1995	949,531
1996	756,000
1997	554,617
1998	854,997
1999	1,182,130
2000	1,113,159
2001	733,882
2002	1,049,255

Return year	Number of eggs taken
2003	901,095
2004	1,311,051
2005	883,669
2006	1,190,757
2007	655,201
2008	1,145,330
2009	1,217,028
Average	***890,379***

Number of acclimation days

The 2008 brood Wenatchee summer Chinook were transferred to Dryden Pond between 9-22 March 2009. These fish received 38-51 days of acclimation on Wenatchee River water before being released on 28 April 2009 (Table 6.7). In recent years, a small proportion of the brood (high ELISA fish) has been reared separately and received no acclimation (i.e., these fish were released directly into the Wenatchee River). These data are not shown in Table 6.7. No such release occurred in 2010.

Table 6.7. Number of days Wenatchee summer Chinook were acclimated at Dryden Pond, brood years 1989-2008. Numbers in parenthesis represents the number of days fish reared at Chiwawa Ponds.

Brood year	Release year	Transfer date	Release date	Number of days
1989	1991	2-Mar	7-May	66
1990	1992	19-Feb	2-May	73
1991	1993	10-Mar	8-May	59
1992	1994	1-Mar	6-May	66
1993	1995	3-Mar	1-May	59
1994	1996	2-Oct	6-May	217 (154)
		5-Mar	6-May	62
1995	1997	16-Oct	8-May	205 (139)
		27-Feb	8-May	70
1996	1998	6-Oct	28-Apr	204 (142)
		25-Feb	28-Apr	62
1997	1999	23-Feb	27-Apr	63
1998	2000	5-Mar	1-May	57
1999	2001	8-Mar	23-Apr	46
2000	2002	1-Mar	6-May	66
2001	2003	19-Feb	23-Apr	63

Brood year	Release year	Transfer date	Release date	Number of days
2002	2004	5-Mar	23-Apr	49
2003	2005	15-Mar	25-Apr	41
2004	2006	25-Mar	27-Apr	33
2005	2007	15-Mar	30-Apr	46
2006	2008	11-14-Mar	28-Apr	45-48
2007	2009	30-31-Mar	29-Apr	29-30
2008	2010	9-12, 15, 22-Mar	28-Apr	38-51

Release Information

Numbers released

The 2008 Wenatchee summer Chinook program achieved 103% of the 864,000 target goal with about 888,811 fish being released (Table 6.8). The slight overage was likely related to above average fecundities while maintaining or exceeding in-hatchery survival goals for the program.

Table 6.8. Numbers of Wenatchee summer Chinook smolts released from the hatchery, 1989-2008. The release target for Wenatchee summer Chinook is 864,000 smolts.

Brood year	Release year	CWT mark rate	Number released with PIT tags	Number of smolts released
1989	1991	0.2013	0	720,000
1990	1992	0.9597	0	124,440
1991	1993	0.9957	0	191,179
1992	1994	0.9645	0	627,331
1993	1995	0.9881	0	900,429
1994	1996	0.9697	0	797,350
1995	1997	0.9725	0	687,439
1996	1998	0.9758	0	600,127
1997	1999	0.9913	0	438,223
1998	2000	0.9869	0	649,612
1999	2001	0.9728	0	1,005,554
2000	2002	0.9723	0	929,496
2001	2003	0.9868	0	604,668
2002	2004	0.9644	0	835,645
2003	2005	0.9778	0	653,764
2004	2006	0.9698	0	892,926
2005	2007	0.9596	0	644,182
2006	2008	0.9676	0	51,550[a]
		0.9676	0	899,107
2007	2009	0.9768	0	456,805

Brood year	Release year	CWT mark rate	Number released with PIT tags	Number of smolts released
2008	2010	0.9664	10,035	888,811
Average		***0.9375***	***10,035***	***667,354***

[a] Represents high Elisa group planted directly in the Wenatchee River at Leavenworth Boat Launch.

Numbers tagged

The 2008 brood Wenatchee summer Chinook were 96.7% CWT and adipose fin-clipped (Table 6.8).

In 2010, a total of about 30,300 summer Chinook (brood year 2009) were PIT tagged at Eastbank Fish Hatchery during 7-9, 14-16, and 21-23 September 2010. Fish were tagged in three groups of about 10,100 per group. One group of PIT-tagged Chinook was placed in standard raceway #13 (Control Group), another group was placed in re-use Circular Pond R-1, and the last group was placed in re-use Circular Pond R-2. Fish were not fed during tagging or for two days before and after tagging. Chinook from the Control Group averaged 84 mm in length and 6.3 g at time of tagging. Fish in R-1 averaged 85 mm in length and 6.4 g, while those in R-2 averaged 90 mm in length and 7.6 g. As of the end of January 2011, a total of 71 tagged Chinook have died (14 from the Control Group, 28 from R-1, and 29 from R-2). Three fish have shed their tags, all from the Control Group.

Table 6.9 summarizes the number of hatchery summer Chinook that have been PIT-tagged and released into the Wenatchee River.

Table 6.9. Summary of PIT-tagging activities for Wenatchee hatchery summer Chinook, brood yearS 2008-2009.

Brood year	Release year	Number of fish tagged	Number of tagged fish that died	Number of tags shed	Number of tagged fish released
2008	2010	10,100	64	1	10,035
2009	2011	10,100 (Control)	NA	NA	NA
		10,100 (R1)	NA	NA	NA
		10,100 (R2)	NA	NA	NA

Fish size and condition at release

About 888,811 summer Chinook from the 2008 brood were released from Dryden Pond using an unmonitored volitional method (i.e., volitional without PIT-tag detection equipment in place) on 28 April 2010. Size at release was 94.3% and 114.5% of the target fork length and weight goals, respectively. This brood year exceeded the target CV for length by 44.4% (Table 6.10). Since the program began, Wenatchee summer Chinook have not met the target length and CV values. The target weight (fish/pound or FPP) of juvenile fish has been met occasionally.

Table 6.10. Mean lengths (FL, mm), weight (g and fish/pound), and coefficient of variation (CV) of Wenatchee summer Chinook smolts released from the hatchery, brood years 1989-2008; NA = not available. Size targets are provided in the last row of the table.

Brood year	Release year	Fork length (cm)		Mean weight	
		Mean	CV	Grams (g)	Fish/pound
1989	1991	158	13.7	45.4	10
1990	1992	155	14.2	45.4	10
1991	1993	156	15.5	42.3	11
1992	1994	152	13.1	40.1	10
1993	1995	149	NA	34.9	13
1994	1996	138	NA	21.7	21
1995	1997	149	12.2	42.5	11
1996	1998	151	16.6	43.2	10
1997	1999	154	10.1	42.8	11
1998	2000	166	9.7	53.1	9
1999	2001	137	16.1	29.0	16
2000	2002	148	14.6	37.1	12
2001	2003	148	NA	38.9	12
2002	2004	146	15.1	37.3	14
2003	2005	147	13.2	36.5	12
2004	2006	147	10.7	35.4	13
2005	2007	153	16.3	40.6	11
2006	2008	136	21.5	29.2	16
2007	2009	163	21.6	49.7	9
2008	2010	166	15.0	52.0	9
Targets		***176***	***9.0***	***45.4***	***10***

Survival Estimates

Overall survival of the 2008 brood Wenatchee summer Chinook from green (unfertilized) egg to release was slightly below the standard set for the program in part because of not meeting standards in ponding-to-release and transport-to-release survivals (Table 6.11).

Table 6.11. Hatchery life-stage survival rates (%) for Wenatchee summer Chinook, brood years 1989-2008. Survival standards or targets are provided in the last row of the table.

Brood year	Collection to spawning		Unfertilized egg-eyed	Eyed egg-ponding	30 d after ponding	100 d after ponding	Ponding to release	Transport to release	Unfertilized egg-release
	Female	Male							
1989	90.0	93.4	90.9	97.0	99.7	99.3	98.5	99.4	86.9
1990	89.7	95.6	80.9	96.6	99.6	99.2	97.7	98.8	76.3
1991	88.2	98.3	86.9	96.1	99.3	98.5	94.9	98.1	77.4
1992	84.3	92.2	79.8	97.8	99.9	99.9	97.1	98.1	75.8

Brood year	Collection to spawning		Unfertilized egg-eyed	Eyed egg-ponding	30 d after ponding	100 d after ponding	Ponding to release	Transport to release	Unfertilized egg-release
	Female	Male							
1993	92.4	95.9	84.2	97.5	99.6	99.3	96.7	98.8	79.4
1994	90.7	95.3	83.7	100	99.2	97.0	95.3	98.4	79.8
1995	94.7	98.2	86.0	100	96.7	96.4	74.9	90.8	72.4
1996	84.6	96.1	84.1	100	97.9	97.7	94.4	97.7	79.4
1997	89.3	98.3	82.6	97.3	97.1	96.9	98.3	98.2	79.0
1998	85.3	94.6	80.9	98.3	99.4	98.6	95.6	99.8	76.0
1999	98.4	98.3	90.4	97.9	98.1	97.9	96.2	99.4	85.1
2000	93.0	96.6	88.3	98.0	99.6	99.3	96.5	98.9	83.5
2001	87.4	91.5	90.6	97.7	99.8	99.6	93.1	93.3	82.4
2002	93.8	94.1	85.1	99.8	98.1	97.6	93.7	96.5	79.6
2003	77.4	85.1	80.5	98.1	99.6	99.1	91.9	93.5	72.6
2004	92.8	97.8	85.7	87.8	99.9	99.6	86.6	92.1	65.1
2005	97.3	89.6	83.5	98.0	99.7	99.4	89.1	99.5	72.9
2006	92.4	95.2	85.6	98.4	99.3	98.4	94.8	97.2	79.8
2007	73.6	97.5	73.7	97.9	99.5	98.7	96.6	99.1	69.7
2008	96.6	97.9	90.4	97.3	99.4	98.7	88.2	89.6	77.6
Standard	***90.0***	***85.0***	***92.0***	***98.0***	***97.0***	***93.0***	***90.0***	***95.0***	***81.0***

6.3 Disease Monitoring

Rearing of the 2008 brood Wenatchee summer Chinook was similar to previous years with fish being held on well water before being transferred to Dryden Pond for final acclimation in March 2010. Fish were transferred to Dryden pond from 9 to 22 March. Increased mortality caused by external fungus began to occur during the acclimation period at Dryden pond at which time a formalin treatment was initiated in an attempt to prevent the fungus from proliferating.

Results of the 2010 adult broodstock bacterial kidney disease (BKD) monitoring indicated that most females (99%) had ELISA values less than 0.199. About 99.5% of females had ELISA values less than 0.120, which would require about 0.05% of the progeny to be reared at densities not to exceed 0.06 fish per pound (Table 6.12).

Table 6.12. Proportion of bacterial kidney disease (BKD) titer groups for the Wenatchee summer Chinook broodstock, brood years 1997-2010. Also included are the proportions to be reared at either 0.125 fish per pound or 0.060 fish per pound.

Brood year[a]	Optical density values by titer group				Proportion at rearing densities (fish per pound, fpp)	
	Very Low (≤ 0.099)	Low (0.1-0.199)	Moderate (0.2-0.449)	High (≥ 0.450)	≤ 0.125 fpp (<0.119)	≤ 0.060 fpp (>0.120)
1997	0.7714	0.0857	0.0381	0.1048	0.8095	0.1905
1998	0.3067	0.2393	0.1656	0.2883	0.4479	0.5521
1999	0.9590	0.0123	0.0123	0.0164	0.9713	0.0287

Brood year[a]	Optical density values by titer group				Proportion at rearing densities (fish per pound, fpp)	
	Very Low (≤ 0.099)	**Low (0.1-0.199)**	**Moderate (0.2-0.449)**	**High (≥ 0.450)**	**≤ 0.125 fpp (<0.119)**	**≤ 0.060 fpp (>0.120)**
2000	0.6268	0.1053	0.1627	0.1053	0.7321	0.2679
2001	0.6513	0.0263	0.0987	0.2237	0.6776	0.3224
2002	0.7868	0.0457	0.0711	0.0964	0.8325	0.1675
2003	0.9825	0.0000	0.0058	0.0117	0.9825	0.0175
2004	0.9593	0.0081	0.0163	0.0163	0.9675	0.0325
2005	0.9833	0.0056	0.0000	0.0111	0.9833	0.0167
2006	0.9134	0.0563	0.0000	0.0303	0.9351	0.0649
2007	0.9535	0.0078	0.0078	0.0310	0.9535	0.0465
2008	0.9868	0.0088	0.0044	0.0000	0.9868	0.0132
2009	0.9957	0.0000	0.0000	0.0043	0.9957	0.0043
2010	0.9897	0.0025	0.0000	0.0025	0.9949	0.0051
Average	*0.8476*	*0.0431*	*0.0416*	*0.0673*	*0.8764*	*0.1236*

[a] Individual ELISA samples were not collected before the 1997 brood.

6.4 Natural Juvenile Productivity

During 2010, juvenile summer Chinook were sampled at the Lower Wenatchee Trap located at the West Monitor Bridge.

Emigrant Estimates

The Lower Wenatchee Trap operated nightly between 4 February and 20 July 2010. During that time period, trap 1 and trap 2 were inoperable for 19 and 68 days, respectively, because of high river flows, debris, snow/ice, or mechanical failure. During the six-month sampling period, a total of 50,685 wild subyearling Chinook were captured at the Lower Wenatchee Trap. Based on capture efficiencies estimated from the flow model, the total number of wild subyearling Chinook that emigrated past the Lower Wenatchee Trap was 6,695,977 (± 2,435,120). Most of these fish emigrated during May (Figure 6.1). Monthly captures and mortalities of all fish collected at the Lower Wenatchee Trap are reported in Appendix B.

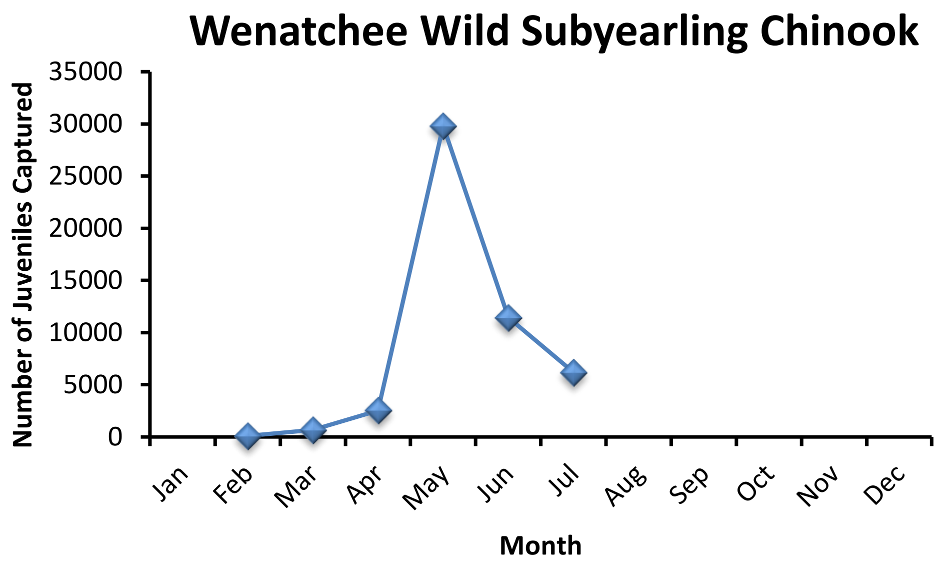


Figure 6.1. Numbers of wild subyearling Chinook captured at the Lower Wenatchee Trap during February to August, 2010.

6.5 Spawning Surveys

Surveys for Wenatchee summer Chinook redds were conducted from late September to mid-November, 2010, in the Wenatchee River and Icicle Creek. Both peak counts and total counts (based on expansion factors; Murdoch and Peven 2005) were conducted in the river (see Appendix G for more details).

Redd Counts

A peak count of 2,564 summer Chinook redds was estimated in 2010 based on ground surveys conducted in the Wenatchee River and Icicle Creek (Table 6.13). A total redd count of 3,261 redds was estimated in 2010 based on expanded peak counts and 3,730 based on the naïve expansion method in the Wenatchee Basin (Table 6.13).

Table 6.13. Peak and total numbers of redds counted in the Wenatchee River, 1989-2010; NA = not available. Total counts are based on two different methods: expanded peak counts and naïve expansion methods (see Appendix G for more information).

Survey year	Peak redd count	Total redd count	
		Peak expansion	Naïve expansion
1989	3,331	4,215	NA
1990	2,479	3,103	NA
1991	2,180	2,748	NA
1992	2,328	2,913	NA
1993	2,334	2,953	NA
1994	2,426	3,077	NA
1995	1,872	2,350	NA
1996	1,435	1,814	NA

Survey year	Peak redd count	Total redd count	
		Peak expansion	Naïve expansion
1997	1,388	1,739	NA
1998	1,660	2,230	NA
1999	2,188	2,738	NA
2000	2,022	2,540	NA
2001	2,857	3,550	NA
2002	5,419	6,836	NA
2003	4,281	5,268	NA
2004	4,003	4,874	NA
2005	2,895	3,538	NA
2006*	7,233	8,896	NA
2007*	1,870	1,970	NA
2008*	2,361	2,800	2,658
2009*	2,688	3,441	2,940
2010*	2,564	3,261	3,730
Average	***2,810***	***3,493***	***3,109***

* Peak and total counts include 68, 13, 23, 21, and 11 redds counted in Icicle Creek in 2006-2010, respectively.

Redd Distribution

Summer Chinook redds were not evenly distributed among reaches within the Wenatchee Basin in 2010 (Table 6.14; Figure 6.2). Most of the spawning occurred upstream from the Leavenworth Bridge in Reaches 6, 9, and 10. The highest density of redds occurred in Reach 6 near the confluence of the Icicle River.

Table 6.14. Peak and total numbers of summer Chinook redds counted in different reaches in the Wenatchee Basin during September through mid-November, 2010. Reach codes are described in Table 2.10.

Survey reach	Peak redd count	Total redd count	
		Peak expansion	Naïve expansion
Wenatchee 1	12	17	18
Wenatchee 2	129	184	111
Wenatchee 3	184	231	463
Wenatchee 4	58	77	153
Wenatchee 5	76	110	87
Wenatchee 6	1,047	1,431	1,394
Wenatchee 7	249	268	221
Wenatchee 8	86	101	100
Wenatchee 9	341	432	562
Wenatchee 10	371	399	610
Icicle Creek	11	11	11
Totals	***2,564***	***3,261***	***3,730***

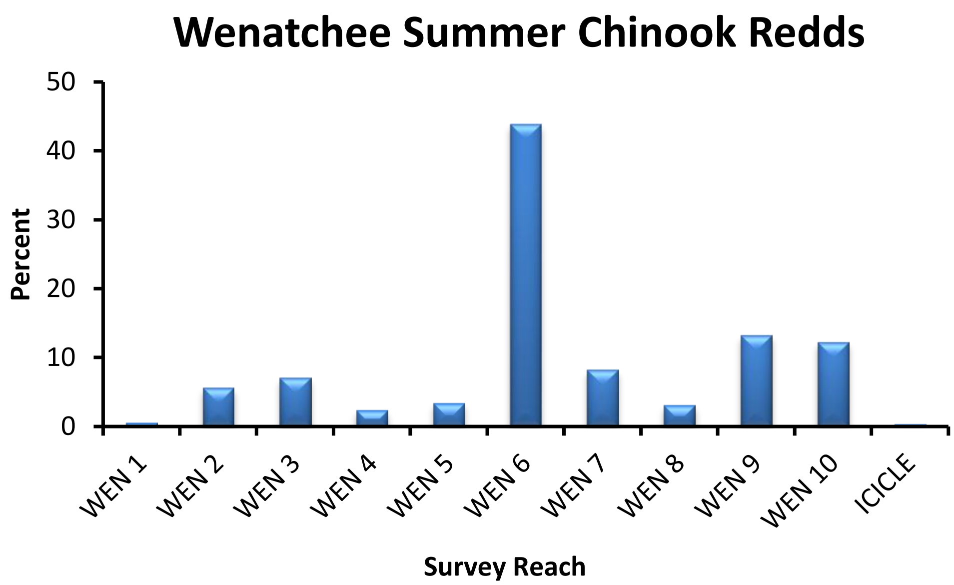


Figure 6.2. Percent of the total number (based on peak expansion) of summer Chinook redds counted in different reaches in the Wenatchee Basin during September through mid-November, 2010. Reach codes are described in Table 2.10.

Spawn Timing

In 2010, spawning in the Wenatchee River began during the first week of October, peaked the third week of October, and ended in early November (Figure 6.3).

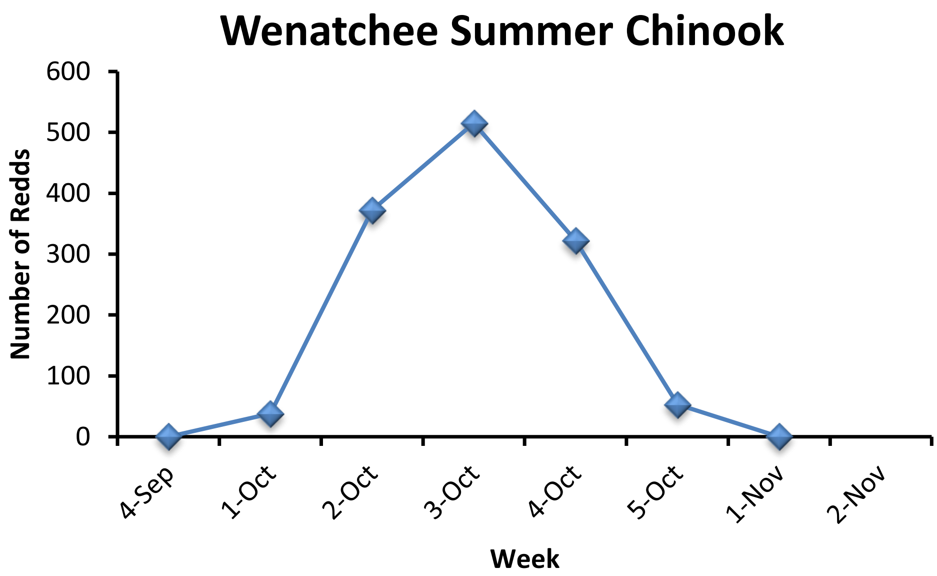


Figure 6.3. Number of new summer Chinook redds counted during different weeks in the Wenatchee River, September through mid-November 2010 (based on mapping counts).

Spawning Escapement

Spawning escapement for Wenatchee summer Chinook was calculated as the total number of redds (expanded peak counts) times the fish per redd ratio estimated from broodstock and fish sampled at adult trapping sites. The estimated fish per redd ratio for summer Chinook in 2010 was 2.29. Multiplying this ratio by the number of redds counted in the Wenatchee Basin resulted in a total spawning escapement of 7,468 summer Chinook (Table 6.15).

Table 6.15. Spawning escapements for summer Chinook in the Wenatchee Basin, return years 1989-2010. Number of redds is based on expanded peak redd counts.

Return year	Fish/Redd	Redds	Total spawning escapement
1989	3.40	4,215	14,331
1990	3.50	3,103	10,861
1991	3.70	2,748	10,168
1992	4.00	2,913	11,652
1993	3.20	2,953	9,450
1994	3.30	3,077	10,154
1995	3.30	2,350	7,755
1996	3.40	1,814	6,168
1997	3.40	1,739	5,913
1998	2.40	2,230	5,352
1999	2.00	2,738	5,476
2000	2.17	2,540	5,512
2001	3.20	3,550	11,360

Return year	Fish/Redd	Redds	Total spawning escapement
2002	2.30	6,836	15,723
2003	2.24	5,268	11,800
2004	2.15	4,874	10,479
2005	2.46	3,538	8,703
2006	2.00	8,896	17,792
2007	2.33	1,970	4,590
2008	2.32	2,800	6,496
2009	2.42	3,441	8,327
2010	2.29	3,261	7,468
Average	***2.79***	***3,493***	***9,341***

6.6 Carcass Surveys

Surveys for Wenatchee summer Chinook carcasses were conducted during late September to mid-November, 2010, in the Wenatchee River and Icicle Creek.

Number sampled

A total of 1,509 summer Chinook carcasses were sampled during October through mid-November in the Wenatchee Basin in 2010 (Table 6.16).

Table 6.16. Numbers of summer Chinook carcasses sampled within each survey reach in the Wenatchee Basin, 1993-2010. Reach codes are described in Table 2.10.

Survey year	Number of summer Chinook carcasses											
	W-1	W-2	W-3	W-4	W-5	W-6	W-7	W-8	W-9	W-10	Icicle	Total
1993	61	138	627	12	77	141	202	38	0	0	0	**1,296**
1994	0	6	22	1	17	48	18	47	125	1	0	**285**
1995	0	10	14	0	0	111	49	36	19	0	0	**239**
1996	0	5	67	39	9	190	26	30	41	0	0	**407**
1997	1	44	118	4	28	288	7	71	67	13	0	**641**
1998	6	74	141	3	0	248	28	346	324	59	0	**1,229**
1999	0	160	97	15	31	857	61	133	171	72	0	**1,597**
2000	7	109	165	7	79	651	75	111	159	193	0	**1,556**
2001	0	45	127	26	0	323	33	110	87	81	0	**832**
2002	0	238	170	0	196	809	0	306	520	155	6	**2,400**
2003	6	323	164	61	132	673	56	237	482	47	36	**2,217**
2004	8	141	181	157	158	975	87	312	428	366	5	**2,818**
2005	8	85	106	39	46	707	70	140	353	257	7	**1,818**
2006	22	140	160	64	112	953	435	343	703	658	18	**3,608**
2007	3	15	49	9	26	475	38	38	96	91	8	**848**
2008	10	34	63	36	36	678	47	42	103	143	8	**1,200**
2009	11	29	43	32	27	389	16	58	240	175	6	**1,026**

Survey year	Number of summer Chinook carcasses											
	W-1	W-2	W-3	W-4	W-5	W-6	W-7	W-8	W-9	W-10	Icicle	Total
2010	3	31	98	57	122	681	136	49	124	193	15	**1,509**
Average	***8***	***90***	***134***	***31***	***61***	***511***	***77***	***136***	***225***	***139***	***6***	***1,418***

Carcass Distribution and Origin

Summer Chinook carcasses were not evenly distributed among reaches within the Wenatchee Basin in 2010 (Table 6.15; Figure 6.4). Most of the carcasses in the Wenatchee Basin were found upstream from the Leavenworth Bridge. The highest percentage of carcasses (36%) was sampled in Reach 6 near the confluence of the Icicle River.

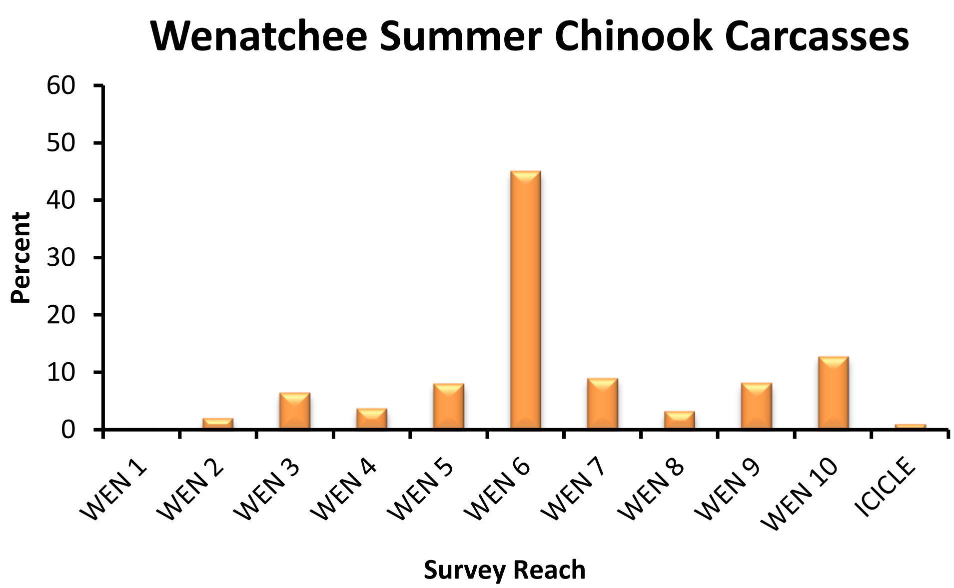


Figure 6.4. Percent of summer Chinook carcasses sampled within different reaches in the Wenatchee Basin during September through mid-November, 2010. Reach codes are described in Table 2.10.

Numbers of wild and hatchery-origin summer Chinook carcasses sampled in 2010 will be available after analysis of CWTs and scales. Based on the available data (1993-2009), most fish, regardless of origin, were found in Reach 6 (Leavenworth Bridge to Icicle Road Bridge) (Table 6.17). However, a larger percentage of hatchery fish were found in that reach than were wild fish (Figure 6.5). In contrast, a larger percentage of wild fish were found in reaches upstream from the Icicle Road Bridge.

Table 6.17. Numbers of wild and hatchery summer Chinook carcasses sampled within different reaches in the Wenatchee Basin, 1993-2009.

Survey year	Origin	Survey reach											Total
		W-1	W-2	W-3	W-4	W-5	W-6	W-7	W-8	W-9	W-10	Icicle	
1993	Wild	52	133	591	11	77	124	200	37	0	0	0	**1,225**
	Hatchery	9	5	36	1	0	17	2	1	0	0	0	**71**
1994	Wild	0	2	15	1	15	34	18	47	124	1	0	**257**
	Hatchery	0	4	7	0	2	14	0	0	1	0	0	**28**
1995	Wild	0	4	11	0	0	99	49	34	19	0	0	**216**
	Hatchery	0	6	3	0	0	12	0	2	0	0	0	**23**
1996	Wild	0	5	65	37	8	181	26	30	41	0	0	**393**
	Hatchery	0	0	2	2	1	9	0	0	0	0	0	**14**
1997	Wild	1	35	104	4	21	242	7	71	66	13	0	**564**
	Hatchery	0	9	14	0	7	46	0	0	1	0	0	**77**
1998	Wild	6	55	106	2	0	169	25	325	297	56	0	**1,041**
	Hatchery	0	19	35	1	0	79	3	21	27	3	0	**188**
1999	Wild	0	79	55	7	14	525	51	124	155	68	0	**1,078**
	Hatchery	0	81	42	8	17	332	10	9	16	4	0	**519**
2000	Wild	4	68	102	6	51	443	68	100	154	186	0	**1,182**
	Hatchery	3	41	63	1	28	208	7	11	5	7	0	**374**
2001	Wild	0	33	88	4	0	230	29	108	83	78	0	**653**
	Hatchery	0	12	39	22	0	93	4	2	4	3	0	**179**
2002	Wild	0	140	110	0	94	440	0	295	514	150	4	**1,747**
	Hatchery	0	98	60	0	102	369	0	11	6	5	2	**653**
2003	Wild	5	218	118	21	94	425	52	223	445	46	11	**1,658**
	Hatchery	1	105	46	40	38	248	4	14	37	1	25	**559**
2004	Wild	7	108	151	102	97	640	74	282	416	357	0	**2,234**
	Hatchery	1	33	30	55	61	335	13	30	12	9	5	**584**
2005	Wild	4	49	78	24	26	397	66	125	336	243	0	**1,348**
	Hatchery	4	36	28	15	20	310	4	15	17	14	7	**470**
2006	Wild	16	108	133	46	80	753	426	336	700	654	5	**3,257**
	Hatchery	6	32	27	18	32	200	9	7	3	4	13	**351**
2007	Wild	1	9	29	2	16	241	36	37	96	91	3	**561**
	Hatchery	2	6	20	7	10	234	2	1	0	0	5	**287**
2008	Wild	7	17	39	25	21	404	43	35	102	142	2	**869**
	Hatchery	3	17	24	11	15	272	4	7	2	1	6	**130**
2009	Wild	6	22	32	23	20	288	13	55	236	173	5	**873**
	Hatchery	5	7	11	9	7	101	3	3	4	2	1	**153**
Average	***Wild***	***6***	***64***	***107***	***19***	***37***	***331***	***70***	***133***	***223***	***133***	***2***	***1,127***
	Hatchery	***2***	***30***	***29***	***11***	***20***	***169***	***4***	***8***	***8***	***3***	***4***	***274***

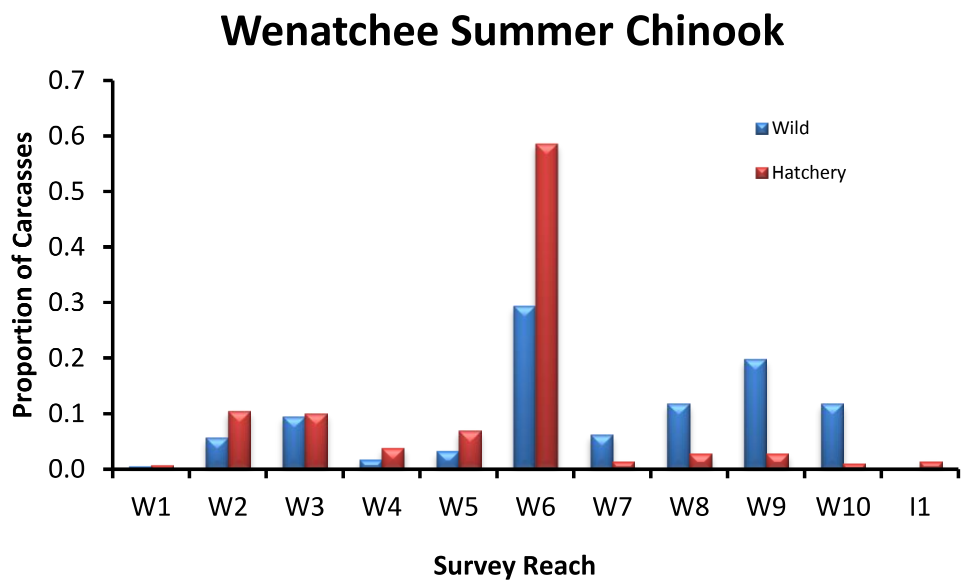


Figure 6.5. Distribution of wild and hatchery produced carcasses in different reaches in the Wenatchee Basin, 1993-2009. Reach codes are described in Table 2.10.

Sampling Rate

If escapement is based on total numbers of redds (based on peak expansion), then about 20% of the total spawning escapement of summer Chinook in the Wenatchee Basin was sampled in 2010 (Table 6.18). Sampling rates among survey reaches varied from 7 to 60%.

Table 6.18. Number of redds and carcasses, total spawning escapement, and sampling rates for summer Chinook in the Wenatchee Basin, 2010.

Sampling reach	Total number of redds	Total number of carcasses	Total spawning escapement	Sampling rate
Wenatchee 1	17	3	39	0.08
Wenatchee 2	184	31	421	0.07
Wenatchee 3	231	98	529	0.19
Wenatchee 4	77	57	176	0.32
Wenatchee 5	110	122	252	0.48
Wenatchee 6	1,431	681	3,277	0.21
Wenatchee 7	268	136	614	0.22
Wenatchee 8	101	49	231	0.21
Wenatchee 9	432	124	989	0.13
Wenatchee 10	399	193	914	0.21
Icicle Creek	11	15	25	0.60
Total	***3,261***	***1,509***	***7,468***	***0.20***

Length Data

Mean lengths (POH, cm) of male and female summer Chinook carcasses sampled during surveys in the Wenatchee Basin in 2010 are provided in Table 6.19. The average size of males and females sampled in the Wenatchee basin were 68 cm and 72 cm, respectively.

Table 6.19. Mean lengths (postorbital-to-hypural length; cm) and standard deviations (in parentheses) of male and female summer Chinook carcasses sampled in different streams/watersheds in the Wenatchee Basin, 2010.

Stream/watershed	Mean length (cm)	
	Male	Female
Wenatchee 1	75.0 (17.0)	NA
Wenatchee 2	66.8 (9.1)	72.3 (4.4)
Wenatchee 3	65.5 (10.3)	68.3 (6.9)
Wenatchee 4	65.5 (12.9)	75.0 (5.9)
Wenatchee 5	62.3 (10.0)	70.5 (5.0)
Wenatchee 6	65.8 (9.3)	68.9 (6.4)
Wenatchee 7	67.8 (9.7)	69.9 (5.0)
Wenatchee 8	65.0 (10.1)	69.5 (5.5)
Wenatchee 9	66.8 (9.6)	69.7 (4.5)
Wenatchee 10	67.1 (7.2)	69.5 (4.4)
Icicle Creek	68.0 (7.8)	71.5 (4.5)
Total	***68.4 (11.7)***	***71.8 (5.4)***

6.7 Life History Monitoring

Life history characteristics of Wenatchee summer Chinook were assessed by examining carcasses on spawning grounds and fish collected or examined at broodstock collection sites, and by reviewing tagging data and fisheries statistics.

Migration Timing

Migration timing of hatchery and wild Wenatchee summer Chinook was determined from broodstock data and stock assessment data collected at Dryden Dam. Sampling at Dryden Dam occurs from early July through mid-October. During that period, hatchery summer Chinook arrived about 1-2 weeks before wild Chinook in 2010 (Table 6.20). This pattern was different in previous years when wild fish arrived about 1-2 weeks earlier than hatchery fish. This latter pattern was also observed when data were pooled for the 2007-2010 survey period.

Table 6.20. The week that 10%, 50% (median), and 90% of the wild and hatchery summer Chinook salmon passed Dryden Dam, 2007-2010. The average week is also provided. Migration timing is based on collection of summer Chinook broodstock at Dryden Dam.

Survey year	Origin	Wenatchee Summer Chinook Migration Time (week)				Sample size
		10 Percentile	50 Percentile	90 Percentile	Mean	
2007	Wild	28	31	37	31	274
	Hatchery	30	33	41	35	305

Survey year	Origin	Wenatchee Summer Chinook Migration Time (week)				Sample size
		10 Percentile	50 Percentile	90 Percentile	Mean	
2008	Wild	29	31	40	32	219
	Hatchery	32	37	41	37	576
2009	Wild	27	29	41	31	469
	Hatchery	28	34	42	35	382
2010	Wild	30	33	35	32	403
	Hatchery	29	30	33	30	268
Average	Wild	***28***	***31***	***36***	***32***	***1,365***
	Hatchery	***29***	***34***	***41***	***35***	***1,531***

Age at Maturity

Most of the wild and hatchery summer Chinook sampled during the period 1993-2009 in the Wenatchee Basin were age-5 fish (total age) (Table 6.21; Figure 6.6). A higher percentage of age-4 wild Chinook returned to the basin than did age-4 hatchery Chinook. In contrast, a higher proportion of age-6 hatchery fish returned than did age-6 wild fish. Thus, a higher percentage of hatchery fish returned at an older age than did wild fish.

Table 6.21. Proportions of wild and hatchery summer Chinook of different ages (total age) sampled on spawning grounds in the Wenatchee Basin, 1993-2009.

Sample year	Origin	Total age						Sample size
		2	3	4	5	6	7	
1993	Wild	0.00	0.03	0.42	0.55	0.00	0.00	1,224
	Hatchery	0.00	0.03	0.91	0.06	0.00	0.00	69
1994	Wild	0.01	0.03	0.44	0.52	0.00	0.00	257
	Hatchery	0.00	0.00	0.12	0.88	0.00	0.00	25
1995	Wild	0.00	0.03	0.19	0.74	0.05	0.00	216
	Hatchery	0.00	0.00	0.00	0.05	0.95	0.00	22
1996	Wild	0.00	0.02	0.36	0.60	0.02	0.00	513
	Hatchery	0.00	0.00	0.45	0.18	0.27	0.09	22
1997	Wild	0.00	0.01	0.38	0.57	0.03	0.00	562
	Hatchery	0.00	0.05	0.20	0.66	0.08	0.00	74
1998	Wild	0.00	0.03	0.34	0.62	0.01	0.00	1,041
	Hatchery	0.00	0.03	0.51	0.40	0.06	0.00	187
1999	Wild	0.00	0.01	0.43	0.55	0.01	0.00	1,087
	Hatchery	0.00	0.01	0.16	0.81	0.03	0.00	512
2000	Wild	0.01	0.04	0.27	0.68	0.00	0.00	1,182
	Hatchery	0.00	0.07	0.12	0.65	0.15	0.00	342
2001	Wild	0.00	0.08	0.59	0.32	0.01	0.00	653
	Hatchery	0.00	0.05	0.76	0.15	0.04	0.00	182
2002	Wild	0.00	0.03	0.66	0.31	0.00	0.00	1,747

Sample year	Origin	Total age						Sample size
		2	3	4	5	6	7	
	Hatchery	0.00	0.01	0.19	0.78	0.02	0.00	643
2003	Wild	0.00	0.02	0.34	0.64	0.00	0.00	1,649
	Hatchery	0.00	0.06	0.11	0.75	0.09	0.00	522
2004	Wild	0.00	0.06	0.13	0.80	0.01	0.00	2,234
	Hatchery	0.00	0.09	0.57	0.25	0.09	0.00	561
2005	Wild	0.00	0.04	0.60	0.32	0.04	0.00	1,186
	Hatchery	0.00	0.02	0.10	0.86	0.02	0.00	451
2006	Wild	0.00	0.01	0.15	0.84	0.01	0.00	2,972
	Hatchery	0.00	0.02	0.17	0.26	0.55	0.00	299
2007	Wild	0.01	0.08	0.20	0.62	0.10	0.00	479
	Hatchery	0.00	0.01	0.15	0.76	0.06	0.03	275
2008	Wild	0.01	0.05	0.74	0.20	0.00	0.00	766
	Hatchery	0.01	0.01	0.16	0.72	0.10	0.00	331
2009	Wild	0.00	0.05	0.52	0.43	0.00	0.00	798
	Hatchery	0.00	0.10	0.39	0.50	0.02	0.00	131
Average	***Wild***	***0.00***	***0.04***	***0.40***	***0.55***	***0.02***	***0.00***	***1,092***
	Hatchery	***0.00***	***0.03***	***0.30***	***0.51***	***0.15***	***0.01***	***273***

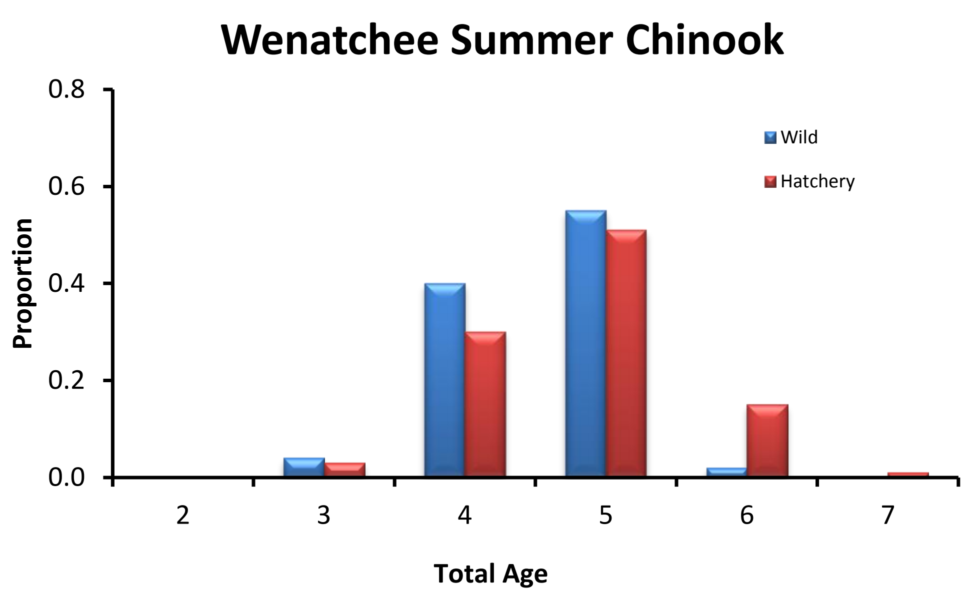


Figure 6.6. Proportions of wild and hatchery summer Chinook of different total ages sampled at broodstock collection sites and on spawning grounds in the Wenatchee Basin for the combined years 1993-2009.

Size at Maturity

On average, hatchery summer Chinook were about 4 cm smaller than wild summer Chinook sampled in the Wenatchee Basin (Table 6.22). This is interesting given that a slightly higher percentage of hatchery fish returned as age-5 and 6 fish than did wild fish. Future analyses will compare sizes of hatchery and wild fish of the same age groups and gender.

Table 6.22. Mean lengths (POH; cm) and variability statistics for wild and hatchery summer Chinook sampled in the Wenatchee Basin, 1993-2009; SD = 1 standard deviation.

Sample year	Origin	Sample size	Summer Chinook length (POH; cm)			
			Mean	SD	Minimum	Maximum
1993	Wild	1,344	73	8	33	94
	Hatchery	68	61	9	37	83
1994	Wild	276	73	8	31	89
	Hatchery	25	70	8	54	85
1995	Wild	225	75	7	48	87
	Hatchery	23	74	7	57	85
1996	Wild	210	74	7	43	92
	Hatchery	9	66	12	52	84
1997	Wild	615	74	8	29	99
	Hatchery	78	69	10	29	83
1998	Wild	1,179	73	8	28	97
	Hatchery	188	67	10	37	87
1999	Wild	1,218	72	8	29	95
	Hatchery	518	71	8	26	94
2000	Wild	1,302	71	10	24	94
	Hatchery	369	69	11	33	91
2001	Wild	730	70	9	30	93
	Hatchery	179	63	10	28	86
2002	Wild	1,914	72	8	39	94
	Hatchery	653	71	8	34	95
2003	Wild	1,950	74	9	24	105
	Hatchery	546	69	10	26	97
2004	Wild	2,571	72	9	32	98
	Hatchery	580	59	11	25	91
2005	Wild	1,352	69	7	41	92
	Hatchery	469	69	8	39	91
2006	Wild	3,249	74	6	29	99
	Hatchery	350	71	9	35	90
2007	Wild	566	73	9	29	92
	Hatchery	269	70	7	45	87
2008	Wild	836	69	8	29	89

Sample year	Origin	Sample size	Summer Chinook length (POH; cm)			
			Mean	SD	Minimum	Maximum
	Hatchery	363	70	9	24	94
2009	Wild	872	71	8	30	94
	Hatchery	153	64	11	32	84
Pooled	***Wild***	***20,409***	***72***	***2***	***24***	***105***
	Hatchery	***4,840***	***68***	***4***	***24***	***97***

Contribution to Fisheries

Most of the harvest on hatchery-origin Wenatchee summer Chinook occurred in the ocean (Table 6.23). Ocean harvest has made up 50% to 100% of all hatchery Wenatchee summer Chinook harvested. Total harvest on early brood years (1990-1996) was lower than for later brood years (1997-2004).

Table 6.23. Estimated number and percent (in parentheses) of hatchery-origin Wenatchee summer Chinook captured in different fisheries, brood years 1989-2004.

Brood year	Ocean fisheries	Columbia River Fisheries			Total
		Tribal	Commercial (Zones 1-5)	Recreational (sport)	
1989	1,461 (50)	1,432 (49)	0 (0)	20 (1)	2,913
1990	30 (100)	0 (0)	0 (0)	0 (0)	30
1991	30 (63)	0 (0)	0 (0)	18 (38)	48
1992	151 (79)	39 (21)	0 (0)	0 (0)	190
1993	40 (62)	25 (38)	0 (0)	0 (0)	65
1994	650 (91)	62 (9)	2 (0)	0 (0)	714
1995	559 (98)	9 (2)	5 (1)	0 (0)	573
1996	195 (96)	3 (1)	0 (0)	6 (3)	204
1997	3,028 (95)	45 (1)	16 (1)	106 (3)	3,195
1998	4,973 (92)	128 (2)	16 (0)	287 (5)	5,404
1999	1,580 (84)	168 (9)	21 (1)	105 (6)	1,874
2000	7,939 (73)	1,248 (11)	447 (4)	1,225 (11)	10,859
2001	1,056 (60)	238 (13)	106 (6)	366 (21)	1,766
2002	1,489 (56)	557 (21)	189 (7)	431 (16)	2,666
2003	823 (50)	485 (29)	89 (5)	257 (16)	1,254
2004	407 (49)	212 (26)	66 (8)	142 (17)	827

Straying

Stray rates were determined by examining CWTs recovered on spawning grounds within and outside the Wenatchee Basin. Targets for strays based on return year (recovery year) and brood year should be less than 5%.

On average, rates of hatchery-origin Wenatchee summer Chinook straying into basins outside the Wenatchee have been low (Table 6.24). Although hatchery-origin Wenatchee summer Chinook have strayed into other spawning areas, straying has generally been less than 5%. In four different years, Wenatchee strays have made up more than 5% of the spawning escapement in the Entiat Basin and Chelan tailrace. Wenatchee strays have made up more than 5% of spawning escapement in the Methow Basin in five different years.

Table 6.24. Number and percent of spawning escapements within other non-target basins that consisted of hatchery-origin Wenatchee summer Chinook, return years 1994-2007. For example, for return year 2000, 3% of the summer Chinook escapement in the Methow Basin consisted of hatchery-origin Wenatchee summer Chinook. Percent strays should be less than 5%.

Return year	Methow		Okanogan		Chelan		Entiat		Hanford Reach	
	Number	%	Number	%	Number	%	Number	%	Number	%
1994	0	0.0	75	1.9	-	-	-	-	-	-
1995	0	0.0	0	0.0	-	-	-	-	-	-
1996	0	0.0	0	0.0	-	-	-	-	-	-
1997	0	0.0	0	0.0	-	-	-	-	-	-
1998	25	3.7	0	0.0	0	0.0	0	0.0	0	0.0
1999	20	2.0	3	0.1	0	0.0	0	0.0	13	0.1
2000	36	3.0	13	0.4	0	0.0	0	0.0	0	0.0
2001	163	5.9	57	0.5	30	3.0	0	0.0	0	0.0
2002	153	3.3	53	0.4	40	6.9	74	14.8	0	0.0
2003	80	2.0	24	0.7	44	10.5	132	19.1	26	0.0
2004	113	5.2	42	0.6	30	7.1	0	0.0	0	0.0
2005	245	9.6	67	0.8	51	11.5	49	13.4	0	0.0
2006	170	6.2	12	0.1	12	2.9	18	3.1	0	0.0
2007	127	9.3	5	0.1	9	4.8	18	7.3	20	0.1
Total	***1,132***	***4.2***	***351***	***0.5***	***216***	***5.0***	***291***	***8.3***	***59***	***0.0***

On average, about 11% of the hatchery-origin Wenatchee summer Chinook returns have strayed into non-target spawning areas, exceeding the target of 5% (Table 6.25). Depending on brood year, percent strays into non-target spawning areas have ranged from 0-19%. In addition, on average, about 5.5% have strayed into non-target hatchery programs, but straying into non-target programs has declined over time.

Table 6.25. Number and percent of hatchery-origin Wenatchee summer Chinook that homed to target spawning areas and the target hatchery program, and number and percent that strayed to non-target spawning areas and non-target hatchery programs, by brood years 1989-2004. Percent stays should be less than 5%.

Brood year	Homing				Straying			
	Target stream		Target hatchery		Non-target streams		Non-target hatcheries	
	Number	%	Number	%	Number	%	Number	%
1989	1,352	62.9	60	2.8	75	3.5	662	30.8
1990	74	84.1	1	1.1	0	0.0	13	14.8
1991	14	60.9	1	4.3	0	0.0	8	34.8
1992	375	84.8	7	1.6	0	0.0	60	13.6
1993	67	72.8	9	9.8	4	4.3	12	13.0
1994	890	71.8	205	16.5	56	4.5	88	7.1
1995	748	74.8	139	13.9	42	4.2	71	7.1
1996	261	70.4	42	11.3	53	14.3	15	4.0
1997	3,609	85.6	171	4.1	396	9.4	38	0.9
1998	1,790	78.5	11	0.5	416	18.2	64	2.8
1999	507	79.7	0	0.0	121	19.0	8	1.3
2000	2,745	83.0	0	0.0	526	15.9	37	1.1
2001	521	82.0	0	0.0	105	16.5	9	1.4
2002	1,521	85.3	10	0.6	244	13.7	8	0.4
2003	1,268	89.3	42	3.0	101	7.1	9	0.6
2004	438	83.4	3	0.6	66	12.6	18	3.4
Total	***16,180***	***80.1***	***703***	***3.5***	***2,217***	***11.0***	***1,106***	***5.5***

Genetics

Genetic studies were conducted to investigate relationships among temporally replicated collections of summer Chinook from the Wenatchee River, Methow River, and Okanogan River in the upper Columbia River basin (Kassler et al. 2100; the entire report is appended as Appendix J). Samples from the Eastbank Hatchery – Wenatchee stock, Eastbank Hatchery – Methow/Okanogan (MEOK) stock, and Wells Hatchery were also included in the analysis. Samples of natural and hatchery-origin summer Chinook were analyzed and compared to determine if the supplementation program has affected the genetic structure of these populations. The study also calculated the effective number of breeders for collection locations of natural and hatchery-origin summer Chinook from 1993 and 2008.

In general, population differentiation was not observed among the temporally replicated collection locations. A single collection from the Okanogan River (1993) was the only collection showing statistically significant differences. The effective number of breeders was not statistically different from the early collection in 1993 in comparison to the late collection in 2008. Overall, these analyses revealed a lack of differentiation among the temporal replicates from the same locations and among the collection from different locations, suggesting the populations have been homogenized or that there has been substantial gene flow among populations. Additional comparisons among summer-run and fall-run Chinook populations in the upper Columbia River were conducted to determine if there was any differentiation between Chinook with different run timing. These analyses revealed pairwise F_{ST} values that were less than 0.01 for the collections of summer Chinook to collections of fall Chinook from Hanford Reach, lower Yakima River, Priest Rapids, and Umatilla. Collections of fall Chinook from Crab Creek, Lyons Ferry Hatchery, Marion Drain, and Snake River had pairwise F_{ST} values that were higher in comparison to the collections of summer Chinook. The consensus clustering analysis did not provide good statistical support to the groupings, but did show relationships among collections based on geographic proximity. Overall the summer and fall run Chinook that have historically been spawned together were not differentiated while fall Chinook from greater geographic distances were differentiated.

Proportion of Natural Influence

Another method for assessing the genetic risk of a supplementation program is to determine the influence of the hatchery and natural environments on the adaptation of the composite population. This is estimated by the proportion of natural-origin fish in the hatchery broodstock (pNOB) and the proportion of hatchery-origin fish in the natural spawning escapement (pHOS). The ratio pNOB/(pHOS+pNOB) is the Proportion of Natural Influence (PNI). The larger the ratio (PNI), the greater the strength of selection in the natural environment relative to that of the hatchery environment. In order for the natural environment to dominate selection, PNI should be greater than 0.5 (HSRG/WDFW/NWIFC 2004).

For brood years 1989-2009, the PNI was consistently greater than 0.5 (Table 6.26). This indicates that the natural environment has a greater influence on adaptation of Wenatchee summer Chinook than does the hatchery environment.

Table 6.26. Proportionate natural influence (PNI) of the Wenatchee summer Chinook supplementation program for brood years 1989-2009. PNI was calculated as the proportion of naturally produced Chinook in the hatchery broodstock (pNOB) divided by the proportion of hatchery Chinook on the spawning grounds (pHOS) plus pNOB. NOS = number of natural-origin Chinook on the spawning grounds; HOS = number of hatchery-origin Chinook on the spawning grounds; NOB = number of natural-origin Chinook collected for broodstock; and HOB = number of hatchery-origin Chinook included in hatchery broodstock.

Brood year	Spawners			Broodstock			PNI
	NOS	HOS	pHOS	NOB	HOB	pNOB	
1989	14,331	0	0.00	290	0	1.00	1.00
1990	10,861	0	0.00	57	0	1.00	1.00
1991	10,168	0	0.00	105	0	1.00	1.00
1992	11,652	0	0.00	274	0	1.00	1.00
1993	8,810	640	0.07	406	44	0.90	0.93
1994	8,378	1,776	0.17	333	54	0.86	0.83
1995	6,813	942	0.12	363	16	0.96	0.89
1996	5,991	177	0.03	263	3	0.99	0.97
1997	5,381	532	0.09	205	13	0.94	0.91

Brood year	Spawners			Broodstock			PNI
	NOS	HOS	pHOS	NOB	HOB	pNOB	
1998	4,003	1,349	0.25	299	78	0.79	0.76
1999	3,971	1,505	0.27	242	236	0.51	0.65
2000	4,381	1,131	0.21	275	180	0.60	0.74
2001	9,262	2,098	0.18	210	136	0.61	0.77
2002	11,691	4,032	0.26	409	10	0.98	0.79
2003	9,760	2,040	0.17	337	7	0.98	0.85
2004	9,085	1,394	0.13	424	2	1.00	0.88
2005	6,862	1,841	0.21	397	3	0.99	0.83
2006	16,060	1,732	0.10	433	4	0.99	0.91
2007	3,173	1,417	0.31	263	3	0.99	0.76
2008	4,794	1,702	0.26	378	69	0.85	0.77
2009	7,113	1,214	0.15	452	8	0.98	0.87
Average	***8,216***	***1,215***	***0.14***	***305***	***41***	***0.90***	***0.87***

Natural and Hatchery Replacement Rates

Natural replacement rates (NRR) were calculated as the ratio of natural-origin recruits (NOR) to the parent spawning population (spawning escapement). For brood years 1989-2003, NRR for summer Chinook in the Wenatchee averaged 0.96 (range, 0.16-2.90) if harvested fish were not include in the estimate and 2.71 (range, 0.36-9.79) if harvested fish were included in the estimate (Table 6.27). NRRs for more recent brood years will be calculated as soon as all tag recoveries and sampling rates have been loaded into the database.

Hatchery replacement rates (HRR) are the hatchery adult-to-adult returns and were calculated as the ratio of hatchery-origin recruits (HOR) to the parent broodstock collected. These rates should be greater than the NRRs and greater than or equal to 5.30 (the calculated target value in Murdoch and Peven 2005). HRRs exceeded NRRs in 11 of the 15 years of data, regardless if harvest was or was not included in the estimate (Table 6.27). Hatchery replacement rates for Wenatchee summer Chinook have exceeded the estimated target value of 5.30 in three or six of the 15 years of data depending on if harvest was or was not included in the estimate.

Table 6.27. Broodstock collected, spawning escapements, natural and hatchery-origin recruits (NOR and HOR), and natural and hatchery replacement rates (NRR and HRR; with and without harvest) for summer Chinook in the Wenatchee Basin, brood years 1989-2003.

Brood year	Broodstock Collected	Spawning Escapement	Harvest not included				Harvest included			
			HOR	NOR	HRR	NRR	HOR	NOR	HRR	NRR
1989	346	14,331	2,149	9,133	6.21	0.64	5,062	21,489	14.63	1.50
1990	87	10,861	88	9,463	1.01	0.87	118	12,805	1.36	1.18
1991	128	10,168	23	5,557	0.18	0.55	71	17,151	0.55	1.69
1992	341	11,652	442	5,876	1.30	0.50	632	8,467	1.85	0.73
1993	524	9,450	92	5,023	0.18	0.53	157	8,572	0.30	0.91

Brood year	Broodstock Collected	Spawning Escapement	Harvest not included				Harvest included			
			HOR	NOR	HRR	NRR	HOR	NOR	HRR	NRR
1994	418	10,154	1,239	3,875	2.96	0.38	1,953	6,122	4.67	0.60
1995	398	7,755	1,000	5,219	2.51	0.67	1,573	8,271	3.95	1.07
1996	334	6,168	371	4,353	1.11	0.71	575	6,802	1.72	1.10
1997	240	5,913	4,214	9,585	17.56	1.62	7,409	16,875	30.87	2.85
1998	472	5,352	2,281	15,514	4.83	2.90	7,685	52,412	16.28	9.79
1999	488	5,476	636	11,855	1.30	2.16	2,510	47,044	5.14	8.59
2000	492	5,512	3,308	3,982	6.72	0.72	14,167	17,090	28.79	3.10
2001	493	11,360	635	19,059	1.29	1.68	2,401	72,468	4.87	6.38
2002	482	15,723	1,783	4,918	3.70	0.31	4,449	12,357	9.23	0.79
2003	496	11,800	1,420	1,942	2.86	0.16	3,074	4,231	6.20	0.36
Average	***383***	***9,445***	***1,312***	***7,690***	***3.58***	***0.96***	***3,456***	***20,810***	***8.70***	***2.71***

Smolt-to-Adult Survivals

Smolt-to-adult survival ratios (SARs) were calculated as the number of hatchery adult recaptures divided by the number of tagged hatchery smolts released. SARs were based on CWT returns. For the available brood years, SARs have ranged from 0.00037 to 0.01696 for hatchery summer Chinook in the Wenatchee basin (Table 6.28).

Table 6.28. Smolt-to-adult ratios (SARs) for Wenatchee hatchery summer Chinook, brood years 1989-2004.

Brood year	Number of tagged smolts released[a]	Estimated adult captures[b]	SAR
1989	144,905	1,017	0.00702
1990	119,214	115	0.00096
1991	190,371	71	0.00037
1992	605,055	617	0.00102
1993	210,626	157	0.00075
1994	452,340	1,928	0.00426
1995	668,409	1,539	0.00230
1996	585,590	567	0.00097
1997	434,645	7,371	0.01696
1998	641,109	7,610	0.01187
1999	988,328	2,487	0.00252
2000	903,368	13,814	0.01528
2001	596,618	2,386	0.00400
2002	805,919	4,319	0.00536
2003	639,381	3,026	0.00473
2004	603,942	1,339	0.00222

Brood year	Number of tagged smolts released[a]	Estimated adult captures[b]	SAR
Average	***536,864***	***3,023***	***0.00563***

[a] Includes all tag codes and CWT released fish (CWT + Ad Clip fish and CWT-only fish).

[b] Includes estimated recoveries (spawning ground, hatcheries, harvest, etc.) and observed recoveries if estimated recoveries were unavailable.

6.8 ESA/HCP Compliance

Broodstock Collection

Per the 2008 broodstock collection protocol, 492 natural-origin (adipose fin present) summer Chinook adults were targeted for collection at Dryden and Tumwater dams. Because of low wild fish abundance and low trap efficiency at Dryden Dam, the actual 2008 collection totaled 472 summer Chinook (400 natural origin and 72 hatchery origin) in combination from Dryden Dam and Tumwater Dam. Trapping began 1 July and ended 8 August 2008.

Summer Chinook and steelhead broodstock collections occurred concurrently at Dryden Dam; therefore, steelhead and spring Chinook encounters at Dryden Dam during Wenatchee summer Chinook broodstock collection were attributable to steelhead broodstock collections authorized under ESA Permit 1395 take authorizations. No steelhead or spring Chinook takes were associated with the Wenatchee summer Chinook collection.

Consistent with impact minimization measures in ESA Permit 1347, all ESA-listed species handled during summer Chinook broodstock collection were subject to water-to-water transfers or anesthetized if removed from water during handling.

Hatchery Rearing and Release

The 2008 Wenatchee summer Chinook program released an estimated 888,811 smolts, representing 102.9% of the 864,000 programmed production and was within the 10% overage allowance identified in ESA permit 1347.

Hatchery Effluent Monitoring

Per ESA Permits 1196, 1347, and 1395, permit holders shall monitor and report hatchery effluents in compliance with applicable National Pollution Discharge Elimination Systems (NPDES) (EPA 1999) permit limitations. There were no NPDES violations reported at Chelan PUD Hatchery facilities during the period 1 January 2010 through 31 December 2010. NPDES monitoring and reporting for Chelan PUD Hatchery Programs during 2010 are provided in Appendix E.

Smolt and Emigrant Trapping

ESA-listed spring Chinook and steelhead were encountered during operation of the Lower Wenatchee Trap. ESA takes are reported in the steelhead (Section 3.8) and spring Chinook (Section 5.8) sections and are not repeated here.

Spawning Surveys

Summer Chinook spawning ground surveys conducted in the Wenatchee Basin during 2010 were consistent with ESA Section 10 Permit No. 1347. Because of the difficulty of quantifying the level of take associated with spawning ground surveys, the Permit does not specify a take level associated with these activities, even though it does authorize implementation of spawning ground surveys. Therefore, no take levels are reported. However, to minimize potential impacts to established redds, wading was restricted to the extent practical, and extreme caution was used to avoid established redds when wading was required.

SECTION 7: METHOW SUMMER CHINOOK

7.1 Broodstock Sampling

This section focuses on results from sampling 2008-2009 Methow summer Chinook broodstock, which were collected in the East Ladder of Wells Dam. Summer Chinook adults collected at Wells Dam are also used in the Okanogan/Similkameen supplementation program. Complete information is not currently available for the 2010 return (this information will be provided in the 2011 annual report).

Origin of Broodstock

Both 2008 and 2009 broodstock consisted almost entirely of natural-origin (adipose fin present) summer Chinook (Table 7.1). These fish were used for both the Methow and Okanogan supplementation programs. In 2009, to meet production goals, hatchery-origin adults were collected in concert with natural-origin fish. About 1% of the 2009 broodstock were comprised of hatchery-origin fish (hatchery-origin was determined by examination of scales and CWTs). However, no hatchery fish were incorporated into the broodstock because of pre-spawn mortality.

Table 7.1. Numbers of wild and hatchery summer Chinook collected for broodstock, numbers that died before spawning, and numbers of Chinook spawned for the Methow/Okanogan programs, 1989-2009. Unknown origin fish (i.e., undetermined by scale analysis, no CWT or fin clips, and no additional hatchery marks) were considered naturally produced. Mortality includes fish that died of natural causes typically near the end of spawning and were not needed for the program and surplus fish killed at spawning.

Brood year	Wild summer Chinook					Hatchery summer Chinook					Total number spawned
	Number collected	Prespawn loss	Mortality	Number spawned	Number released	Number collected	Prespawn loss	Mortality	Number spawned	Number released	
1989[a]	1,419	72	-	1,297	-	341	17	-	312	-	1,609
1990[a]	864	34	-	828	-	214	8	-	206	-	1,034
1991[a]	1,003	59	-	924	-	341	20	-	314	-	1,238
1992[a]	312	6	-	297	-	428	9	-	406	-	703
1993[a]	813	48	-	681	-	464	28	-	388	-	1,069
1994	385	33	11	341	12	266	15	7	244	1	585
1995	254	13	10	173	58	351	28	9	240	74	413
1996	316	15	11	290	0	234	2	9	223	0	513
1997	214	11	5	198	0	308	24	20	264	0	462
1998	239	28	58	153	0	348	18	119	211	0	364
1999	248	5	19	224	0	307	2	16	289	0	513
2000	184	15	5	164	0	373	17	17	339	0	503
2001	135	8	36	91	0	423	29	128	266	0	357
2002	270	2	21	247	0	285	11	33	241	0	488
2003	449	14	53	381	0	112	2	9	101	0	482
2004	541	23	12	506	0	17	0	1	16	0	522
2005	551	29	76	391	55	12	2	0	9	1	400

Brood year	Wild summer Chinook					Hatchery summer Chinook					Total number spawned
	Number collected	Prespawn loss	Mortality	Number spawned	Number released	Number collected	Prespawn loss	Mortality	Number spawned	Number released	
2006	579	50	10	500	19	12	2	0	10	0	510
2007	504	22	26	456	0	19	0	2	17	0	473
2008	418	5	9	404	0	41	0	0	41	0	445
2009	553	31	15	507	0	5	5	0	0	0	507
Average[b]	***488***	***25***	***24***	***431***	***9***	***233***	***11***	***23***	***197***	***5***	***628***

[a] Number of fish spawned and collected during these years included fish retained from the right- and left-bank ladder traps at Wells Dam and fish collected from the volunteer channel. There was no distinction made between fish collected at trap locations and program (i.e., aggregated population used for Wells, Methow, and Okanogan summer Chinook programs).

[b] Because of bias from aggregating the spawning population from 1989-1993, averages are based on adult numbers collected from 1994-2006.

Age/Length Data

Ages of summer Chinook broodstock were determined from analysis of scales and/or CWTs. Broodstock collected from the 2008 return consisted primarily of age-3 and 4 natural-origin Chinook (85%) and age-4 and 5 hatchery-origin Chinook (95%). Age-2, 5, and 6 natural-origin fish collectively made up 15% of the broodstock (Table 7.2). Age-3 and 6 hatchery-origin Chinook collectively made up 5% of the broodstock.

Broodstock collected from the 2009 return consisted primarily of age-4 and 5 natural-origin Chinook (89%) and age-5 hatchery-origin Chinook (100%). Age-2 and 3 natural-origin fish collectively made up 15% of the broodstock (Table 7.2). Age-3 and 6 hatchery-origin Chinook collectively made up 11% of the broodstock (Table 7.2).

Table 7.2. Percent of hatchery and wild summer Chinook of different ages (total age) collected from broodstock for the Methow/Okanogan programs, 1991-2009.

Return Year	Origin	Total age				
		2	3	4	5	6
1991	Wild	0.5	6.8	35.1	55.4	2.2
	Hatchery	0.5	5.1	36.2	49.0	9.2
1992	Wild	0.0	13.1	36.2	50.7	0.0
	Hatchery	0.0	0.0	0.0	0.0	0.0
1993	Wild	0.0	3.9	75.3	20.8	0.0
	Hatchery	0.0	1.0	85.9	13.1	0.0
1994	Wild	3.1	9.7	26.3	60.3	0.6
	Hatchery	0.0	14.7	11.3	74.0	0.0
1995	Wild	0.0	4.6	15.2	75.6	4.6
	Hatchery	0.0	0.4	13.0	25.6	61.0
1996	Wild	0.0	8.4	56.6	30.4	4.6
	Hatchery	0.0	3.0	31.0	47.0	19.0
1997	Wild	1.0	9.3	52.9	34.8	2.0
	Hatchery	0.0	20.7	10.8	62.0	6.5
1998	Wild	2.0	14.1	54.8	29.1	0.0
	Hatchery	2.3	18.5	56.6	15.9	6.7

Return Year	Origin	Total age				
		2	3	4	5	6
1999	Wild	4.7	5.1	53.7	36.0	0.5
	Hatchery	0.3	3.6	28.0	66.1	2.0
2000	Wild	0.6	14.0	28.7	56.1	0.6
	Hatchery	0.0	27.0	14.3	54.3	4.3
2001	Wild	7.1	26.0	52.0	11.8	3.1
	Hatchery	0.3	19.8	68.1	9.5	2.3
2002	Wild	0.4	17.4	66.0	16.2	0.0
	Hatchery	0.0	2.4	39.4	58.2	0.0
2003	Wild	0.7	3.9	65.9	29.5	0.0
	Hatchery	0.9	5.6	18.5	69.4	5.6
2004	Wild	0.8	15.3	11.6	72.1	0.2
	Hatchery	0.0	6.7	53.3	33.3	6.7
2005	Wild	0.0	17.2	69.9	11.0	1.9
	Hatchery	0.0	1.0	40.0	50.0	0.0
2006	Wild	1.6	3.0	41.0	52.9	1.5
	Hatchery	0.0	16.7	25.0	50.0	8.3
2007	Wild	1.8	15.3	8.2	70.2	4.5
	Hatchery	0.0	0.0	21.1	57.9	21.0
2008	Wild	0.3	17.1	67.8	13.6	1.2
	Hatchery	0.0	2.6	52.7	42.1	2.6
2009	Wild	1.3	10.0	68.3	20.4	0.0
	Hatchery	0.0	0.0	0.0	100.0	0.0
Average	***Wild***	***1.4***	***11.3***	***46.6***	***39.3***	***1.4***
	Hatchery	***0.2***	***7.8***	***31.9***	***46.2***	***8.2***

Mean lengths of natural-origin summer Chinook of a given age differed little between 2008 and 2009 (Table 7.3). Average fork lengths for age-5 natural-origin adults were 20 cm longer than that of age-5 hatchery fish (Table 7.3). These differences may be related to the small sample size of hatchery-origin fish (i.e., few hatchery fish were included in the broodstock).

Table 7.3. Mean fork length (cm) at age (total age) of hatchery and wild Methow/Okanogan summer Chinook collected from broodstock for the Methow/Okanogan programs, 1991-2009; N = sample size and SD = 1 standard deviation.

Return year	Origin	Summer Chinook fork length (cm)														
		Age-2			Age-3			Age-4			Age-5			Age-6		
		Mean	N	SD	Mean	N	SD	Mean	N	SD	Mean	N	SD	Mean	N	SD
1991	Wild	47	1	-	68	15	6	82	78	10	94	123	8	97	5	5
	Hatchery	47	1	-	49	10	6	78	71	5	91	96	8	96	18	6
1992	Wild	-	0	-	55	9	5	69	25	6	78	35	6	-	0	-
	Hatchery	-	0	-	-	0	-	-	0	-	-	0	-	-	0	-

Return year	Origin	Summer Chinook fork length (cm)														
		Age-2			Age-3			Age-4			Age-5			Age-6		
		Mean	N	SD	Mean	N	SD	Mean	N	SD	Mean	N	SD	Mean	N	SD
1993	Wild	-	0	-	72	3	4	86	58	7	98	16	5	-	0	-
	Hatchery	-	0	-	42	1	-	76	85	8	88	13	6	-	0	-
1994	Wild	42	10	6	51	31	7	80	84	9	93	193	8	104	2	13
	Hatchery	-	0	-	49	38	5	76	29	7	88	191	7	-	0	-
1995	Wild	-	0	-	67	6	8	79	20	9	96	99	5	94	6	5
	Hatchery	-	0	-	52	1	-	73	32	9	89	63	9	95	150	8
1996	Wild	-	0	-	68	22	9	83	149	8	95	80	7	101	12	5
	Hatchery	-	0	-	52	7	10	77	72	7	90	109	8	100	44	7
1997	Wild	36	2	6	60	19	7	85	108	8	96	71	7	98	4	11
	Hatchery	-	0	-	45	63	5	71	33	9	92	189	7	97	20	7
1998	Wild	43	4	6	59	23	6	83	107	7	96	58	7	-	0	-
	Hatchery	42	8	7	50	64	6	74	190	8	92	54	8	98	23	5
1999	Wild	38	10	3	64	11	8	82	115	8	96	77	6	104	1	-
	Hatchery	37	1	-	53	11	9	75	92	7	91	204	6	98	6	5
2000	Wild	39	1	-	66	23	7	83	47	6	96	92	5	95	1	-
	Hatchery	-	0	-	54	100	7	78	53	8	93	201	6	99	16	6
2001	Wild	40	9	3	65	33	8	87	66	8	93	15	5	97	4	16
	Hatchery	44	1	-	51	79	7	78	271	8	93	38	7	102	9	5
2002	Wild	56	1	-	65	44	7	88	167	6	100	41	7	-	0	-
	Hatchery	-	0	-	45	6	5	76	100	7	95	148	5	-	0	-
2003	Wild	43	3	6	61	16	6	87	268	7	99	120	6	-	0	-
	Hatchery	49	1	-	55	6	9	73	20	8	91	75	7	102	6	9
2004	Wild	51	4	4	67	78	6	81	59	6	97	368	7	99	1	-
	Hatchery	-	0	-	52	1	-	70	8	5	97	5	8	109	1	-
2005	Wild	-	0	-	68	89	6	83	363	8	94	57	6	101	10	7
	Hatchery	-	0	-	55	1	-	70	4	4	89	5	4	-	0	-
2006	Wild	48	9	3	69	16	4	88	222	7	97	286	6	97	8	6
	Hatchery	-	0	-	52	2	0	80	3	3	88	6	7	94	1	-
2007	Wild	50	8	6	69	69	9	85	37	8	98	317	6	96	20	8
	Hatchery	-	0	-	-	0	-	70	4	2	94	11	7	91	4	18
2008	Wild	52	1	-	70	67	6	87	265	6	95	53	7	103	5	7
	Hatchery	-	0	-	55	1	-	79	20	5	89	16	7	104	1	-
2009	Wild	49	7	6	69	54	7	91	368	6	99	110	6	-	0	-
	Hatchery	-	0	-	-	0	-	-	0	-	79	1	-	-	0	-

Sex Ratios

Male summer Chinook in the 2008 broodstock made up about 49% of the adults collected, resulting in an overall male to female ratio of 0.94:1.00 (Table 7.4.). In 2009, males made up about 47% of the adults collected, resulting in an overall male to female ratio of 0.89:1.00 (Table

7.4). The ratio for both 2008 and 2009 broodstock was below the assumed 1:1 ratio goal in the broodstock protocol.

Table 7.4. Numbers of male and female wild and hatchery summer Chinook collected for broodstock at Wells Dam for the Methow/Okanogan programs, 1991-2009. Ratios of males to females are also provided.

Return year	Number of wild summer Chinook			Number of hatchery summer Chinook			Total M/F ratio
	Males (M)	Females (F)	M/F	Males (M)	Females (F)	M/F	
1989[a]	752	667	1.13:1.00	181	160	1.13:1.00	1.13:1.00
1990[a]	381	482	0.79:1.00	95	120	0.79:1.00	0.79:1.00
1991[a]	443	559	0.79:1.00	151	191	0.79:1.00	0.79:1.00
1992[a]	349	318	1.10:1.00	38	35	1.09:1.00	1.10:1.00
1993[a]	513	300	1.71:1.00	293	171	1.71:1.00	1.71:1.00
1994	205	180	1.14:1.00	165	101	1.63:1.00	1.32:1.00
1995	103	149	0.69:1.00	158	197	0.80:1.00	0.75:1.00
1996	178	138	1.29:1.00	132	102	1.29:1.00	1.29:1.00
1997	102	112	0.91:1.00	174	134	1.30:1.00	1.12:1.00
1998	130	109	1.19:1.00	263	85	3.09:1.00	2.03:1.00
1999	138	110	1.25:1.00	161	146	1.10:1.00	1.17:1.00
2000	82	102	0.80:1.00	243	130	1.87:1.00	1.40:1.00
2001	89	46	1.93:1.00	311	112	2.78:1.00	2.53:1.00
2002	166	104	1.60:1.00	149	136	1.10:1.00	1.31:1.00
2003	255	194	1.31:1.00	61	51	1.20:1.00	1.29:1.00
2004	263	278	0.95:1.00	12	5	2.40:1.00	0.97:1.00
2005	365	186	1.96:1.00	6	6	1.00:1.00	1.93:1.00
2006	287	292	0.98:1.00	9	3	3.00:1.00	1.00:1.00
2007	228	276	0.83:1.00	11	8	1.38:1.00	0.84:1.00
2008	210	208	1.01:1.00	13	28	0.46:1.00	0.94:1.00
2009	261	292	0.89:1.00	2	3	0.67:1.00	0.89:1.00
Total[b]	***2,857***	***2,776***	***1.03:1.00***	***1,870***	***1,247***	***1.50:1.00***	***1.17:1.00***

[a] Numbers and male to female ratios were derived from the aggregate population collected at Wells Fish Hatchery volunteer channel and left- and right-ladder traps at Wells Dam.

[b] Total values were derived from 1994-present data to exclude aggregate population bias from 1989-1993 returns.

Fecundity

Fecundities for the 2008 and 2009 summer Chinook broodstock averaged 4,787 and 5,115 eggs per female, respectively (Table 7.5). These values are close to the overall average of 4,985 eggs per female. Mean observed fecundity for the 2008 return was slightly below the expected fecundity of 5,000 eggs per female assumed in the broodstock protocol; the 2009 return was slightly above the broodstock protocol.

Table 7.5. Mean fecundity of wild, hatchery, and all female summer Chinook collected for broodstock at Wells Dam for the Methow/Okanogan programs, 1989-2009; NA = not available.

Return year	Mean fecundity		
	Wild	Hatchery	Total
1989*	NA	NA	4,750
1990*	NA	NA	4,838
1991*	NA	NA	4,819
1992*	NA	NA	4,804
1993*	NA	NA	4,849
1994*	NA	NA	5,907
1995*	NA	NA	4,930
1996*	NA	NA	4,870
1997	5,166	5,296	5,237
1998	5,043	4,595	4,833
1999	4,897	4,923	4,912
2000	5,122	5,206	5,170
2001	5,040	4,608	4,735
2002	5,306	5,258	5,279
2003	5,090	4,941	5,059
2004	5,130	5,118	5,130
2005	4,545	4,889	4,553
2006	4,854	4,824	4,854
2007	5,265	5,093	5,260
2008	4,814	4,588	4,787
2009	5,115	-	5,115
Average	***5,030***	***4,945***	***4,985***

* Individual fecundities were not assigned to females until 1997 brood.

7.2 Hatchery Rearing

Rearing History

Number of eggs taken

Based on the unfertilized egg-to-release survival standard of 81%, a total of 493,827 eggs are needed to meet the program release goal of 400,000 smolts. From 1989 through 2009, the egg take goal was reached in seven of those years (Table 7.6).

Table 7.6. Numbers of eggs taken from summer Chinook broodstock collected at Wells Dam for the Methow/Okanogan programs, 1989-2009.

Return year	Number of eggs taken
1989	482,800
1990	464,097
1991	586,594

Return year	Number of eggs taken
1992	486,260
1993	531,490
1994	595,390
1995	491,000
1996	448,000
1997	401,162
1998	389,346
1999	483,726
2000	403,268
2001	279,272
2002	466,530
2003	473,681
2004	537,210
2005	305,826
2006	509,334
2007	549,802
2008	441,778
2009	560,602
Average	***470,818***

Number of acclimation days

Rearing of the 2008 brood Methow summer Chinook was similar to previous years with fish being held on well water before being transferred to Carlton Pond for final acclimation on Methow River water in March 2010 (Table 7.7). Groups of the 1994 and 1995 broods were reared for longer durations at Methow FH on Methow River water.

Table 7.7. Number of days Methow summer Chinook were acclimated at Carlton Pond, brood years 1989-2008.

Brood year	Release year	Transfer date	Release date	Number of days
1989	1991	15-Mar	6-May	52
1990	1992	26-Feb	28-Apr	61
1991	1993	10-Mar	23-Apr	44
1992	1994	4-Mar	21-Apr	48
1993	1995	18-Mar	2-May	45
1994	1996	25-Sep	28-Apr	215
		19-Mar	28-Apr	40
1995	1997	22-Oct	8-Apr	168
		19-Mar	22-Apr	34

Brood year	Release year	Transfer date	Release date	Number of days
1996	1998	9-Mar	14-Apr	36
1997	1999	10-Mar	20-Apr	41
1998	2000	19-Mar	2-May	44
1999	2001	18-Mar	18-Apr	31
2000	2002	28-Mar	1-May	34
2001	2003	27-Mar	24-Apr	28
2002	2004	16-Mar	24-Apr	39
2003	2005	18-Mar	21-Apr	34
2004	2006	12-Mar	22-Apr	41
2005	2007	12-Mar	15-Apr – 8-May	34-57
2006	2008	4-7-Mar	16-Apr – 2 May	40-59
2007	2009	18-24-Mar	21-Apr	28-34
2008	2010	4-5, 8-9-Mar	4-21-Apr	33-50

Release Information

Numbers released

The 2008 brood Methow summer Chinook program achieved 99.4% of the 400,000 target goal with about 397,554 fish being forcibly released on 4-21 April 2010 (Table 7.8).

Table 7.8. Numbers of Methow summer Chinook smolts released from the hatchery, brood years 1989-2008. The release target for Methow summer Chinook is 400,000 smolts.

Brood year	Release year	CWT mark rate	Number of smolts released
1989	1991	0.8529	420,000
1990	1992	0.9485	391,650
1991	1993	0.6972	540,900
1992	1994	0.9752	402,641
1993	1995	0.4623	433,375
1994	1996	0.9851	406,560
1995	1997	0.9768	353,182
1996	1998	0.9221	298,844
1997	1999	0.9884	384,909
1998	2000	0.9429	205,269
1999	2001	0.9955	424,363
2000	2002	0.9928	336,762
2001	2003	0.9902	248,595
2002	2004	0.9913	399,975
2003	2005	0.9872	354,699

Brood year	Release year	CWT mark rate	Number of smolts released
2004	2006	0.9848	400,579
2005	2007	0.9897	263,723
2006	2008	0.9783	419,734
2007	2009	0.9837	433,256
2008	2010	0.9394	397,554
Average		***0.9292***	***375,829***

Numbers tagged

The 2008 brood Methow summer Chinook were 93.9% CWT and adipose fin-clipped (Table 7.8).

In 2010, a total of about 5,050 summer Chinook (brood year 2009) were PIT tagged at Eastbank Fish Hatchery on 1-2 September. Fish were not fed during tagging or for two days before and after tagging. Fish averaged 78 mm in length and 5.0 g at time of tagging. As of the end of January 2011, a total of 11 tagged Chinook have died and nine others have shed their tags, leaving 5,030 tagged summer Chinook alive at the end of the month.

Table 7.9 summarizes the number of hatchery summer Chinook that have been PIT-tagged and released into the Methow River.

Table 7.9. Summary of PIT-tagging activities for Methow hatchery summer Chinook, brood years 2008-2009.

Brood year	Release year	Number of fish tagged	Number of tagged fish that died	Number of tags shed	Number of tagged fish released
2008	2010	10,100	4	0	10,096
2009	2011	5,050	NA	NA	NA

Fish size and condition at release

Fish were volitionally released as yearling smolts during the period 4-21 April 2010. Size at release of the acclimated population was 88.1% and 92.5% of the respective target fork length and weight goals (Table 7.10). This brood year exceeded the CV of length goal by 58%.

Table 7.10. Mean lengths (FL, mm), weight (g and fish/pound), and coefficient of variation (CV) of Methow summer Chinook smolts released from the hatchery, brood years 1991-2008. Size targets are provided in the last row of the table.

Brood year	Release year	Fork length (mm)		Mean weight	
		Mean	CV	Grams (g)	Fish/pound
1991	1993	152	13.6	40.3	11
1992	1994	145	16.0	37.2	12
1993	1995	154	8.6	37.1	12
1994	1996	163	8.2	48.2	9
1995	1997	141	9.6	37.0	12

Brood year	Release year	Fork length (mm)		Mean weight	
		Mean	CV	Grams (g)	Fish/pound
1996	1998	199	13.1	105.1	4
1997	1999	153	7.6	39.5	12
1998	2000	164	8.7	51.7	9
1999	2001	153	9.3	41.5	11
2000	2002	170	10.2	54.2	8
2001	2003	167	7.4	52.7	9
2002	2004	148	13.1	35.7	13
2003	2005	148	10.1	35.5	13
2004	2006	142	9.8	31.1	15
2005	2007	158	15.0	42.2	11
2006	2008	156	18.0	42.8	11
2007	2009	138	21.0	32.1	14
2008	2010	155	14.2	42.0	11
Targets		***176***	***9.0***	***45.4***	***10***

Survival Estimates

Overall survival of the Methow summer Chinook from green (unfertilized) egg-to-release was above the standard set for the program (Table 7.11). This high survival was because of all but one (unfertilized egg-eyed) of the survival categories exceeding the standards set by the program. Currently, it is unknown if gamete viability is gender biased or is uniform between sexes and more influenced by between-year environmental variations.

It is important to note that the Methow summer Chinook program typically receives progeny from the highest ELISA females, while the lowest titer progeny are reserved for the Okanogan program. The inability to effectively manage bacterial kidney disease at Similkameen Pond during the winter months precludes an even mix of progeny for a given brood year between the two programs. As a result, in some years poor survival performance at any level may be more directly related to this procedure than a function of the overall program.

Table 7.11. Hatchery life-stage survival rates (%) for Methow summer Chinook, brood years 1989-2008. Survival standards or targets are provided in the last row of the table.

Brood year	Collection to spawning		Unfertilized egg-eyed	Eyed egg-ponding	30 d after ponding	100 d after ponding	Ponding to release	Transport to release	Unfertilized egg-release
	Female	Male							
1989[a]	89.8	99.5	89.9	96.7	99.7	99.4	73.3	98.5	87.0
1990[a]	93.9	99.0	84.9	97.1	81.2	80.6	97.7	99.5	84.4
1991[a]	93.1	95.5	88.2	98.0	99.4	99.1	97.5	99.6	92.2
1992[a]	96.9	99.0	87.8	98.0	99.9	99.9	90.9	98.3	82.8
1993[a]	82.2	99.4	85.4	97.6	99.8	99.5	92.0	99.4	81.5
1994	96.1	90.0	86.6	100.0	98.1	97.4	73.1	99.1	68.3
1995	91.9	96.2	98.2	84.1	96.5	96.2	92.7	89.6	71.9

Brood year	Collection to spawning		Unfertilized egg-eyed	Eyed egg-ponding	30 d after ponding	100 d after ponding	Ponding to release	Transport to release	Unfertilized egg-release
	Female	Male							
1996	95.4	98.1	83.2	100.0	97.7	96.9	86.5	89.0	66.7
1997	91.9	94.6	86.1	98.4	98.7	98.3	98.8	99.7	95.9
1998	84.0	96.2	54.1	98.0	99.4	98.9	96.6	99.9	52.7
1999	98.8	98.7	92.9	96.9	98.0	97.6	96.9	99.9	87.7
2000	90.5	96.9	89.2	98.1	98.5	98.3	94.6	94.4	83.5
2001	96.2	92.3	89.1	97.6	97.2	97.1	97.5	99.8	89.0
2002	97.1	98.1	88.3	99.9	97.7	97.5	96.7	99.9	85.7
2003	96.7	97.5	82.8	98.2	99.7	99.2	93.7	99.9	74.9
2004	93.6	98.2	84.0	97.8	99.6	99.2	98.3	98.5	74.6
2005	97.0	89.6	88.0	95.5	99.6	98.9	96.6	99.9	86.2
2006	92.9	89.5	86.3	98.3	99.6	98.7	97.2	99.5	82.4
2007	92.6	99.6	84.1	98.5	99.7	99.5	98.9	99.8	81.9
2008	99.6	97.9	91.9	99.5	99.3	98.9	98.5	99.9	90.0
Standard	***90.0***	***85.0***	***92.0***	***98.0***	***97.0***	***93.0***	***90.0***	***95.0***	***81.0***

[a] Survival rates were calculated from aggregate population collected at Wells Fish Hatchery volunteer channel and left- and right-ladder traps at Wells Dam.

7.3 Disease Monitoring

Results of adult broodstock bacterial kidney disease (BKD) monitoring indicated that most females (99.6%) had ELISA values less than 0.199. All females had ELISA values less than 0.120, which means that none of the progeny need to be reared at densities not to exceed 0.06 fish per pound (Table 7.12).

Table 7.12. Proportion of bacterial kidney disease (BKD) titer groups for the Methow/Okanogan summer Chinook broodstock, brood years 1997-2010. Also included are the proportions to be reared at either 0.125 fish per pound or 0.060 fish per pound.

Brood year[a]	Optical density values by titer group				Proportion at rearing densities (fish per pound, fpp)	
	Very Low (≤ 0.099)	Low (0.1-0.199)	Moderate (0.2-0.449)	High (≥ 0.450)	≤ 0.125 fpp (<0.119)	≤ 0.060 fpp (>0.120)
1997	0.6267	0.1333	0.0622	0.1778	0.6844	0.3156
1998	0.9632	0.0184	0.0123	0.0061	0.9816	0.0184
1999	0.9444	0.0198	0.0238	0.0119	0.9643	0.0357
2000	0.7476	0.0952	0.0238	0.1333	0.8000	0.2000
2001	0.9801	0.0199	0.0000	0.0000	1.0000	0.0000
2002	0.9567	0.0130	0.0130	0.0173	0.9740	0.0260
2003	0.9620	0.0127	0.0169	0.0084	0.9747	0.0253
2004	0.9585	0.0151	0.0075	0.0189	0.9736	0.0264
2005	0.9884	0.0000	0.0000	0.0116	0.9884	0.0116

Brood year[a]	Optical density values by titer group				Proportion at rearing densities (fish per pound, fpp)	
	Very Low (≤ 0.099)	Low (0.1-0.199)	Moderate (0.2-0.449)	High (≥ 0.450)	≤ 0.125 fpp (<0.119)	≤ 0.060 fpp (>0.120)
2006	0.9962	0.0038	0.0000	0.0000	0.9962	0.0038
2007	0.9202	0.0266	0.0152	0.0380	0.9354	0.0646
2008	1.0000	0.0000	0.0000	0.0000	1.0000	0.0000
2009	0.9891	0.0073	0.0037	0.0000	0.9927	0.0073
2010	0.9960	0.0040	0.0000	0.0000	1.0000	0.0000
Average	*0.9307*	*0.0264*	*0.0127*	*0.0302*	*0.9475*	*0.0525*

[a] Individual ELISA samples were not collected before the 1997 brood.

7.4 Spawning Surveys

Surveys for Methow summer Chinook redds were conducted from late September to mid-November, 2010, in the Methow River. Total redd counts (not peak counts) were conducted in the river (see Appendix K for more details).

Redd Counts

A total of 887 summer Chinook redds were counted in the Methow River in 2010 (Table 7.13). This was higher than the overall average of 614 redds.

Table 7.13. Total number of redds counted in the Methow River, 1989-2010.

Survey year	Total redd count
1989	149*
1990	418*
1991	153
1992	107
1993	154
1994	310
1995	357
1996	181
1997	205
1998	225
1999	448
2000	500
2001	675
2002	2,013
2003	1,624
2004	973
2005	874
2006	1,353

Survey year	Total redd count
2007	620
2008	599
2009	692
2010	887
Average	***614***

* Total counts based on expanded aerial counts.

Redd Distribution

Summer Chinook redds were not evenly distributed among the seven reaches in the Methow River. Most redds (73%) were located in reaches downstream from the town of Twisp and in Reach 5 between Methow Valley Irrigation Diversion (MVID) and the Winthrop Bridge (Table 7.14; Figure 7.1). Few summer Chinook spawned upstream from the Winthrop Bridge in Reaches 6 and 7.

Table 7.14. Total number of summer Chinook redds counted in different reaches on the Methow River during September through early November, 2010. Reach codes are described in Table 2.11.

Survey reach	Total redd count	Percent
Methow 1	166	18.7
Methow 2	244	27.5
Methow 3	236	26.6
Methow 4	103	11.6
Methow 5	129	14.5
Methow 6	5	0.6
Methow 7	4	0.5
Totals	***887***	***100.0***

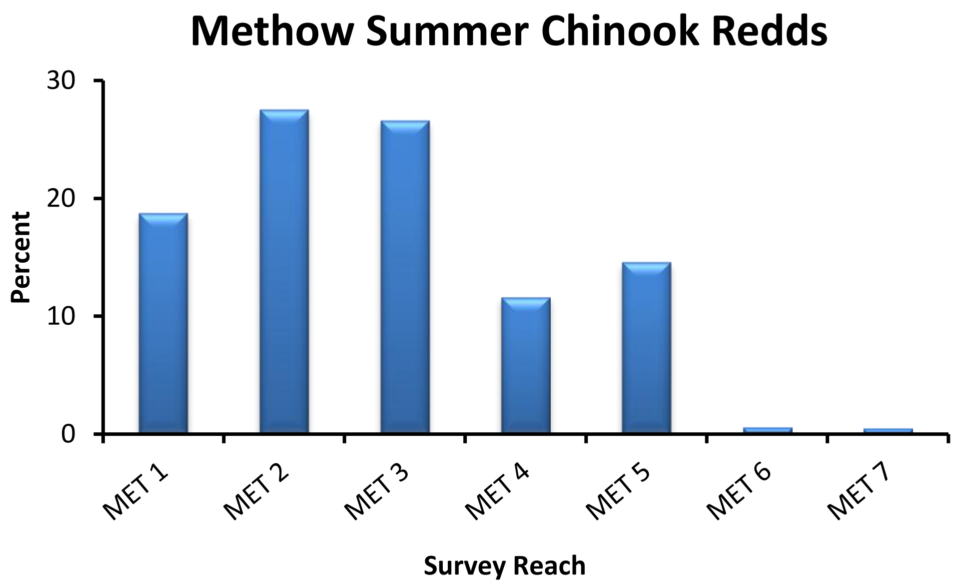


Figure 7.1. Percent of the total number of summer Chinook redds counted in different reaches on the Methow River during September through mid-November, 2010. Reach codes are described in Table 2.11.

Spawn Timing

Spawning in 2010 began the last week of September, peaked the second week of October, and ended after the second week of November (Figure 7.2). Stream temperatures in the Methow River, when spawning began, varied from 6.5-12.0°C. Peak spawning occurred in the upper reaches of the Methow River during the second week of October and in the lower reaches the following week.

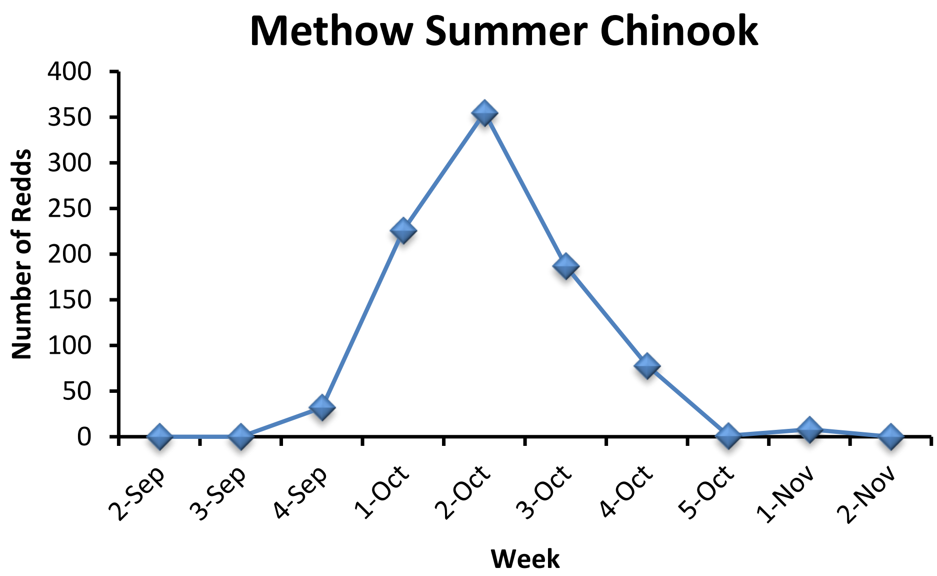


Figure 7.2. Number of new summer Chinook redds counted during different weeks in the Methow River, September through mid-November 2010.

Spawning Escapement

Spawning escapement for Methow summer Chinook was calculated as the total number of redds times the fish per redd ratio estimated from fish sampled at Wells Dam. The estimated fish per redd ratio for Methow summer Chinook in 2010 was 2.81. Multiplying this ratio by the number of redds counted in the Methow River resulted in a total spawning escapement of 2,492 summer Chinook (Table 7.15).

Table 7.15. Spawning escapements for summer Chinook in the Methow River for return years 1989-2010.

Return year	Fish/Redd	Redds	Total spawning escapement
1989*	3.30	149	492
1990*	3.40	418	1,421
1991*	3.70	153	566
1992*	4.30	107	460
1993*	3.30	154	508
1994*	3.50	310	1,085
1995*	3.40	357	1,214
1996*	3.40	181	615
1997*	3.40	205	697
1998	3.00	225	675
1999	2.20	448	986
2000	2.40	500	1,200
2001	4.10	675	2,768

Return year	Fish/Redd	Redds	Total spawning escapement
2002	2.30	2,013	4,630
2003	2.42	1,624	3,930
2004	2.25	973	2,189
2005	2.93	874	2,561
2006	2.02	1,353	2,733
2007	2.20	620	1,364
2008	3.25	599	1,947
2009	2.54	692	1,758
2010	2.81	887	2,492
Average	***3.01***	***614***	***1,650***

* Spawning escapement was calculated using the "Modified Meekin Method" (i.e., 3.1 x jack multiplier).

7.5 Carcass Surveys

Surveys for Methow summer Chinook carcasses were conducted during late September to mid-November, 2010, in the Methow River (see Appendix K for more details).

Number sampled

A total of 577 summer Chinook carcasses were sampled during September through mid-November in the Methow River (Table 7.15).

Table 7.15. Numbers of summer Chinook carcasses sampled within each survey reach on the Methow River, 1991-2010. Reach codes are described in Table 2.11.

Survey year	Number of summer Chinook carcasses							
	M-1	M-2	M-3	M-4	M-5	M-6	M-7	Total
1991	0	12	8	4	2	0	0	**26**
1992	8	8	19	0	17	1	0	**53**
1993	19	25	14	2	5	0	0	**65**
1994[a]	43	33	20	5	13	0	0	**114**
1995	14	33	58	7	7	0	0	**119**
1996	6	30	46	5	2	0	0	**89**
1997	6	12	38	2	19	1	0	**78**
1998	90	84	99	17	30	0	0	**320**
1999	47	144	232	32	37	12	2	**506**
2000	62	118	105	9	99	5	0	**398**
2001	392	275	88	14	76	11	1	**857**
2002	551	318	518	164	219	34	10	**1,814**
2003	115	383	317	115	128	5	0	**1,063**
2004	40	173	187	82	92	2	1	**577**
2005	154	173	182	42	112	3	0	**666**
2006	121	149	111	56	146	3	1	**587**
2007	135	131	108	27	55	0	0	**456**

Survey year	Number of summer Chinook carcasses							
	M-1	**M-2**	**M-3**	**M-4**	**M-5**	**M-6**	**M-7**	**Total**
2008	64	128	197	33	57	3	0	**482**
2009	144	158	159	36	94	0	0	**591**
2010	105	180	185	38	63	5	1	**577**
Average	***106***	***128***	***135***	***35***	***64***	***4***	***1***	***472***

[a] An additional 113 carcasses were sampled, but reach was not identified.

Carcass Distribution and Origin

Summer Chinook carcasses were not evenly distributed among reaches within the Methow River in 2010 (Table 7.15; Figure 7.3). Most of the carcasses in the Methow River were found downstream from Twisp.

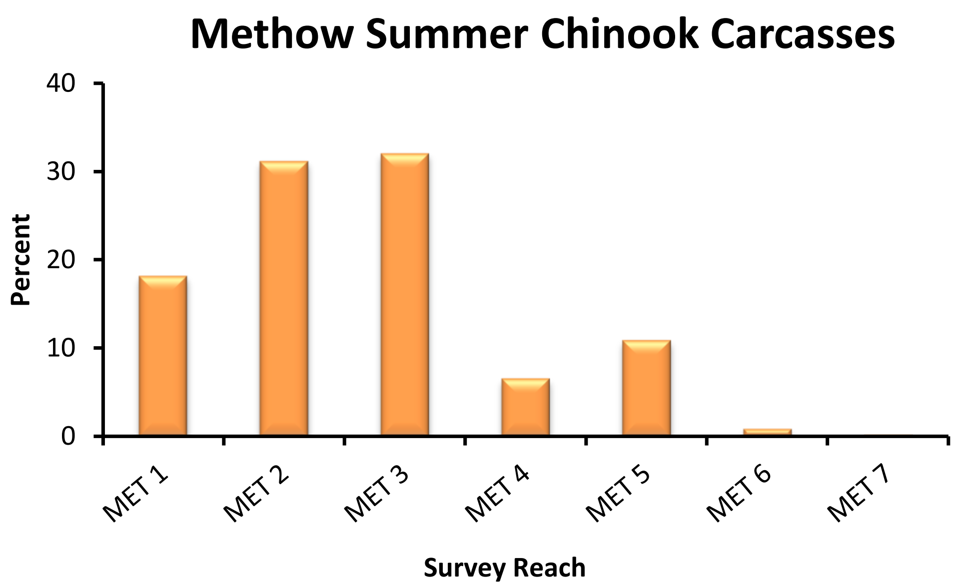


Figure 7.3. Percent of summer Chinook carcasses sampled within different reaches on the Methow River during September through mid-November, 2010. Reach codes are described in Table 2.11.

Numbers of wild and hatchery-origin summer Chinook carcasses sampled in 2010 will be available after analysis of CWTs and scales. Based on the available data (1991-2009), hatchery and wild summer Chinook carcasses were not distributed equally among the reaches in the Methow River (Table 7.16). A larger percentage of hatchery carcasses occurred in the lower reaches, while a larger percentage of wild summer Chinook carcasses occurred in upstream reaches (Figure 7.4).

Table 7.16. Numbers of wild and hatchery summer Chinook carcasses sampled within different reaches on the Methow River, 1991-2010.

Survey year	Origin	Survey reach							Total
		M-1	M-2	M-3	M-4	M-5	M-6	M-7	
1991	Wild	0	12	8	4	2	0	0	**26**
	Hatchery	0	0	0	0	0	0	0	**0**
1992	Wild	8	8	19	0	17	1	0	**53**
	Hatchery	0	0	0	0	0	0	0	**0**
1993	Wild	11	15	9	0	3	0	0	**38**
	Hatchery	8	7	5	2	2	0	0	**24**
1994	Wild	21	17	8	4	9	0	0	**59**
	Hatchery	20	15	11	0	3	0	0	**49**
1995	Wild	6	9	27	7	5	0	0	**54**
	Hatchery	7	24	25	0	1	0	0	**57**
1996	Wild	1	20	29	4	2	0	0	**56**
	Hatchery	5	7	11	1	0	0	0	**24**
1997	Wild	5	5	28	1	17	0	0	**56**
	Hatchery	1	4	7	1	2	1	0	**16**
1998	Wild	41	46	70	9	23	0	0	**189**
	Hatchery	48	36	28	6	5	0	0	**123**
1999	Wild	27	79	110	14	17	4	2	**253**
	Hatchery	15	57	102	17	13	7	0	**211**
2000	Wild	23	78	74	7	72	3	0	**257**
	Hatchery	37	33	20	1	16	2	0	**109**
2001	Wild	49	102	54	9	66	11	1	**292**
	Hatchery	330	157	32	4	6	0	0	**529**
2002	Wild	124	163	362	129	183	34	9	**1,004**
	Hatchery	412	141	138	24	22	0	1	**738**
2003	Wild	33	123	176	63	85	3	0	**483**
	Hatchery	80	122	127	38	36	2	0	**405**
2004	Wild	14	108	144	61	73	1	0	**401**
	Hatchery	24	52	28	17	12	1	1	**135**
2005	Wild	62	99	133	33	107	3	0	**437**
	Hatchery	92	74	49	9	5	0	0	**229**
2006	Wild	68	103	83	49	131	3	1	**438**
	Hatchery	53	46	28	7	15	0	0	**149**
2007	Wild	52	71	62	19	45	0	0	**249**
	Hatchery	93	60	47	9	10	0	0	**219**
2008	Wild	15	69	158	29	54	2	0	**327**
	Hatchery	49	59	39	4	3	1	0	**155**
2009	Wild	54	91	104	28	86	0	0	**363**
	Hatchery	90	67	55	8	8	0	0	**228**
Average	***Wild***	***32***	***64***	***87***	***25***	***52***	***3***	***1***	***265***

Survey year	Origin	Survey reach							Total
		M-1	M-2	M-3	M-4	M-5	M-6	M-7	
	Hatchery	*72*	*51*	*40*	*8*	*8*	*1*	*0*	*179*

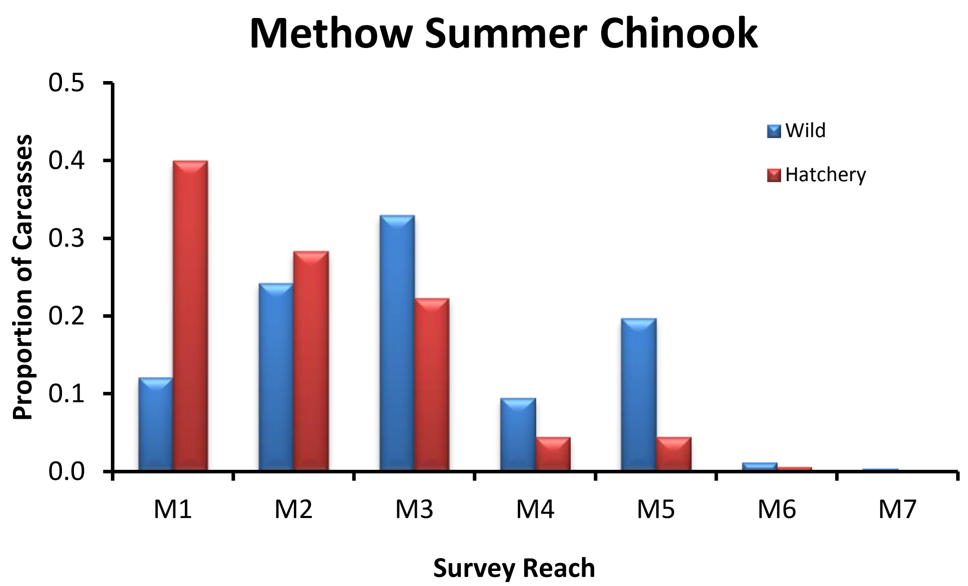


Figure 7.4. Distribution of wild and hatchery produced carcasses in different reaches on the Methow River, 1993-2009. Reach codes are described in Table 2.11.

Sampling Rate

Overall, 23% of the total spawning escapement of summer Chinook in the Methow Basin was sampled in 2010 (Table 7.17). Sampling rates among survey reaches varied from 9 to 36%.

Table 7.17. Number of redds and carcasses, total spawning escapement, and sampling rates for summer Chinook in the Methow Basin, 2010. Reach codes are described in Table 2.11.

Survey reach	Total number of redds	Total number of carcasses	Total spawning escapement	Sampling rate
Methow 1	166	105	466	0.23
Methow 2	244	180	686	0.26
Methow 3	236	185	663	0.28
Methow 4	103	38	289	0.13
Methow 5	129	63	363	0.17
Methow 6	5	5	14	0.36
Methow 7	4	1	11	0.09
Total	***887***	***577***	***2,492***	***0.23***

Length Data

Mean lengths (POH, cm) of male and female summer Chinook carcasses sampled during surveys on the Methow River in 2010 are provided in Table 7.18. The average size of males and females sampled in the Methow River were 62 cm and 70 cm, respectively.

Table 7.18. Mean lengths (postorbital-to-hypural length; cm) and standard deviations (in parentheses) of male and female summer Chinook carcasses sampled in different reaches on the Methow River, 2010. Reach codes are described in Table 2.11.

Stream/watershed	Mean length (cm)	
	Male	Female
Methow 1	59.5 (9.1)	69.3 (6.9)
Methow 2	60.2 (10.4)	71.4 (5.3)
Methow 3	62.9 (9.8)	67.8 (6.2)
Methow 4	64.1 (9.8)	71.5 (7.5)
Methow 5	67.5 (8.5)	71.7 (4.7)
Methow 6	73.3 (2.3)	70.0 (1.4)
Methow 7	-	68.0 (0.0)
Total	***62.0 (10.0)***	***69.8 (6.1)***

7.6 Life History Monitoring

Life history characteristics of Methow summer Chinook were assessed by examining carcasses on spawning grounds and fish collected or examined at broodstock collection sites, and by reviewing tagging data and fisheries statistics.

Migration Timing

Migration timing of hatchery and wild Methow/Okanogan summer Chinook was determined from broodstock data collected at Wells Dam. Counting of summer/fall Chinook at Wells Dam occurs from 29 June to 15 November. Broodstock collection at the Dam occurs from early July (week 27) to mid-September (week 37) (Table 2.1). Based on broodstock sampling in 2010, both wild and hatchery summer Chinook arrived at Wells Dam about the same time (Table 7.19). This was true throughout most of the migration period. This pattern was also observed when data were pooled for the 2007-2010 survey period.

Table 7.19. The week that 10%, 50% (median), and 90% of the wild and hatchery summer Chinook salmon passed Wells Dam, 2007-2010. The average week is also provided. Migration timing is based on collection of summer Chinook broodstock at Wells Dam.

Survey year	Origin	Methow/Okanogan Summer Chinook Migration Time (week)				Sample size
		10 Percentile	50 Percentile	90 Percentile	Mean	
2007	Wild	27	30	34	30	485
	Hatchery	27	30	33	30	433
2008	Wild	28	30	34	30	542
	Hatchery	28	30	36	31	884
2009	Wild	27	29	34	30	585

Survey year	Origin	Methow/Okanogan Summer Chinook Migration Time (week)				Sample size
		10 Percentile	50 Percentile	90 Percentile	Mean	
	Hatchery	27	29	33	29	708
2010	Wild	27	29	33	29	377
	Hatchery	27	29	32	29	801
Average	Wild	***27***	***29***	***34***	***30***	***1,989***
	Hatchery	***27***	***29***	***34***	***30***	***2,826***

Age at Maturity

Most of the wild and hatchery summer Chinook sampled during the period 1993-2009 in the Methow River were age-4 and 5 fish (total age) (Table 7.20; Figure 7.5). A higher percentage of age-4 wild Chinook returned to the basin than did age-4 hatchery Chinook. In contrast, a higher proportion of age-6 hatchery fish returned than did age-6 wild fish. Thus, a higher percentage of hatchery fish returned at an older age than did wild fish.

Table 7.20. Proportions of wild and hatchery summer Chinook of different ages (total age) sampled on spawning grounds in the Methow River, 1993-2009.

Survey year	Origin	Total age						Sample size
		2	3	4	5	6	7	
1993	Wild	0.00	0.05	0.34	0.58	0.03	0.00	38
	Hatchery	0.00	0.00	1.00	0.00	0.00	0.00	20
1994	Wild	0.01	0.02	0.53	0.44	0.00	0.00	101
	Hatchery	0.00	0.00	0.07	0.93	0.00	0.00	111
1995	Wild	0.00	0.02	0.07	0.89	0.02	0.00	54
	Hatchery	0.00	0.02	0.04	0.43	0.52	0.00	56
1996	Wild	0.00	0.04	0.46	0.41	0.09	0.00	56
	Hatchery	0.00	0.00	0.04	0.48	0.43	0.04	23
1997	Wild	0.00	0.00	0.36	0.63	0.02	0.00	56
	Hatchery	0.00	0.13	0.06	0.56	0.25	0.00	16
1998	Wild	0.00	0.13	0.52	0.34	0.00	0.00	188
	Hatchery	0.00	0.02	0.52	0.42	0.03	0.00	123
1999	Wild	0.00	0.02	0.59	0.39	0.01	0.00	253
	Hatchery	0.00	0.00	0.07	0.90	0.03	0.00	209
2000	Wild	0.00	0.05	0.15	0.80	0.00	0.00	257
	Hatchery	0.00	0.10	0.22	0.57	0.11	0.00	97
2001	Wild	0.01	0.15	0.59	0.24	0.02	0.00	292
	Hatchery	0.00	0.11	0.60	0.26	0.04	0.00	528
2002	Wild	0.00	0.04	0.66	0.29	0.00	0.00	1,004
	Hatchery	0.00	0.01	0.41	0.57	0.01	0.00	733
2003	Wild	0.00	0.01	0.43	0.55	0.00	0.00	483
	Hatchery	0.00	0.02	0.07	0.88	0.03	0.00	394

Survey year	Origin	Total age						Sample size
		2	3	4	5	6	7	
2004	Wild	0.00	0.04	0.08	0.86	0.01	0.00	401
	Hatchery	0.00	0.08	0.29	0.30	0.33	0.00	134
2005	Wild	0.00	0.03	0.58	0.34	0.05	0.00	410
	Hatchery	0.00	0.08	0.30	0.61	0.01	0.00	220
2006	Wild	0.00	0.02	0.18	0.78	0.02	0.00	379
	Hatchery	0.00	0.00	0.22	0.48	0.29	0.00	129
2007	Wild	0.02	0.08	0.19	0.64	0.07	0.00	209
	Hatchery	0.00	0.04	0.14	0.73	0.08	0.01	189
2008	Wild	0.02	0.11	0.72	0.14	0.01	0.00	302
	Hatchery	0.09	0.13	0.42	0.23	0.13	0.00	151
2009	Wild	0.01	0.08	0.42	0.49	0.00	0.00	334
	Hatchery	0.00	0.18	0.37	0.43	0.02	0.00	225
Average	***Wild***	***0.00***	***0.05***	***0.40***	***0.52***	***0.02***	***0.00***	***283***
	Hatchery	***0.01***	***0.05***	***0.28***	***0.52***	***0.14***	***0.00***	***198***

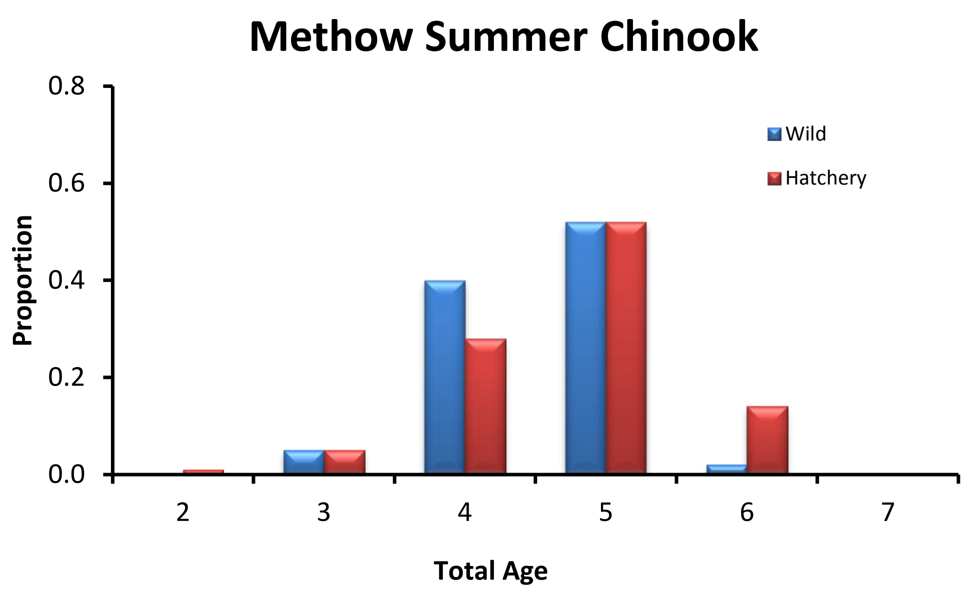


Figure 7.5. Proportions of wild and hatchery summer Chinook of different total ages sampled at broodstock collection sites and on spawning grounds in the Methow River for the combined years 1993-2009.

Size at Maturity

On average, hatchery summer Chinook were about 4 cm smaller than wild summer Chinook sampled in the Methow Basin (Table 7.21). This is interesting given that a slightly higher percentage of hatchery fish returned as age-6 fish than did wild fish. Future analyses will compare sizes of hatchery and wild fish of the same age groups and gender.

Table 7.21. Mean lengths (POH; cm) and variability statistics for wild and hatchery summer Chinook sampled in the Methow Basin, 1993-2009; SD = 1 standard deviation.

Survey year	Origin	Sample size	Summer Chinook length (POH; cm)			
			Mean	SD	Minimum	Maximum
1993	Wild	41	74	9	51	89
	Hatchery	24	62	8	36	80
1994	Wild	112	69	8	35	87
	Hatchery	114	67	5	43	77
1995	Wild	62	74	6	52	88
	Hatchery	57	73	7	46	85
1996	Wild	64	70	11	34	91
	Hatchery	23	72	7	58	85
1997	Wild	62	76	9	35	90
	Hatchery	16	68	15	33	87
1998	Wild	196	67	10	38	97
	Hatchery	123	63	10	37	87
1999	Wild	293	66	8	43	99
	Hatchery	211	66	7	26	89
2000	Wild	288	74	8	37	89
	Hatchery	109	68	12	24	87
2001	Wild	328	67	10	29	86
	Hatchery	529	63	10	31	87
2002	Wild	1,076	70	8	37	94
	Hatchery	738	67	9	33	87
2003	Wild	543	71	8	35	88
	Hatchery	405	69	8	35	89
2004	Wild	442	73	7	38	89
	Hatchery	135	65	12	34	85
2005	Wild	437	69	8	45	86
	Hatchery	229	64	9	36	79
2006	Wild	438	73	7	35	92
	Hatchery	149	69	8	38	91
2007	Wild	249	72	11	33	89
	Hatchery	219	69	9	22	84
2008	Wild	384	69	8	30	90
	Hatchery	210	63	15	23	86
2009	Wild	363	71	9	32	88
	Hatchery	228	63	12	30	83
Pooled	***Wild***	***5,378***	***71***	***9***	***29***	***99***
	Hatchery	***3,519***	***67***	***10***	***22***	***91***

Contribution to Fisheries

Most of the harvest on hatchery-origin Methow summer Chinook occurred in the Ocean (Table 7.22). Ocean harvest has made up 13% to 99% of all hatchery-origin Methow summer Chinook harvested. Brood years 1989 and 1998 provided the largest harvests, while brood years 1996 and 1999 provided the lowest.

Table 7.22. Estimated number and percent (in parentheses) of hatchery-origin Methow summer Chinook captured in different fisheries, brood years 1989-2004.

Brood year	Ocean fisheries	Columbia River Fisheries			Total
		Tribal	Commercial (Zones 1-5)	Recreational (sport)	
1989	1,057 (53)	884 (44)	0 (0)	66 (3)	2,007
1990	63 (61)	41 (39)	0 (0)	0 (0)	104
1991	12 (20)	49 (80)	0 (0)	0 (0)	61
1992	17 (55)	14 (45)	0 (0)	0 (0)	31
1993	14 (58)	8 (33)	2 (8)	0 (0)	24
1994	153 (81)	34 (18)	1 (1)	1 (1)	189
1995	77 (99)	0 (0)	1 (1)	0 (0)	78
1996	13 (93)	1 (7)	0 (0)	0 (0)	14
1997	221 (89)	7 (3)	0 (0)	21 (8)	249
1998	1,764 (83)	101 (5)	14 (1)	234 (11)	2,113
1999	2 (13)	13 (87)	0 (0)	0 (0)	15
2000	364 (71)	88 (17)	27 (5)	33 (6)	512
2001	320 (52)	97 (16)	43 (7)	160 (26)	620
2002	272 (48)	69 (17)	61 (11)	132 (24)	561
2003	54 (57)	17 (18)	7 (7)	17 (18)	95
2004	133 (67)	21 (11)	9 (5)	36 (18)	199

Straying

Stray rates were determined by examining CWTs recovered on spawning grounds within and outside the Methow Basin. Targets for strays based on return year (recovery year) and brood year should be less than 5%.

Rates of hatchery-origin Methow summer Chinook straying into basins outside the Methow have been very low (Table 7.23). Although a few hatchery-origin Methow summer Chinook have strayed into the Okanogan Basin, Entiat Basin, Chelan tailrace, and Hanford Reach, staying has consistently been less than 5%.

Table 7.23. Number and percent of spawning escapements within other non-target basins that consisted of hatchery-origin Methow summer Chinook, return years 1994-2007. For example, for return year 2002, 0.4% of the summer Chinook escapement in the Okanogan Basin consisted of hatchery-origin Methow summer Chinook. Percent strays should be less than 5%.

Return year	Wenatchee		Okanogan		Chelan		Entiat		Hanford Reach	
	Number	%	Number	%	Number	%	Number	%	Number	%
1994	0	0.0	72	1.8	-	-	-	-	-	-
1995	0	0.0	9	0.3	-	-	-	-	-	-
1996	0	0.0	0	0.0	-	-	-	-	-	-
1997	0	0.0	0	0.0	-	-	-	-	-	-
1998	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
1999	0	0.0	6	0.2	0	0.0	0	0.0	7	0.0
2000	0	0.0	3	0.1	0	0.0	0	0.0	0	0.0
2001	0	0.0	0	0.0	0	0.0	0	0.0	7	0.0
2002	0	0.0	54	0.4	0	0.0	0	0.0	0	0.0
2003	0	0.0	1	0.0	6	1.4	0	0.0	0	0.0
2004	0	0.0	7	0.1	3	0.7	0	0.0	0	0.0
2005	0	0.0	24	0.3	0	0.0	0	0.0	0	0.0
2006	0	0.0	12	0.1	0	0.0	0	0.0	0	0.0
2007	0	0.0	17	0.4	2	1.1	1	0.4	0	0.0
Total	***0***	***0.0***	***205***	***0.3***	***11***	***0.3***	***1***	***0.0***	***14***	***0.0***

On average, about 4.0% of the returns have strayed into non-target spawning areas, falling below the target of 5% (Table 7.24). Depending on brood year, percent strays into non-target spawning areas have ranged from 0-14.7%. Few (<2% on average) have strayed into non-target hatchery programs.

Table 7.24. Number and percent of hatchery-origin Methow summer Chinook that homed to target spawning areas and the target hatchery program, and number and percent that strayed to non-target spawning areas and non-target hatchery programs, by brood years 1989-2004. Percent stays should be less than 5%.

Brood year	Homing				Straying			
	Target stream		Target hatchery		Non-target streams		Non-target hatcheries	
	Number	%	Number	%	Number	%	Number	%
1989	773	55.7	459	33.0	81	5.8	76	5.5
1990	199	70.6	81	28.7	0	0.0	2	0.7
1991	82	65.6	43	34.4	0	0.0	0	0.0
1992	68	63.0	40	37.0	0	0.0	0	0.0
1993	25	65.8	10	26.3	3	7.9	0	0.0
1994	419	79.7	94	17.9	13	2.5	0	0.0
1995	126	81.8	28	18.2	0	0.0	0	0.0

Brood year	Homing				Straying			
	Target stream		Target hatchery		Non-target streams		Non-target hatcheries	
	Number	%	Number	%	Number	%	Number	%
1996	57	93.4	4	6.6	0	0.0	0	0.0
1997	379	93.8	7	1.7	18	4.5	0	0.0
1998	1,653	94.7	32	1.8	60	3.4	0	0.0
1999	18	100.0	0	0.0	0	0.0	0	0.0
2000	239	93.0	4	1.6	14	5.4	0	0.0
2001	272	88.3	6	1.9	29	9.4	1	0.3
2002	316	95.2	4	1.2	12	3.6	0	0.0
2003	117	99.2	1	0.8	0	0.0	0	0.0
2004	81	85.3	0	0.0	14	14.7	0	0.0
Total	***4,824***	***80.9***	***813***	***13.6***	***244***	***4.1***	***79***	***1.3***

Genetics

Genetic studies were conducted to investigate relationships among temporally replicated collections of summer Chinook from the Wenatchee River, Methow River, and Okanogan River in the upper Columbia River basin (Kassler et al. 2100; the entire report is appended as Appendix J). Samples from the Eastbank Hatchery – Wenatchee stock, Eastbank Hatchery – Methow/Okanogan (MEOK) stock, and Wells Hatchery were also included in the analysis. Samples of natural and hatchery-origin summer Chinook were analyzed and compared to determine if the supplementation program has affected the genetic structure of these populations. The study also calculated the effective number of breeders for collection locations of natural and hatchery-origin summer Chinook from 1993 and 2008.

In general, population differentiation was not observed among the temporally replicated collection locations. A single collection from the Okanogan River (1993) was the only collection showing statistically significant differences. The effective number of breeders was not statistically different from the early collection in 1993 in comparison to the late collection in 2008. Overall, these analyses revealed a lack of differentiation among the temporal replicates from the same locations and among the collection from different locations, suggesting the populations have been homogenized or that there has been substantial gene flow among populations. Additional comparisons among summer-run and fall-run Chinook populations in the upper Columbia River were conducted to determine if there was any differentiation between Chinook with different run timing. These analyses revealed pairwise F_{ST} values that were less than 0.01 for the collections of summer Chinook to collections of fall Chinook from Hanford Reach, lower Yakima River, Priest Rapids, and Umatilla. Collections of fall Chinook from Crab Creek, Lyons Ferry Hatchery, Marion Drain, and Snake River had pairwise F_{ST} values that were higher in comparison to the collections of summer Chinook. The consensus clustering analysis did not provide good statistical support to the groupings, but did show relationships among collections based on geographic proximity. Overall the summer and fall run Chinook that have historically been spawned together were not differentiated while fall Chinook from greater geographic distances were differentiated.

Proportion of Natural Influence

Another method for assessing the genetic risk of a supplementation program is to determine the influence of the hatchery and natural environments on the adaptation of the composite population. This is estimated by the proportion of natural-origin fish in the hatchery broodstock (pNOB) and the proportion of hatchery-origin fish in the natural spawning escapement (pHOS). The ratio pNOB/(pHOS+pNOB) is the Proportion of Natural Influence (PNI). The larger the ratio (PNI), the greater the strength of selection in the natural environment relative to that of the hatchery environment. In order for the natural environment to dominate selection, PNI should be greater than 0.5 (HSRG/WDFW/NWIFC 2004).

For brood years 1989-2009, the PNI was equal to or greater than 0.5 in all but three years (Table 7.25). This indicates that the natural environment has a greater influence on adaptation of Methow summer Chinook than does the hatchery environment.

Table 7.25. Proportionate natural influence (PNI) of the Methow summer Chinook supplementation program for brood years 1989-2009. PNI was calculated as the proportion of naturally produced Chinook in the hatchery broodstock (pNOB) divided by the proportion of hatchery Chinook on the spawning grounds (pHOS) plus pNOB. NOS = number of natural-origin Chinook on the spawning grounds; HOS = number of hatchery-origin Chinook on the spawning grounds; NOB = number of natural-origin Chinook collected for broodstock; and HOB = number of hatchery-origin Chinook included in hatchery broodstock.

Brood year	Spawners			Broodstock			PNI
	NOS	HOS	pHOS	NOB	HOB	pNOB	
1989	492	0	0.00	1,297	312	0.81	1.00
1990	1,421	0	0.00	828	206	0.80	1.00
1991	566	0	0.00	924	314	0.75	1.00
1992	460	0	0.00	297	406	0.42	1.00
1993	309	199	0.39	681	388	0.64	0.62
1994	573	512	0.47	341	244	0.58	0.55
1995	563	651	0.54	173	240	0.42	0.44
1996	424	191	0.31	290	223	0.57	0.65
1997	512	185	0.27	198	264	0.43	0.61
1998	432	243	0.36	153	211	0.42	0.54
1999	537	449	0.46	224	289	0.44	0.49
2000	838	362	0.30	164	339	0.33	0.52
2001	1,052	1,716	0.62	91	266	0.25	0.29
2002	2,505	2,125	0.46	247	241	0.51	0.53
2003	2,224	1,706	0.43	381	101	0.79	0.65
2004	1,609	580	0.26	506	16	0.97	0.79
2005	1,672	889	0.35	391	9	0.98	0.74
2006	2,039	694	0.25	500	10	0.98	0.80
2007	764	600	0.44	456	17	0.96	0.69
2008	1,293	654	0.34	404	41	0.91	0.73
2009	1,093	665	0.38	553	5	0.99	0.72

Brood year	Spawners			Broodstock			PNI
	NOS	HOS	pHOS	NOB	HOB	pNOB	
Average	***1,018***	***591***	***0.32***	***433***	***197***	***0.66***	***0.68***

Natural and Hatchery Replacement Rates

Natural replacement rates (NRR) were calculated as the ratio of natural-origin recruits (NOR) to the parent spawning population (spawning escapement). For brood years 1989-2003, NRR for summer Chinook in the Methow averaged 1.22 (range, 0.10-4.74) if harvested fish were not include in the estimate and 2.38 (range, 0.18-10.52) if harvested fish were included in the estimate (Table 7.26). NRRs for more recent brood years will be calculated as soon as all tag recoveries and sampling rates have been loaded into the database.

Hatchery replacement rates (HRR) are the hatchery adult-to-adult returns and were calculated as the ratio of hatchery-origin recruits (HOR) to the parent broodstock collected. These rates should be greater than the NRRs and greater than or equal to 5.30 (the calculated target value in Murdoch and Peven 2005). HRRs exceeded NRRs in eight out of the 15 years of data, regardless if harvest was or was not included in the estimate (Table 7.26). Hatchery replacement rates for Methow summer Chinook have exceeded the estimated target value of 5.30 in two of the 15 years of data, regardless if harvest is or is not included in the estimate.

Table 7.26. Broodstock collected, spawning escapements, natural and hatchery-origin recruits (NOR and HOR), and natural and hatchery replacement rates (NRR and HRR; with and without harvest) for wild summer Chinook in the Methow Basin, brood years 1989-2003.

Brood year	Broodstock Collected	Spawning Escapement	Harvest not included				Harvest included			
			HOR	NOR	HRR	NRR	HOR	NOR	HRR	NRR
1989	202	492	1,389	620	6.88	1.26	3,396	1,509	16.81	3.07
1990	202	1,421	282	933	1.40	0.66	386	1,285	1.91	0.90
1991	266	566	125	276	0.47	0.49	186	413	0.70	0.73
1992	214	460	108	598	0.50	1.30	139	772	0.65	1.68
1993	234	508	38	420	0.16	0.83	62	685	0.26	1.35
1994	260	1,085	526	521	2.02	0.48	715	710	2.75	0.65
1995	242	1,214	154	1,149	0.64	0.95	232	1,730	0.96	1.43
1996	220	615	61	420	0.28	0.68	75	518	0.34	0.84
1997	209	697	404	1,448	1.93	2.08	653	2,351	3.12	3.37
1998	235	675	1,745	3,202	7.43	4.74	3,858	7,100	16.42	10.52
1999	222	986	18	2,827	0.08	2.87	33	5,187	0.15	5.26
2000	222	1,200	257	812	1.16	0.68	769	2,438	3.46	2.03
2001	223	2,768	308	2,856	1.38	1.03	928	8,655	4.16	3.13
2002	222	4,630	332	1,073	1.50	0.23	893	2,900	4.02	0.63
2003	224	3,930	118	397	0.53	0.10	213	717	0.95	0.18
Average	***226***	***1,416***	***391***	***1,170***	***1.76***	***1.22***	***836***	***2,465***	***3.78***	***2.38***

Smolt-to-Adult Survivals

Smolt-to-adult survival ratios (SARs) were calculated as the number of hatchery adult recaptures divided by the number of tagged hatchery smolts released. SARs were based on CWT returns. For the available brood years, SARs have ranged from 0.00008 to 0.01888 for hatchery summer Chinook in the Methow Basin (Table 7.27).

Table 7.27. Smolt-to-adult ratios (SARs) for Methow summer Chinook, brood years 1989-2004.

Brood year	Number of tagged smolts released[a]	Estimated adult captures[b]	SAR
1989	358,237	2,882	0.00804
1990	371,483	369	0.00099
1991	377,097	130	0.00034
1992	392,636	138	0.00035
1993	200,345	62	0.00031
1994	400,488	710	0.00177
1995	344,974	229	0.00066
1996	289,880	74	0.00026
1997	380,430	649	0.00171
1998	202,559	3,824	0.01888
1999	422,473	33	0.00008
2000	334,337	768	0.00230
2001	246,159	923	0.00375
2002	310,846	890	0.00286
2003	353,495	213	0.00060
2004	394,490	293	0.00074
Average	***336,246***	***762***	***0.00227***

[a] Includes all tag codes and CWT released fish (CWT + Ad Clip fish and CWT-only fish).

[b] Includes estimated recoveries (spawning ground, hatcheries, harvest, etc.) and observed recoveries if estimated recoveries were unavailable.

7.7 ESA/HCP Compliance

Broodstock Collection

Summer Chinook adults collected at Wells Dam are used for both the Methow and Okanogan supplementation programs. Per the 2008 broodstock collection protocol, 556 natural-origin (adipose fin present) adults were targeted for collection between 1 July and 14 September at the East Ladder of Wells Dam. Actual collections occurred between 2 July and 10 September and totaled 459 summer Chinook. ESA Permit 1347 provides authorization to collect Methow and Okanogan summer Chinook at Wells Dam three days per week and up to 16 hours per day from July through November. During 2008, broodstock collection activities encompassed a total of 32 days, representing 100% of the allowable trapping days allowed under ESA Permit 1347.

Collection of Methow and Okanogan summer Chinook broodstock at Wells Dam occurred concurrently with collection of summer steelhead for the Wells steelhead program authorized under ESA Section 10 Permit 1395. Encounters with steelhead and spring Chinook during Methow and Okanogan summer Chinook broodstock collections did not result in takes that were outside those authorized in Permit 1347 and in Permit 1395 for the Wells Steelhead program. Steelhead encountered during summer Chinook collections that were not required for steelhead broodstock were passed at the trap site and were not physically handled. Any spring Chinook encountered during summer Chinook broodstock activities were also passed without handling.

Hatchery Rearing and Release

The 2008 brood Methow/Okanogan summer Chinook reared throughout their juvenile life-stages at Eastbank Fish Hatchery and the Carlton Acclimation pond without incident (see Section 7.2). The 2008 brood smolt release totaled 397,554 summer Chinook, representing 99.4% of the production objective and was compliant with the 10% overage allowable in ESA Section 10 Permit 1347.

Hatchery Effluent Monitoring

Per ESA Permits 1196, 1347, and 1395, permit holders shall monitor and report hatchery effluents in compliance with applicable National Pollution Discharge Elimination Systems (NPDES) (EPA 1999) permit limitations. There were no NPDES violations reported at Chelan PUD Hatchery facilities during the period 1 January 2010 through 31 December 2010. NPDES monitoring and reporting for Chelan PUD Hatchery Programs during 2010 are provided in Appendix E.

Spawning Surveys

Summer Chinook spawning ground surveys conducted in the Methow Basin during 2010 were consistent with ESA Section 10 Permit No. 1347. Because of the difficulty of quantifying the level of take associated with spawning ground surveys, the Permit does not specify a take level associated with these activities, even though it does authorize implementation of spawning ground surveys. Therefore, no take levels are reported. However, to minimize potential impacts to established redds, wading was restricted to the extent practical, and extreme caution was used to avoid established redds when wading was required.

SECTION 8: OKANOGAN/SIMILKAMEEN SUMMER CHINOOK

8.1 Broodstock Sampling

Summer Chinook broodstock for the Okanogan/Similkameen and Methow programs is collected in the East Ladder of Wells Dam. Refer to Section 7.1 for information on the origin, age and length, sex ratios, and fecundity of summer Chinook broodstock collected at Wells Dam.

8.2 Hatchery Rearing

Rearing History

Number of eggs taken

Based on the unfertilized egg-to-release survival standard of 81%, a total of 711,111 eggs are required to meet the program release goal of 576,000 smolts. From 1989 through 2009, the egg take goal was reached in 12 of those years (Table 8.1).

Table 8.1. Numbers of eggs taken from summer Chinook broodstock collected at Wells Dam for the Okanogan program, 1989-2009.

Return year	Number of eggs taken
1989	724,200
1990	696,144
1991	879,892
1992	729,389
1993	797,234
1994	893,086
1995	736,500
1996	672,000
1997	601,744
1998	584,018
1999	725,589
2000	645,403
2001	418,907
2002	718,599
2003	710,521
2004	805,814
2005	452,928
2006	757,350
2007	824,703
2008	662,668
2009	840,902
Average	***708,457***

Number of acclimation days

Summer Chinook were released volitionally from Similkameen Pond as yearling smolts beginning in April and ending in May 2010. Fish acclimated at Similkameen were held for 176 to 201 days (Table 8.2). Summer Chinook at Bonaparte Pond were released volitionally between 19 April and 5 May. Fish acclimated at Bonaparte Pond were held for 165-185 days before release.

Table 8.2. Number of days Okanogan summer Chinook broods were acclimated at Similkameen and Bonaparte ponds, brood years 1989-2008.

Brood year	Release year	Rearing facility	Transfer date	Release date	Number of days
1989	1991	Similkameen	29-Oct	7-May	190
1990	1992	Similkameen	5-Nov	25-Apr	171
1991	1993	Similkameen	1-Nov	9-Apr	159
1992	1994	Similkameen	2-Nov	1-Apr	150
			26-Feb	1-Apr	34
1993	1995	Similkameen	24-Oct	1-Apr	159
			24-Feb	1-Apr	36
1994	1996	Similkameen	30-Oct	6-Apr	158
			14-Mar	6-Apr	23
1995	1997	Similkameen	1-Oct	1-Apr	182
1996	1998	Similkameen	10-Oct	15-Mar	156
1997	1999	Similkameen	7-Oct	19-Apr	194
1998	2000	Similkameen	5-Oct	19-Apr	196
1999	2001	Similkameen	5-Oct	18-Apr	195
2000	2002	Similkameen	10-Oct	8-Apr	180
2001	2003	Similkameen	1-Oct	29-Apr	210
2002	2004	Similkameen	9-Nov	23-Apr	165
2003	2005	Similkameen	19-Oct	28-Apr	191
2004	2006	Similkameen	26-Oct	23-Apr	179
2005	2007	Bonaparte	6-Nov	11-Apr	156
		Similkameen	25-Oct	18-Apr – 9-May	179-200
2006	2008	Similkameen	15-17-Oct	16-Apr – 7-May	182-205
2007	2009	Bonaparte	3-4-Nov	10-22-Apr	157-170
		Similkameen	20-24-Oct	14-Apr – 9-May	172-201
2008	2010	Bonaparte	2-4-Nov	19-Apr – 5-May	167-185

Brood year	Release year	Rearing facility	Transfer date	Release date	Number of days
		Similkameen	26-28-Oct	19-Apr – 14-May	176-201

Release Information

Numbers released

The 2008 Okanogan summer Chinook program achieved 90.2% of the 576,000 target goal with about 519,357 fish being released volitionally in the Similkameen and Okanogan rivers. About 175,729 summer Chinook were released volitionally from the Bonaparte Pond between 19 April and 5 May, while 343,628 fish were released volitionally from the Similkameen facility between 19 April and 14 May (Table 8.3).

Table 8.3. Numbers of Okanogan summer Chinook smolts released from the Similkameen and Bonaparte ponds, brood years 1989-2008; NA = not available. The release target for Okanogan summer Chinook is 576,000 smolts.

Brood year	Release year	Rearing facility	CWT mark rate	Number of smolts released
1989	1991	Similkameen	0.5732	352,600
1990	1992	Similkameen	0.6800	540,000
1991	1993	Similkameen	0.5335	675,500
1992	1994	Similkameen	0.9819	548,182
1993	1995	Similkameen	0.6470	586,000
1994	1996	Similkameen	0.4176	536,299
1995	1997	Similkameen	0.9785	587,000
1996	1998	Similkameen	0.9769	507,913
1997	1999	Similkameen	0.9711	589,591
1998	2000	Similkameen	0.9825	293,191
1999	2001	Similkameen	0.9689	630,463
2000	2002	Similkameen	0.9928	532,453
2001	2003	Similkameen	0.9877	26,642
2002	2004	Similkameen	0.9204	388,589
2003	2005	Similkameen	0.9929	579,019
2004	2006	Similkameen	0.9425	703,359
2005	2007	Bonaparte	0	0 (assumed)
		Similkameen	0.9862	275,919
2006	2008	Bonaparte	NA	NA
		Similkameen	0.9878	604,035
2007	2009	Bonaparte	0.9920	102,099
		Similkameen	0.9914	513,039
2008	2010	Bonaparte	0.9947	175,729
		Similkameen	0.9947	343,628
Average			***0.8476***	***458,693***

Numbers tagged

The 2008 brood Okanogan summer Chinook from the Similkameen and Bonaparte facilities were respectively 99.5% CWT and adipose fin-clipped (Table 8.3).

In 2010, a total of about 5,100 Similkameen summer Chinook (brood year 2009) were PIT tagged at Eastbank Fish Hatchery on 26-28 July. Fish were not fed during tagging or for two days before and after tagging. Fish averaged 69 mm in length and 3.8 g at time of tagging. As of the end of January 2011, a total of 11 tagged Chinook have died; no fish have shed their tags. These left 5,030 tagged summer Chinook alive at the end of the month.

Table 8.4 summarizes the number of hatchery summer Chinook that have been PIT-tagged and released into the Okanogan Basin.

Table 8.4. Summary of PIT-tagging activities for Okanogan hatchery summer Chinook, brood years 2008-2009.

Brood year	Release year	Number of fish tagged	Number of tagged fish that died	Number of tags shed	Number of tagged fish released
2008	2010	5,700 (high density)	1,169	0	4,531
		5,700 (low density)	1,407	0	4,293
2009	2011	5,100	NA	NA	NA

Fish size and condition at release

Size at release of the Similkameen population was 79.5% and 77.3% of the target fork length and weight, respectively. The target CV for fork length was exceeded by 37% (Table 8.5). No information was available for the Bonaparte acclimation group.

Table 8.5. Mean lengths (FL, mm), weight (g and fish/pound), and coefficient of variation (CV) of Okanogan summer Chinook smolts released from the hatchery, brood years 1989-2008. Size targets are provided in the last row of the table.

Brood year	Release year	Fork length (mm)		Mean weight	
		Mean	CV	Grams (g)	Fish/pound
1989	1991	-	-	41.3	11
1990	1992	143	9.5	37.8	12
1991	1993	125	15.5	22.4	20
1992	1994	120	15.4	20.7	22
1993	1995	132	-	23.2	20
1994	1996	136	16.0	29.6	15
1995	1997	137	8.2	32.8	14
1996	1998	127	12.8	26.2	17
1997	1999	144	9.9	36.0	13
1998	2000	148	5.9	41.0	11
1999	2001	141	15.7	35.4	13

Brood year	Release year	Fork length (mm)		Mean weight	
		Mean	CV	Grams (g)	Fish/pound
2000	2002	121	13.4	20.4	22
2001	2003	132	8.2	25.7	18
2002	2004	119	13.4	20.8	22
2003	2005	133	10.6	28.9	16
2004	2006	132	9.9	29.8	15
2005	2007	132	9.6	25.9	18
2006	2008	120	12.3	20.9	22
2007	2009	124	12.6	21.9	21
2008	2010	140	12.3	35.1	13
Targets		***176***	***9.0***	***45.4***	***10***

Survival Estimates

Overall survival of Okanogan summer Chinook from green (unfertilized) egg to release was below the standard set for the program (Table 8.6). Lower than expected transport-to-release survival had the greatest effect on the overall survival performance. Currently, it is unknown if gamete viability is gender biased or is uniform between sexes and more influenced by between-year environmental variations.

Table 8.6. Hatchery life-stage survival rates (%) for Okanogan summer Chinook, brood years 1989-2008. Survival standards or targets are provided in the last row of the table.

Brood year	Rearing facility	Collection to spawning		Unfertilized egg-eyed	Eyed egg-ponding	30 d after ponding	100 d after ponding	Ponding to release	Transport to release	Unfertilized egg-release
		Female	Male							
1989[a]	Similkameen	89.8	99.5	89.9	96.7	99.7	99.4	73.3	57.4	48.7
1990[a]	Similkameen	93.9	99.0	84.9	97.1	81.2	80.6	97.7	98.6	77.6
1991[a]	Similkameen	93.1	95.5	88.2	97.1	99.4	99.1	98.4	97.1	76.8
1992[a]	Similkameen	96.9	99.0	87.0	98.0	99.9	99.9	91.7	92.6	75.2
1993[a]	Similkameen	82.2	99.4	85.4	97.6	99.8	99.5	92.0	90.2	73.5
1994	Similkameen	96.1	90.0	86.6	100.0	98.1	97.4	73.1	89.8	60.1
1995	Similkameen	91.9	96.2	98.2	84.1	96.5	96.2	92.7	98.2	79.7
1996	Similkameen	95.4	98.1	83.2	100.0	97.7	96.9	86.5	92.5	75.6
1997	Similkameen	91.9	94.6	86.1	98.4	98.7	98.3	98.8	99.4	98.0
1998	Similkameen	84.0	96.2	54.1	98.0	99.4	98.9	96.6	99.6	50.2
1999	Similkameen	98.8	98.7	92.9	96.9	98.0	97.6	96.9	99.0	86.9
2000	Similkameen	90.5	96.9	89.2	98.5	98.2	98.0	93.6	97.2	82.5
2001	Similkameen	96.2	92.3	89.1	97.6	99.7	99.5	7.4	11.9	6.4
2002	Similkameen	97.1	98.1	89.8	98.0	99.7	99.5	51.6	52.2	54.1
2003	Similkameen	96.7	97.5	86.8	97.6	99.3	98.5	98.0	98.8	81.5
2004	Similkameen	93.6	98.2	84.0	97.6	99.6	99.3	97.8	98.8	80.2
	Bonaparte	93.6	98.2	84.0	97.6	99.6	99.3	97.9	98.9	80.3
2005	Similkameen	97.0	89.6	88.0	99.5	99.5	99.0	93.5	94.6	81.8

Brood year	Rearing facility	Collection to spawning		Unfertilized egg-eyed	Eyed egg-ponding	30 d after ponding	100 d after ponding	Ponding to release	Transport to release	Unfertilized egg-release
		Female	Male							
	Bonaparte	97.0	89.6	88.0	99.5	99.5	99.0	0.0	0.0	0.0
2006	Similkameen	92.9	89.5	86.3	98.3	99.6	99.3	94.1	95.5	79.8
2007	Similkameen	92.6	99.6	80.8	99.1	99.5	99.1	97.0	98.1	77.7
	Bonaparte	92.6	99.6	80.8	99.1	99.5	99.1	95.6	96.7	76.6
2008	Similkameen	97.9	99.6	91.2	96.8	99.7	99.3	89.8	90.5	79.3
	Bonaparte	97.9	99.6	91.2	96.8	99.7	99.3	86.9	87.8	76.7
Standard		***90.0***	***85.0***	***92.0***	***98.0***	***97.0***	***93.0***	***90.0***	***95.0***	***81.0***

[a] Survival rates were calculated from the aggregate population collected at Wells Fish Hatchery volunteer channel and left- and right-ladder traps at Wells Dam.

8.3 Disease Monitoring

Rearing of the 2008 brood Okanogan summer Chinook was similar to previous years with fish being held on well water before being transferred for final acclimation on Similkameen or Okanogan river water. The Similkameen and Bonaparte groups were transferred in late October and early November, respectively. The Bonaparte group began developing bacterial gill disease infections in December 2009. No further problems developed after treatment. Fish acclimating at the Similkameen facility were diagnosed with having an external fungus and bacterial gill disease in November. They were treated through March with minimal results. No further problems developed after treatment. It was believed but not confirmed that considerable mortality was possibly due to a low level influx of toxins associated with increased runoff. No additional disease-related problems were noted before the fish were released.

Results of adult broodstock bacterial kidney disease (BKD) monitoring for Methow/Okanogan summer Chinook are shown in Table 7.11 in Section 7.3.

8.4 Spawning Surveys

Surveys for Okanogan/Similkameen summer Chinook redds were conducted from late September to mid-November, 2010, in the Okanogan and Similkameen rivers. Total redd counts (not peak counts) were conducted in the rivers (see Appendix K for more details).

Redd Counts

A total of 2,118 summer Chinook redds were counted in the Okanogan Basin in 2010 (Table 8.7). This was greater than the overall average of 1,721 redds.

Table 8.7. Total number of redds counted in the Okanogan Basin, 1989-2010.

Survey year	Number of summer Chinook redds		
	Okanogan River	Similkameen River	Total count
1989	151	370	535
1990	99	147	255
1991	64	91	155
1992	53	57	110
1993	162	288	450

Survey year	Number of summer Chinook redds		
	Okanogan River	Similkameen River	Total count
1994	375*	777	1,152
1995	267*	616	883
1996	116	419	535
1997	158	486	644
1998	88	276	364
1999	369	1,275	1,644
2000	549	993	1,542
2001	1,108	1,540	2,648
2002	2,667	3,358	6,025
2003	1,035	378	1,413
2004	1,327	1,660	2,987
2005	1,611	1,423	3,034
2006	2,592	1,666	4,258
2007	1,301	707	2,008
2008	1,146	1,000	2,146
2009	1,672	1,298	2,970
2010	1,011	1,107	2,118
Average	***815***	***906***	***1,721***

* Reach-expanded aerial counts.

Redd Distribution

Summer Chinook redds were not evenly distributed among the survey reaches in the Okanogan Basin. Most redds (90%) were located in the upper Okanogan and lower Similkameen reaches (reaches upstream of the Riverside Bridge) (Table 8.8; Figure 8.1). Relatively few summer Chinook spawned downstream of the Riverside Bridge on the Okanogan River (Reaches 1-4).

Table 8.8. Total number of summer Chinook redds counted in different reaches in the Okanogan Basin during September through mid-November, 2010. Reach codes are described in Table 2.11.

Survey reach	Total redd count	Percent
Okanogan 1	9	0.004
Okanogan 2	58	0.027
Okanogan 3	67	0.032
Okanogan 4	89	0.042
Okanogan 5	357	0.169
Okanogan 6	431	0.203
Similkameen 1	895	0.423
Similkameen 2	212	0.100
Totals	***2,118***	***1.000***

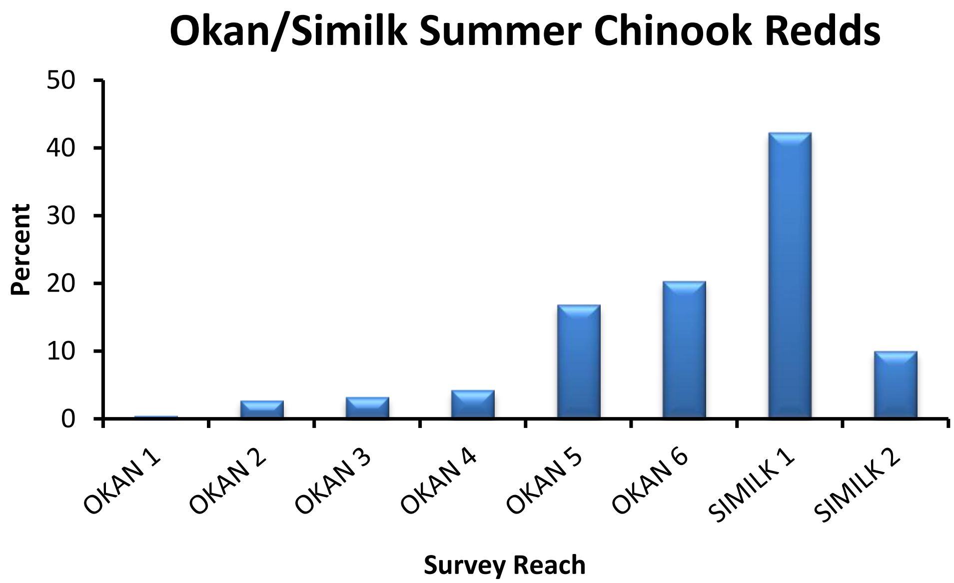


Figure 8.1. Percent of the total number of summer Chinook redds counted in different reaches in the Okanogan Basin during September through mid-November, 2010. Reach codes are described in Table 2.11.

Spawn Timing

Spawning in 2010 began the last week of September in the Similkameen and Okanogan rivers, and peaked during the second week of October in both rivers (Figure 8.2). Spawning began when stream temperature varied from 8.5-16°C.

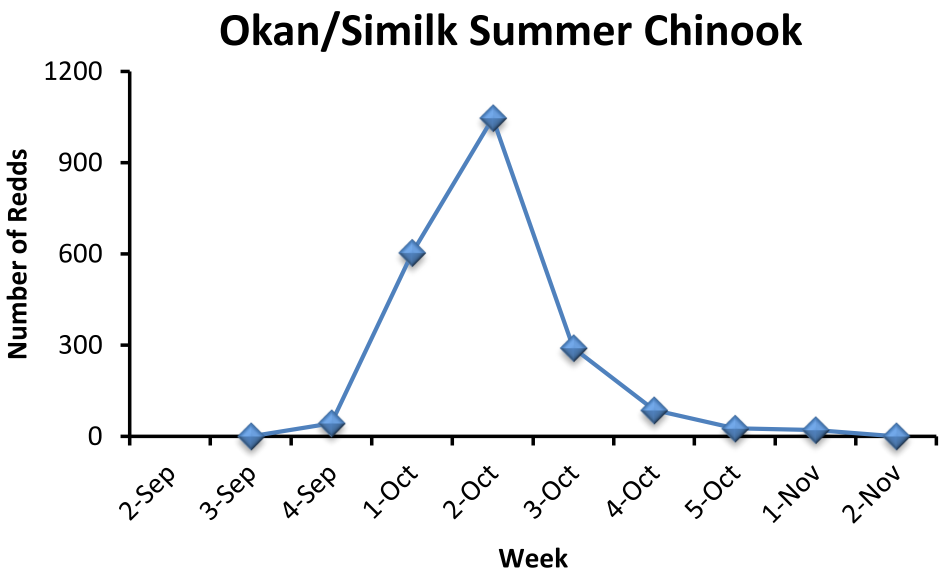


Figure 8.2. Number of new summer Chinook redds counted during different weeks in the Okanogan Basin, September through mid-November, 2010.

Spawning Escapement

Spawning escapement for Okanogan/Similkameen summer Chinook was calculated as the total number of redds times the fish per redd ratio estimated from fish sampled at Wells Dam. The estimated fish per redd ratio for Okanogan/Similkameen summer Chinook in 2010 was 2.81. Multiplying this ratio by the number of redds counted in the Okanogan and Similkameen rivers resulted in a total spawning escapement of 5,952 summer Chinook (Table 8.9).

Table 8.9. Spawning escapements for summer Chinook in the Okanogan and Similkameen rivers for return years 1989-2010.

Return year	Fish/Redd	Spawning escapement		
		Okanogan	Similkameen	Total
1989*	3.30	498	1,221	1,765
1990*	3.40	337	500	868
1991*	3.70	237	337	574
1992*	4.30	228	245	473
1993*	3.30	535	950	1,485
1994*	3.50	1,313	2,720	4,033
1995*	3.40	908	2,094	3,002
1996*	3.40	394	1,425	1,819
1997*	3.40	537	1,652	2,189
1998	3.00	264	828	1,092
1999	2.20	812	2,805	3,617
2000	2.40	1,318	2,383	3,701

Return year	Fish/Redd	Spawning escapement		
		Okanogan	**Similkameen**	**Total**
2001	4.10	4,543	6,314	10,857
2002	2.30	6,134	7,723	13,857
2003	2.42	2,505	915	3,420
2004	2.25	2,986	3,735	6,721
2005	2.93	4,720	4,169	8,889
2006	2.02	5,236	3,365	8,601
2007	2.20	2,862	1,555	4,417
2008	3.25	3,725	3,250	6,975
2009	2.54	4,247	3,297	7,544
2010	2.81	2,841	3,111	5,952
Average	***3.01***	***2,145***	***2,482***	***4,626***

* Spawning escapement was calculated using the "Modified Meekin Method" (i.e., 3.1 x jack multiplier).

8.5 Carcass Surveys

Surveys for summer Chinook carcasses were conducted during late September to mid-November, 2010, in the Okanogan and Similkameen rivers (see Appendix K for more details).

Number sampled

A total of 1,453 summer Chinook carcasses were sampled during September through mid-November in the Okanogan Basin (Table 8.10). A total of 678 were sampled in the Okanogan River and 775 in the Similkameen River.

Table 8.10. Numbers of summer Chinook carcasses sampled within each survey reach in the Okanogan Basin, 1993-2010. Reach codes are described in Table 2.11.

Survey year	Number of summer Chinook carcasses								
	Okanogan						**Similkameen**		**Total**
	O-1	**O-2**	**O-3**	**O-4**	**O-5**	**O-6**	**S-1**	**S-2**	
1993[a]	0	2	3	0	23	13	73	1	**115**
1994[b]	0	4	4	0	27	5	318	60	**418**
1995	0	0	2	0	30	0	239	15	**286**
1996	0	0	0	2	5	2	226	0	**235**
1997	0	0	2	0	9	3	225	1	**240**
1998	0	1	8	1	7	7	340	4	**368**
1999	0	0	3	2	23	53	766	48	**895**
2000	0	2	20	15	47	16	727	41	**868**
2001	0	26	75	10	127	112	1,141	105	**1,596**
2002	10	32	83	35	204	573	1,265	259	**2,461**
2003[c]	0	0	26	0	15	208	180	8	**437**
2004	0	4	31	24	146	283	1,392	298	**2,178**

Survey year	Number of summer Chinook carcasses								
	Okanogan						Similkameen		Total
	O-1	O-2	O-3	O-4	O-5	O-6	S-1	S-2	
2005	0	8	93	37	371	431	731	276	**1,947**
2006	4	3	31	16	120	291	513	100	**1,078**
2007	2	1	48	1	459	519	657	29	**1,716**
2008	4	10	40	36	248	665	859	157	**2,019**
2009	2	7	31	32	348	500	702	150	**1,772**
2010	3	10	30	42	241	352	627	148	**1,453**
Average	***1***	***6***	***29***	***14***	***136***	***224***	***610***	***94***	***1,116***

[a] 25 additional carcasses were sampled on the Similkameen and 46 on the Okanogan without any reach designation.
[b] One additional carcasses was sampled on the Similkameen without any reach designation.
[c] 793 carcasses were sampled on the Similkameen before initiation of spawning (pre-spawn mortality) and an additional 40 carcasses were sampled on the Okanogan. The cause of the high mortality (*Ichthyophthirius multifilis* and *Flavobacterium columnarae*) was exacerbated by high river temperatures.

Carcass Distribution and Origin

Summer Chinook carcasses were not evenly distributed among reaches within the Okanogan Basin in 2010 (Table 8.9; Figure 8.3). Most of the carcasses in the basin were found in the upper Okanogan River and lower Similkameen River. The highest percentage of carcasses (43%) was sampled in Reach 1 on the Similkameen River between the Driscoll Channel and Oroville Bridge.

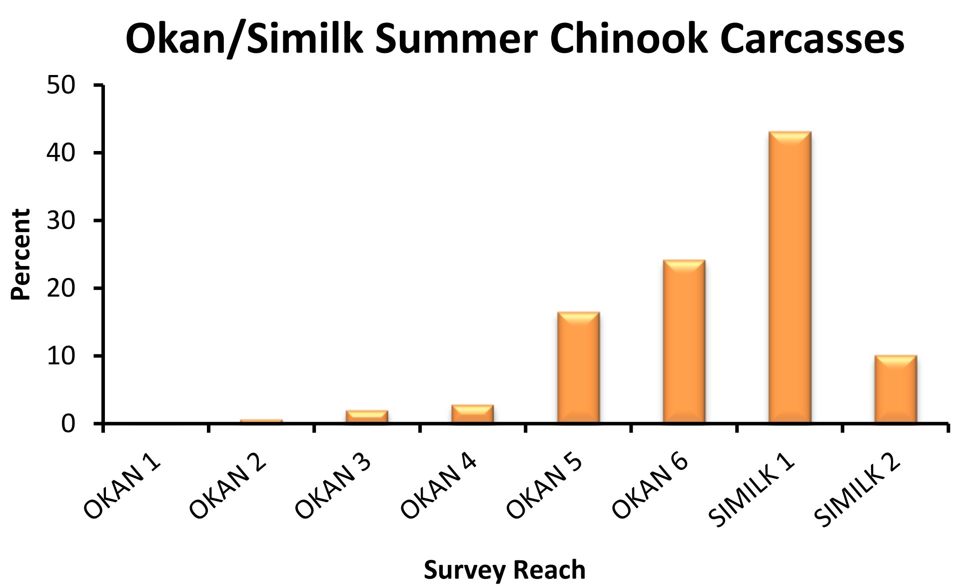


Figure 8.3. Percent of summer Chinook carcasses sampled within different reaches in the Okanogan Basin during September through mid-November, 2010. Reach codes are described in Table 2.11.

Numbers of wild and hatchery-origin summer Chinook carcasses sampled in 2010 will be available after analysis of CWTs and scales. Based on the available data (1991-2009), most fish, regardless of origin, were found in Reach 1 on the Similkameen River (Driscoll Channel to Oroville Bridge) (Table 8.11). However, a slightly larger percentage of hatchery fish were found in reaches on the Similkameen River than were wild fish (Figure 8.4). In contrast, a larger percentage of wild fish were found in reaches on the Okanogan River.

Table 8.11. Numbers of wild and hatchery summer Chinook carcasses sampled within different reaches in the Okanogan Basin, 1993-2009.

Survey year	Origin	Survey reach								Total
		O-1	O-2	O-3	O-4	O-5	O-6	S-1	S-2	
1993	Wild	0	0	3	0	13	4	48	1	**69**
	Hatchery	0	2	0	0	10	9	25	0	**46**
1994	Wild	0	0	1	0	8	1	113	22	**145**
	Hatchery	0	4	3	0	19	4	205	38	**273**
1995	Wild	0	0	1	0	10	0	66	4	**81**
	Hatchery	0	0	1	0	20	0	173	11	**205**
1996	Wild	0	0	0	1	3	1	53	0	**58**
	Hatchery	0	0	0	1	2	1	173	0	**177**
1997	Wild	0	0	1	0	0	2	83	0	**86**
	Hatchery	0	0	1	0	9	0	142	1	**153**
1998	Wild	0	1	3	1	6	5	162	4	**182**
	Hatchery	0	0	5	0	1	2	178	0	**186**
1999	Wild	0	0	0	0	9	24	298	10	**341**
	Hatchery	0	0	3	2	14	29	468	38	**554**
2000	Wild	0	0	8	8	24	11	189	4	**244**
	Hatchery	0	2	12	7	23	5	538	37	**624**
2001	Wild	0	10	23	5	67	42	390	54	**591**
	Hatchery	0	16	52	5	60	70	751	51	**1,005**
2002	Wild	6	14	20	10	81	212	340	72	**755**
	Hatchery	4	18	63	25	123	360	925	187	**1,705**
2003	Wild	0	0	13	0	12	149	221	116	**511**
	Hatchery	0	0	15	0	5	91	364	257	**732**
2004	Wild	0	2	19	19	108	225	1,126	260	**1,759**
	Hatchery	0	2	12	5	38	58	266	38	**419**
2005	Wild	0	5	51	21	256	364	532	176	**1,405**
	Hatchery	0	3	42	16	115	67	199	100	**542**
2006	Wild	2	2	23	11	110	271	70	78	**567**
	Hatchery	2	1	8	5	10	20	443	22	**511**
2007	Wild	1	0	33	1	303	347	441	21	**1,147**
	Hatchery	1	0	22	0	150	172	217	8	**570**
2008	Wild	2	1	16	11	121	341	361	44	**897**
	Hatchery	2	9	24	25	127	324	498	113	**1,122**
2009	Wild	2	3	14	15	192	352	341	76	**995**

Survey year	**Origin**	**Survey reach**								**Total**
		O-1	**O-2**	**O-3**	**O-4**	**O-5**	**O-6**	**S-1**	**S-2**	
	Hatchery	0	4	17	17	156	148	362	74	**778**
Average	***Wild***	***1***	***2***	***13***	***6***	***78***	***138***	***284***	***55***	***578***
	Hatchery	***1***	***4***	***16***	***6***	***52***	***80***	***349***	***57***	***565***

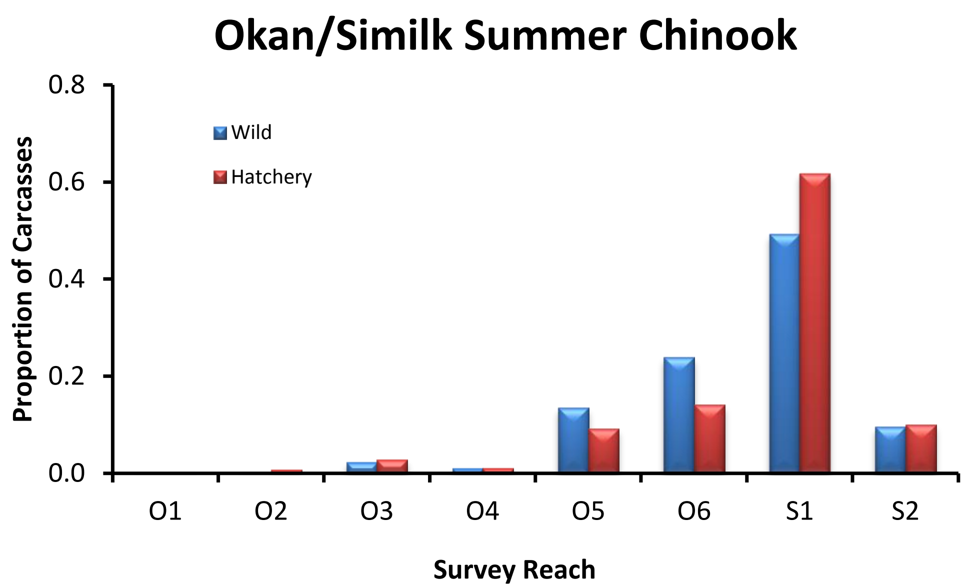


Figure 8.4. Distribution of wild and hatchery produced carcasses in different reaches in the Okanogan Basin, 1993-2009. Reach codes are described in Table 2.11.

Sampling Rate

Overall, 24% of the total spawning escapement of summer Chinook in the Okanogan Basin was sampled in 2010 (Table 8.12). This was above the target of 20%. Sampling rates among survey reaches varied from 6 to 29%.

Table 8.12. Number of redds and carcasses, total spawning escapement, and sampling rates for summer Chinook in the Okanogan Basin, 2010.

Sampling reach	**Total number of redds**	**Total number of carcasses**	**Total spawning escapement**	**Sampling rate**
Okanogan 1	9	3	26	0.12
Okanogan 2	58	10	163	0.06
Okanogan 3	67	30	188	0.16
Okanogan 4	89	42	250	0.17
Okanogan 5	357	241	1,003	0.24
Okanogan 6	431	352	1,211	0.29
Similkameen 1	895	627	2,515	0.25

Sampling reach	Total number of redds	Total number of carcasses	Total spawning escapement	Sampling rate
Similkameen 2	212	148	596	0.25
Total	***2,118***	***1,453***	***5,952***	***0.24***

Length Data

Mean lengths (POH, cm) of male and female summer Chinook carcasses sampled during surveys on the Okanogan and Similkameen rives in 2010 are provided in Table 8.13. The average size of males and females sampled in the Okanogan Basin were 63 cm and 72 cm, respectively.

Table 8.13. Mean lengths (postorbital-to-hypural length; cm) and standard deviations (in parentheses) of male and female summer Chinook carcasses sampled in different reaches in the Okanogan Basin, 2010.

Stream/watershed	Mean length (cm)	
	Male	Female
Okanogan 1	57.3 (4.2)	-
Okanogan 2	55.8 (8.6)	68.0 (4.9)
Okanogan 3	58.9 (7.4)	73.7 (5.4)
Okanogan 4	59.7 (6.4)	70.6 (5.5)
Okanogan 5	64.7 (10.2)	69.7 (6.0)
Okanogan 6	60.1 (9.6)	70.0 (5.8)
Similkameen 1	64.3 (11.1)	73.7 (6.5)
Similkameen 2	64.2 (12.5)	72.3 (5.9)
Total	***62.6 (10.5)***	***72.1 (6.4)***

8.6 Life History Monitoring

Life history characteristics of Okanogan/Similkameen summer Chinook were assessed by examining carcasses on spawning grounds and fish collected or examined at broodstock collection sites, and by reviewing tagging data and fisheries statistics.

Migration Timing

Migration timing for Okanogan/Similkameen summer Chinook is described in Section 7.6.

Age at Maturity

Most of the wild and hatchery summer Chinook sampled during the period 1993-2009 in the Okanogan Basin were age-4 and 5 fish (total age) (Table 8.14; Figure 8.5). A higher percentage of age-3 and 4 wild Chinook returned to the basin than did age-3 and 4 hatchery Chinook. In contrast, a higher proportion of age-5 and 6 hatchery fish returned than did age-5 and 6 wild fish. Thus, a higher percentage of hatchery fish returned at an older age than did wild fish.

Table 8.14. Proportions of wild and hatchery summer Chinook of different ages (total age) sampled on spawning grounds in the Okanogan Basin, 1993-2009.

Sample year	Origin	Total age						Sample size
		2	3	4	5	6	7	
1993	Wild	0.00	0.00	0.76	0.24	0.00	0.00	63
	Hatchery	0.00	0.02	0.97	0.02	0.00	0.00	61
1994	Wild	0.00	0.03	0.42	0.55	0.00	0.00	135
	Hatchery	0.00	0.02	0.09	0.89	0.00	0.00	292
1995	Wild	0.00	0.01	0.26	0.72	0.00	0.00	68
	Hatchery	0.00	0.01	0.16	0.35	0.48	0.00	204
1996	Wild	0.00	0.14	0.50	0.36	0.00	0.00	36
	Hatchery	0.00	0.02	0.21	0.55	0.20	0.01	177
1997	Wild	0.00	0.00	0.05	0.66	0.29	0.00	73
	Hatchery	0.00	0.00	0.03	0.86	0.12	0.00	153
1998	Wild	0.00	0.03	0.64	0.34	0.00	0.00	151
	Hatchery	0.01	0.05	0.50	0.23	0.22	0.00	185
1999	Wild	0.00	0.00	0.33	0.66	0.00	0.00	275
	Hatchery	0.00	0.00	0.12	0.86	0.01	0.00	545
2000	Wild	0.01	0.07	0.28	0.63	0.02	0.00	216
	Hatchery	0.00	0.12	0.03	0.75	0.10	0.00	545
2001	Wild	0.02	0.15	0.75	0.07	0.00	0.00	531
	Hatchery	0.00	0.05	0.88	0.02	0.05	0.00	1,005
2002	Wild	0.01	0.11	0.65	0.23	0.00	0.00	692
	Hatchery	0.00	0.01	0.21	0.78	0.00	0.00	1,681
2003	Wild	0.01	0.02	0.76	0.21	0.00	0.00	478
	Hatchery	0.00	0.03	0.06	0.79	0.12	0.00	653
2004	Wild	0.00	0.12	0.11	0.76	0.01	0.00	1,529
	Hatchery	0.00	0.01	0.32	0.46	0.21	0.00	381
2005	Wild	0.00	0.08	0.76	0.14	0.02	0.00	1,282
	Hatchery	0.00	0.03	0.13	0.69	0.14	0.00	526
2006	Wild	0.00	0.01	0.47	0.51	0.01	0.00	839
	Hatchery	0.01	0.06	0.26	0.27	0.40	0.00	112
2007	Wild	0.01	0.07	0.10	0.80	0.02	0.00	1,061
	Hatchery	0.01	0.21	0.31	0.45	0.02	0.01	519
2008	Wild	0.01	0.31	0.63	0.04	0.01	0.00	848
	Hatchery	0.01	0.02	0.60	0.35	0.02	0.00	1,108
2009	Wild	0.01	0.02	0.81	0.16	0.00	0.00	948
	Hatchery	0.00	0.06	0.07	0.85	0.03	0.00	761
Average	***Wild***	***0.00***	***0.07***	***0.49***	***0.42***	***0.02***	***0.00***	***9,225***
	Hatchery	***0.00***	***0.04***	***0.29***	***0.54***	***0.12***	***0.00***	***8,908***

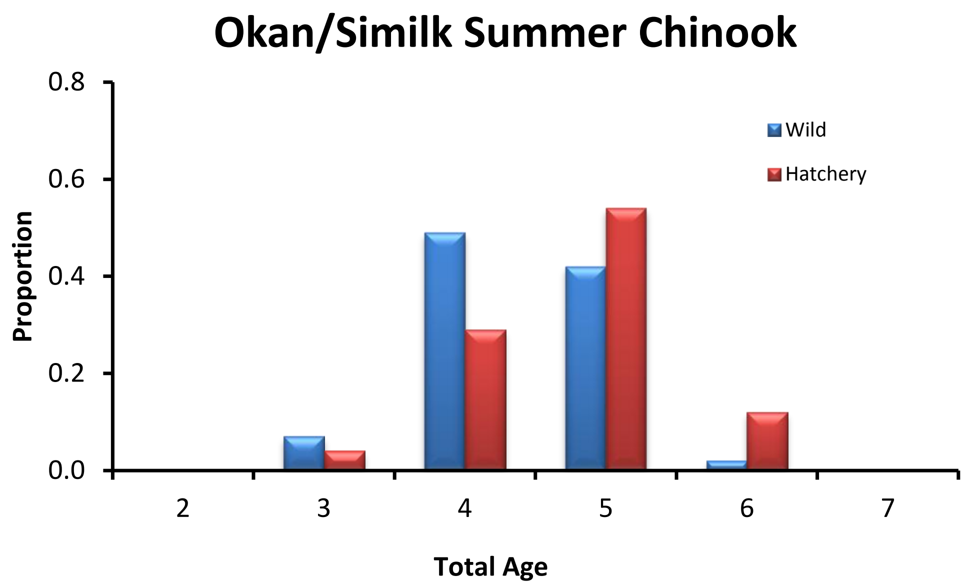


Figure 8.5. Proportions of wild and hatchery summer Chinook of different total ages sampled at broodstock collection sites and on spawning grounds in the Okanogan Basin for the combined years 1993-2009.

Size at Maturity

On average, hatchery summer Chinook were about 2 cm smaller than wild summer Chinook sampled in the Okanogan Basin (Table 8.15). This is interesting given that a slightly higher percentage of hatchery fish returned as age-5 and 6 fish than did wild fish. Future analyses will compare sizes of hatchery and wild fish of the same age groups and gender.

Table 8.15. Mean lengths (POH; cm) and variability statistics for wild and hatchery summer Chinook sampled in the Okanogan Basin, 1993-2009; SD = 1 standard deviation.

Sample year	Origin	Sample size	Summer Chinook length (POH; cm)			
			Mean	SD	Minimum	Maximum
1993	Wild	69	73	7	52	90
	Hatchery	59	62	6	47	75
1994	Wild	164	71	7	40	86
	Hatchery	300	69	8	30	84
1995	Wild	81	75	6	54	87
	Hatchery	201	73	8	39	87
1996	Wild	22	68	14	22	85
	Hatchery	26	75	8	60	88
1997	Wild	87	71	7	44	85
	Hatchery	148	74	6	48	88
1998	Wild	182	70	8	45	94
	Hatchery	186	65	12	30	87

Sample year	Origin	Sample size	Summer Chinook length (POH; cm)			
			Mean	SD	Minimum	Maximum
1999	Wild	340	73	7	56	91
	Hatchery	554	71	7	23	84
2000	Wild	241	70	10	32	86
	Hatchery	624	69	12	24	92
2001	Wild	579	67	9	26	90
	Hatchery	997	61	8	32	90
2002	Wild	755	69	9	28	91
	Hatchery	1,705	70	8	33	87
2003	Wild	533	68	9	30	93
	Hatchery	732	69	10	26	90
2004	Wild	1,757	71	10	33	94
	Hatchery	416	66	9	41	92
2005	Wild	1,407	66	7	41	99
	Hatchery	542	68	8	31	85
2006	Wild	940	72	6	31	91
	Hatchery	138	70	10	33	86
2007	Wild	1,147	75	9	27	99
	Hatchery	570	63	13	30	85
2008	Wild	897	65	9	29	86
	Hatchery	1,122	65	8	32	89
2009	Wild	995	70	7	28	89
	Hatchery	777	70	9	35	86
Pooled	***Wild***	***10,196***	***70***	***8***	***22***	***99***
	Hatchery	***9,097***	***68***	***9***	***23***	***92***

Contribution to Fisheries

Most of the harvest on hatchery-origin Okanogan/Similkameen summer Chinook occurred in the Ocean (Table 8.16). Ocean harvest has made up 38-100% of all hatchery-origin Okanogan/Similkameen summer Chinook harvested. Brood years 1989, 1997-2000, and 2002-2004 provided the largest harvests, while brood year 1996 provided the lowest.

Table 8.16. Estimated number and percent (in parentheses) of hatchery-origin Okanogan/Similkameen summer Chinook captured in different fisheries, brood years 1989-2004.

Brood year	Ocean fisheries	Columbia River Fisheries			Total
		Tribal	Commercial (Zones 1-5)	Recreational (sport)	
1989	2,379 (80)	553 (19)	0 (0)	42 (1)	2,974
1990	349 (88)	34 (9)	0 (0)	12 (3)	395
1991	224 (86)	37 (14)	0 (0)	0 (0)	261

Brood year	Ocean fisheries	Columbia River Fisheries			Total
		Tribal	Commercial (Zones 1-5)	Recreational (sport)	
1992	439 (92)	28 (6)	2 (0)	10 (2)	479
1993	24 (80)	6 (20)	0 (0)	0 (0)	30
1994	385 (92)	23 (6)	2 (0)	7 (2)	417
1995	656 (93)	9 (1)	12 (2)	25 (4)	702
1996	5 (100)	0 (0)	0 (0)	0 (0)	5
1997	6,658 (92)	133 (2)	36 (0)	416 (6)	7,246
1998	4,359 (89)	251 (5)	45 (1)	219 (4)	4,874
1999	1,356 (68)	224 (11)	31 (2)	383 (19)	1,994
2000	3,127 (69)	533 (12)	222 (5)	664 (15)	4,546
2001	183 (57)	81 (25)	31 (10)	24 (8)	319
2002	680 (55)	200 (16)	90 (7)	258 (21)	1,228
2003	697 (38)	568 (31)	117 (6)	459 (25)	1,841
2004	2,786 (43)	1,457 (22)	483 (7)	1,774 (27)	6,500

Straying

Stray rates were determined by examining CWTs recovered on spawning grounds within and outside the Okanogan Basin. Targets for strays based on return year (recovery year) and brood year should be less than 5%.

Rates of hatchery-origin Okanogan summer Chinook straying into basins outside the Okanogan have been very low (Table 8.17). Although a few hatchery-origin Okanogan summer Chinook have strayed into other spawning areas, straying, on average, has been less than 5%. The Chelan tailrace has received the largest number of Okanogan strays.

Table 8.17. Number and percent of spawning escapements within other non-target basins that consisted of hatchery-origin Okanogan summer Chinook, return years 1994-2007. For example, for return year 2002, 1% of the summer Chinook spawning escapement in the Entiat Basin consisted of hatchery-origin Okanogan summer Chinook. Percent strays should be less than 5%.

Return year	Wenatchee		Methow		Chelan		Entiat		Hanford Reach	
	Number	%	Number	%	Number	%	Number	%	Number	%
1994	0	0.0	0	0.0	-	-	-	-	-	-
1995	0	0.0	0	0.0	-	-	-	-	-	-
1996	0	0.0	0	0.0	-	-	-	-	-	-
1997	0	0.0	0	0.0	-	-	-	-	-	-
1998	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
1999	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
2000	0	0.0	6	0.5	30	4.5	0	0.0	3	0.0
2001	12	0.1	0	0.0	10	1.0	0	0.0	0	0.0
2002	0	0.0	3	0.1	4	0.7	5	1.0	0	0.0
2003	0	0.0	8	0.2	22	5.3	14	2.0	0	0.0

Return year	Wenatchee		Methow		Chelan		Entiat		Hanford Reach	
	Number	%	Number	%	Number	%	Number	%	Number	%
2004	0	0.0	0	0.0	5	1.2	0	0.0	0	0.0
2005	5	0.1	27	1.1	36	8.1	7	1.9	8	0.0
2006	0	0.0	5	0.2	4	1.0	2	0.3	0	0.0
2007	0	0.0	3	0.2	4	2.1	0	0.0	0	0.0
Total	***17***	***0.0***	***52***	***0.2***	***115***	***2.6***	***28***	***0.8***	***11***	***0.0***

On average, less than 1% of the returns have strayed into non-target spawning areas, falling below the target of 5% (Table 8.18). Depending on brood year, percent strays into non-target spawning areas have ranged from 0-4.2%. Few (<1% on average) have strayed into non-target hatchery programs.

Table 8.18. Number and percent of hatchery-origin Okanogan summer Chinook that homed to target spawning areas and the target hatchery, and number and percent that strayed to non-target spawning areas and non-target hatchery programs, by brood years 1989-2004. Percent stays should be less than 5%.

Brood year	Homing				Straying			
	Target stream		Target hatchery		Non-target streams		Non-target hatcheries	
	Number	%	Number	%	Number	%	Number	%
1989	3,132	69.7	1,328	29.6	2	0.0	31	0.7
1990	729	71.4	291	28.5	0	0.0	1	0.1
1991	1,125	71.3	453	28.7	0	0.0	0	0.0
1992	1,264	68.5	572	31.0	8	0.4	1	0.1
1993	54	62.1	32	36.8	0	0.0	1	1.1
1994	924	80.8	203	17.7	16	1.4	1	0.1
1995	1,883	85.4	271	12.3	50	2.3	0	0.0
1996	27	100.0	0	0.0	0	0.0	0	0.0
1997	11,659	97.1	309	2.6	35	0.3	2	0.0
1998	2,784	95.4	102	3.5	31	1.1	2	0.1
1999	828	96.7	18	2.1	10	1.2	0	0.0
2000	2,091	93.8	29	1.3	94	4.2	15	0.7
2001	105	98.1	2	1.9	0	0.0	0	0.0
2002	702	96.2	17	2.3	11	1.5	0	0.0
2003	1,576	96.2	47	2.9	15	0.9	0	0.0
2004	4,391	94.9	179	3.9	54	1.2	2	0.0
Total	***33,274***	***88.7***	***3,853***	***10.3***	***326***	***0.9***	***56***	***0.1***

Genetics

Genetic studies were conducted to investigate relationships among temporally replicated collections of summer Chinook from the Wenatchee River, Methow River, and Okanogan River in the upper Columbia River basin (Kassler et al. 2100; the entire report is appended as Appendix J). Samples from the Eastbank Hatchery – Wenatchee stock, Eastbank Hatchery – Methow/Okanogan (MEOK) stock, and Wells Hatchery were also included in the analysis. Samples of natural and hatchery-origin summer Chinook were analyzed and compared to determine if the supplementation program has affected the genetic structure of these populations. The study also calculated the effective number of breeders for collection locations of natural and hatchery-origin summer Chinook from 1993 and 2008.

In general, population differentiation was not observed among the temporally replicated collection locations. A single collection from the Okanogan River (1993) was the only collection showing statistically significant differences. The effective number of breeders was not statistically different from the early collection in 1993 in comparison to the late collection in 2008. Overall, these analyses revealed a lack of differentiation among the temporal replicates from the same locations and among the collection from different locations, suggesting the populations have been homogenized or that there has been substantial gene flow among populations. Additional comparisons among summer-run and fall-run Chinook populations in the upper Columbia River were conducted to determine if there was any differentiation between Chinook with different run timing. These analyses revealed pairwise F_{ST} values that were less than 0.01 for the collections of summer Chinook to collections of fall Chinook from Hanford Reach, lower Yakima River, Priest Rapids, and Umatilla. Collections of fall Chinook from Crab Creek, Lyons Ferry Hatchery, Marion Drain, and Snake River had pairwise F_{ST} values that were higher in comparison to the collections of summer Chinook. The consensus clustering analysis did not provide good statistical support to the groupings, but did show relationships among collections based on geographic proximity. Overall the summer and fall run Chinook that have historically been spawned together were not differentiated while fall Chinook from greater geographic distances were differentiated.

Proportion of Natural Influence

Another method for assessing the genetic risk of a supplementation program is to determine the influence of the hatchery and natural environments on the adaptation of the composite population. This is estimated by the proportion of natural-origin fish in the hatchery broodstock (pNOB) and the proportion of hatchery-origin fish in the natural spawning escapement (pHOS). The ratio pNOB/(pHOS+pNOB) is the Proportion of Natural Influence (PNI). The larger the ratio (PNI), the greater the strength of selection in the natural environment relative to that of the hatchery environment. In order for the natural environment to dominate selection, PNI should be greater than 0.5 (HSRG/WDFW/NWIFC 2004).

For brood years 1989-2009, the PNI was equal to or greater than 0.5 in 12 out of the 21 years (Table 8.19). This indicates that in those years the natural environment has had a relatively greater influence on adaptation of Okanogan/Similkameen summer Chinook than has the hatchery environment.

Table 8.19. Proportionate natural influence (PNI) of the Okanogan/Similkameen summer Chinook supplementation program for brood years 1989-2009. PNI was calculated as the proportion of naturally produced Chinook in the hatchery broodstock (pNOB) divided by the proportion of hatchery Chinook on the spawning grounds (pHOS) plus pNOB. NOS = number of natural-origin Chinook on the spawning grounds; HOS = number of hatchery-origin Chinook on the spawning grounds; NOB = number of natural-origin Chinook collected for broodstock; and HOB = number of hatchery-origin Chinook included in hatchery broodstock.

Brood year	Spawners			Broodstock			PNI
	NOS	HOS	pHOS	NOB	HOB	pNOB	
1989	1,719	0	0.00	1,297	312	0.81	1.00
1990	837	0	0.00	828	206	0.80	1.00
1991	574	0	0.00	924	314	0.75	1.00
1992	473	0	0.00	297	406	0.42	1.00
1993	915	570	0.38	681	388	0.64	0.63
1994	1,323	2,710	0.67	341	244	0.58	0.46
1995	979	2,023	0.67	173	240	0.42	0.39
1996	568	1,251	0.69	290	223	0.57	0.45
1997	862	1,327	0.61	198	264	0.43	0.41
1998	600	492	0.45	153	211	0.42	0.48
1999	1,275	2,342	0.65	224	289	0.44	0.40
2000	1,174	2,527	0.68	164	339	0.33	0.33
2001	4,306	6,551	0.60	91	266	0.25	0.29
2002	4,358	9,499	0.69	247	241	0.51	0.43
2003	1,932	1,488	0.44	381	101	0.79	0.64
2004	5,309	1,412	0.21	506	16	0.97	0.82
2005	6,441	2,448	0.28	391	9	0.98	0.78
2006	5,507	3,094	0.36	500	10	0.98	0.73
2007	2,983	1,434	0.32	456	17	0.96	0.75
2008	2,998	3,977	0.57	404	41	0.91	0.61
2009	4,204	3,340	0.44	507	0	1.00	0.69
Average	***2,349***	***2,214***	***0.41***	***431***	***197***	***0.66***	***0.62***

Natural and Hatchery Replacement Rates

Natural replacement rates (NRR) were calculated as the ratio of natural-origin recruits (NOR) to the parent spawning population (spawning escapement). For brood years 1989-2003, NRR for summer Chinook in the Okanogan averaged 1.19 (range, 0.16-3.79) if harvested fish were not include in the estimate and 2.47 (range, 0.35-10.17) if harvested fish were included in the estimate (Table 8.20). NRRs for more recent brood years will be calculated as soon as all tag recoveries and sampling rates have been loaded into the database.

Hatchery replacement rates (HRR) are the hatchery adult-to-adult returns and were calculated as the ratio of hatchery-origin recruits (HOR) to the parent broodstock collected. These rates should be greater than the NRRs and greater than or equal to 5.30 (the calculated target value in Murdoch and Peven 2005). HRRs exceeded NRRs in 12 of the 15 years of data, regardless if harvest was or was not included in the estimate (Table 8.20). Hatchery replacement rates for Okanogan summer Chinook have exceeded the estimated target value of 5.30 in six or nine of the 15 years of data depending on if harvest was or was not included in the estimate.

Table 8.20. Broodstock collected, spawning escapements, natural and hatchery-origin recruits (NOR and HOR), and natural and hatchery replacement rates (NRR and HRR; with and without harvest) for wild summer Chinook in the Okanogan Basin, brood years 1989-2003.

Brood year	Broodstock Collected	Spawning Escapement	Harvest not included				Harvest included			
			HOR	NOR	HRR	NRR	HOR	NOR	HRR	NRR
1989	304	1,719	4,493	2,139	14.78	1.24	7,467	3,565	24.56	2.07
1990	288	837	1,021	1,477	3.55	1.76	1,416	2,057	4.92	2.46
1991	364	574	1,578	883	4.34	1.54	1,839	1,024	5.05	1.78
1992	304	473	1,845	1,069	6.07	2.26	2,324	1,350	7.64	2.85
1993	328	1,485	87	474	0.27	0.32	117	637	0.36	0.43
1994	302	4,033	1,144	1,397	3.79	0.35	1,561	1,911	5.17	0.47
1995	385	3,002	2,204	1,357	5.72	0.45	2,906	1,795	7.55	0.60
1996	330	1,819	27	730	0.08	0.40	32	870	0.10	0.48
1997	313	2,189	12,005	4,418	38.35	2.02	19,251	7,103	61.50	3.24
1998	352	1,092	2,919	4,144	8.29	3.79	7,793	11,110	22.14	10.17
1999	333	3,617	856	6,679	2.57	1.85	2,850	22,338	8.56	6.18
2000	334	3,701	2,229	1,729	6.67	0.47	6,775	5,271	20.28	1.42
2001	335	10,857	107	8,994	0.32	0.83	426	35,976	1.27	3.31
2002	333	13,857	730	6,045	2.19	0.44	1,958	16,250	5.88	1.17
2003	337	3,420	1,638	558	4.86	0.16	3,479	1,187	10.32	0.35
Average	***329***	***3,512***	***2,192***	***2,806***	***6.79***	***1.19***	***4,013***	***7,496***	***12.35***	***2.47***

Smolt-to-Adult Survivals

Smolt-to-adult survival ratios (SARs) were calculated as the number of hatchery adult recaptures divided by the number of tagged hatchery smolts released. SARs were based on CWT returns. For the available brood years, SARs have ranged from 0.00006 to 0.03272 for hatchery summer Chinook in the Okanogan Basin (Table 8.21).

Table 8.21. Smolt-to-adult ratios (SARs) for Okanogan/Similkameen summer Chinook, brood years 1989-2004.

Brood year	Number of tagged smolts released[a]	Estimated adult captures[b]	SAR
1989	202,125	4,298	0.02126
1990	367,207	969	0.00264
1991	360,380	977	0.00271
1992	537,190	2,299	0.00428

Brood year	Number of tagged smolts released[a]	Estimated adult captures[b]	SAR
1993	379,139	117	0.00031
1994	217,818	1,538	0.00706
1995	574,197	2,855	0.00497
1996	487,776	31	0.00006
1997	572,531	18,731	0.03272
1998	287,948	7,684	0.02669
1999	610,868	2,779	0.00455
2000	528,639	6,748	0.01276
2001	26,315	424	0.01611
2002	245,997	1,953	0.00794
2003	574,908	3,464	0.00603
2004	579,570	10,730	0.01851
Average	***409,538***	***4,100***	***0.01001***

[a] Includes all tag codes and CWT released fish (CWT + Ad Clip fish and CWT-only fish).

[b] Includes estimated recoveries (spawning ground, hatcheries, harvest, etc.) and observed recoveries if estimated recoveries were unavailable.

8.7 ESA/HCP Compliance

Broodstock Collection

Because summer Chinook adults collected at Wells Dam are used for both the Methow and Okanogan supplementation programs, please refer to Section 7.7 for information on ESA compliance during broodstock collection.

Hatchery Rearing and Release

The 2008 brood Okanogan/Similkameen summer Chinook reared throughout their juvenile life-stages at Eastbank Fish Hatchery and Similkameen and Bonaparte Acclimation ponds without significant incident; although, there was some elevated mortality associated with bacterial cold-water disease and bacterial gill disease (see Section 8.3). The 2008 brood smolt release from the Similkameen and Bonaparte ponds totaled 519,357 summer Chinook, representing 90.8% of the production objective for the Okanogan/Similkameen program and was compliant with the 10% overage in production allowable in ESA Section 10 Permit 1347.

Hatchery Effluent Monitoring

Per ESA Permits 1196, 1347, and 1395, permit holders shall monitor and report hatchery effluents in compliance with applicable National Pollution Discharge Elimination Systems (NPDES) (EPA 1999) permit limitations. There were no NPDES violations reported at Chelan PUD Hatchery facilities during the period 1 January 2010 through 31 December 2010. NPDES monitoring and reporting for Chelan PUD Hatchery Programs during 2010 are provided in Appendix E.

Spawning Surveys

Summer Chinook spawning ground surveys conducted in the Okanogan Basin during 2010 were consistent with ESA Section 10 Permit No. 1347. Because of the difficulty of quantifying the level of take associated with spawning ground surveys, the Permit does not specify a take level associated with these activities, even though it does authorize implementation of spawning ground surveys. Therefore, no take levels are reported. However, to minimize potential impacts to established redds, wading was restricted to the extent practical, and extreme caution was used to avoid established redds when wading was required.

SECTION 9: TURTLE ROCK SUMMER CHINOOK

9.1 Broodstock Sampling

Broodstock for the Turtle Rock programs (yearling and sub-yearling) are collected as part of the Wells summer Chinook volunteer program. Refer to Snow et al. (2007) for information related to adults collected for these programs.

9.2 Hatchery Rearing

Rearing History

Number of eggs taken

Broodstock for the Turtle Rock summer Chinook are collected at Wells Dam and consist of volunteers to the hatchery. In recent years some naturally produced fish have been incorporated into the brood. Eyed eggs are transferred from Wells FH to Eastbank FH for rearing. As such, the number of green (unfertilized) eggs collected for this program is reported as egg inventory and distribution reports provided by Wells FH personnel.

Disease

Within the normal and accelerated subyearling program, the primary cause of mortality in the early life stages (swim-up to early ponding) continues to be coagulated yolk as a result of lack of chilled water during incubation. No additional significant health concerns were encountered with the two subyearling groups during rearing and no treatments were recommended. External fungus was diagnosed in the yearling program in December. No further issue developed after treatment. No additional disease-related problems were noted before the fish were released.

Number of acclimation days

Rearing of the 2008-brood normal and accelerated subyearling Turtle Rock summer Chinook was similar to previous years with fish being held on well water before being transferred to Turtle Rock for final acclimation on 11 May 2009. Both rearing groups were released on 11 June 2009 after 32 days of acclimation on Columbia River water. One group of yearling Turtle Rock summer Chinook was released on 7 May 2010, after 180 days of acclimation on Columbia River water. The Chelan River net pen group was released on 29 April, after 165 days of acclimation on Chelan River water.

Release Information

Numbers released

The 2009 subyearling Turtle Rock summer Chinook program achieved 88.0% of the 810,000 target goal with about 713,130 fish being released (Table 9.1). The accelerated subyearling summer Chinook program was discontinued; however, releases of accelerated subyearling Chinook in past years are shown in Table 9.2. It is important to note that the subyearling program has been terminated. Production (400,000 fish) from the subyearling programs was converted to the yearling program.

The 2008 yearling summer Chinook program achieved 75.6% of the 600,000 target goal with about 453,761 fish being released (252,762 from Turtle Rock and 200,999 from the Chelan River net pens) (Table 9.3). Releases of 2009 yearling Chinook will be reported in the 2011 report.

Table 9.1. Numbers of Turtle Rock summer Chinook subyearlings released from the hatchery, 1995-2010. The release target for Turtle Rock summer Chinook subyearlings is 810,000 fish.

Brood year	Release year	CWT mark rate	Number of subyearlings released
1995	1996	0.1873	1,074,600
1996	1997	0.9653	385,215
1997	1998	0.9780	508,060
1998	1999	0.6453	301,777
1999	2000	0.9748	369,026
2000	2001	0.3678	604,892
2001	2002	0.9871	214,059
2002	2003	0.3070	656,399
2003	2004	0.4138	491,480
2004	2005	0.4591	411,707
2005	2006	0.4337	490,074
2006	2007	0.3388	538,392
2007	2008	0.4385	439,806
2008	2009	0.6355	309,003
2009	2010	NA	713,130
2010	2011	Discontinued	
Average		***0.6111***	***500,508***

Table 9.2. Numbers of Turtle Rock summer Chinook accelerated subyearlings released from the hatchery, 1995-2009. The release target for Turtle Rock summer Chinook accelerated subyearlings is 810,000 fish.

Brood year	Release year	CWT mark rate	Number of subyearlings released
1995	1996	0.9834	169,000
1996	1997	0.4163	477,300
1997	1998	0.3767	521,480
1998	1999	0.6033	307,571
1999	2000	0.9556	347,946
2000	2001	0.4331	449,329
2001	2002	0.4086	480,584
2002	2003	0.5492	364,461
2003	2004	0.6414	289,696
2004	2005	0.5471	364,453
2005	2006	0.9783	457,340

Brood year	Release year	CWT mark rate	Number of subyearlings released
2006	2007	0.5510	342,273
2007	2008	0.4745	392,024
2008	2009	0.5295	372,320
2009	2010	Discontinued	
Average		***0.6034***	***381,127***

Table 9.3. Numbers of Turtle Rock summer Chinook yearling smolts released from the hatchery, 1995-2008. The release target for Turtle Rock summer Chinook is 200,000 smolts.

Brood year	Release year	Acclimation facility	CWT mark rate	Number of smolts released
1995	1997	Turtle Rock	0.9688	150,000
1996	1998	Turtle Rock	0.9582	202,727
1997	1999	Turtle Rock	0.9800	202,989
1998	2000	Turtle Rock	0.9337	217,797
1999	2001	Turtle Rock	0.9824	285,707
2000	2002	Turtle Rock	0.9948	165,935
2001	2003	Turtle Rock	0.9824	203,279
2002	2004	Turtle Rock	0.9799	195,851
2003	2005	Turtle Rock	0.9258	215,366
2004	2006	Turtle Rock	0.9578	206,734
2005	2007	Turtle Rock	0.9810	204,644
2006	2008	Chelan	0.9752	99,271
		Turtle Rock	0.9752	43,943
2007	2009	Chelan	0.9426	112,604
		Turtle Rock	0.9426	61,003
2008	2010	Chelan	0.9818	200,999
		Turtle Rock	0.9818	252,762
Average			***0.9673***	***177,742***

Numbers tagged

About 53.0% of the 2008 Turtle Rock accelerated subyearling Chinook and 63.6% of the normal subyearling Chinook were adipose fin-clipped and CWT. The remaining fish were released untagged and unmarked. The 2008 yearling Chinook were 98.2% CWT and adipose fin-clipped.

In 2010, a total of 10,101 summer Chinook from the 2009 brood were PIT tagged at Ringold Fish Hatchery during 24-25 and 25-26 August. Fish were tagged in two groups of about 5,050 per group. One group consisted of Turtle Rock Hatchery fish and the other Chelan River Net Pens fish. Fish were not fed during tagging or for 1-2 days before and after tagging. Chinook from the Turtle Rock group averaged 88 mm in length and 7.6 g at time of tagging. Those from the Chelan Net Pens group averaged 82 mm in length and 6.6 g. As of the end of January 2011, 101 tagged Chinook have died (100 from the Turtle Rock group and one from the Chelan Net Pens group). No fish have shed their tags. This leaves 10,000 tagged summer Chinook alive at the end of the month.

Table 9.4 summarizes the number of yearling summer Chinook that have been PIT-tagged and released from the Turtle Rock Program.

Table 9.4. Summary of PIT-tagging activities for Turtle Rock yearling summer Chinook, brood years 2007-2009.

Brood year	Release year	Raceway/Program	Number of fish tagged	Number of tagged fish that died	Number of tags shed	Number of tagged fish released
2007	2009	Circular Reuse	10,104	128	1	9,975
		Standard	10,102	162	3	9,937
2008	2010	Circular Reuse	11,102	15	0	11,087
		Standard	11,100	18	2	11,080
2009	2011	Turtle Rock	5,050			
		Chelan Net Pens	5,050			

Fish size and condition at release

Size at release of the 2008 normal subyearling Turtle Rock summer Chinook was 76.8% and 69.3% of the target fork length and weight, respectively. This brood year was below the target CV for length by 12% (Table 9.5).

Table 9.5. Mean lengths (FL, mm), weight (g and fish/pound), and coefficient of variation (CV) of Turtle Rock summer Chinook subyearlings released from the hatchery, 1995-2008. Size targets are provided in the last row of the table.

Brood year	Release year	Fork length (mm)		Mean weight	
		Mean	CV	Grams (g)	Fish/pound
1995	1996	102	6.3	12.6	36
1996	1997	87	8.0	7.4	62
1997	1998	98	6.2	10.2	45
1998	1999	96	6.3	10.7	43
1999	2000	90	9.0	9.8	46
2000	2001	100	7.1	11.3	40
2001	2002	104	7.2	13.4	34
2002	2003	97	7.3	11.8	39
2003	2004	101	8.0	12.0	43
2004	2005	100	7.8	11.4	40
2005	2006	100	6.5	12.5	36
2006	2007	95	7.2	9.5	48
2007	2008	79	7.4	5.6	81
2008	2009	86	7.9	7.9	57

Brood year	Release year	Fork length (mm)		Mean weight	
		Mean	CV	Grams (g)	Fish/pound
Targets		***112***	***9.0***	***11.4***	***40***

Size at release of the 2008 accelerated subyearling Turtle Rock Chinook was 86.6% and 93.0% of the target fork length and weight, respectively. This brood year was below the target CV for length by 4% (Table 9.6).

Table 9.6. Mean lengths (FL, mm), weight (g and fish/pound), and coefficient of variation (CV) of Turtle Rock summer Chinook accelerated subyearlings released from the hatchery, 1995-2008. Size targets are provided in the last row of the table.

Brood year	Release year	Fork length (mm)		Mean weight	
		Mean	CV	Grams (g)	Fish/pound
1995	1996	129	7.1	27.3	17
1996	1997	107	6.5	15.6	29
1997	1998	117	6.0	18.9	24
1998	1999	119	8.0	18.9	24
1999	2000	114	6.7	19.0	24
2000	2001	111	7.0	16.8	27
2001	2002	117	8.4	19.5	23
2002	2003	116	11.3	21.2	21
2003	2004	113	14.9	17.0	30
2004	2005	117	11.3	20.1	23
2005	2006	119	9.1	22.2	21
2006	2007	118	8.3	19.1	24
2007	2008	95	7.7	10.0	45
2008	2009	97	8.6	10.6	43
Targets		***112***	***9.0***	***11.4***	***40***

Size at release of the 2008 yearling summer Chinook was 83.0% and 89.4% of the target fork length and weight, respectively, for the Chelan Falls group. This group also exceeded the target CV for length by 154%. The Turtle Rock group was 97.7% and 129.0% of the target fork length and weight, respectively, and exceeded the target CV for length by 77% (Table 9.7).

Table 9.7. Mean lengths (FL, mm), weight (g and fish/pound), and coefficient of variation (CV) of Turtle Rock summer Chinook yearlings released from the hatchery, 1995-2008. Size targets are provided in the last row of the table.

Brood year	Release year	Acclimation facility	Fork length (mm)		Mean weight	
			Mean	CV	Grams (g)	Fish/pound
1995	1997	Turtle Rock	-	-	-	-
1996	1998	Turtle Rock	166	14.2	60.9	7
1997	1999	Turtle Rock	198	4.6	91.3	5

Brood year	Release year	Acclimation facility	Fork length (mm)		Mean weight	
			Mean	CV	Grams (g)	Fish/pound
1998	2000	Turtle Rock	161	11.9	53.9	8
1999	2001	Turtle Rock	164	18.6	59.0	8
2000	2002	Turtle Rock	170	15.3	59.0	8
2001	2003	Turtle Rock	154	22.3	48.6	9
2002	2004	Turtle Rock	157	16.7	44.0	12
2003	2005	Turtle Rock	173	13.8	54.7	8
2004	2006	Turtle Rock	176	20.6	45.3	7
2005	2007	Turtle Rock	158	11.0	43.5	10
2006	2008	Chelan	172	14.5	58.4	8
		Turtle Rock	157	25.8	54.1	8
2007	2009	Chelan	153	18.8	45.7	10
		Turtle Rock	167	14.6	49.3	9
2008	2010	Chelan	146	22.9	40.6	11
		Turtle Rock	172	15.9	58.5	8
Targets			***176***	***9.0***	***45.4***	***10***

Survival Estimates

Normal subyearling releases

Overall survival of the normal subyearling Turtle Rock summer Chinook program from green egg to release was below the standard set for the program (Table 9.8). Lower than expected survival at ponding and post-ponding reduced the overall program performance.

Table 9.8. Hatchery life-stage survival rates (%) for Turtle Rock subyearling (zero program) summer Chinook, brood years 2004-2008. Survival standards or targets are provided in the last row of the table.

Brood year	Collection to spawning		Unfertilized egg-eyed	Eyed egg-ponding	30 d after ponding	100 d after ponding	Ponding to release	Transport to release	Unfertilized egg-release
	Female	Male							
2004	NA	NA	93.5	74.4	93.9	91.4	90.8	99.7	63.1
2005	NA	NA	94.4	87.9	85	84.8	84.2	99.4	69.8
2006	NA	NA	97.8	87.9	85.0	84.8	84.2	99.4	72.4
2007	NA	NA	92.7	84.9	88.5	86.7	84.8	99.6	66.7
2008	NA	NA	78.8	95.0	80.7	79.3	79.9	99.8	59.8
Standard	***90.0***	***85.0***	***92.0***	***98.0***	***97.0***	***93.0***	***90.0***	***95.0***	***81.0***

Accelerated subyearling releases

Overall survival of the accelerated subyearling Turtle Rock summer Chinook program from green egg to release was below the standard set for the program (Table 9.9). Lower than expected survival in post-ponding reduced the overall program performance.

Table 9.9. Hatchery life-stage survival rates (%) for Turtle Rock subyearling (accelerated program) summer Chinook, brood years 2004-2008. Survival standards or targets are provided in the last row of the table.

Brood year	Collection to spawning		Unfertilized egg-eyed	Eyed egg-ponding	30 d after ponding	100 d after ponding	Ponding to release	Transport to release	Unfertilized egg-release
	Female	Male							
2004	NA	NA	92.5	98.3	93.4	92.4	90.0	97.8	81.8
2005	NA	NA	93.8	94.6	83.7	83.4	81.7	98.8	72.5
2006	NA	NA	86.1	94.6	83.7	83.4	81.7	98.8	66.5
2007	NA	NA	93.4	95.4	78.4	77.5	76.3	98.9	67.9
2008	NA	NA	93.4	95.0	79.8	78.8	78.2	99.3	67.1
Standard	***90.0***	***85.0***	***92.0***	***98.0***	***97.0***	***93.0***	***90.0***	***95.0***	***81.0***

Yearling releases

Overall survival of the yearling Turtle Rock summer Chinook program from green egg to release was above the standard set for the program (Table 9.10). Higher than expected survivals in all life stages contributed to the increased program performance.

Table 9.10. Hatchery life-stage survival rates (%) for Turtle Rock yearling summer Chinook, brood years 2004-2008. Survival standards or targets are provided in the last row of the table.

Brood year	Collection to spawning		Un-fertilized egg-eyed	Eyed egg-ponding	30 d after ponding	100 d after ponding	Ponding to release	Transport to release	Un-fertilized egg-release
	Female	Male							
2004	NA	NA	92.9	97.7	96.8	96.4	95.5	99.6	86.7
2005	NA	NA	89.1	97.5	98.1	97.8	96.6	99.1	83.9
2006	NA	NA	86.2	78.8	97.6	97.1	95.2	98.7	64.8
2007 (Turtle Rock)	NA	NA	80.3	97.6	98.8	98.2	95.4	99.1	74.8
2007 (Chelan Falls)	NA	NA	80.3	97.6	98.8	98.2	94.9	97.1	74.4
2008 (Turtle Rock)	NA	NA	93.5	98.0	99.4	97.2	95.9	98.8	87.8
2008 (Chelan Falls)	NA	NA	93.5	98.0	97.6	98.7	96.4	99.3	88.2
Standard	***90.0***	***85.0***	***92.0***	***98.0***	***97.0***	***93.0***	***90.0***	***95.0***	***81.0***

9.3 Life History Monitoring

Life history characteristics of Turtle Rock summer Chinook were assessed by examining carcasses on spawning grounds and by reviewing tagging data and fisheries statistics.

Contribution to Fisheries

Normal subyearling releases

Most of the harvest on Turtle Rock summer Chinook (normal subyearling releases) occurred in the Ocean (10-100% of the fish harvested; Table 9.11). Brood year 1995, 1999, and 2001 provided the largest total harvests, while brood year 1997 and 2003 provided the lowest.

Table 9.11. Estimated number and percent (in parentheses) of Turtle Rock summer Chinook (normal subyearling releases) captured in different fisheries, brood years 1995-2004.

Brood year	Ocean fisheries	Columbia River Fisheries			Total
		Tribal	Commercial (Zones 1-5)	Recreational (sport)	
1995	693 (84)	106 (13)	11 (1)	16 (2)	826
1996	74 (80)	0 (0)	5 (5)	13 (14)	92
1997	10 (100)	0 (0)	0 (0)	0 (0)	10
1998	21 (100)	0 (0)	0 (0)	0 (0)	21
1999	184 (64)	26 (9)	4 (1)	75 (26)	289
2000	36 (55)	8 (12)	8 (12)	14 (21)	66
2001	164 (64)	30 (12)	20 (8)	44 (17)	258
2002	23 (20)	33 (29)	3 (3)	56 (49)	115
2003	9 (10)	55 (61)	2 (2)	24 (27)	90
2004	42 (37)	29 (25)	2 (2)	42 (37)	115

Accelerated subyearling releases

Most of the harvest on Turtle Rock summer Chinook (accelerated subyearling releases) occurred in ocean fisheries (Table 9.12). Ocean harvest has made up 27% to 100% of all Turtle Rock summer Chinook harvested (no fish from the 2003 brood year were harvested). Brood year 1999 provided the largest total harvest, while brood years 1995, 1997, 2002, and 2003 provided the lowest.

Table 9.12. Estimated number and percent (in parentheses) of Turtle Rock summer Chinook (accelerated subyearling releases) captured in different fisheries, brood years 1995-2004.

Brood year	Ocean fisheries	Columbia River Fisheries			Total
		Tribal	Commercial (Zones 1-5)	Recreational (sport)	
1995	3 (100)	0 (0)	0 (0)	0 (0)	3
1996	77 (89)	5 (6)	5 (6)	0 (0)	87
1997	3 (100)	0 (0)	0 (0)	0 (0)	3
1998	97 (95)	2 (2)	3 (3)	0 (0)	102
1999	1,029 (76)	142 (10)	12 (1)	178 (13)	1,361
2000	117 (100)	0 (0)	0 (0)	0 (0)	117
2001	205 (59)	49 (14)	13 (4)	80 (23)	347
2002	9 (100)	0 (0)	0 (0)	0 (0)	9
2003	0 (0)	0 (0)	0 (0)	0 (0)	0
2004	45 (27)	80 (48)	6 (4)	34 (21)	165

Yearling releases

Most of the harvest on Turtle Rock summer Chinook (yearling releases) occurred in ocean fisheries (Table 9.13). Ocean harvest has made up 43% to 95% of all Turtle Rock summer

Chinook harvested. Brood year 1998 provided the largest harvest, while brood year 1995 provided the lowest.

Table 9.13. Estimated number and percent (in parentheses) of Turtle Rock summer Chinook (yearling releases) captured in different fisheries, brood years 1995-2004.

Brood year	Ocean fisheries	Columbia River Fisheries			Total
		Tribal	Commercial (Zones 1-5)	Recreational (sport)	
1995	451 (75)	51 (8)	32 (5)	70 (12)	604
1996	770 (95)	14 (2)	2 (0)	21 (3)	807
1997	2,836 (91)	61 (2)	27 (1)	176 (6)	3,100
1998	4,299 (90)	224 (5)	16 (0)	230 (5)	4,769
1999	1,660 (73)	233 (10)	7 (0)	382 (17)	2,282
2000	1,123 (73)	129 (8)	48 (3)	244 (16)	1,544
2001	1,918 (59)	453 (14)	178 (5)	728 (22)	3,277
2002	1,008 (50)	384 (19)	102 (5)	536 (26)	2,030
2003	749 (47)	421 (26)	69 (4)	360 (23)	1,599
2004	837 (43)	516 (26)	96 (5)	502 (26)	1,951

Straying

Normal subyearling releases

Rates of Turtle Rock summer Chinook (normal subyearling releases) straying into spawning areas in the upper basin have been low (Table 9.14). Although a few Turtle Rock summer Chinook have strayed into other spawning areas, straying, on average, has been less than 5%. The Chelan tailrace has received the largest number of Turtle Rock strays.

Table 9.14. Number (No.) and percent of spawning escapements within other non-target basins that consisted of Turtle Rock summer Chinook (normal subyearling releases), return years 1998-2007. For example, for return year 2003, 0.6% of the summer Chinook spawning escapement in the Okanogan Basin consisted of Turtle Rock summer Chinook. Percent strays should be less than 5%.

Return year	Wenatchee		Methow		Okanogan		Chelan		Entiat		Hanford Reach	
	No.	%	No.	%	No.	%	No.	%	No.	%	No.	%
1998	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
1999	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
2000	8	0.1	3	0.3	13	0.4	63	9.5	0	0.0	0	0.0
2001	0	0.0	5	0.2	13	0.1	0	0.0	0	0.0	0	0.0
2002	0	0.0	0	0.0	13	0.1	0	0.0	0	0.0	0	0.0
2003	7	0.1	7	0.2	19	0.6	6	1.4	0	0.0	0	0.0
2004	5	0.0	4	0.2	13	0.2	6	1.4	0	0.0	0	0.0
2005	5	0.1	0	0.0	5	0.1	0	0.0	2	0.5	0	0.0
2006	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
2007	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0

Return year	Wenatchee		Methow		Okanogan		Chelan		Entiat		Hanford Reach	
	No.	%	No.	%	No.	%	No.	%	No.	%	No.	%
Total	***25***	***0.03***	***19***	***0.08***	***76***	***0.12***	***75***	***1.72***	***2***	***0.06***	***0***	***0.00***

On average, about 31% of the brood year returns have strayed into spawning areas in the upper basin (Table 9.15). Depending on brood year, percent strays into spawning areas have ranged from 0-100%. Few (0.9% on average) have strayed into non-target hatchery programs.

Table 9.15. Number and percent of Turtle Rock summer Chinook (normal subyearling releases) that homed to the target hatchery and strayed to non-target spawning areas and non-target hatchery programs, by brood years 1995-2004.

Brood year	Homing				Straying			
	Target stream		Target hatchery		Non-target streams		Non-target hatcheries	
	Number	%	Number	%	Number	%	Number	%
1995	-	-	197	74.1	64	24.1	5	1.9
1996	-	-	54	54.5	44	44.4	1	1.0
1997	-	-	2	28.6	5	71.4	0	0.0
1998	-	-	0	0.0	24	100.0	0	0.0
1999	-	-	40	43.5	52	56.5	0	0.0
2000	-	-	5	50.0	5	50.0	0	0.0
2001	-	-	56	77.8	16	22.2	0	0.0
2002	-	-	10	100.0	0	0.0	0	0.0
2003	-	-	27	100.0	0	0.0	0	0.0
2004	-	-	71	100.0	0	0.0	0	0.0
Total	***-***	***-***	***462***	***68.1***	***210***	***31.0***	***6***	***0.9***

Accelerated subyearling releases

Rates of Turtle Rock summer Chinook (accelerated subyearling releases) straying into spawning areas in the upper basin have been low (Table 9.16). Although a few Turtle Rock summer Chinook have strayed into other spawning areas, straying, on average, has been less than 2%. The Chelan tailrace, Entiat Basin, and Methow Basin have received the largest number of Turtle Rock strays.

Table 9.16. Number (No.) and percent of spawning escapements within other non-target basins that consisted of Turtle Rock summer Chinook (accelerated subyearling releases), return years 1998-2007. For example, for return year 2001, 0.2% of the summer Chinook spawning escapement in the Methow Basin consisted of Turtle Rock summer Chinook. Percent strays should be less than 5%.

Return year	Wenatchee		Methow		Okanogan		Chelan		Entiat		Hanford Reach	
	No.	%	No.	%	No.	%	No.	%	No.	%	No.	%
1998	3	0.1	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
1999	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0

Return year	Wenatchee		Methow		Okanogan		Chelan		Entiat		Hanford Reach	
	No.	%	No.	%	No.	%	No.	%	No.	%	No.	%
2000	7	0.1	0	0.0	0	0.0	24	3.6	0	0.0	0	0.0
2001	0	0.0	12	0.4	31	0.3	0	0.0	0	0.0	0	0.0
2002	0	0.0	5	0.1	0	0.0	0	0.0	0	0.0	0	0.0
2003	0	0.0	45	1.1	0	0.0	22	5.3	13	1.9	16	0.0
2004	0	0.0	7	0.3	0	0.0	14	3.3	0	0.0	18	0.0
2005	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
2006	0	0.0	0	0.0	0	0.0	0	0.0	2	0.3	0	0.0
2007	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
Total	***10***	***0.01***	***69***	***0.30***	***31***	***0.05***	***60***	***1.38***	***15***	***0.43***	***34***	***0.01***

On average, about 41% of the brood year returns have strayed into spawning areas in the upper basin (Table 9.17). Depending on brood year, percent strays into spawning areas have ranged from 0-83%. Few (<1% on average) have strayed into non-target hatchery programs.

Table 9.17. Number and percent of Turtle Rock summer Chinook (accelerated subyearling releases) that homed to the target hatchery and strayed to non-target spawning areas and non-target hatchery programs, by brood years 1995-2004.

Brood year	Homing				Straying			
	Target stream		Target hatchery		Non-target streams		Non-target hatcheries	
	Number	%	Number	%	Number	%	Number	%
1995	-	-	7	70.0	3	30.0	0	0.0
1996	-	-	33	54.5	69	67.6	0	0.0
1997	-	-	6	28.6	0	0.0	0	0.0
1998	-	-	2	16.7	10	83.3	0	0.0
1999	-	-	138	54.1	117	45.9	0	0.0
2000	-	-	12	40.0	18	60.0	0	0.0
2001	-	-	57	96.6	2	3.4	0	0.0
2002	-	-	0	0.0	0	0.0	0	0.0
2003	-	-	3	100.0	0	0.0	0	0.0
2004	-	-	90	76.9	27	23.1	0	0.0
Total	***-***	***-***	***348***	***58.6***	***246***	***41.4***	***0***	***0.0***

Yearling releases

Rates of Turtle Rock summer Chinook (yearling releases) straying into spawning areas in the upper basin have varied widely depending on spawning area (Table 9.18). Most of these fish strayed to spawning areas within the Chelan tailrace, Entiat Basin, and Methow Basin. Relatively few, on average, have strayed to spawning areas in the Okanogan Basin, Wenatchee Basin, and the Hanford Reach.

Table 9.18. Number (No.) and percent of spawning escapements within other non-target basins that consisted of Turtle Rock summer Chinook (yearling releases), return years 1998-2007. For example, for return year 2003, 4.3% of the summer Chinook spawning escapement in the Methow Basin consisted of Turtle Rock summer Chinook. Percent strays should be less than 5%.

Return year	Wenatchee		Methow		Okanogan		Chelan		Entiat		Hanford Reach	
	No.	%	No.	%	No.	%	No.	%	No.	%	No.	%
1998	0	0.0	2	0.3	0	0.0	0	0.0	0	0.0	0	0.0
1999	3	0.1	2	0.2	0	0.0	0	0.0	0	0.0	0	0.0
2000	18	0.3	57	4.8	167	4.5	73	11.0	0	0.0	10	0.0
2001	109	1.0	523	18.9	334	3.1	316	32.1	0	0.0	7	0.0
2002	92	0.6	437	9.4	194	1.4	191	32.8	136	27.1	0	0.0
2003	64	0.5	170	4.3	14	0.4	165	39.4	180	26.0	9	0.0
2004	10	0.1	51	2.3	116	1.7	75	17.9	0	0.0	0	0.0
2005	5	0.1	73	2.9	73	0.8	88	19.8	42	11.4	0	0.0
2006	0	0.0	100	3.7	25	0.3	64	15.2	9	1.6	0	0.0
2007	0	0.0	65	4.8	31	0.7	40	21.2	20	8.2	19	0.1
Total	***301***	***0.31***	***1,480***	***6.42***	***954***	***1.46***	***1,012***	***23.24***	***387***	***11.02***	***45***	***0.01***

On average, about 66% of the brood year returns have strayed into spawning areas in the upper basin (Table 9.19). Depending on brood year, percent strays into spawning areas have ranged from 37-86%. Few (<1% on average) have strayed into non-target hatchery programs.

Table 9.19. Number and percent of Turtle Rock summer Chinook (yearling releases) that homed to the target hatchery and strayed to non-target spawning areas and non-target hatchery programs, by brood years 1995-2004.

Brood year	Homing				Straying			
	Target stream		Target hatchery		Non-target streams		Non-target hatcheries	
	Number	%	Number	%	Number	%	Number	%
1995	-	-	180	39.3	278	60.7	0	0.0
1996	-	-	218	27.2	583	72.8	0	0.0
1997	-	-	254	14.2	1,531	85.6	3	0.2
1998	-	-	166	16.1	864	83.8	1	0.1
1999	-	-	181	42.7	243	57.3	0	0.0
2000	-	-	89	27.4	236	72.6	0	0.0
2001	-	-	389	59.8	261	40.2	0	0.0
2002	-	-	303	57.8	220	42.0	1	0.2
2003	-	-	373	62.8	220	37.0	1	0.2
2004	-	-	279	57.9	203	42.1	0	0.0
Total	***-***	***-***	***2,432***	***34.4***	***4,639***	***65.6***	***6***	***0.1***

Smolt-to-Adult Survivals

Subyearling-to-adult and smolt-to-adult survival ratios (SARs) were calculated as the number of hatchery adult recaptures divided by the number of tagged hatchery subyearling or yearling Chinook released. SARs were based on CWT returns.

Normal subyearling releases

For the available brood years, SARs for normal subyearling-released Chinook have ranged from 0.000034 to 0.001562 (Table 9.20).

Table 9.20. Subyearling-to-adult ratios (SARs) for Turtle Rock normal subyearling-released summer Chinook, brood years 1995-2004.

Brood year	Number released[a]	Estimated adult captures[b]	SAR
1995	201,230	205	0.001019
1996	371,848	190	0.000511
1997	496,904	17	0.000034
1998	194,723	28	0.000144
1999	197,793	203	0.001026
2000	222,460	28	0.000126
2001	211,306	330	0.001562
2002	200,163	38	0.000190
2003	203,410	49	0.000241
2004	198,019	90	0.000455
Average	***249,786***	***118***	***0.000472***

[a] Includes all tag codes and CWT released fish (CWT + Ad Clip fish and CWT-only fish).

[b] Includes estimated recoveries (spawning ground, hatcheries, harvest, etc.) and observed recoveries if estimated recoveries were unavailable.

Accelerated subyearling releases

For the available brood years, SARs for accelerated subyearling-released Chinook have ranged from 0.000011 to 0.004619 (Table 9.21).

Table 9.21. Subyearling-to-adult ratios (SARs) for Turtle Rock accelerated subyearling-released summer Chinook, brood years 1995-2004.

Brood year	Number released[a]	Estimated adult captures[b]	SAR
1995	166,203	13	0.000078
1996	198,720	79	0.000398
1997	196,459	3	0.000015
1998	185,551	69	0.000372
1999	192,665	890	0.004619
2000	194,603	63	0.000324
2001	196,355	167	0.000851
2002	200,165	5	0.000025
2003	185,834	2	0.000011

Brood year	Number released[a]	Estimated adult captures[b]	SAR
2004	203,255	156	0.000768
Average	***191,981***	***145***	***0.000754***

[a] Includes all tag codes and CWT released fish (CWT + Ad Clip fish and CWT-only fish).

[b] Includes estimated recoveries (spawning ground, hatcheries, harvest, etc.) and observed recoveries if estimated recoveries were unavailable.

Yearling releases

For the available brood years, SARs for yearling-released Chinook have ranged from 0.007184 to 0.026799 (Table 9.22).

Table 9.22. Smolt-to-adult ratios (SARs) for Turtle Rock yearling-released summer Chinook, brood years 1995-2004.

Brood year	Number released[a]	Estimated adult captures[b]	SAR
1995	145,318	1,044	0.007184
1996	194,251	1,557	0.008015
1997	198,924	4,814	0.024200
1998	215,646	5,779	0.026799
1999	280,683	2,673	0.009523
2000	165,072	1,868	0.011316
2001	199,694	3,884	0.019450
2002	192,234	2,525	0.013135
2003	199,386	2,045	0.010256
2004	202,682	2,404	0.011861
Average	***199,389***	***2,859***	***0.014340***

[a] Includes all tag codes and CWT released fish (CWT + Ad Clip fish and CWT-only fish).

[b] Includes estimated recoveries (spawning ground, hatcheries, harvest, etc.) and observed recoveries if estimated recoveries were unavailable.

9.4 ESA/HCP Compliance

Broodstock Collection

The 2008 brood Turtle Rock summer Chinook program is supported through adult collections at the volunteer trap at Wells Fish Hatchery and in conjunction with the Wells summer Chinook collections. During 2008, broodstock collections at the volunteer trap were consistent with the 2008 Upper Columbia River Salmon and Steelhead Broodstock Objectives and site-based broodstock collection protocols as required in ESA permit 1347. The 2008 collection totaled 1,388 summer Chinook (combined Wells Fish Hatchery and Turtle Rock Fish Hatchery programs), representing 99.6% of the targeted 1,393 broodstock collection objective. The minor difference in adult broodstock was a result of enumeration errors during collection.

Hatchery Rearing and Release

Brood year 2008 releases totaled 1,135,084 fish, including yearling, regular subyearling, and accelerated subyearling releases (453,761, 309,003, and 372,320 juveniles, respectively). These releases represented 62.3% of the Rocky Reach HCP and ESA Section 10 Permit 1347 production for the combined Turtle Rock yearling and subyearling production.

Consistent with ESA Permit 1347, a total of 393,856 normal and accelerated subyearling Chinook were adipose fin clipped and coded-wire tagged, representing 98.5% of the 400,000 adipose clipped and CWT target for sub-yearling production. The remainder of the subyearling production was released untagged and unmarked. The yearling Chinook were 98.2% CWT and adipose fin-clipped. About 22,167 2008 brood Turtle Rock yearling summer Chinook were PIT tagged. See Section 9.2 for specific rearing, tagging, and release information related to the 2008 brood Turtle Rock summer Chinook program.

Hatchery Effluent Monitoring

Per ESA Permits 1196, 1347, and 1395, permit holders shall monitor and report hatchery effluents in compliance with applicable National Pollution Discharge Elimination Systems (NPDES) (EPA 1999) permit limitations. There were no NPDES violations reported at Chelan PUD Hatchery facilities during the period 1 January 2010 through 31 December 2010. NPDES monitoring and reporting for Chelan PUD Hatchery Programs during 2010 are provided in Appendix E.

SECTION 10: REFERENCES

Blankenship, S. M., J. Von Bargen, K. I Warheit, and A R. Murdoch. 2007. Assessing the genetic diversity of natural Chiwawa River spring Chinook salmon and evaluating the effectiveness of its supportive hatchery supplementation program. Washington Department of Fish and Wildlife Molecular Genetics Lab, Olympia, WA.

Environmental Protection Agency (EPA). 1999. National pollutant discharge elimination systems (NPDES) permit program.

Hays, S., T. Hillman, T. Kahler, R. Klinge, R. Langshaw, B. Lenz, A. Murdoch, K. Murdoch, and C. Peven. 2006. Analytical framework for monitoring and evaluating PUD hatchery programs. Final report to the HCP Hatchery Committee, Wenatchee, WA.

Hillman, T., J. Mullan, and J. Griffith. 1992. Accuracy of underwater counts of juvenile Chinook salmon, coho salmon, and steelhead. North American Journal of Fisheries Management 12:589-603.

Hillman, T. and M. Miller. 2004. Abundance and total numbers of Chinook salmon and trout in the Chiwawa River Basin, Washington, 2004. BioAnalysts, Inc. Report to Chelan County PUD, Wenatchee, WA.

HSRG/WDFW/NWIFC. 2004. Integrated hatchery programs. HSRG/WDFW/NWIFC Technical discussion paper #1, 21 June 2004, Portland, OR.

Hyatt, K., M. Stockwell, H. Wright, K. Long, J. Tamblyn, and M. Walsh. 2006. Fish and water management tool project assessments: Okanogan adult sockeye salmon (Oncorhynchus nerka) abundance and biological traits in 2005. Draft report to JSID-SRe 3-05, Salmon and Freshwater Ecosystems Division, Fisheries and Oceans Canada, Nanaimo, B.C.

Kassler, W., S. Blankenship, and A. Murdoch. 2011. Genetic structure of upper Columbia River summer Chinook and evaluation of the effects of supplementation programs. Washington Department of Fish and Wildlife Molecular Genetics Lab, Olympia, WA.

Miller, T. 2008. 2007 Chiwawa and Wenatchee River smolt estimates. Technical memorandum from Todd Miller, WDFW to the HCP Hatchery Committee, 13 February 2008, Wenatchee, WA.

Miller, T. and M. Tonseth. 2008. The integrated status and effectiveness monitoring program: expansion of smolt trapping and steelhead spawning survey. Annual report to the U.S. Department of Energy, Bonneville Power Administration, Division of Fish and Wildlife, Portland, OR.

Murdoch, A. and C. Peven. 2005. Conceptual approach to monitoring and evaluating the Chelan County Public Utility District hatchery programs. Final report. Prepared for the Chelan PUD Habitat Conservation Plan's Hatchery Committee, Wenatchee, WA.

Murdoch, A., T. Pearsons, T. Maitland, M. Ford, and K. Williamsons. 2006. Monitoring the reproductive success of naturally spawning hatchery and natural spring Chinook salmon in the Wenatchee River. BPA Project No. 2003-039-00, Department of Energy, Bonneville Power Administration, Portland, OR.

Murdoch, A., T. Pearsons, T. Maitland, C. Deason, M. Ford, and K. Williamsons. 2007. Monitoring the reproductive success of naturally spawning hatchery and natural spring Chinook salmon in the Wenatchee River. BPA Project No. 2003-039-00, Contract No. 00020391, Department of Energy, Bonneville Power Administration, Portland, OR.

Murdoch, A., T. Pearsons, T. Maitland, M. Ford, and K. Williamsons. 2008. Monitoring the reproductive success of naturally spawning hatchery and natural spring Chinook salmon in the Wenatchee River. BPA Project No. 2003-039-00, Contract No. 00032138, Department of Energy, Bonneville Power Administration, Portland, OR.

NMFS (National Marine Fisheries Service). 2003. Section 10(a)(1)(b) Permit for takes of endangered/threatened species. Incidental Take Permit 1347 for the artificial propagation of unlisted salmon. Portland, OR.

NMFS (National Marine Fisheries Service). 2004. Biological Opinion and Magnuson-Stevens Fishery Conservation and Management Act Consultation Interim Protection Plan for Operation of the Priest Rapids Hydroelectric Project FERC Project No. 2114 Columbia River, Grant and Kittitas Counties, Washington Action Agency: Federal Energy Regulatory Commission Consultation Conducted by: NOAA Fisheries Northwest Region Hydropower Division NOAA Fisheries Log Number: 1999/01878. May 3, 2004.

Peven, C. 2007. Chelan County PUD Hatchery monitoring and evaluation implementation plan, 2008. Chelan County Public Utility District. Prepared for the Chelan PUD Habitat Conservation Plan's Hatchery Committee, Wenatchee, WA.

Snow, C. 2007. Wells Hatchery summer Chinook salmon production; 1997 brood year summary report. Washington Department of Fish and Wildlife. Prepared for Douglas County Public Utility District, East Wenatchee, WA.

Truscott, K. 2005. Memo to Habitat Conservation Plan (HCP) Hatchery Committee (HC). Brood year 2005-2013 Upper Columbia steelhead stocking allotments for releases in the Wenatchee River basin. February 28, 2005 memo from K. Truscott, Washington Department of Fish and Wildlife, Wenatchee, WA.

Washington Department of Fish and Wildlife (WDFW). 2006. Memo to Habitat Conservation Plan (HCP) Hatchery Committee (HC). 2006 Upper Columbia River salmon and steelhead broodstock objectives and site-based broodstock collection protocols. Memo from K. Truscott, Washington Department of Fish and Wildlife, Wenatchee, WA.

SECTION 11: APPENDICES

Appendix A: **Abundance and Total Numbers of Chinook Salmon and Trout in the Chiwawa River Basin, Washington, 2010.**

Appendix B: **Fish Trapping at the Chiwawa, Upper Wenatchee, and Lower Wenatchee Smolt Traps during 2010.**

Appendix C: **Summary of ISEMP PIT Tagging Activities in the Wenatchee Basin, 2010.**

Appendix D: **Wenatchee Steelhead Spawning Ground Surveys, 2010.**

Appendix E: **NPDES Hatchery Effluent Monitoring, 2010.**

Appendix F: **Steelhead Stock Assessment at Priest Rapids Dam, 2010.**

Appendix G: **Wenatchee Sockeye and Summer Chinook Spawning Ground Surveys, 2010.**

Appendix H: **Genetic Diversity of Wenatchee Sockeye Salmon.**

Appendix I: **Genetic Diversity of Natural Chiwawa River Spring Chinook Salmon.**

Appendix J: **Genetic Diversity of Upper Columbia Summer Chinook Salmon.**

Appendix K: **Summer Chinook Spawning Ground Surveys in the Methow and Okanogan Basin, 2010.**

APPENDIX A

Abundance and Total Numbers of Chinook Salmon and Trout in the Chiwawa River Basin, Washington, 2010.

BioAnalysts, Inc.℠
4725 North Cloverdale Road, Ste 102
Boise Idaho 83713

January 25, 2011

TO: HCP Hatchery Committee

FROM: Tracy Hillman

Subject: Abundance and Total Numbers of Chinook Salmon and Trout in the Chiwawa River Basin, Washington, 2010

The Chelan County Public Utility District (PUD) hatchery program is operated through a habitat conservation program (HCP) that was incorporated into the PUD's license in 2004. The HCP directed the signatories to develop a monitoring and evaluation plan within one year of the effective date. This resulted in the development of the Conceptual Approach to Monitoring and Evaluating the Chelan County Public Utility District Hatchery Programs (Murdoch and Peven 2005). This study will help the HCP Hatchery Committee determine if it is meeting Objective 7 in the monitoring and evaluation plan (Murdoch and Peven 2005).

Objective 7: *Determine if the proportion of hatchery fish on the spawning grounds affects the freshwater productivity (i.e., number of juveniles per redd) of supplemented streams when compared to non-supplemented streams.*

We estimated densities and total numbers of age-0 spring Chinook salmon *Oncorhynchus tshawytscha*, trout *Oncorhynchus* sp., and char *Salvelinus* sp. in the Chiwawa River Basin, Washington, in August 2010. This was the 18th year of an ongoing study to assess the freshwater productivity (juveniles/redd) of Chinook salmon in the Chiwawa Basin. We used landscape classification to stratify streams in the basin that supported juvenile Chinook salmon (Hillman and Miller 2004). Classification "explained" most of the variability in fish numbers caused by geology, land type, valley bottom type, stream state condition, and habitat type. We identified ten reaches on the lower 31 miles (50 km) of the Chiwawa River and one reach in each of Phelps, Rock, Chikamin, Big Meadow, Alder, Brush, Clear, Y, and Unnamed[1] creeks (Figure 1). Each reach consisted of several combinations of state-type and habitat-type strata. We used classification to find reference areas for reaches in the Chiwawa River. We matched Reach 3 and Reach 8 of the Chiwawa River with a moderately-confined section of Nason Creek (RM 0.62-1.70) and an unconfined area of the Little Wenatchee River (RM 4.39-8.55), respectively

[1]Unnamed tributary that drains the eastside of Chiwawa Ridge. Its confluence with the Chiwawa River is about 1 mile (1.6 km) downstream from the mouth of Phelps Creek.

(Hillman and Miller 2004). Following methods described in Hillman and Miller (2004), we used underwater observations to estimate numbers of fish in 189 randomly selected sites.

During sampling in August 2010, discharge in the Chiwawa River averaged 333 cubic feet per second (cfs) and ranged from 182 to 641 cfs (Figure 2). Stream temperatures for the study period ranged from 9.0 to 18.5°C. Fish species observed in the Chiwawa Basin and reference areas during the 1992-2010 survey period[2] included: spring Chinook salmon, coho salmon *O. kisutch*, sockeye salmon *O. nerka* (in the Little Wenatchee River reference area), steelhead/rainbow trout *O. mykiss* (hatchery rainbow were present only in 1992 and 1993), cutthroat trout *O. clarki lewisi*, bull trout *S. confluentus*, brook trout *S. fontinalis*, mountain whitefish *Prosopium williamsoni*, dace *Rhinichthys* sp., suckers *Catostomus* sp., and sculpin *Cottus* sp. The age-0 spring Chinook that we observed in the Chiwawa Basin during the 2010 survey were produced from 421 redds counted in the fall of 2009 (Hillman et al. 2010). Assuming a mean fecundity of 4,573 eggs per female Chinook (from females collected for broodstock), and that no female produced more than one redd (Murdoch et al. 2009), we estimated that the Chiwawa River Basin was seeded with 1,925,233 eggs in 2009 (Appendix A).

In 2010, riffles made up the largest fraction of habitat types in reaches of the Chiwawa Basin (53% of the total stream surface area) (Table 1). Pools (23%), glides (8%), and multiple channels (16%) constituted the remaining 47% of the stream surface area. We consistently found woody debris associated with multiple-channel habitat.

Chinook Salmon Abundance

Chinook salmon were the most abundant salmonid in the Chiwawa Basin. We estimated, based on surface area, that age-0 Chinook salmon numbered 128,220 (±14% of the estimated total) in the Chiwawa River Basin in August 2010 (Table 2). Extrapolating based on volume of habitat types, age-0 Chinook numbered 132,526 (±26%) in the Chiwawa Basin. About 8% of the juvenile Chinook were in tributaries to the Chiwawa River. During the 1992-2010 surveys, numbers of age-0 Chinook ranged from 5,815 to 134,874 in the Chiwawa Basin (Figure 3; Appendix B). Most of the difference in juvenile numbers among years resulted from different seeding levels (Figure 4). Numbers of Chinook redds in the Chiwawa Basin during 1992-2010 ranged from 13 to 1,046, resulting in seeding levels of 66,248 to 4,836,704 eggs (Appendix A).

As in most years, age-0 Chinook in 2010 were distributed contagiously among reaches in the Chiwawa River (Table 2). In the Chiwawa River, densities of age-0 Chinook were highest in the upper reaches (Reaches 7-10). The highest densities in the Chiwawa Basin were in tributaries to the Chiwawa River (Table 2). Age-0 Chinook were most abundant in multiple channels and least abundant in glides and riffles. We found the majority of the Chinook associated with woody debris in multiple channels (multiple channel use index = 2.82)[3]. These sites (multiple channels)

---

[2] The study period 1992-2010 includes only 18 years of sampling because there was no sampling in 2000.

[3] The habitat use index was calculated as follows: Multiple channel use = ($parr_{mc}/parr_t$) / ($area_{mc}/area_t$), where $parr_{mc}$ = the number of parr counted in multiple channel habitat, $parr_t$ = the total number of parr counted within all habitat types, $area_{mc}$ = the area of multiple channel habitat within the sampling frame, and $area_t$ = the total area of the sampling frame. A multiple channel use index value of 1 would indicate that parr were uniformly distributed among habitat types and exhibited no preference for multiple habitat types. Values of the use index greater than 1 indicate

made up 16% of the total area of the Chiwawa Basin, but they provided habitat for 53% of all the age-0 Chinook in the basin in 2010 (Appendix C). In contrast, riffles made up 53% of the total area, but provided habitat for only 11% of all age-0 Chinook in the Chiwawa Basin (riffle use index = 0.25). Pools made up 23% of the total area and provided habitat for 34% of all age-0 Chinook in the basin (pool use index = 1.50). Few Chinook used glides that lacked woody debris (glide use index = 0.26).

As noted earlier, we assumed that the Chiwawa River was seeded with 1,925,233 Chinook eggs (421 redds times 4,573 eggs/female) in fall, 2009, and that at least 128,220 of those survived to August 2010. This means that the egg-to-parr survival was at least 6.7% (95% confidence bound 5.7-7.6%). During 1992-2010, egg-to-parr survival averaged 9.0% (range 2.7-19.1%) in the Chiwawa Basin (Appendix A). This survival rate comports with those from other streams. For example, Mullan et al. (1992) estimated an egg-to-parr survival rate of 9.8% for spring Chinook salmon in Icicle Creek, a tributary of the Wenatchee River. Using a Beverton and Holt model, Hubble (1993) estimated that egg-to-parr survival of Chinook in the Chewuck River, a tributary to the Methow River, ranged between 13% and 32%, depending on percent seeding level in the basin. Kiefer and Forster (1991) estimated a mean egg-to-parr survival rate of 5.5% (range 5.1-6.7%) for naturally-spawning spring Chinook salmon in the entire upper Salmon River. They also noted that egg-to-parr survival of natural spawners and adult outplants in the headwater streams of the upper Salmon River averaged 24.4% (range 16.1-32.0%). Petrosky (1990) reported an egg-to-parr survival range of 1.2-29.0% for Chinook in the upper Salmon River, Idaho. Konopacky et al. (1986) estimated egg-to-parr survival of Chinook in Bear Valley Creek, Idaho, as 8.1-9.4%. Work by Richards and Cernera (1987) in Bear Valley Creek indicated an egg-to-parr survival of 2.1%.

Mean densities of age-0 Chinook salmon in two reaches of the Chiwawa River were generally less than those in corresponding reference areas (Figure 5). Within both the Chiwawa River and its reference areas, pools and multiple channels consistently had the highest densities of age-0 Chinook.

We estimated a total of 291 (±31% of the estimated total) age-1+ Chinook salmon in the Chiwawa Basin in August 2010 (Table 3). In August 1992-2010, numbers of age-1+ Chinook ranged from 5 to 563 in the Chiwawa River Basin (Figure 3; Appendix B). These fish occurred throughout the Chiwawa River. We found relatively few age-1+ Chinook in tributaries. Age-1+ Chinook were most abundant in multiple channels and pools.

Juvenile Chinook Salmon Productivity (Fish/Redd)

Freshwater productivity of juvenile Chinook salmon was estimated as the number of parr (age-0 Chinook) per redd in the Chiwawa Basin. Theoretically, the relationship between number of parr and redds can be explained mathematically provided the relationship between the two parameters goes through the origin, increases monotonically at low spawning levels, and shows some level of density dependence at high spawning levels. We identified five alternative hypotheses that may explain the relationship between spawning level (redds) and numbers of age-0 Chinook:

---

use of multiple channels to a greater extent than the average, while scores between 0 and 1 indicate below-average use of multiple channel habitat.

1. The first hypothesis assumed that because of low spawner escapements, the number of juvenile Chinook increases linearly with increasing numbers of redds. This hypothesis assumes that there is no density dependence because of low seeding levels. This hypothesis was modeled with a density-independent function that took the form:

$$\boldsymbol{J = \alpha R}$$

where $\boldsymbol{J}$ is the number of juvenile (age-0) Chinook, $\boldsymbol{R}$ is the number or redds, and $\boldsymbol{\alpha}$ is the increase in numbers of juveniles with each incremental increase in redds.

2. The second hypothesis assumed that the number of juveniles increases constantly toward an asymptote as the number of redds increases. After the asymptote is reached, the number of juveniles neither increases nor decreases. The asymptote represents the maximum number of juveniles the system can support (i.e., carrying capacity for the system). This hypothesis was modeled with a Beverton-Holt curve that took the form:

$$\boldsymbol{J = \frac{(\alpha R)}{(\beta + R)}}$$

where $\boldsymbol{J}$ and $\boldsymbol{R}$ are as above, $\boldsymbol{\alpha}$ is the maximum number of juveniles produced, and $\boldsymbol{\beta}$ is the number of redds needed to produce (on average) juveniles equal to one-half the maximum number of juveniles.

3. The third hypothesis, like the second, assumed that the number of juveniles increases toward an asymptote (carrying capacity) as the number of redds increases. After the carrying capacity is reached, the number of juveniles neither increases nor decreases. The carrying capacity represents the maximum number of juveniles the system can support. This hypothesis was modeled with a smooth hockey stick function that took the form:

$$\boldsymbol{J = J_{\infty}\left(1 - e^{-\left(\frac{\alpha}{J_{\infty}}\right)R}\right)}$$

where $\boldsymbol{J}$ and $\boldsymbol{R}$ are as above, $\boldsymbol{\alpha}$ is the slope at the origin of the spawner-recruitment curve, and $\boldsymbol{J_{\infty}}$ is the carrying capacity of juveniles.

4. The fourth hypothesis assumed that the number of juveniles increases to a maximum and then declines as the number or redds increases. In this case, mortality rate of juveniles (or eggs) is proportional to the initial number of redds. Higher mortality rate is associated with density-dependent growth coupled with size-dependent predation. This hypothesis was modeled with a Ricker curve that took the form:

$$\boldsymbol{J = \alpha R e^{-\beta R}}$$

where $\boldsymbol{J}$ and $\boldsymbol{R}$ are as above, $\boldsymbol{\alpha}$ is the number of juveniles per redd at low spawning levels, and $\boldsymbol{\beta}$ describes how quickly the juveniles per redd drop as the number of redds increases.

5. The fifth hypothesis, like the second, assumed that the number of juveniles increases constantly, but unlike the second, the number of juveniles does not reach an asymptote. Rather, the number of juveniles increases indefinitely, but at a slowing rate of increase. This hypothesis was modeled with both a Cushing curve and a Gamma function. The

Cushing curve took the form:

$$J = \alpha R^{\gamma}$$

where J and R are as above, α is the number of juveniles per redd at low spawning levels, and γ describes the level of density dependence at high spawning levels. The Gamma function is a three-parameter model that has the form:

$$J = \alpha R^{\gamma} e^{-\beta R}.$$

This is an un-normalized gamma function that is similar to the Cushing curve when $\beta = 0$.

We used Akaike's Information Criterion for small sample size (AIC_c) to determine which model(s) best explained the productivity of juvenile Chinook in the Chiwawa Basin. AIC_c was estimated as:

$$AIC_c = -2log\big(£(\theta|data)\big) + 2K + \left(\frac{2K(K+1)}{n-K-1}\right)$$

where $log(£(\theta|data))$ is the maximum likelihood estimate, K is the number of estimable parameters (structural parameters plus the residual variance parameter), and n is the sample size (Burnham and Anderson 2002). We used least-squares methods to estimate $log(£(\theta|data))$, which was calculated as $log(\sigma^2)$, where σ^2 = residual sum of squares divided by the sample size ($\sigma^2 = RSS/n$). AIC_c assesses model fit in relation to model complexity (number of parameters). The model with the smallest AIC_c value represents the "best approximating" model within the model set. Remaining models were ranked relative to the best model using AIC_c difference scores (ΔAIC_c), Akaike weights (w_i), and evidence ratios. Models with ΔAIC_c values less than 2 indicate that there is substantial support for these models as being the best-fitting models within the set (Burnham and Anderson 2002). Models with values greater than 2 have less support. Akaike weights are probabilities estimating the strength of the evidence supporting a particular model as being the best model within the model set. Models with small w_i values are less plausible as competing models (Burnham and Anderson 2002). If no single model could be specified as the best model, a "best subset" of competing models was identified using (1) AIC_c differences to indicate the level of empirical support each model had as being the best model, (2) evidence ratios based on Akaike weights to indicate the relative probability that any model is the best model, and (3) coefficients of determination (R^2) assessing the explanatory power of each model.

The use of AIC_c indicated that the Beverton-Holt model best approximated the information in the juveniles/redd data (Table 4; Figure 6). The estimated structural parameters for this model were:

$$Juveniles = \frac{(133{,}561 \times Redds)}{(158 + Redds)}$$

where the estimated standard errors of the two parameters were 24,529 and 81,561, respectively. The adjusted $R^2 = 0.81$. The second-best model was the Ricker model, which was 5.99 AIC_c units from the best model (Table 4; Figure 6). The estimated parameters for this model were:

$$Juveniles = 603 \times Redds \times e^{-(0.00187 \times Redds)}$$

where the estimated standard errors of the two parameters were 77 and 0.00035, respectively, and the R^2 = 0.73. The AIC_c difference scores, Akaike weights, and evidence ratios indicated that there was substantial support for the Beverton-Holt model (Table 4). There was less support for the remaining models (Ricker, Gamma[4], Cushing, smooth hockey stick, and Density Independent), which were > 4 AIC_c units from the best model. This was further supported by the fact that, relative to the best model, the remaining models had evidence ratios greater than 6.

Although the Beverton-Holt, Ricker, and smooth hockey stick models have different biological assumptions, they all indicated a density-dependent relationship between spawning levels (redds) and juvenile Chinook production. This was not only evident in the best approximating model, but there was also a significant negative relationship between juveniles per redd and numbers of redds in the Chiwawa Basin (Figure 7). Although data at high seeding levels are lacking, the Beverton-Holt model would limit the production of juvenile Chinook to less than about 250,000 parr in the basin (upper 95% CI of $\boldsymbol{\alpha}$ in the Beverton-Holt model). In contrast, the smooth hockey stick model, which did not fit the data as well as the Beverton-Holt model, would limit the carrying capacity for juvenile Chinook to about 210,000 parr (upper 95% CI of $\boldsymbol{J_\infty}$ in the smooth hockey stick model). Additional information at high spawning escapements is needed to determine more precisely the maximum juvenile productivity in the Chiwawa Basin.

Steelhead/Rainbow Abundance

Based on stream surface area, we estimated a total of 25,018 (±15% of the estimated total) age-0 steelhead/rainbow (<4 in) in reaches of the Chiwawa Basin in August 2010 (Table 5). During the 1992-2010 survey period, numbers of age-0 steelhead/rainbow ranged from 1,410 to 45,727 in the Chiwawa River Basin (Figure 8; Appendix B). In 1992-2010, numbers of age-0 steelhead/rainbow varied among reaches, but were typically highest in the lower reaches of the Chiwawa River. In all years they most often used riffle and multiple channel habitats in the Chiwawa River, although we also found them associated with woody debris in pool and glide habitat. In tributaries they were generally most abundant in small pools. Those that we observed in riffles selected stations in quiet water behind small and large boulders or occupied stations in quiet water along the stream margin. In pool and multiple-channel habitats, we found age-0 steelhead/rainbow using the same kinds of habitat as age-0 Chinook salmon.

We estimated that 9,616 (±13% of the estimated total) age-1+ steelhead/rainbow (4-8 in) lived in reaches of the Chiwawa Basin in August 2010 (Table 6). During the survey period 1992-2010, numbers of age-1+ steelhead/rainbow ranged from 2,533 to 22,130 (Figure 8; Appendix B). In most years we found these fish in nearly all reaches, but they were typically most numerous in lower reaches of the Chiwawa River. We observed age-1+ steelhead/rainbow mostly in pool, riffle, and multiple-channel habitats. Those that we observed in pools were usually in deeper water than age-0 steelhead/rainbow and Chinook. Like age-0 steelhead/rainbow, age-1+ steelhead/rainbow selected stations in quiet water behind boulders in riffles, but we generally did not find the two age groups together. Age-1+ steelhead/rainbow appeared to use deeper and

[4] The γ parameter in the Gamma model was greater than 0, which means that this model is nearly identical to the Ricker model. The reason it did not rank higher is because it contains an extra parameter, which means that it has less bias and greater variance than the Ricker model.

faster water than did age-0 steelhead/rainbow.

We estimated that steelhead/rainbow larger than 8 inches numbered 63 (±27% of the estimated total) in the Chiwawa Basin in August 2010 (Table 7). During the period 1992-2010, steelhead/rainbow numbers ranged from 8 to 1,869 (Appendix B). Steelhead/rainbow larger than 8 inches were most abundant in the lower Chiwawa River; however, in 1992 and 1993, they were most abundant near campgrounds in Reaches 8, 9, and 10 (these were mostly hatchery fish planted near the campgrounds). We found very few in tributary survey reaches. Most of the steelhead/rainbow larger than 8 inches used deep pools (>5 feet), and occupied stations near the bottom at the upstream end of pools.

Bull Trout Abundance

We estimated, based on surface area, that at least 79 (±32% of the estimated total) juvenile (2-8 in) bull trout lived in reaches of the Chiwawa River Basin in August 2010 (Table 8). We found most of these fish in the upper-most reaches and in tributaries of the Chiwawa River. During 1992-2010, numbers of juvenile bull trout ranged from 79 to 505 (Figure 9; Appendix B). These estimates and those for adult bull trout are incomplete because we did not sample the entire range of bull trout in all tributaries. We did not extend our surveys into the headwaters of the Chiwawa River because there were no juvenile Chinook there. Areas beyond the distribution of juvenile Chinook salmon are known to support bull trout, steelhead/rainbow, and cutthroat trout (USFS 1993). In addition, our estimates of bull trout abundance were based on daytime snorkel surveys, which may underestimate the actual abundance of bull trout.[5] Several studies (e.g., Goetz 1994; Thurow and Schill 1996; Hillman and Chapman 1996; Bonar et al. 1997) have found bull trout population estimates based on nighttime snorkeling to be in some cases more accurate than daytime snorkeling, especially for juvenile bull trout. Our estimates of adult bull trout numbers may be more accurate than those for juveniles.

In all years we found most juvenile bull trout in the upstream reaches of the Chiwawa River. Of the reaches we surveyed, they were most numerous in Reaches 8-10 on the Chiwawa River. We found the majority of these fish in multiple channels, pools, and riffles, and few in glides. They consistently occupied stations close to the stream bottom over rubble and small boulder substrate or near woody debris. This is similar to the observation of Pratt (1984) in the upper Flathead River Basin in Montana. She found that juvenile bull trout lay close to instream cover and that they tended to conceal themselves. As a result, she found it difficult to accurately estimate their numbers. Although this implies that we underestimated numbers of juvenile bull trout in the Chiwawa River, the relative distribution of juvenile bull trout is valid if we assume that we saw the same fraction of juveniles in all reaches (i.e., detection probability was the same across survey sites).

We estimated a total of 547 (±15% of the estimated total) adult (>8 in) bull trout in reaches of the Chiwawa Basin in August 2010 (Table 9). In previous years, numbers ranged from 76 to 900 (Figure 9; Appendix B). As with juvenile bull trout, we found most of the adult bull trout

---

[5] Because there are no estimates for probability of detecting bull trout with daytime underwater observation methods in the Chiwawa Basin, we could not adjust bull trout numbers based on detectability. Therefore, the numbers reported in this report likely underestimate the “true” number of bull trout in the survey area.

upstream from Reach 6; although they were found in nearly all reaches on the Chiwawa River. We found relatively few adult bull trout in tributaries of the Chiwawa River. Adult bull trout primarily used pools and multiple channel habitat, although most of the smaller adults (<10 in) used riffles. In all years we found few adult bull trout near campgrounds. There also appeared to be an inverse association between numbers of adult bull trout and numbers of age-0 Chinook salmon in pools in Reaches 7-10. That is, where we found large bull trout we generally observed few juvenile Chinook salmon.

Abundance of Other Salmonids

In August 2010, we estimated that at least 147 brook trout, an exotic species closely related to the bull trout, occurred in the Chiwawa River, Chikamin Creek, Big Meadow Creek, Minnow Creek, and in the Little Wenatchee River survey areas. Brook trout occurred in the lower seven reaches on the Chiwawa River. In both the Chiwawa and Little Wenatchee rivers, brook trout usually used multiple channels. Few appeared to be bull trout/brook trout hybrids. In Chikamin, Minnow, and Big Meadow creeks, brook trout were most abundant in pools. Brook trout lengths ranged from 2-8 inches.

At least 254 westslope cutthroat trout occurred in the Chiwawa River, Rock Creek, and Phelps Creek survey areas in August 2010. These fish most often occurred in pools and multiple channel habitats. They ranged in size from 2-18 inches. Juvenile coho salmon were observed in Nason Creek.

We observed both juvenile and adult mountain whitefish in the Chiwawa River, Rock Creek, Phelps Creek, Nason Creek, and the Little Wenatchee River survey areas. In sum, at least 6,655 adult and 1,169 juvenile whitefish lived in these streams in August 2010. We found few whitefish in most tributaries to the Chiwawa River.

Conclusion

This was the 18th year of a study to monitor trends in juvenile spring Chinook production in the Chiwawa River Basin. As shown in Figure 3, numbers of juvenile Chinook salmon in the Chiwawa Basin have fluctuated widely over the 18-year period. Numbers of juveniles in 2001 and 2002 were some of the highest recorded, while numbers in the mid-1990s were some of the lowest. Interestingly, the highest spawning escapements (highest redd numbers) resulted in the lowest egg-parr survival rates (Appendix A). This is supported by the fact that the best approximating model clearly demonstrates a density-dependent relationship between seeding levels and juvenile production. Indeed, there is a significant negative relationship between parr per redd and numbers of redds in the Chiwawa Basin. This is an important observation because Objectives 1, 3, 4, and 7 and their associated hypotheses in the monitoring and evaluation plan (Murdoch and Peven 2005) are only valid when the supplemented population is below its carrying capacity.

The presence of density dependence in the early life stages of spring Chinook is not surprising. Rarely does density dependence appear in numbers of adult spring Chinook or on their spawning grounds. The Chiwawa Basin appears to have plenty of spawning habitat, as indicated by the large numbers of spawners and redds widely distributed throughout the basin during 2001 and 2002. However, those large spawning escapements did not translate into large numbers of juveniles or smolts. Thus, density-dependent regulation appears to occur sometime during the early life stages of the fish, likely at the fry stage. It is possible that physical habitat (space) during higher flows when fry are emerging may limit juvenile Chinook production in the basin. Low nutrient levels and its effects on food (macroinvertebrates) production may also be a limiting factor in the basin. If spawning escapements remain relatively high, marine-derived nutrients should increase in the basin, resulting in more food for juvenile Chinook salmon.

References

Bonar, S. A., M. Divens, and B. Bolding. 1997. Methods for sampling the distribution and abundance of bull trout and Dolly Varden. Washington Department of Fish and Wildlife, Research Report No. RAD97-05. Olympia, WA.

Burnham, K. P. and D. R. Anderson. 2002. Model selection and multimodel inference: a practical information-theoretic approach. Second edition. Springer, New York, N.Y.

Goetz, F. A. 1994. Distribution and juvenile ecology of bull trout (*Salvelinus confluentus*) in the Cascade Mountains. Master's thesis. Oregon State University, Corvallis.

Hillman, T. W. and D. W. Chapman. 1996. Comparison of underwater methods and electrofishing for estimating fish populations in the upper Blackfoot River Basin. Report to Seven-Up Pete Joint Venture, Lincoln, MT.

Hillman, T. W. and M. D. Miller. 2004. Abundance and total numbers of Chinook salmon and trout in the Chiwawa River Basin, Washington, 2004. Report to Chelan Public Utility District, Wenatchee, WA. BioAnalysts, Inc., Boise, ID.

Hillman, T, M. Miller, J. Miller, M. Tonseth, T. Miller, and A. Murdoch. 2010. Monitoring and evaluation of the Chelan County PUD Hatchery programs: 2009 annual report. Report to the HCP Hatchery Committee, Wenatchee, WA.

Hubble, J. 1993. Methow valley spring Chinook supplementation project. Yakima Indian Nation. Annual report to Douglas County Public Utility District, East Wenatchee, WA.

Kiefer, R. and K. Forster. 1991. Idaho habitat and natural production monitoring. Idaho Department of Fish and Game, Annual Report 1989, Project No. 83-7, Contract No. DE-BI79-84BP13381.

Konopacky, R. C., P. J. Cernera, and E. C. Bowles. 1986. Natural propagation and habitat improvement, Idaho: Salmon River habitat enhancement. Subproject I, Bear Valley Creek: inventory, 1984 and 1985. Shoshone-Bannock Tribes, Fort Hall, ID. Report to U.S. Department of Energy, Bonneville Power Administration, Division of Fish and Wildlife, Project No. 83-359, Contract No. DE-A179-84BP14383, Portland, OR.

Mullan, J. W., K. R. Williams, G. Rhodus, T. W. Hillman, and J. D. McIntyre. 1992. Production and habitat of salmonids in mid-Columbia River tributary streams. U.S. Fish and Wildlife Service, Monograph I. 489 p.

Murdoch, A. and C. Peven. 2005. Conceptual approach to monitoring and evaluating the Chelan County Public Utility District hatchery programs. Chelan County Public Utility District and the Washington Department of Fish and Wildlife, Wenatchee, WA.

Murdoch, A., T. Pearsons, and T. Maitland. 2009. The number of redds constructed per female spring Chinook salmon in the Wenatchee River Basin. North American Journal of Fisheries Management 29:441-446.

Petrosky, C. E. 1990. Estimating spring Chinook parr and smolt abundance in wild and natural production areas. Pages 57-61 *in*: D. L. Park, editor. Status and future of spring Chinook salmon in the Columbia River basin--conservation and enhancement. Spring Chinook salmon workshop, U.S. Dept. Comm. NOAA Tech. Mem. NMFS F/NWD-187.

Pratt, K. L. 1984. Habitat use and species interactions of juvenile cutthroat *Salmo clarki lewisi* and bull trout *Salvelinus confluentus* in the upper Flathead River Basin. Masters thesis. University of Idaho, Moscow, ID. 95 p.

Richards, C. and P. J. Cernera. 1987. Salmon River habitat enhancement, annual report, 1986. Shoshone-Bannock Tribes, Fort Hall, ID. Report to Bonneville Power Administration, Project No. 83-359, Contract No. DE-A179-84BP14383, Portland, OR.

Thurow, R. F. and D. J. Schill. 1996. Comparison of day snorkeling, night snorkeling, and electrofishing to estimate bull trout abundance and size structure in a second-order Idaho stream. North American Journal of Fisheries Management 16:314-323.

USFS (United States Forest Service). 1993. Upper Chiwawa River stream survey report. Wenatchee National Forest, Wenatchee, WA.

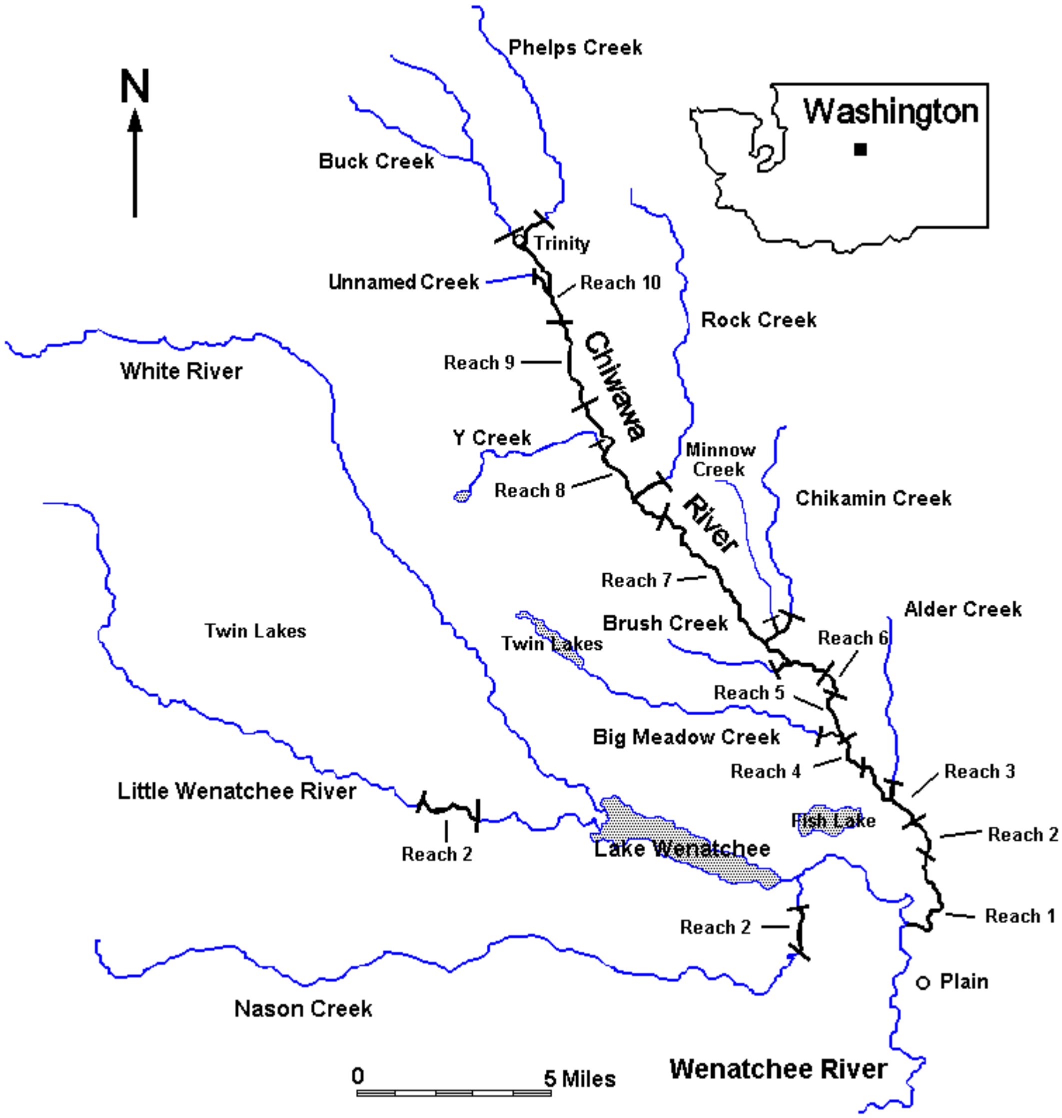


Figure 1. Location of study reaches on the Chiwawa River, and Chikamin, Rock, Big Meadow, Unnamed, Alder, Brush and Phelps creeks, Chelan County, Washington. Reach 2 on Nason Creek and Reach 2 on the Little Wenatchee River were matched with Reaches 3 and 8 on the Chiwawa River, respectively.

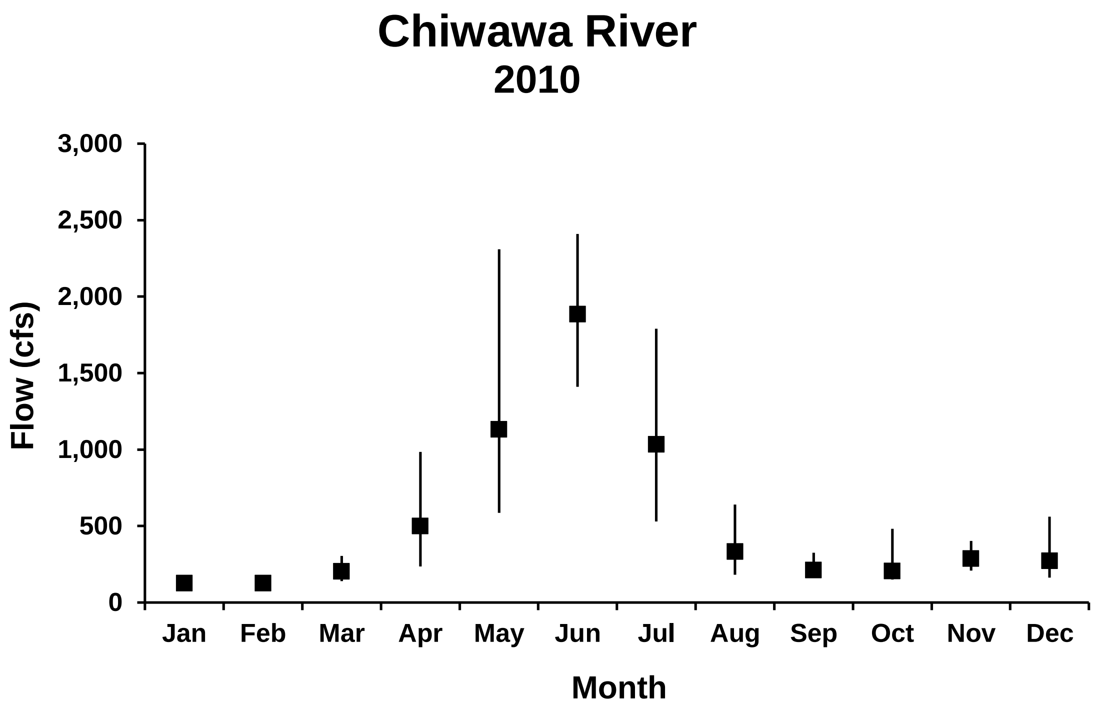


Figure 2. Mean, minimum, and maximum monthly flows in the Chiwawa River for 2010.

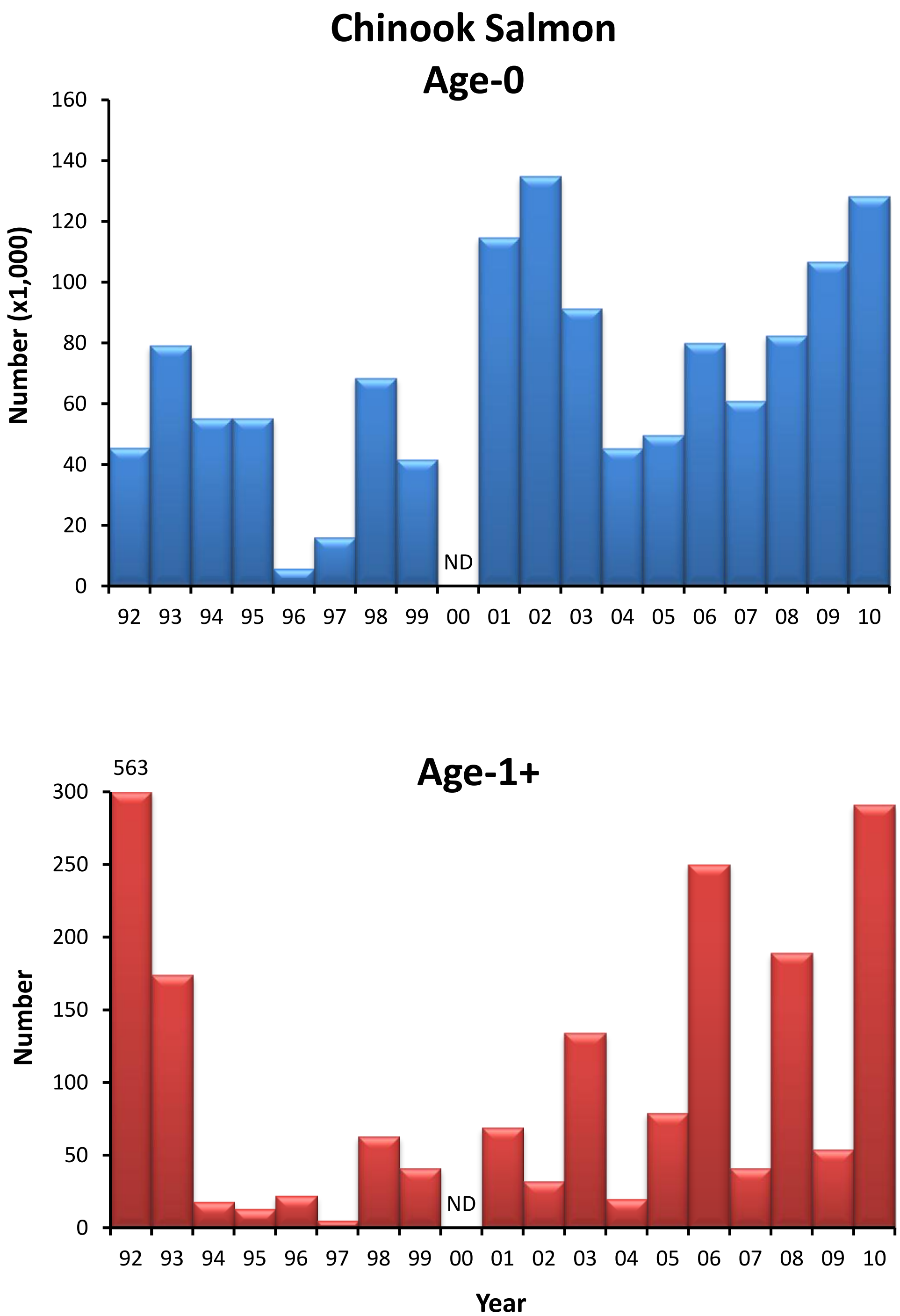


Figure 3. Numbers of age-0 and age-1+ Chinook salmon within the Chiwawa River Basin in August 1992-2010; ND = no data.

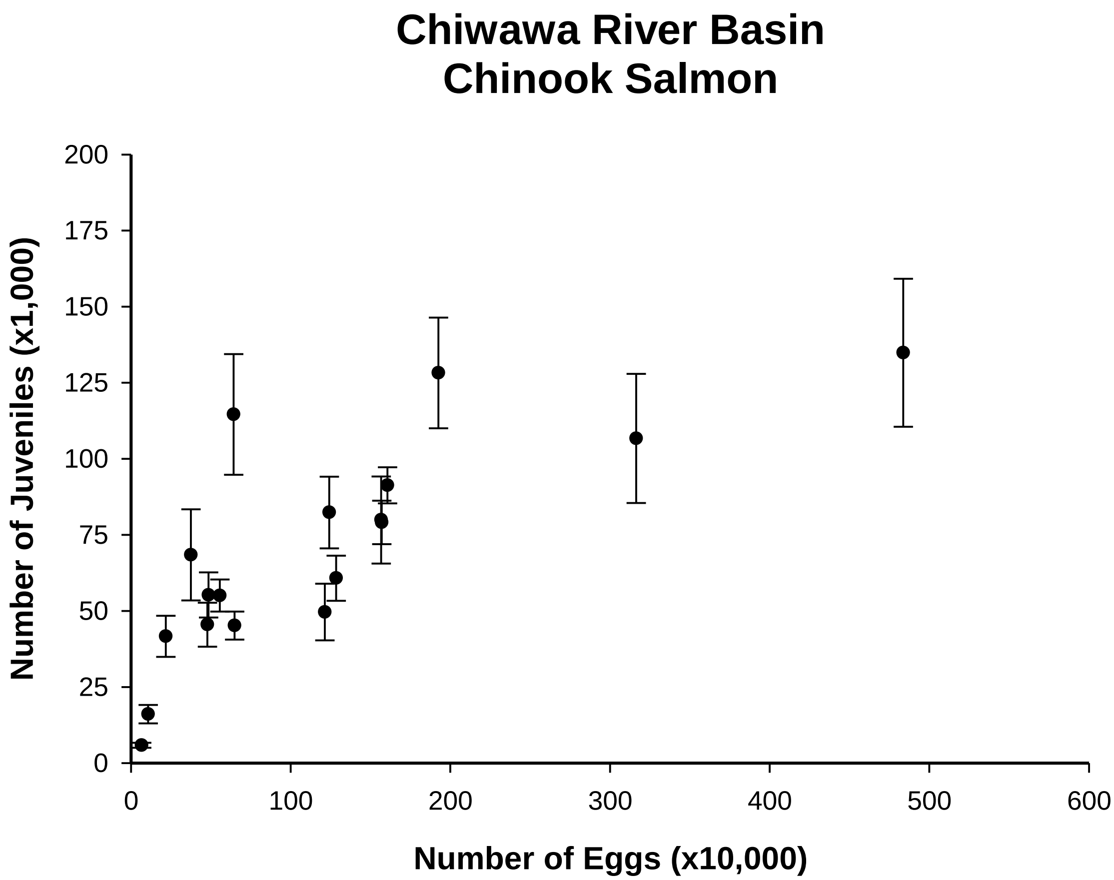


Figure 4. Relationship between total numbers of age-0 Chinook salmon (based on fish/ha) and numbers of eggs in the Chiwawa River Basin. Vertical bars indicate 95% confidence bounds.

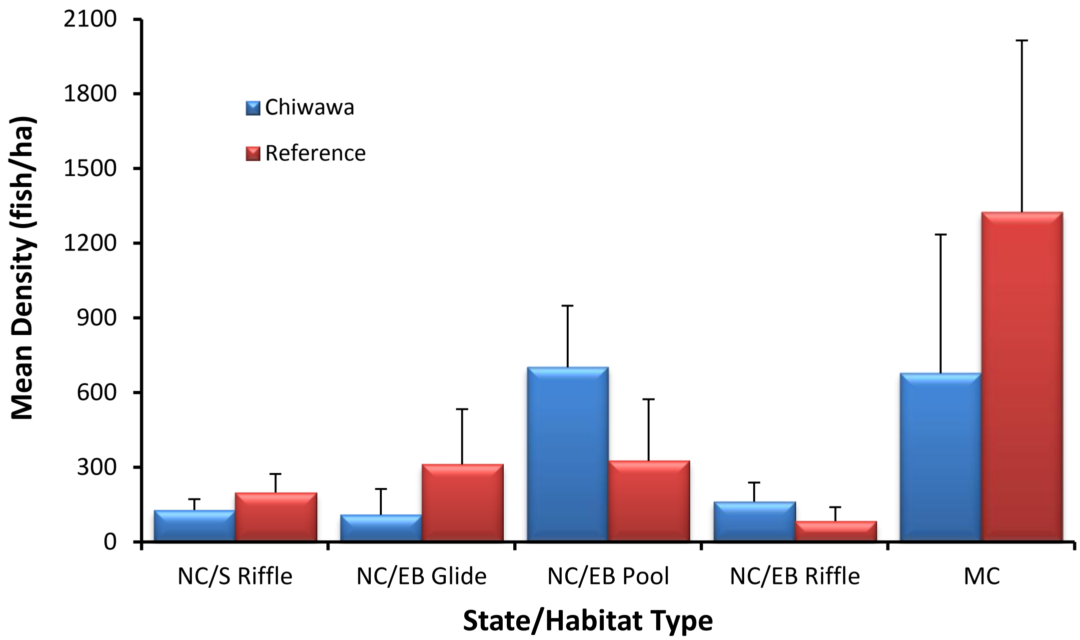


Figure 5. Comparison of the 17-year means (95% CI) of age-0 Chinook salmon densities (fish/ha) within state/habitat types in Reaches 3 and 8 of the Chiwawa River and their matched reference areas on Nason Creek and the Little Wenatchee River. There was no sampling in 2000 and no sampling in reference areas in 1992.

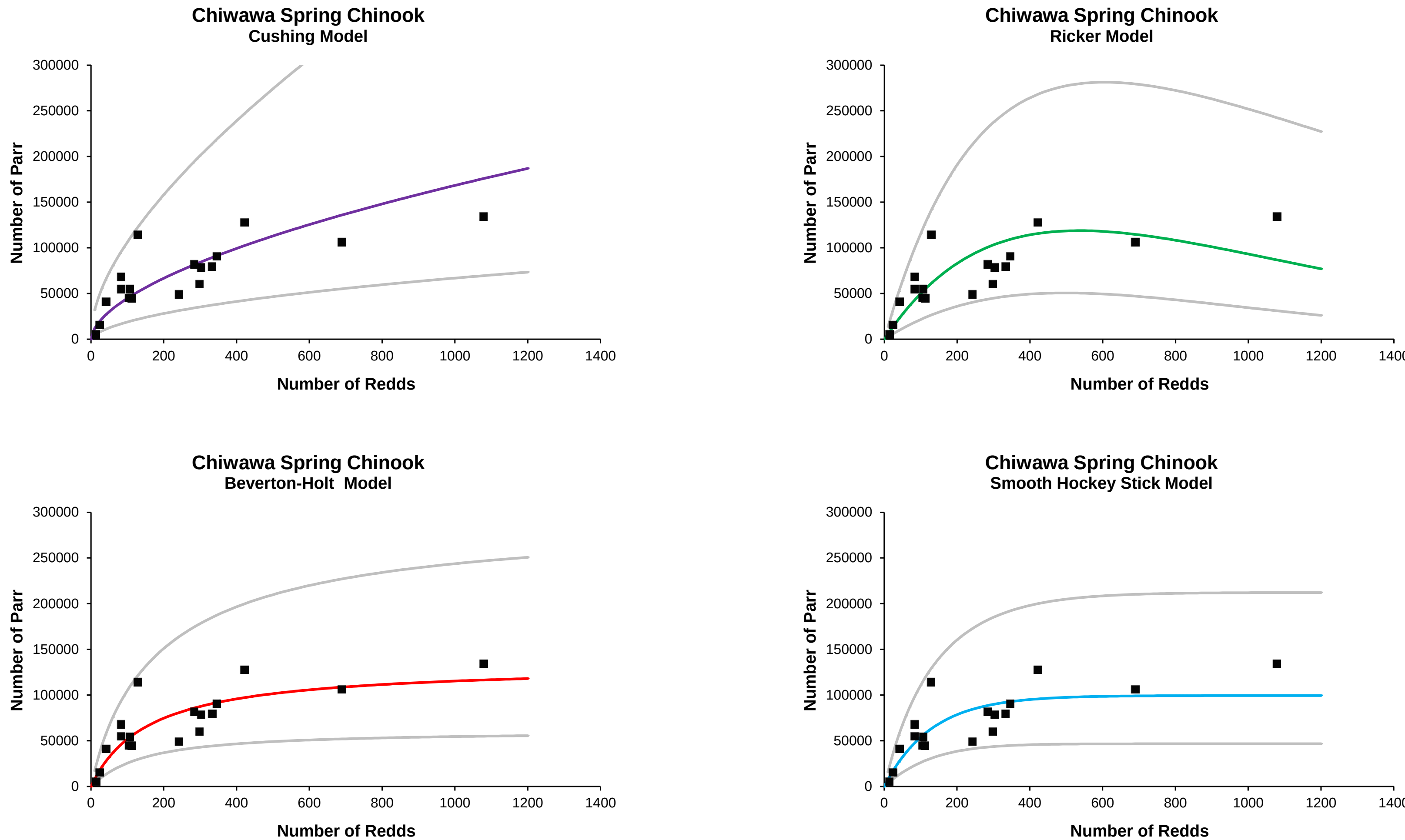


Figure 6. Relationship between numbers of juvenile (age-0) Chinook and redds in the Chiwawa Basin, 1992-2010 (no sampling occurred in 2000). Figures show the fit of the Cushing model, Beverton-Holt model, Ricker model, and the smooth hockey stick model to the data. Gray lines indicate the upper and lower 95% C.B.

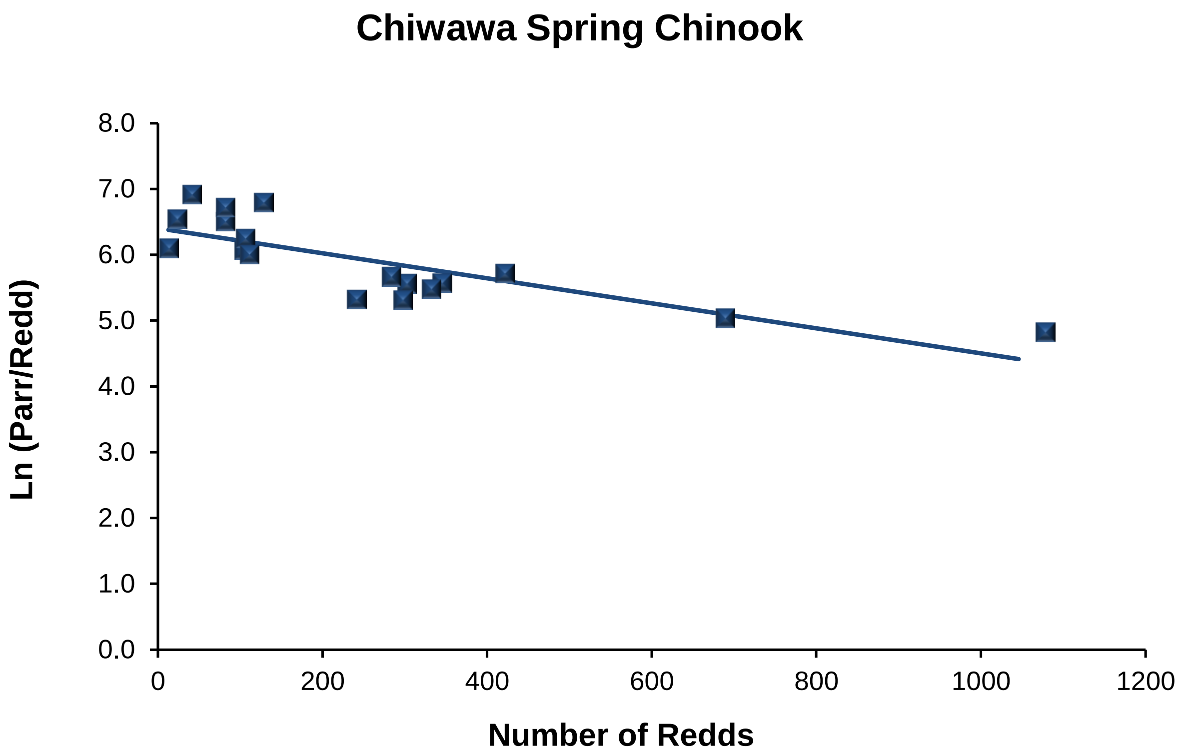
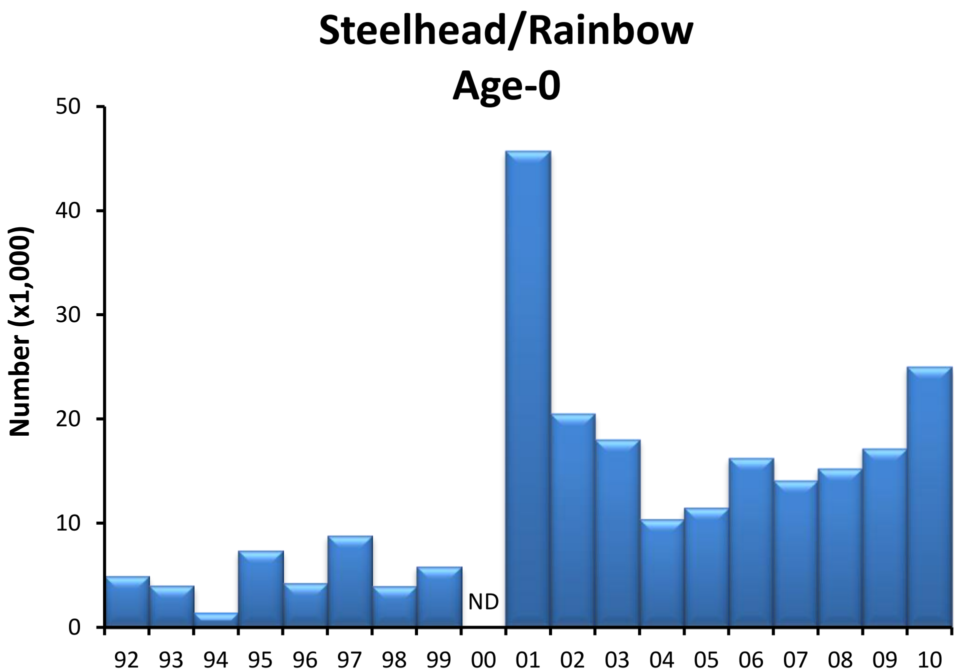


Figure 7. Relationship between natural log parr/redd and numbers of redds in the Chiwawa River Basin, 1992-2010. No sampling was conducted in 2000. Estimates for 1992-2010 included the Chiwawa River and its tributaries; the 1992 estimate included only the Chiwawa River. The linear relationship LN(P/R) = 6.40 – 0.002(Redds) was significant with P = 0.0001; R^2 = 0.644.



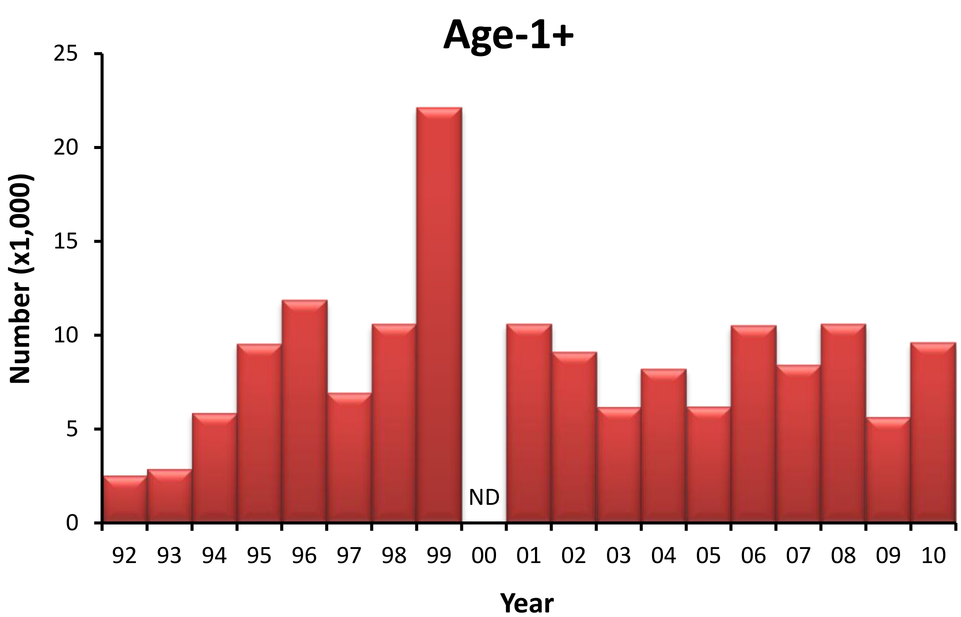


Figure 8. Numbers of age-0 (<4 in) and age-1+ (4-8 in) steelhead/rainbow within the Chiwawa River Basin in August 1992-2010; ND = no data.

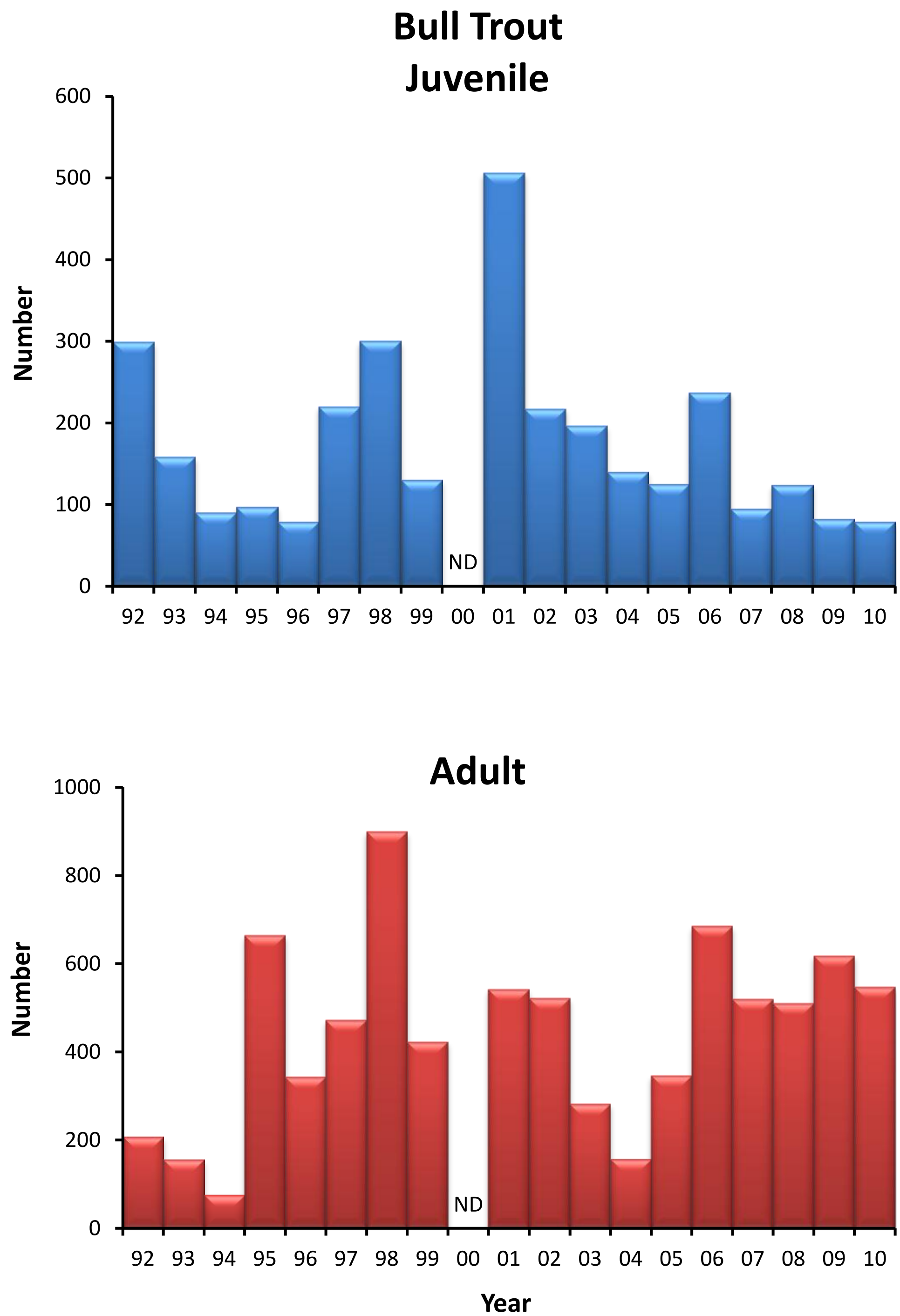


Figure 9. Numbers of juvenile (2-8 inches) and adult (>8 inches) bull trout within the Chiwawa River Basin in August 1992-2010; ND = no data.

Table 1. Description, location (river mile), and area (hectares) of land-class strata (reaches) used by age-0 Chinook salmon in the Chiwawa River Basin, 2010. Reaches were classified according to geologic district, landtype association, valley-bottom type, stream state-type, and habitat type within the Cascade Ecoregion; MCV = moderately confined valley, CC = confined canyon, UCV = unconfined valley, NC = natural channel, EB = eroded banks, S = straight, G = glide, P = pool, R = riffle, and MC = multiple channel. See Hillman and Miller (2004) for definitions of stream state codes.

Reach	RM	Gradient	Geologic district	Landtype association	Valley bottom type	Stream state type	Habitat type	Area (ha)	
								Total	Sample
Chiwawa River									
1	0.00-3.77	0.007	Glacial Drift over Chumstick Formation	Glacial Valley	MCV Alluvial	NC/EB	G	0.59	0.59
						NC/EB	P	1.43	1.06
						NC/EB	R	18.38	1.78
2	3.77-5.51	0.010	Glacial Drift over Chumstick Formation	Glacial Canyon	CC Fluvial	NC/EB	G	0.31	0.31
						NC/EB	P	0.71	0.24
						NC/EB	R	6.66	0.62
3	5.51-7.88	0.009	Glacial Drift over Chumstick Formation	Glacial Valley	MCV Alluvial	NC/S	R	5.91	0.81
						NC/EB	G	0.13	0.13
						NC/EB	R	4.47	0.55
						MC	MC	0.38	0.38
4	7.88-8.90	0.007	Glacial Drift over Chumstick Formation	Glacial Canyon	CC Fluvial	NC/EB	P	0.47	0.35
						NC/EB	R	3.21	0.57
						MC	MC	0.51	0.51
5	8.90-10.83	0.011	Glacial Drift over Chumstick Formation	Glacial Valley	MCV Alluvial	NC/EB	P	0.13	0.13
						NC/EB	R	8.92	0.96
6	10.83-11.80	0.008	Glacial Drift over Chumstick Formation	Glacial Canyon	CC Fluvial	NC/EB	P	0.41	0.41
						NC/EB	R	3.81	1.01
						MC	MC	0.34	0.34
7	11.80-20.03	0.001	Glacial Drift over Chumstick Formation	Glacial Valley	UCV Alluvial	NC	G	2.50	0.59
						NC	P	5.96	0.67
						NC	R	1.50	0.57
						NC/EB	G	3.38	1.09
						NC/EB	P	8.25	1.26
						NC/EB	R	5.24	1.10
						MC	MC	4.59	1.67
8	20.03-25.42	0.003	Glacial Drift over Swakane Gneiss	Glacial Valley	UCV Alluvial	NC/EB	G	3.25	1.37
						NC/EB	P	7.68	1.60
						NC/EB	R	4.88	0.93
						EB	P	0.23	0.23
						EB	R	0.40	0.40
						MC	MC	6.84	3.12
9	25.42-28.81	0.007	Glacial Drift over Swakane Gneiss	Glacial Valley	MCV Alluvial	NC	G	0.25	0.25
						NC	P	3.43	1.11
						NC	R	3.25	0.45
						MC	MC	3.73	1.11
10	28.81-31.11	0.011	Pre-upper Jurassic Gneiss	Glacial Valley	MCV Alluvial	NC	P	1.03	0.44
						NC	R	2.73	0.81
						MC	MC	3.83	0.65

Table 1. Concluded.

Reach	RM	Gradient	Geologic district	Landtype association	Valley bottom type	Stream state type	Habitat type	Area (ha) Total	Area (ha) Sampled
Phelps Creek									
1	0.00-0.35	0.043	Pre-upper Jurassic Gneiss	Glacial Valley	MCV Alluvial	NC	P	0.03	0.03
						NC	R	0.18	0.18
						NC	MC	0.05	0.05
Chikamin Creek[1]									
1	0.00-0.94	0.013	Glacial Drift over Chumstick Formation	Glacial Valley	UCV Alluvial	NC	G	0.03	0.03
						NC	P	0.21	0.06
						NC	R	0.43	0.16
						MC	MC	0.14	0.14
Rock Creek									
1	0.00-0.73	0.020	Glacial Drift over Swakane Gneiss	Glacial Valley	UCV Alluvial	NC	P	0.19	0.04
						NC	R	0.33	0.07
						MC	MC	0.11	0.11
Unnamed Creek									
1	0.00-0.05		Pre-upper Jurassic Gneiss	Glacial Valley	MCV Alluvial	NC	P	0.03	0.03
						NC	R	0.01	0.01
Big Meadow Creek									
1	0.00-0.35	0.025	Glacial Drift over Chumstick Formation	Glacial Valley	MCV Alluvial	NC	G	0.01	0.01
						NC	P	0.21	0.04
						NC	R	0.04	0.01
						MC	MC	0.02	0.02
Alder Creek									
1	0.00-0.01		Glacial Drift over Chumstick Formation	Glacial Valley	MCV Alluvial	NC	P	0.007	0.007
						NC	R	0.009	0.009
Brush Creek									
1	0.00-0.01		Glacial Drift over Chumstick Formation	Glacial Valley	UCV Alluvial	NC	P	0.002	0.002
						NC	R	0.006	0.006
Clear Creek									
1	0.00-0.05		Glacial Drift over Chumstick Formation	Glacial Valley	UCV Alluvial	NC	P	0.002	0.002
						NC	R	0.003	0.003
Y Creek									
1	0.00-0.05		Glacial Drift over Swakane Gneiss	Glacial Valley	UCV Alluvial	NC	P	0.000	0.000
						NC	R	0.000	0.000

[1] Includes the lower 0.2 miles of Minnow Creek

Table 2. Estimated mean densities (fish/hectare and fish/m^3), total numbers, 95% confidence bounds on total numbers, and error of the estimated total number of age-0 Chinook salmon in reaches in the Chiwawa River Basin, Washington, August 2010.

Reach	Mean density		Surface area (ha)			Volume (m^3)		
	Fish/ha	Fish/m^3	Total No.	95% C.B.	± Error	Total No.	95% C.B.	± Error
Chiwawa River								
1	302.2	0.084	6,165	±2,208	0.36	6,079	±2,107	0.35
2	267.1	0.070	2,051	±381	0.19	2,462	±567	0.23
3	189.4	0.045	2,063	±76	0.04	2,154	±89	0.04
4	548.9	0.107	2,300	±107	0.05	2,444	±124	0.05
5	206.6	0.041	1,870	±46	0.03	2,143	±73	0.03
6	382.2	0.086	1,743	±49	0.03	1,746	±88	0.05
7	1,026.1	0.161	32,240	±3,303	0.10	33,631	±2,957	0.09
8	990.7	0.162	23,064	±5,358	0.23	22,066	±6,342	0.29
9	2,010.8	0.380	21,435	±16,104	0.75	19,861	±33,129	1.67
10	3,236.9	0.801	24,568	±4,902	0.20	27,364	±4,305	0.16
Phelps Creek								
1	2,023.1	1.005	526	±0	0.00	526	±0	0.00
Chikamin Creek[1]								
1	5,643.2	3.324	4,571	±685	0.15	5,511	±757	0.14
Rock Creek								
1	6,431.7	2.898	4,052	±1,448	0.36	4,881	±1,369	0.28
Unnamed Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Big Meadow Creek								
1	5,193.5	1.673	1,449	±287	0.20	1,535	±506	0.33
Alder Creek								
1	3,500.0	2.213	56	±0	0.00	56	±0	0.00
Brush Creek								
1	5,250.0	6.774	42	±0	0.00	42	±0	0.00
Clear Creek								
1	5,000.0	4.310	25	±0	0.00	25	±0	0.00
Y Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Grand Total	**973.3**	**0.193**	**128,220**	**±18,185**	**0.14**	**132,526**	**±34,242**	**0.26**

[1] Includes lower 0.2 miles of Minnow Creek.

Table 3. Estimated mean densities (fish/hectare and fish/m^3), total numbers, 95% confidence bounds on total numbers, and error of the estimated total number of age-1+ Chinook salmon in reaches in the Chiwawa River Basin, Washington, August 2010.

Reach	Mean density		Surface area (ha)			Volume (m^3)		
	Fish/ha	Fish/m^3	Total No.	95% C.B.	± Error	Total No.	95% C.B.	± Error
Chiwawa River								
1	1.7	0.001	35	±17	0.49	36	±54	1.50
2	4.3	0.001	33	±11	0.33	35	±26	0.74
3	0.0	0.000	0	±0	0.00	0	±0	0.00
4	1.9	0.000	8	±5	0.63	7	±10	1.43
5	0.4	0.000	4	±0	0.00	5	±0	0.00
6	0.9	0.000	4	±0	0.00	4	±0	0.00
7	0.0	0.000	0	±0	0.00	0	±0	0.00
8	1.8	0.000	41	±51	1.24	41	±54	1.32
9	0.0	0.000	0	±0	0.00	0	±0	0.00
10	10.8	0.003	82	±38	0.46	85	±117	1.38
Phelps Creek								
1	103.8	0.052	27	±0	0.00	27	±0	0.00
Chikamin Creek[1]								
1	23.5	0.012	19	±18	0.95	20	±19	0.95
Rock Creek								
1	60.3	0.031	38	±56	1.47	52	±41	0.79
Unnamed Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Big Meadow Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Alder Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Brush Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Clear Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Y Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Grand Total	**2.2**	**0.001**	**291**	**±90**	**0.31**	**312**	**±149**	**0.48**

[1] Includes lower 0.2 miles of Minnow Creek.

Table 4. Summary of the six productivity models of juvenile (age-0) Chinook salmon in the Chiwawa Basin. Models are shown, including the number of parameters (*K*), AIC_c values, AIC_c difference scores (Δ_i), the likelihood of the model given the data ($£(g_i|x)$), Akaike weights (w_i), and adjusted R^2 values. The sample size (*n*) for all models was 18. Models describe the relationship between juvenile Chinook numbers (dependent variable) and redd numbers (independent variable).

Model	K^a	AIC_c	Δ_i	$£(g_i\|x)$	w_i	Adj R^2
Beverton-Holt	3	-87.11	0.00	1.00	0.90	0.81
Ricker	3	-81.11	5.99	0.05	0.05	0.73
Gamma[b]	4	-80.14	6.97	0.03	0.03	0.75
Cushing	3	-79.85	7.26	0.03	0.02	0.71
Smooth Hockey Stick	3	-45.13	41.98	0.00	0.00	0.80
Density Independent	2	25.09	112.19	0.00	0.00	-0.06

[a] ***K*** is the number of structural parameters in the model plus 1 for σ^2.
[b] The γ parameter in the Gamma model was greater than 0, which means that this model is nearly identical to the Ricker model. The reason it did not rank higher than the Ricker model is because the Gamma model contains an extra parameter, which means that it has less bias and greater variance than the Ricker model (less parsimonious).

Table 5. Estimated mean densities (fish/hectare and fish/m^3), total numbers, 95% confidence bounds on total numbers, and error of the estimated total number of age-0 (<4 in) steelhead/rainbow in reaches in the Chiwawa River Basin, Washington, August 2010.

Reach	Mean density		Surface area (ha)			Volume (m^3)		
	Fish/ha	Fish/m^3	Total No.	95% C.B.	± Error	Total No.	95% C.B.	± Error
Chiwawa River								
1	138.2	0.038	2,819	±161	0.06	2,750	±169	0.06
2	204.0	0.059	1,567	±135	0.09	2,068	±244	0.12
3	250.5	0.059	2,728	±201	0.07	2,847	±197	0.07
4	99.0	0.021	415	±74	0.18	481	±66	0.14
5	139.7	0.029	1,264	±54	0.04	1,521	±80	0.05
6	141.7	0.032	646	±71	0.11	652	±38	0.06
7	184.5	0.028	5,797	±2,859	0.49	5,881	±3,020	0.51
8	84.0	0.014	1,956	±2,188	1.12	1,858	±2,191	1.18
9	35.6	0.006	380	±669	1.76	318	±1,157	3.64
10	0.0	0.000	0	±0	0.00	0	±0	0.00
Phelps Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Chikamin Creek[1]								
1	3,543.2	2.050	2,870	±492	0.17	3,399	±478	0.14
Rock Creek								
1	2,346.0	1.017	1,478	±879	0.59	1,713	±1,061	0.62
Unnamed Creek								
1	500.0	0.082	5	±0	0.00	5	±0	0.00
Big Meadow Creek								
1	10,189.9	3.313	2,843	±201	0.07	3,039	±597	0.20
Alder Creek								
1	11,375.0	7.194	182	±0	0.00	182	±0	0.00
Brush Creek								
1	4,375.0	5.645	35	±0	0.00	35	±0	0.00
Clear Creek								
1	6,600.0	5.690	33	±0	0.00	33	±0	0.00
Y Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Grand Total	**189.9**	**0.039**	**25,018**	**±3,816**	**0.15**	**26,782**	**±4,136**	**0.15**

[1] Includes lower 0.2 miles of Minnow Creek.

Table 6. Estimated mean densities (fish/hectare and fish/m^3), total numbers, 95% confidence bounds on total numbers, and error of the estimated total number of age-1+ (4-8 in) steelhead/rainbow in reaches in the Chiwawa River Basin, Washington, August 2010.

Reach	Mean density		Surface area (ha)			Volume (m^3)		
	Fish/ha	Fish/m^3	Total No.	95% C.B.	± Error	Total No.	95% C.B.	± Error
Chiwawa River								
1	126.0	0.035	2,570	±180	0.07	2,511	±195	0.08
2	92.7	0.026	712	±76	0.11	923	±126	0.14
3	73.6	0.017	801	±71	0.09	827	±77	0.09
4	64.0	0.013	268	±14	0.05	307	±42	0.14
5	72.2	0.015	653	±47	0.07	784	±59	0.08
6	65.8	0.015	300	±8	0.03	302	±38	0.13
7	92.6	0.014	2,910	±1,171	0.40	2,972	±1,301	0.44
8	4.7	0.001	110	±170	1.55	96	±200	2.08
9	0.0	0.000	0	±0	0.00	0	±0	0.00
10	0.0	0.000	0	±0	0.00	0	±0	0.00
Phelps Creek								
1	123.1	0.061	32	±0	0.00	32	±0	0.00
Chikamin Creek[1]								
1	451.9	0.265	366	±80	0.22	439	±77	0.18
Rock Creek								
1	623.8	0.298	393	±345	0.88	502	±255	0.51
Unnamed Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Big Meadow Creek								
1	1,720.4	0.561	480	±188	0.39	515	±149	0.29
Alder Creek								
1	1,312.5	0.830	21	±0	0.00	21	±0	0.00
Brush Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Clear Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Y Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Grand Total	**73.0**	**0.015**	**9,616**	**±1,267**	**0.13**	**10,231**	**±1,375**	**0.13**

[1] Includes lower 0.2 miles of Minnow Creek.

Table 7. Estimated mean densities (fish/hectare and fish/m^3), total numbers, 95% confidence bounds on total numbers, and error of the estimated total number of steelhead/rainbow larger than 8 inches in reaches in the Chiwawa River Basin, Washington, August 2010.

Reach	Mean density		Surface area (ha)			Volume (m^3)		
	Fish/ha	Fish/m^3	Total No.	95% C.B.	± Error	Total No.	95% C.B.	± Error
Chiwawa River								
1	0.7	0.000	15	±7	0.47	14	±21	1.50
2	0.8	0.000	6	±1	0.17	7	±6	0.86
3	0.0	0.000	0	±0	0.00	0	±0	0.00
4	1.4	0.000	6	±8	1.33	7	±10	1.43
5	0.0	0.000	0	±0	0.00	0	±0	0.00
6	1.1	0.000	5	±0	0.00	4	±0	0.00
7	0.9	0.000	27	±12	0.44	21	±27	1.29
8	0.0	0.000	0	±0	0.00	0	±0	0.00
9	0.0	0.000	0	±0	0.00	0	±0	0.00
10	0.3	0.000	2	±3	1.50	3	±3	1.00
Phelps Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Chikamin Creek[1]								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Rock Creek								
1	3.2	0.001	2	±0	0.00	2	±0	0.00
Unnamed Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Big Meadow Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Alder Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Brush Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Clear Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Y Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Grand Total	**0.5**	**0.000**	**63**	**±17**	**0.27**	**58**	**±37**	**0.64**

[1] Includes lower 0.2 miles of Minnow Creek.

Table 8. Estimated mean densities (fish/hectare and fish/m^3), total numbers, 95% confidence bounds on total numbers, and error of the estimated total number of juvenile bull trout (2-8 in) in reaches in the Chiwawa River Basin, Washington, August 2010.

Reach	Mean density		Surface area (ha)			Volume (m^3)		
	Fish/ha	Fish/m^3	Total No.	95% C.B.	± Error	Total No.	95% C.B.	± Error
Chiwawa River								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
2	0.0	0.000	0	±0	0.00	0	±0	0.00
3	0.0	0.000	0	±0	0.00	0	±0	0.00
4	0.0	0.000	0	±0	0.00	0	±0	0.00
5	0.0	0.000	0	±0	0.00	0	±0	0.00
6	0.0	0.000	0	±0	0.00	0	±0	0.00
7	0.0	0.000	0	±0	0.00	0	±0	0.00
8	0.0	0.000	0	±0	0.00	0	±0	0.00
9	1.5	0.000	16	±24	1.50	16	±21	1.31
10	1.3	0.000	10	±8	0.80	10	±7	0.70
Phelps Creek								
1	119.2	0.059	31	±0	0.00	31	±0	0.00
Chikamin Creek[1]								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Rock Creek								
1	34.9	0.014	22	±4	0.18	23	±6	0.26
Unnamed Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Big Meadow Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Alder Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Brush Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Clear Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Y Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Grand Total	**0.6**	**0.000**	**79**	**±25**	**0.32**	**80**	**±23**	**0.29**

[1] Includes lower 0.2 miles of Minnow Creek.

Table 9. Estimated mean densities (fish/hectare and fish/m^3), total numbers, 95% confidence bounds on total numbers, and error of the estimated total number of adult bull trout (>8 in) in reaches in the Chiwawa River Basin, Washington, August 2010.

Reach	Mean density		Surface area (ha)			Volume (m^3)		
	Fish/ha	Fish/m^3	Total No.	95% C.B.	± Error	Total No.	95% C.B.	± Error
Chiwawa River								
1	1.1	0.000	23	±5	0.22	22	±31	1.41
2	1.6	0.000	12	±1	0.08	14	±11	0.79
3	0.3	0.000	3	±0	0.00	5	±0	0.00
4	3.8	0.001	16	±4	0.25	18	±12	0.67
5	0.3	0.000	3	±0	0.00	5	±0	0.00
6	1.5	0.000	7	±0	0.00	6	±0	0.00
7	5.7	0.001	180	±53	0.29	188	±98	0.52
8	5.0	0.001	117	±50	0.43	109	±83	0.76
9	6.8	0.001	72	±29	0.40	68	±119	1.75
10	14.8	0.004	112	±14	0.13	123	±105	0.85
Phelps Creek								
1	7.7	0.004	2	±0	0.00	2	±0	0.00
Chikamin Creek[1]								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Rock Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Unnamed Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Big Meadow Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Alder Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Brush Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Clear Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Y Creek								
1	0.0	0.000	0	±0	0.00	0	±0	0.00
Grand Total	**4.2**	**0.001**	**547**	**±80**	**0.15**	**560**	**±207**	**0.37**

[1] Includes lower 0.2 miles of Minnow Creek.

APPENDIX A. Numbers of redds, eggs, age-0 Chinook salmon, parr per redd, and percent egg-to-parr survival in the Chiwawa River Basin, brood years 1991-2009; NS = not sampled. Numbers of eggs were calculated as the number of redds times the mean fecundity of females collected for broodstock.

Brood Year	Chinook Salmon			Parr/Redd	Egg-to-parr survival (%)
	Redds	Eggs	Age-0 (parr)		
1991	104	478,400	45,483	437	9.5
1992	302	1,570,098	79,113	262	5.0
1993	106	556,394	55,056	519	9.9
1994	82	485,686	55,240	674	11.4
1995	13	66,248	5,815	447	8.8
1996	23	106,835	16,066	699	15.0
1997	82	374,740	68,415	834	18.3
1998	41	218,325	41,629	1,015	19.1
1999	34	166,090	NS	NS	NS
2000	128	642,944	114,617	895	17.8
2001	1,078	4,984,672	134,874	125	2.7
2002	345	1,605,630	91,278	265	5.7
2003	111	648,684	45,177	407	7.0
2004	241	1,156,559	49,631	206	4.3
2005	332	1,436,564	79,902	241	5.6
2006	297	1,284,228	60,752	205	4.7
2007	283	1,256,803	82,351	291	6.6
2008	689	3,163,888	106,705	155	3.4
2009	421	1,925,233	128,220	305	6.7
Average	**248**	**1,164,633**	**70,018**	**443**	**9.0**

APPENDIX B. Estimated numbers of salmonids (based on fish/ha) in the Chiwawa River Basin, Washington, 1992-2010; NS = not sampled.

Survey year	Chinook salmon		Steelhead/Rainbow			Bull trout	
	Age-0	Age-1+	Age-0	Age-1+	>8 in[1]	2-8 in	>8 in
1992[2]	45,483	563	4,927	2,533	1,869	299	208
1993	79,113	174	4,004	2,860	768	158	156
1994	55,056	18	1,410	5,856	67	90	76
1995	55,241	13	7,357	9,517	140	97	664
1996	5,815	22	4,245	11,849	78	79	343
1997	16,066	5	8,823	6,905	48	220	472
1998	68,415	63	3,921	10,585	78	300	900
1999	41,629	41	5,838	22,130	33	130	423
2000	NS	NS	NS	NS	NS	NS	NS
2001	114,617	69	45,727	10,623	420	505	542
2002	134,874	32	20,521	9,090	181	217	521
2003	91,278	134	18,020	6,179	49	196	282
2004	45,177	21	10,380	8,190	8	140	157
2005	49,631	79	11,463	6,188	48	125	346
2006	79,902	388	16,245	10,533	50	238	686
2007	60,752	41	14,073	8,448	77	95	520
2008	82,351	189	15,230	10,576	144	124	510
2009	106,705	54	17,179	5,629	85	82	618
2010	128,220	291	25,018	9,616	63	79	547

[1]During 1992-1993, numbers included both hatchery and wild rainbow trout. Thereafter, only wild trout were observed.
[2]Only the Chiwawa River was sampled in 1992. No tributaries were sampled in that year.

APPENDIX C. Proportion of total habitat available, fraction of all age-0 Chinook within each habitat type, and densities (fish/ha) and numbers of age-0 Chinook within each habitat type in the Chiwawa River Basin, survey years 1992-2010; NS = not sampled.

Habitat	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002
Proportion of total habitat available											
Glide	0.10	0.09	0.10	0.10	0.10	0.09	0.09	0.09	NS	0.07	0.08
Pool	0.19	0.19	0.21	0.18	0.18	0.17	0.16	0.17	NS	0.15	0.16
Riffle	0.61	0.61	0.57	0.59	0.57	0.57	0.58	0.55	NS	0.49	0.48
M. Chan	0.10	0.11	0.12	0.14	0.14	0.17	0.17	0.19	NS	0.29	0.28
Fraction of all age-0 Chinook within habitat types											
Glide	0.07	0.03	0.02	0.01	0.02	0.01	0.01	0.01	NS	0.03	0.01
Pool	0.30	0.28	0.22	0.21	0.30	0.16	0.17	0.14	NS	0.23	0.24
Riffle	0.19	0.16	0.12	0.11	0.43	0.23	0.08	0.11	NS	0.18	0.15
M. Chan	0.45	0.53	0.64	0.67	0.24	0.60	0.74	0.74	NS	0.57	0.60
Densities of age-0 Chinook within habitat types (fish/ha)											
Glide	254	251	93	55	11	12	78	13	NS	351	187
Pool	584	1,049	619	541	82	122	607	257	NS	1,392	1,468
Riffle	116	188	124	91	38	52	79	62	NS	336	300
M. Chan	1,710	3,408	2,985	2,328	84	449	2,620	1,201	NS	1,820	2,069
Number of age-0 Chinook within habitat types											
Glide	2,967	2,458	857	623	137	130	837	157	NS	3,231	1,931
Pool	13,468	21,814	12,131	11,294	1,755	2,553	11,454	5,933	NS	25,890	32,612
Riffle	8,531	12,616	6,698	6,197	2,525	3,699	5,392	4,626	NS	20,629	19,754
M. Chan	20,517	42,225	35,370	36,965	1,396	9,682	50,728	30,912	NS	64,866	80,576

APPENDIX C. Concluded.

Habitat	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	Mean
Proportion of total habitat available											
Glide	0.07	0.07	0.08	0.08	0.07	0.09	0.08	0.08			**0.08**
Pool	0.17	0.16	0.16	0.16	0.17	0.23	0.22	0.23			**0.18**
Riffle	0.49	0.50	0.47	0.47	0.47	0.51	0.54	0.53			**0.53**
M. Chan	0.26	0.27	0.29	0.30	0.29	0.17	0.15	0.16			**0.21**
Fraction of all age-0 Chinook within habitat types											
Glide	0.02	0.01	0.01	0.03	0.02	0.03	0.02	0.02			**0.02**
Pool	0.23	0.07	0.19	0.31	0.46	0.40	0.36	0.34			**0.27**
Riffle	0.15	0.14	0.07	0.12	0.12	0.11	0.11	0.11			**0.13**
M. Chan	0.60	0.77	0.73	0.54	0.40	0.45	0.51	0.53			**0.58**
Densities of age-0 Chinook within habitat types (fish/ha)											
Glide	200	58	49	237	113	238	230	286			**148**
Pool	951	155	492	1,240	1,211	1,210	1,453	1,436			**859**
Riffle	216	101	60	166	118	156	175	200			**142**
M. Chan	1,626	1,008	1,057	1,147	603	1,872	2,993	3,293			**1,613**
Number of age-0 Chinook within habitat types											
Glide	1,884	540	442	2,498	1,120	2,668	2,371	3,164			**1,556**
Pool	21,091	3,183	9,626	26,754	28,851	34,314	39,382	44,765			**19,271**
Riffle	13,783	6,501	3,367	10,753	7,809	9,773	11,558	14,446			**9,370**
M. Chan	54,519	34,952	36,196	46,580	25,409	38,275	55,607	69,609			**40,799**

APPENDIX B

Fish Trapping at the Chiwawa, Upper Wenatchee, and Lower Wenatchee Smolt Traps during 2010.

STATE OF WASHINGTON
DEPARTMENT OF FISH AND WILDLIFE
FISH PROGRAM -SCIENCE DIVISION
SUPPLEMENTATION RESEARCH TEAM
3515 Chelan HWY, Wenatchee, WA 98801
Voice (509) 664-3148   FAX (509) 662-6606

February 11, 2011

To: HCP Hatchery Committee

From: Todd Miller and John Walter

Cc: Distribution List

Subject: 2010 Chiwawa and Wenatchee River Smolt Estimates

Smolt monitoring programs in the Wenatchee Basin were intended to estimate the number of naturally produced migrating smolts at either the subbasin (i.e., Wenatchee) or watershed scale (i.e., Chiwawa) depending on the target stock (Table 1). In addition, population estimates of hatchery sockeye emigrating from Lake Wenatchee were used to calculate post release survival (i.e., subyearling parr to yearling smolt). The size of smolt traps operated was determined by water depth and river discharge at each of the locations. The number of smolt traps operated was determined by the expected trap efficiency. Smolt traps were located downstream from all (i.e., Chiwawa spring Chinook, Wenatchee spring Chinook, and Wenatchee sockeye), or the majority (i.e., Wenatchee summer Chinook and Wenatchee steelhead) of the spawning areas (Figure 1).

Table 1. Target stocks and corresponding smolt trapping locations used in 2010.

Stock	Smolt trap location	Smolt trap	
		Number	Diameter (m)
Chiwawa spring Chinook	Chiwawa	1	2.6
Wenatchee sockeye	Lake Wenatchee	2	1.5
Wenatchee spring Chinook	Monitor (Lower Wenatchee)	2	2.6
Wenatchee summer Chinook	Monitor (Lower Wenatchee)	2	2.6
Wenatchee steelhead	Monitor (Lower Wenatchee)	2	2.6

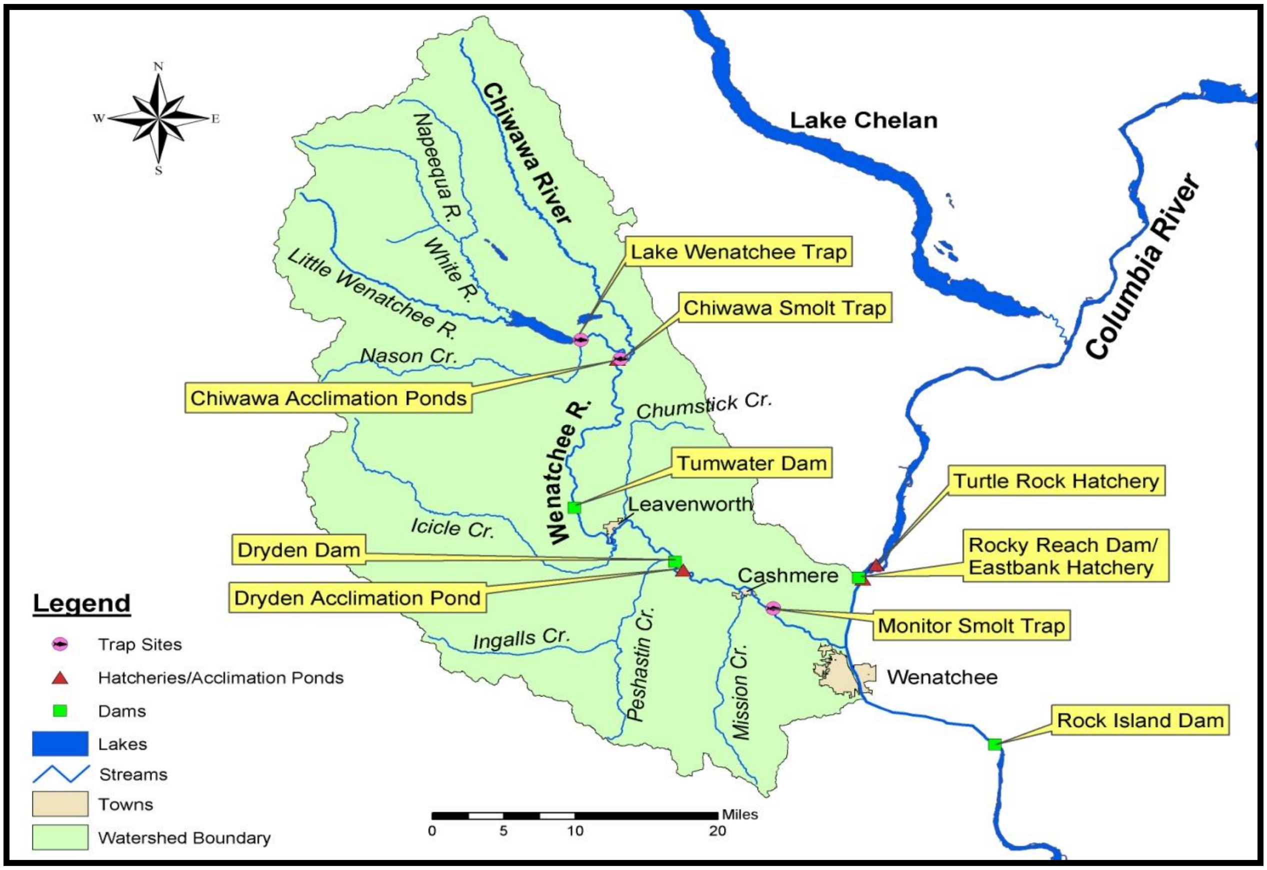


Figure 1. Locations of the upper Wenatchee (Lake Wenatchee Trap), Chiwawa, and lower Wenatchee River (Monitor Smolt Trap) smolt traps.

Methods

Fish were removed from the trap at a minimum every morning and placed in an anesthetic solution of MS-222. Fish were identified to species and counted. Non-target species were allowed to fully recover in fresh water prior to being released in an area of calm water downstream from the smolt trap. Target species were held in separate live boxes when needed for mark/recapture efficiency trials conducted in the evening.

Fork length was measured to the nearest millimeter and weight to the nearest 0.1 g. A Fulton type condition factor ($WH10^5/FL^3$) was calculated for all target species. The degree of smoltification (parr, transitional, or smolt) was assessed by visual examination. Juvenile spring Chinook and steelhead were classified as parr if parr marks were distinct, transitional if parr marks were not distinct, and smolts if parr marks were not visible and the fish exhibited a silvery appearance.

Mark/recapture efficiency trials were conducted throughout the trapping season. The frequency of mark/recapture trials was dependent on the number of fish captured (i.e., no less than 100) and the river discharge. These trials were conducted over the widest range of discharge possible (interval depends on trap location). Fish utilized for mark/recapture trials were marked by clipping the tip of either the upper or lower lobe of the caudal fin or were PIT tagged by Chelan County PUD personnel. Chinook fry (i.e., FL < 50 mm) used in mark/recapture trials were dyed using a Bismark brown solution. Marked fish were distributed evenly on both sides of the river in pools or in calm pockets of water around boulders. In the case of the upper Wenatchee River trap, marked fish were transported and released into Lake Wenatchee. Marked fish were released between 1800 h and 2000 h. All recaptures of marked fish typically occurred within 48 h after each trial. Emigration estimates were calculated using estimated daily trap efficiency derived from the regression formula using trap efficiency (dependent variable) and discharge (independent variable).

Trap efficiency was calculated using the following formula:

$$\text{Trap efficiency} = E_i = R / Mi,$$

Where E_i is the trap efficiency during time period i; M_i is the number of marked fish released during time period i; and R_i is the number of marked fish recaptured during time period i. The number of fish captured was expanded by the estimated daily trap efficiency (e) to estimate the daily number of fish migrating past the trap (N_i) using the following formula:

$$\text{Estimated daily migration} = \hat{N}_i = C_i / \hat{e}_i$$

where N_i is the estimated number of fish passing the trap during time period i; C_i is the number of unmarked fish captured during time period i; and e_i is the estimated trap efficiency for time period i based on the regression equation.

The variance for the total daily number of fish migrating past the trap will be calculated using the following formulas:

$$\text{Variance of daily migration estimate} = \operatorname{var}\left[\hat{N}_i\right] = \hat{N}_i^2 \frac{\text{MSE}\left(1 + \frac{1}{n} + \frac{\left(X_i - \overline{X}\right)^2}{(n-1)s_X^2}\right)}{\hat{e}_i^2}$$

where X_i is the discharge for time period i, and n is the sample size. If a relationship between discharge and trap efficiency was not present (i.e., $P < 0.05$; r^2 ~0.5), a pooled trap efficiency was used to estimate daily emigration:

$$\text{Pooled trap efficiency} = e_p = \sum R / \sum M$$

The daily emigration estimate was calculated using the formula:

$$\text{Daily emigration estimate} = \hat{N}_i = C_i / e_p$$

The variance for daily emigration estimates using the pooled trap efficiency was calculated using the formula:

Variance for daily emigration estimate = $\mathrm{var}\left[\hat{N}_i\right] = \hat{N}_i^2 \dfrac{e_p(1-e_p)\big/\sum M}{e_p^2}$

The total emigration estimate and confidence interval was calculated using the following formulas:

Total emigration estimate = $\sum \hat{N}_i$

95% confidence interval = $1.96 \times \sqrt{\sum \mathrm{var}\left[\hat{N}_i\right]}$

Results

Chiwawa River Smolt Trap

2008 Brood Year

The Chiwawa River smolt trap was located approximately 1 km upstream from the confluence with the Wenatchee River. The smolt trap operated between 5 March and 22 November. During that time period the trap was inoperable for 20 days as a result of high river flows, debris, snow/ice, mechanical failure, or statewide furlough days. During breaks in operation, the estimated number of Chinook captured was calculated from the mean number of fish captured two days prior and two days after the break in operation. The trap was operated in two positions dependent on river discharge (i.e., lower > 12 m^3/s and upper < 12 m^3/s). Daily trap efficiencies were estimated from two regression models (independent variable = discharge) depending on trap position and age class (i.e., subyearling and yearling Chinook).

Wild yearling spring Chinook (2008 brood) were primarily captured between 5 March and 1 June (Figure 2). 6,482 yearling Chinook were captured (Appendix A) and an estimated 6,779 yearling Chinook would have been captured if the trap had operated without interruption. Mortality for the season totaled 23 yearling spring Chinook (0.4 %). Seven mark/recapture efficiency trials were conducted in the lower position with a mean (SD) trap efficiency of 27.3 (0.04) %. In 2010, mark/recapture trials could not be conducted at all required discharge levels due to large catch rates of hatchery Chinook. Therefore, efficiency trials were combined with 2007, 2008, and 2009 trials in order to expand the population models utility over a greater range of river discharge. The 2010 regression model for the lower position ($r^2 = 0.70$, $P < 0.001$) was used to estimate yearling Chinook emigration. The estimated number (95% C.I.) of yearling Chinook that emigrated from the Chiwawa River in 2010 was 35,023 (±9,438).

2009 Brood Year

Wild subyearling spring Chinook were captured between March 5 and November 22, with major peaks occurring in August, September, and November (Figure 2). We captured 13,344 subyearling Chinook and estimated 14,101 subyearling Chinook would have been captured if the trap had operated without interruption (Figure 2). Mortality for the season totaled 64 subyearling spring Chinook (0.48%). Thirteen mark/recapture efficiency trials were conducted with a mean (SD) trap efficiency of 15.4 (0.08)%, which provided a current year regression model (i.e., upper trap position; $r^2 = 0.55$, $P < 0.01$). However, subyearling Chinook were also captured while the trap was operated in the lower position. Hence, a separate regression model from 2002 was used for that time period ($r^2 = 0.62$, $P < 0.01$). In 2010, the estimated number (95% C.I.) of subyearling spring Chinook (including fry) that moved downstream of the Chiwawa River smolt trap during the sampling period was 103,185 (± 15,166).

The proportion of subyearling Chinook that were captured and classified as fry, was greater in 2010 (58%) than in 2009 (45%) or in 2008 (16%). Typically the number of fry captured comprises less than 3% of the total number of Chinook captured for any given brood year. The large proportion of fry captured in 2010 and 2009 was attributed to a combination of large escapement, proximity of redds to the trapping location, high water velocity and discharge during the emergence period. As of yet, we have not determined if fry captured in the smolt trap migrate upstream at a later date and rear in the Chiwawa River or reside downstream of the smolt trap until the following spring and emigrate as yearling smolts. Hillman and Miller (2002) reported large numbers of subyearling Chinook in tributaries of the Chiwawa River where no spawning had been reported. These data suggest considerable movement during the summer rearing period. Due to the high likelihood that fry do migrate upstream and reside in the Chiwawa River, fry have not been included in our emigrant production estimates. Excluding the fry from the estimate, the number of subyearling spring Chinook that emigrated from the Chiwawa River was 31,913 (± 5,779).

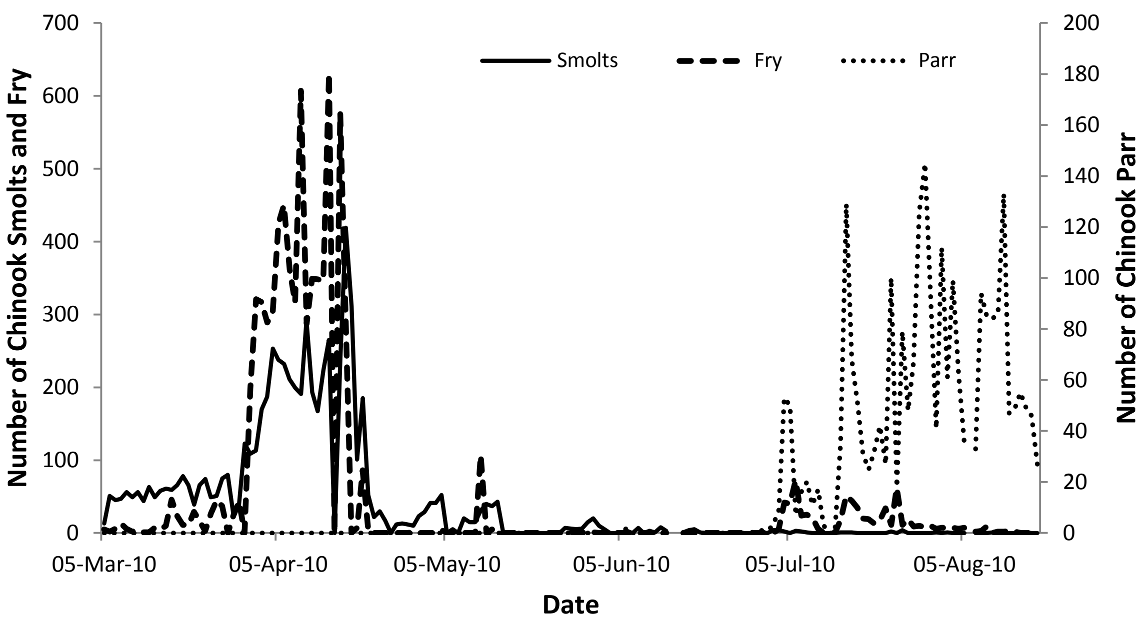


Figure 2. Daily number of Chiwawa River spring Chinook smolts, parr, and fry captured in 2010.

Emigrant Survival

The estimated total egg deposition was calculated by multiplying the mean fecundity of the 2008 brood spawners (WDFW, unpublished data) by the total number of redds found during surveys in the Chiwawa River basin in 2008 (Murdoch et al. 2008). Egg-to-emigrant survival was calculated by dividing the estimated egg deposition by the total number of subyearling (excluding fry) that emigrated in 2009 and yearling spring Chinook that emigrated in 2010. The estimated egg-to-emigrant survival for the 2008 brood Chiwawa spring Chinook was 3.8% (Table 2).

Length and Weight

Individual length and weight measurements were recorded from a sample of the daily catch. The mean fork length (SD) of captured yearling and subyearling Chinook (fry excluded) was 91.52 (7.81) mm and 74.58 (13.04) mm, respectively (Table 3).

Table 2. Estimated egg deposition (# of redds x mean broodstock fecundity) and egg-to-emigrant survival rates for Chiwawa River spring Chinook salmon.

Brood year	Number of redds	Estimated egg deposition	Estimated number			Egg-to-emigrant survival (%)
			Subyearling	Yearling	Total emigrants	
1992	302	1,570,098	25,818	39,723	65,541	4.2
1993	106	556,394	14,036	8,662	22,698	4.1
1994	82	485,686	8,595	16,472	25,067	5.2
1995	13	66,248	2,121	3,830	5,951	9.0
1996	23	106,835	3,708	15,475	19,183	18.0
1997	82	374,740	16,228	28,334	44,562	11.9
1998	39	207,675	2,855	23,068	25,923	12.5
1999	34	166,090	4,988	10,661	15,649	9.4
2000	128	642,944	14,854	40,831	55,685	8.7
2001	1,046	4,836,704	459,784	86,482	546,266	11.3
2002	345	1,605,630	93,331	90,948	184,279	11.5
2003	111	648,684	16,881	16,755	33,637	5.2
2004	241	1,156,559	44,079	72,080	116,158	10.0
2005	362	1,436,564	108,595	69,064	177,659	12.4
2006	297	1,284,228	62,922	45,050	107,972	8.4
2007	283	1,241,521	60,196	25,809	86,006	6.9
2008	689	3,163,199	85,161	35,023	120,184	3.8
2009	423	1,934,379	31,913	-----	----	---

Table 3. Mean fork lengths (mm), weights (g), and body condition factor of spring Chinook salmon captured in the Chiwawa River smolt trap during 2010.

	Yearling			Subyearling*		
	Mean	SD	*N*	Mean	SD	*N*
Fork length	91.52	7.81	*6,297*	74.58	13.04	*4,654*
Weight	8.93	2.39	*6,212*	5.36	2.41	*3,880*
K factor	1.15	0.13	*6,212*	1.11	0.16	*3,880*

* Parr only

Nontarget Salmonids

During the trapping period, 210 steelhead smolts and 1,016 steelhead/rainbow parr were captured. Mortality for the season totaled 8 steelhead juveniles (0.65%). The mean fork length (SD) of steelhead parr and smolts captured was 90.15 (39.46) mm and 124.38 (34.47) mm, respectively (Table 4). Bull trout also comprised a large proportion of incidental species captured. During the trapping period, 45 adult (>300mm) and 499 juvenile bull trout were captured (Table 5). Low numbers of fish captured prevented us from estimating the total number of steelhead and bull trout that emigrated from the Chiwawa River during the sampling period. Mortality for the season totaled 10 juvenile bull trout (2.0%) and 2 adult bull trout (4.4%). The monthly totals of all fish captured are listed in Appendix A.

Table 4. Mean fork lengths (mm), weights (g), and body condition factor of juvenile steelhead captured in the Chiwawa River smolt trap during 2010.

	Parr			Smolts		
	Mean	SD	*N*	Mean	SD	*N*
Fork length	90.15	39.46	*944*	124.38	34.47	*210*
Weight	12.79	18.81	*923*	24.31	19.82	*210*
K factor	1.09	0.16	*923*	1.04	0.10	*210*

Table 5. Mean fork lengths (mm), weights (g), and body condition factor of bull trout captured in the Chiwawa River smolt trap during 2010. Weights were not measured on adults.

	Juvenile			Adult		
	Mean	SD	*N*	Mean	SD	*N*
Fork length	188.34	33.51	*468*	406.4	110.7	*31*
Weight	70.89	39.07	*438*	--	--	--
K factor	0.98	0.22	*438*	--	--	--

Upper Wenatchee River Smolt Trap

The upper Wenatchee River smolt traps were located approximately 0.5 km below the outlet of Lake Wenatchee. The trap operated nightly between 12 March and 8 July 2010. We captured 60,792 wild and 1,909 hatchery sockeye smolts during the sampling period (Figure 3). Mortality during the season totaled 480 wild sockeye (0.79%) and 2 hatchery sockeye (0.10%). We also captured 569 wild spring Chinook smolts, and 95 juvenile Steelhead. Mortality totaled six wild juvenile Steelhead (6.3%) and 5 wild yearling Chinook (0.87%). There was no mortality of bull trout captured during the sampling period. The monthly totals of all fish captured are listed in Appendix B.

Eight mark/recapture efficiency trials with wild and hatchery sockeye were conducted during the sampling period. A combined total of 7,410 wild and hatchery sockeye were marked (i.e., caudal fin clip) and released into Lake Wenatchee. A combined total of 39 wild and hatchery sockeye were recaptured. A delay in migration and subsequent recapture of the marked fish from Lake Wenatchee negatively affected the relationship between discharge and trap efficiency (i.e., unequal probability of recapture). Both the hatchery and wild sockeye smolt production estimates were calculated using a wild and hatchery pooled daily trap efficiency (0.53%). The estimated smolt production (95% C.I.) for wild sockeye was 11,551,430 (±805,182). Age classes of wild sockeye were determined from scales collected randomly from the run (Table 6). Egg deposition was calculated based on the female to male ratio and spawning escapement determined at Tumwater Dam multiplied by fecundity of the broodstock (C. Deason, WDFW, personal communication). Historical egg-to-smolt survival rates for wild Wenatchee sockeye have ranged between 1.2% and 21.2% (Table 7).

The estimated number (95% CI) of hatchery sockeye that emigrated from Lake Wenatchee was 368,600 (±30,120), greater than the actual number of hatchery sockeye released (154,772). This was the fourth brood year in which all hatchery sockeye parr were released at a similar size and time since 1999, and the fourth brood year since 1995 where estimated emigration exceeded actual release. Due to our estimate being greater than the actual number of hatchery parr released we adjusted our emigrant estimate and assumed that survival was 100% (Table 8). Overestimation of the smolt migration is likely due to an underestimate of actual trap efficiency and probability of trap avoidance. Additional studies are needed to determine the source of error in trap efficiency estimates and possible alternatives.

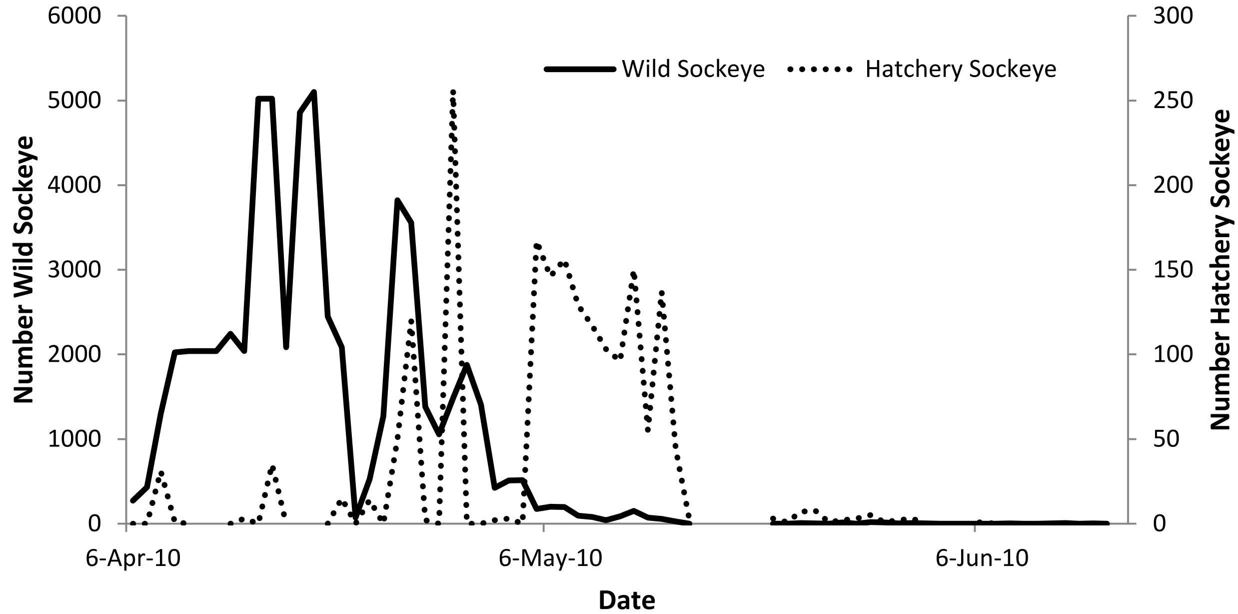


Figure 3. Number of wild and hatchery sockeye captured at the upper Wenatchee smolt trap, 2010.

Table 6. Age composition derived from scale samples and estimated number of wild sockeye smolts emigrating from Lake Wenatchee.

Run year	Proportion of wild smolts			Total emigrants
	Age 1+	Age 2+	Age 3+	
1997	0.075	0.906	0.019	55,359
1998	0.955	0.037	0.008	1,447,259
1999	0.619	0.381	0.000	1,944,966
2000	0.599	0.400	0.001	985,490
2001	0.943	0.051	0.006	39,353
2002	0.961	0.039	0.000	729,716
2003	0.740	0.026	0.000	5,439,032
2004	0.929	0.071	0.000	5,771,187
2005	0.230	0.748	0.022	723,413
2006	0.994	0.006	0.000	1,266,971
2007	0.996	0.004	0.000	2,797,313
2008	0.804	0.195	0.001	549,682
2009	0.927	0.073	0.000	732,686
2010*	0.975	0.024	0.001	11,551,430

* Ages not confirmed by scales.

Table 7. Estimated egg deposition (mean fecundity x estimated # of females) and egg-to-emigrant survival rates for Lake Wenatchee sockeye salmon.

Brood year	Estimated egg deposition	Estimated number of wild smolts				Egg-to-smolt survival (%)
		Age 1+	Age 2+	Age 3+	Total	
1995	4,902,120	4,174	53,549	0	57,723	1.18
1996	10,035,288	1,382,133	741,032	985	2,124,150	21.17
1997	13,223,588	1,203,934	394,196	236	1,598,366	12.09
1998	5,692,106	590,309	2,007	0	592,316	10.41
1999	1,188,488	37,110	28,459	0	65,569	5.52
2000	30,506,949	701,257	1,378,795	0	2,080,052	6.82
2001	64,187,600	4,024,884	409,754	15,915	4,450,553	6.93
2002	49,197,456	5,361,433	541,113	0	5,902,546	12.00
2003	7,576,738	166,385	7,602	0	173,987	2.30
2004	38,749,845	1,259,369	11,189	275	1,270,833	3.28
2005	15,946,506	2,786,123	107,243	0	2,893,366	18.14
2006	7,296,032	442,164	53,413	4,621	500,197	6.86
2007[a]	6,232,804	679,273	280,469	--	959,742	15.40
2008[a]	30,084,691	11,266,110	--	--	11,266,110	37.45

[a] Incomplete brood year.

Table 8. Release-to-smolt survival rates for Lake Wenatchee hatchery sockeye.

Brood year	Releas e year	Run year	Number of fish released	Fork length (mm) at release (SD)	Date of release	Number of fish captured	Estimated number of smolts	Release to smolt survival
1995	1996	1997	150,808	106.0(6.2)	25 Oct	130	28,828	19.12%
1996	1997	1998	284,630	106.5(7.4)	22 Oct	279	55,985	19.67%
1997	1998	1999	197,195	122.1(7.4)	09 Nov	586	112,524	57.06%
1998	1999	2000	121,344	112.3(7.6)	29 Oct	66	24,684	20.34%
1999	2000	2001	84,466	94.4(8.9)	28 Aug	319	30,326	35.90%
1999	2000	2001	83,489	134.3(15.4)	01 Nov	548	63,720	76.32%
2000	2001	2002	92,055	122.6(7.9)	27 Aug	142	30,918	33.59%
2000	2001	2002	98,119	146.3(12.2)	27 Sept	416	90,593	92.33%
2001	2002	2003	96,486	117.9(8.7)	28 Aug	162	36,484	37.81%
2001	2002	2003	104,452	134.8(8.7)	23 Sept	465	103,838	99.41%
2002	2003	2004	98,509	72.7(5.0)	16 Jun	31	5,192	4.41%
2002	2003	2004	104,855	118.1(9.1)	25 Aug	376	98,412	85.88%
2002	2003	2004	112,419	145.4(13.7)	22 Oct	292	112,419	100.0%

2003	2004	2005	32,755	78.7(3.6)	15 Jun	0	0	0.00%
2003	2004	2005	104,879	118.4(7.0)	25 Aug	229	19,574	18.66%
2003	2004	2005	102,825	158.2(12.8)	03 Nov	1,185	102,825	100.0%
2004	2005	2006	81,428	115.8(6.7)	29 Aug	1,500	159,500	92.2%
2004	2005	2006	91,495	150.7(7.0)	02 Nov			
2005	2006	2007	140,542	148.9(14.0)	30 Oct	516	140,542	100.0%
2006	2007	2008	225,670	137.8(14.7)	31 Oct	1,367	102,907	45.60%
2007	2008	2009	252,133	137.2(6.8)	29 Oct	263	247,098	98.00%
2008	2009	2010	154,772	138.0(13.2)	28 Oct	1,909	154,772	100.0%

Lower Wenatchee River Smolt Trap

The lower Wenatchee River smolt traps were located at the West Monitor Bridge (rkm 9.6). The trap operated nightly between 4 February and 20 July. However, due to heavy debris and/or high flow, both traps were not operational for 19 days (i.e., 17 May through 21 May, 3 June through 6 June, 9 June through 11 June, 14 June through 16 June, 25 June through 26 June, and 12 July through 13 July). One trap was not operational for an additional 68 days (i.e., 21 April through 25 April, 15 May through 6 July, and 8 July through 17 July).

We captured 1,079 wild spring Chinook (Figure 4) and 484 parr and smolt steelhead (Figure 5). A total of 215 steelhead fry were captured. A total of 50,685 subyearling Chinook were captured (Figure 4) comprising 97.9% of the total number of wild juvenile Chinook captured in 2010. We also captured 3,153 wild sockeye (Figure 6). Mortality during the trapping period consisted of 5 yearling Chinook (0.5%), 361 wild subyearling Chinook (0.7%), and two steelhead fry (0.9%). Hatchery fish captured totaled 43,613 yearling Chinook, 2,735 steelhead and 440 sockeye. The monthly totals of all fish captured are listed in Appendix C. Smolt production estimates for salmon and steelhead were calculated using efficiency trials conducted with subyearling Chinook, yearling hatchery Chinook, and yearling hatchery coho. Mark/recapture trials were conducted when river discharge changed between 14 and 28 m^3/s or the trap position had changed. Low abundance of other target species precluded their use in mark/recapture trials.

Smolt production estimates were calculated using separate regression models (independent variable = river discharge) for each trap position and species. However, when too few trials for a given position or species were conducted, efficiency trials from previous years were incorporated into the regression model. Until the relative abundance of wild yearling Chinook and steelhead increases, or trap efficiency significantly increases such that an adequate number of the target species are captured, surrogates must be used in trap efficiency trials. Estimates for yearling Chinook and steelhead incorporated regression models developed with hatchery coho and hatchery Chinook for both the trap positions ($r^2 = 0.43$, $P < 0.01$; $r^2 = 0.65$, $P < 0.01$). Subyearling Chinook were captured in sufficient numbers such that regression models were developed using only subyearling Chinook when the trap was operated in both operating positions, however to encompass a wider range of river discharge, previous year mark groups were also used ($r^2 = 0.30$, $P < 0.01$; $r^2 = 0.89$, $P < 0.01$). The smolt production estimate (95% CI) for wild yearling and subyearling Chinook was 82,137 (± 87,931) and 6,695,977 (± 2,435,120), respectively. The 2008 brood egg-to-smolt survival for Wenatchee spring Chinook was 1.27% (Table 9). The smolt production estimate for Wenatchee steelhead was 36,826 (±22,782) and the 2006 brood emigration, completed in 2010, had an egg-to-smolt survival of 1.72% (Table 10).

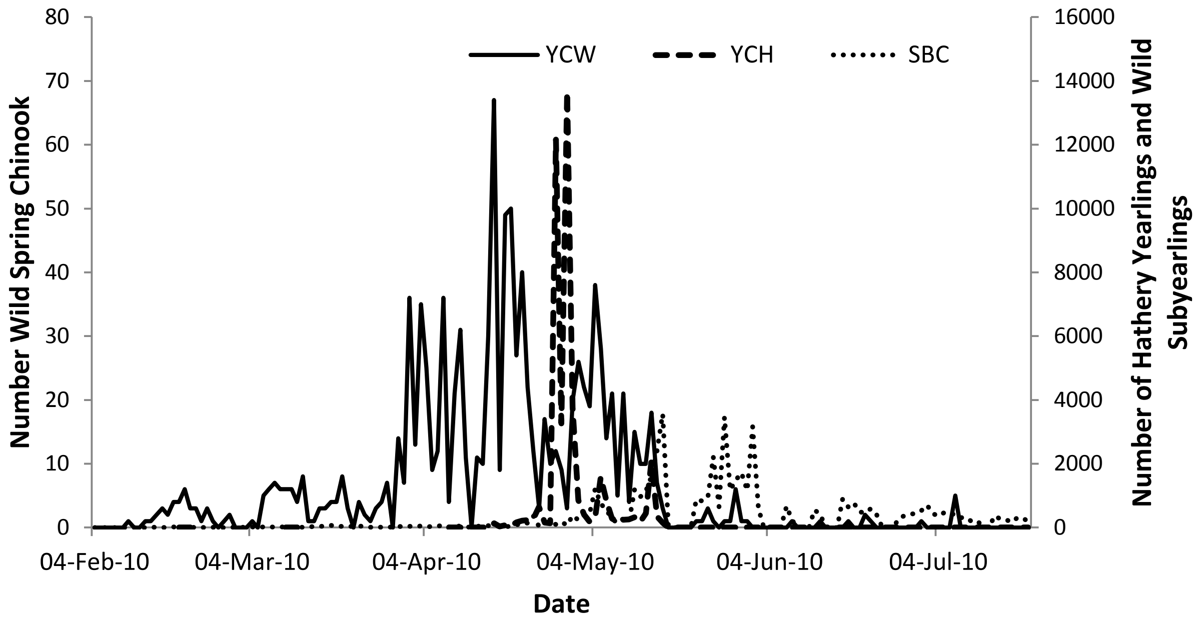


Figure 4. Daily capture of wild and hatchery yearling Chinook and subyearling summer Chinook at the lower Wenatchee River trap in 2010.

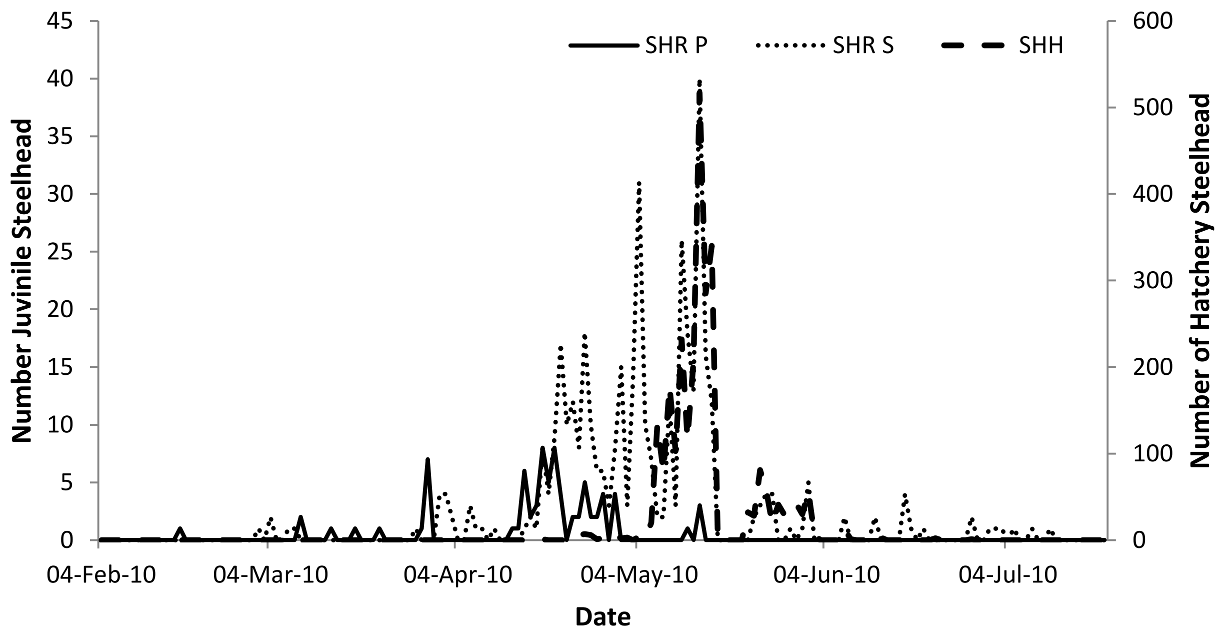


Figure 5. Daily capture of wild and hatchery juvenile steelhead at the lower Wenatchee smolt trap in 2010 (SHR S = steelhead smolt, SHR P = steelhead parr, SHH = hatchery steelhead).

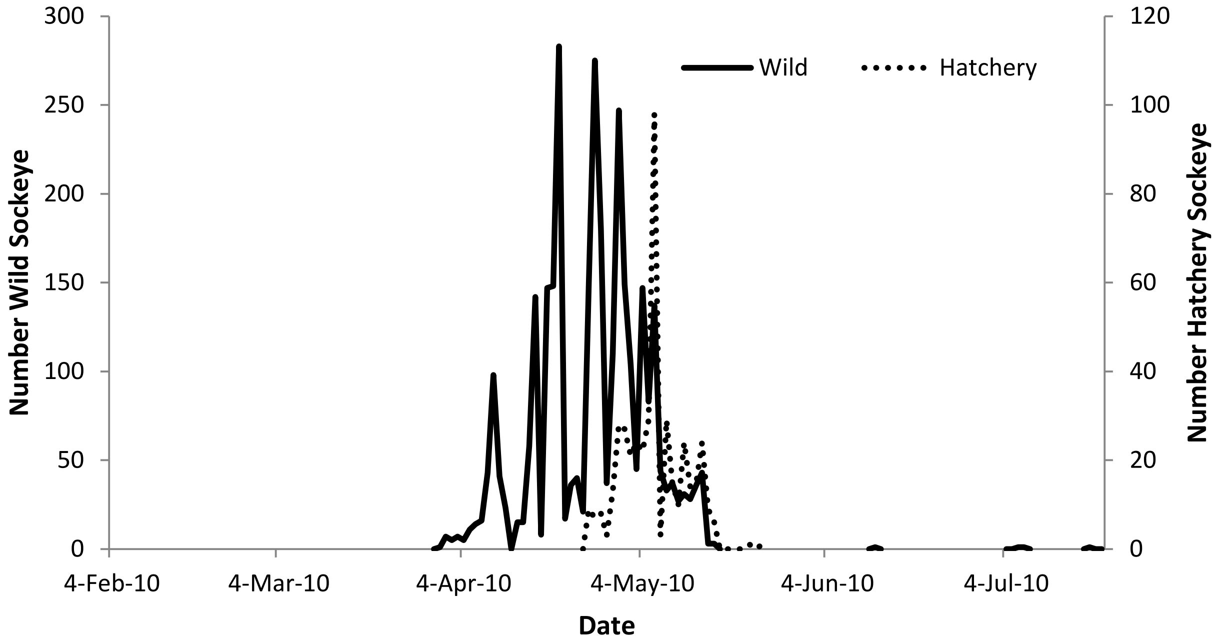


Figure 6. Daily capture of wild and hatchery sockeye at the lower Wenatchee smolt trap in 2010.

Table 9. Estimated egg deposition (# of redds x mean broodstock fecundity) and egg-to-smolt survival rates for Wenatchee Basin spring Chinook salmon.

Brood year	Number of redds	Estimated egg deposition	Estimated number	
			Total emigrants	Egg-to-smolt survival (%)
2000	350	1,758,050	76,643	4.36
2001	1,876	8,674,624	243,516	2.81
2002	1,139	5,300,906	165,116	3.11
2003	323	1,887,612	70,738	3.75
2004	555	2,663,445	55,619	2.09
2005	829	3,587,083	302,116	8.42
2006	588	2,542,512	85,558	3.37
2007	466	2,069,506	60,219	2.91
2008	1,411	6,479,312	82,137	1.27

Table 10. Estimated egg deposition (mean fecundity x estimated # of females) and egg-to-emigrant survival rates for Wenatchee Basin steelhead.

Brood year	Estimated egg deposition	Estimated number of wild smolts				Egg-to-smolt survival (%)
		Age 1+	Age 2+	Age 3+	Total	
1998[a]		16,628	14,799	4,293	35,720	
1999[a]		5,691	24,528	4,203	34,422	
2000[a]		7,972	26,462	5,857	40,292	
2001[b]	858,990	1,930	21,522	8,142	31,594	3.68
2002	2,674,250	4,712	28,153	1,708	34,573	1.29
2003	2,919,420	4,887	6,828	5,520	17,235	0.59
2004	1,933,560	8,963	51,608	944	61,515	3.18
2005	5,620,120	28,307	14,480	5,968	48,755	0.87
2006	2,126,240	16,474	13,922	6,279	36,674	1.72
2007[c]	899,940	7,624	18,988	--	--	--
2008[c]	1,553,838	11,560	--	--	--	--

[a] No redd counts
[b] Partial basin redd counts
[c] Incomplete brood year

Discussion

Upper Wenatchee River Smolt Trap

Wild and hatchery Sockeye were used in eight mark/recapture efficiency trials. While significant numbers of sockeye were caught to perform trials at variable discharge levels, a flow stratified linear model was not obtained (i.e. $P > 0.05$ & $R^2 < 0.50$). A delay in migration and subsequent recapture of the marked fish from Lake Wenatchee negatively affected the relationship between discharge and trap efficiency (i.e., unequal probability of recapture). Therefore, the pooled trap efficiency of 0.53% was used to calculate sockeye smolt production estimates. It is likely this is an underestimate of actual trap efficiency, due to the unequal probability of recapture, and thus led to overestimated smolt migrations. The pooled trap efficiency for 2010 was also significantly lower than previous years that ranged from 0.9% to 1.0%. This contributed to a high measure of inaccuracy in our estimate of both wild and hatchery Sockeye. The trap site will remain the same for 2011 but be moved approximately 8 km downstream for 2012 with the goals of obtaining a flow stratified model, reducing migration delays and predation during efficiency trials, and increasing our catch of Sockeye and other salmonids.

Lower Wenatchee River Smolt Trap

Low abundance of spring Chinook and steelhead precluded their use for mark/recapture trials. Hatchery Chinook were used as surrogates for mark/recapture trials, which were conducted at various levels of river discharge or if the trap position had changed. Smolt production estimates were calculated using separate regression models (independent variable = river discharge; dependent variable = trap efficiency) for each of the two trap positions. Mark/recapture trials conducted in 2010 were too few at the varying river discharge to obtain a useable model. Therefore, trials from previous years (i.e., 2001-2009) were used to increase the sample size in the model.

Hatchery Coho catch numbers were significantly lower in 2010 than previous years while hatchery Chinook numbers were significantly higher (Appendix C), therefore mark/recapture trials were carried out with hatchery Chinook only. Previously, high abundance of hatchery Coho permitted their use as surrogates in mark/recapture trials. Hatchery Chinook and Coho will continue to be used as surrogates in trap efficiency trials until the relative abundance of wild spring Chinook and steelhead increase sufficiently to allow species-specific trials.

The high confidence interval for yearling spring Chinook in 2010 (82,137 (± 87,931)) can be explained by low trap efficiency which inversely contributes to high variance in the estimate. A large portion of the yearling Chinook catch occurred while discharge ranged from 42.5 to 85.0 m^3/s, where efficiencies ranged from 0.95% to 1.96%. Fish were also caught outside the discharge range of our model, adding to inaccuracy. The majority of wild Steelhead smolts were captured at discharge ranges (85.0-141.6 m^3/s) where the trap experienced higher efficiencies (2.0-3.8%). This resulted in a comparatively lower confidence interval for migrating Steelhead smolts (36,826 (±22,782)). This same trend can be applied to sub yearling Chinook estimates, where large catch numbers during discharge ranges resulting in higher efficiencies led to a comparatively lower confidence interval (6,695,977 (± 2,435,120)).

Although the high variability in discharge leads to high confidence intervals we feel our estimates are acceptable because the regression models used to generate them are significant (yearling estimates, $r^2 = 0.43$, $P < 0.01$; $r^2 = 0.65$, $P < 0.01$; sub yearling estimates, $r^2 = 0.30$, $P < 0.01$; $r^2 = 0.89$, $P < 0.01$). Improvements to our variance equation will continue to be explored along with other variables that may influence mark/recapture trials and subsequently affect our confidence intervals. Investigation of such parameters and vigilance in sampling methods will continue to be the focus of upcoming seasons.

Chiwawa River Smolt Trap

The 2009 brood year subyearling spring Chinook model was developed with 2010 mark/recapture trials only. A significant relationship was obtained between river discharge and trap efficiency ($r^2 = 0.55$, $P < 0.01$). Thirty-nine trapping days fell out of the discharge range of the model, however during these time periods only 58 subyearling parr were caught. This resulted in small variance during these discharge ranges.

Only five mark/recapture trials were conducted for the 2008 brood yearling spring Chinook estimate and a relationship between discharge and efficiency was significant. However, discharge for that model only ranged from 5.3 to 8.9 m^3/s. Therefore, mark groups from 2010 were incorporated into a combined 2007 through 2010 linear regression ($r^2 = 0.70$, $P < 0.01$). This enabled the models utility over a range of discharges from 3.8 to 32.5 m^3/s.

Since the spring of 2008 an instream PIT tag antennae array has been in operation directly upstream from the Chiwawa trap site. We have collected numerous amounts of data including all mark recapture efficiency trials conducted at the trap site, adult spawning migration and other juvenile movement detections. Analysis of these data will begin in 2011 with emphasis on exploring subyearling Chinook movement during winter months.

References

Miller, J., A. Murdoch, M. Tonseth, T. Miller, T. Hillman, M. Miller. 2009. Monitoring and Evaluation of the Chelan County PUD Hatchery Programs, 2009 Annual Report prepared for HCP Hatchery Committee, Wenatchee, Washington.

Hillman, T.W. and M.D. Miller. 2002. Abundance and total numbers of Chinook salmon and trout in the Chiwawa River Basin, Washington, 2001. Report to Chelan county Public Utility District, Wenatchee, Washington.

Murdoch, A.R., T.N. Pearsons, T.W. Maitland, M.F. Ford, and K. Williamson. 2007. Monitoring the reproductive success of naturally spawning hatchery and natural spring Chinook salmon in the Wenatchee River. BPA Project No. 2003-039-00. Bonneville Power Administration, Portland, Oregon.

Deason, C. 2010, Personal communication. Washington Department of Fish and Wildlife, Science division, Supplementation research team, Wenatchee WA.

Appendix A. Monthly total juvenile capture information for the Chiwawa River trap.

	2010									
Species/Origin	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Total
Chinook										
Wild yearling	1,589	4,383	428	52	26	4	0	0	0	6,482
Wild subyearling	575	6,302	126	4	1,981	1,784	493	853	1,226	13,344
Hatchery yearling	0	15,285	7,149	0	2	29	10	4	2	22,481
Steelhead										
Wild	19	272	244	123	61	148	218	101	40	1,226
Smolt	14	74	56	44	4	18	0	0	0	210
Parr	5	198	188	79	57	130	218	101	40	1,016
Hatchery	1	1	9,857	24	0	12	17	8	1	9,921
Coho										
Wild yearling	0	3	0	0	0	0	0	1	0	4
Wild subyearling	0	0	0	3	2	0	0	0	0	5
Hatchery yearling	0	3	0	0	0	0	0	0	0	3
Bull trout										
Juvenile	10	4	14	27	19	29	100	183	113	499
Adult	0	0	0	0	1	1	28	14	1	45
Cutthroat	0	0	2	7	0	26	15	2	2	54
Eastern brook	0	0	0	0	0	0	0	0	0	0
Whitefish	33	54	5	0	36	432	196	15	7	778
Northern pikeminnow	0	0	0	0	0	2	2	1	0	5
Longnose dace	2	23	71	263	149	63	597	215	10	1,393
Sucker spp.	0	0	0	0	0	0	0	0	0	0
Redside shiner	0	0	0	0	0	0	0	0	0	0
Yellow perch	0	0	0	0	0	0	0	0	0	0
Sculpin spp.	1	6	3	1	6	8	13	11	2	51

Appendix B. Monthly total juvenile capture information for the upper Wenatchee River trap.

2010											
Species/Origin	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec	Total
Chinook											
Wild yearling	38	280	231	20	0	--	--	--	--	--	569
Wild subyearling	18	181	20	12	26	--	--	--	--	--	254
Hatchery yearling	0	17	175	52	1	--	--	--	--	--	245
Steelhead											
Wild	8	48	21	11	7	--	--	--	--	--	95
Smolt	1	16	14	5	7	--	--	--	--	--	43
Parr	7	32	7	6	0	--	--	--	--	--	52
Hatchery	0	13	341	3	0	--	--	--	--	--	357
Sockeye											
Wild	74	56,583	4,096	34	5	--	--	--	--	--	60,792
Hatchery	0	558	1,346	5	0	--	--	--	--	--	1,909
Coho											
Wild yearling	2	1	1	0	0	--	--	--	--	--	4
Wild subyearling	0	4	4	7	0	--	--	--	--	--	15
Hatchery yearling	21	61	532	18	0	--	--	--	--	--	632
Bull trout											
Juvenile	1	0	2	1	0	--	--	--	--	--	4
Adult	0	0	0	0	0	--	--	--	--	--	0
Cutthroat	0	0	1	1	0	--	--	--	--	--	2
Whitefish	4	70	6	1	0	--	--	--	--	--	81
Northern pikeminnow	10	82	84	18	7	--	--	--	--	--	201
Longnose dace	1	2	0	4	2	--	--	--	--	--	9
Sucker spp.	0	3	1	6	4	--	--	--	--	--	14
Redside shiner	0	42	14	5	5	--	--	--	--	--	66
Yellow perch	0	0	0	0	0	--	--	--	--	--	0

Appendix C. Monthly total juvenile capture information for the lower Wenatchee River trap.

2010											
Species/Origin	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Total
Chinook											
Wild yearling	38	118	634	277	6	6	--	--	--	--	1,079
Wild subyearling	86	663	2,525	29,806	11,427	6,178	--	--	--	--	50,685
Hatchery yearling	1	2	34,941	8,653	8	8	--	--	--	--	43,613
Steelhead											
Wild	1	19	198	243	17	6	--	--	--	--	484
Smolt	0	6	139	239	17	6	--	--	--	--	407
Parr	1	13	59	4	0	0	--	--	--	--	77
Hatchery	0	0	28	2,615	92	0	--	--	--	--	2,735
Sockeye											
Wild	0	1	2,198	950	1	3	--	--	--	--	3,153
Hatchery	0	0	68	372	0	0	--	--	--	--	440
Coho											
Wild yearling	1	12	47	84	18	26	--	--	--	--	188
Wild subyearling	4	18	366	730	201	793	--	--	--	--	2,112
Hatchery yearling	0	6	5,772	2,128	107	0	--	--	--	--	8,013
Bull trout											
Juvenile	0	0	0	2	0	0	--	--	--	--	2
Adult	0	0	0	0	0	0	--	--	--	--	0
Cutthroat	0	0	0	0	0	0	--	--	--	--	0
White fish	1	0	0	6	2	39	--	--	--	--	48
Northern pikeminnow	1	30	45	54	43	25	--	--	--	--	198
Longnose dace	49	126	88	114	80	186	--	--	--	--	643
Speckled dace	0	0	0	0	0	0	--	--	--	--	0
Umatilla dace	0	0	0	0	0	0	--	--	--	--	0
Sucker spp.	6	19	89	104	35	137	--	--	--	--	390
Peamouth	1	3	3	0	8	47	--	--	--	--	62
Chiselmouth	0	1	0	0	0	0	--	--	--	--	1
Redside shiner	3	10	30	85	14	428	--	--	--	--	570
Yellow bullhead	0	0	0	1	0	0	--	--	--	--	1
Pacific lamprey	30	71	256	223	39	61	--	--	--	--	680
River lamprey	0	0	0	0	0	0	--	--	--	--	0
Sculpin spp.	6	20	16	9	9	10	--	--	--	--	70
Stickleback (3 spined)	1	1	0	0	1	1	--	--	--	--	4

Appendix D. Yearly total juvenile capture information for the Chiwawa river trap.

Species/Origin	2009	2008	2007	2006	2005	2004	2003	2002	2001	2000	1999	1998	1997
Chinook													
Wild yearling	3,765	8,711	4,433	4,974	2,874	4,326	8,012	1,423	2,763	1,791	3,917	3,460	880
Wild subyearling	30,641	12,728	16,250	14,542	11,049	5,266	25,096	53,672	5,177	1,483	557	3,843	744
Hatchery yearling	14,097	22,367	17,634	9,796	3,965	7,557	5,893	2,926	0	6	60	97	0
Steelhead													
Wild	1,957	1,700	1,211	1,789	1,672	2,441	1,662	778	1,091	326	253	622	260
Smolt	248	448	152	53	45	280	32	86	63	181	133	160	105
Parr	1,709	1,250	1,056	1,736	1,627	2,161	1,630	692	1,028	145	120	462	155
Hatchery	2,708	2,684	1,964	1,384	2,104	9,678	5,886	2,720	134	45	78	3	0
Coho													
Wild yearling	0	0	0	3	4	0	0	0	0	0	0	0	0
Wild subyearling	1	13	12	2	0	0	0	0	0	0	0	0	0
Hatchery yearling	3	1	0	126	8	0	0	0	2	0	0	0	0
Bull Trout *Juvenile*	496	513	250	125	175	238	438	339	264	421	234	605	233
Bull Trout *Adult*	24	33	29	39	41	12	6	8	25	19	16	57	23
Cutthroat	--	52	40	56	44	45	28	37	183	22	13	34	22
Eastern brook	--	4	3	4	4	2	6	7	25	10	9	17	24
Whitefish	3,340	2,672	2,186	2,267	3,672	3,669	1,212	871	1,825	837	317	1,565	525
Northern pikeminnow	47	7	15	0	0	13	1	3	14	12	2	54	3
Longnose dace	2,081	2,934	2,349	1,951	3,133	3,162	1,557	604	1,217	1,456	130	1,481	579
Sucker spp.	7	9	1	8	10	5	4	0	6	40	3	11	0
Redside shiner	0	0	0	1	2	1	1	0	0	0	0	0	0
Yellow perch	0	0	0	0	0	0	0	1	14	0	1	4	0
Sculpin spp.	78	143	73	104	23	34	13	58	77	56	24	119	42

Appendix E. Yearly total juvenile capture information for the upper Wenatchee river trap.

Species/Origin	2009	2008	2007	2006	2005	2004	2003	2002	2001	2000	1999	1998	1997
Chinook													
Wild yearling	323	194	1,597	138	61	355	257	34	62	49	228	90	12
Wild subyearling	312	71	213	2,012	2,541	139	40	5	118	10	84	0	0
Hatchery yearling	1,074	398	750	10	6	1	0	0	0	0	5	0	0
Steelhead													
Wild	66	28	80	42	36	55	14	2	37	1	9	4	7
Smolt	37	14	15	10	1	1	0	2	4	1	1	3	1
Parr	29	14	65	32	35	54	14	0	33	0	8	1	6
Hatchery	637	61	178	160	354	27	43	41	0	0	0	0	0
Sockeye													
Wild	7,314	9,133	38,628	20,309	6,580	37,953	25,165	3,299	848	2,635	9,887	6,926	265
Hatchery	2,444	1,367	2,387	1,500	1,416	1,866	668	558	1,581	66	572	268	138
Coho													
Wild yearling	9	6	3	10	2	1	0	0	0	0	0	0	0
Wild subyearling	1	16	0	0	5	0	0	0	0	0	0	0	0
Hatchery yearling	585	120	311	125	340	81	98	27	119	11	10	0	0
Bull Trout *Juvenile*	9	3	5	1	5	0	0	1	3	6	4	1	3
Bull Trout *Adult*	0	0	2	0	3	1	0	0	2	0	0	0	0
Cutthroat	2	2	1	0	1	2	0	0	12	0	0	1	0
Whitefish	78	35	49	3	26	19	6	4	16	4	16	10	20
Northern pikeminnow	234	106	113	46	17	46	23	5	28	26	43	33	125
Longnose dace	42	8	24	2	53	58	0	0	20	3	6	2	0
Sucker spp.	30	3	18	2	28	47	12	0	23	5	25	6	5
Redside shiner	90	21	37	21	47	62	14	0	21	15	23	12	34
Yellow perch	0	0	1	0	0	0	0	0	0	0	0	0	0
Sculpin spp.	--	251	201	35	85	68	34	12	96	46	67	59	58

Appendix F. Yearly total juvenile capture information for the lower Wenatchee river trap.

Species/Origin	2009	2008	2007	2006	2005	2004	2003	2002	2001	2000
Chinook										
Wild yearling	5,346	612	1,906	652	333	1,061	1,619	336	206	284
Wild subyearling	37,568	30,547	86,142	63,580	224,858	225,549	110,528	39,714	70,952	72,244
Hatchery yearling	6,709	19,440	45,467	35,261	23,709	11,846	20,939	3,421	8,758	2,753
Steelhead										
Wild	264	319	495	151	246	360	413	252	341	468
Smolt	216	220	433	105	210	299	343	187	273	426
Parr	48	99	62	45	36	61	70	76	68	42
Hatchery	1,949	2,106	2,697	3,769	2,013	3,465	2,175	2,260	1,711	2,219
Sockeye										
Wild	1,259	216	6,340	5,204	202	3,224	7,544	5,042	58	1,114
Hatchery	263	207	248	68	79	335	271	281	131	12
Coho										
Wild yearling	114	111	292	103	189	58	199	72	0	0
Wild subyearling	515	1,013	431	1,460	1,846	927	29	1,443	191	0
Hatchery yearling	9,709	4,296	29,305	13,627	11,943	15,455	8,034	12,363	11,265	12,305
Bull Trout *Juvenile*	0	1	2	1	3	2	0	1	1	4
Bull Trout *Adult*	0	0	0	0	0	0	0	0	0	0
Cutthroat	1	1	0	0	0	0	0	0	2	0
Whitefish	52	67	23	118	9	34	115	31	78	73
Northern pikeminnow	13	57	135	475	90	75	21	93	10	9
Longnose dace	383	568	1,820	801	659	2,374	488	593	445	319
Speckled dace	0	1	0	0	0	5	4	3	7	17
Umatilla dace	0	2	0	0	0	2	1	12	36	17
Sucker spp.	63	612	339	3,420	203	208	172	169	201	121
Peamouth	1	2	1	0	0	0	0	0	0	11
Chiselmouth	0	0	1	32	0	7	2	7	1	6

Redside shiner	18	69	84	952	166	100	14	47	47	8
Yellow bullhead	0	0	0	0	0	0	0	0	0	1
Pacific lamprey	1,245	1,431	2,876	1,933	685	650	922	978	1,267	1,393
River lamprey	0	0	0	0	0	0	1	0	18	20
Sculpin spp.	123	49	64	118	171	86	71	97	55	76
Stickleback (3 spined)	7	4	39	78	51	85	18	48	246	0

APPENDIX C

Summary of ISEMP PIT Tagging Activities in the Wenatchee Basin, 2010.

Appendix C. Numbers of fish captured, PIT tagged, lost, and released in the Wenatchee Basin during February through November, 2010.

Sampling Location	Species and Life Stage	Number held	Number of recaptures	Number tagged	Number died	Shed Tags	Total released	Percent mortality
Chiwawa Trap	Wild Subyearling Chinook	3,637	127	3,326	2	0	3,324	0.05
	Wild Yearling Chinook	6,741	292	6,285	4	0	6,281	0.06
	Wild Steelhead/Rainbow	988	7	931	1	0	930	0.10
	Hatchery Steelhead/Rainbow	3	0	2	0	0	2	0.00
	Wild Coho	0	0	0	0	0	0	--
	Total	**11,369**	**426**	**10,544**	**7**	**0**	**10,537**	**0.06**
Chiwawa Remote	Wild Subyearling Chinook	574	12	532	0	1	531	0.00
	Wild Yearling Chinook	4	0	4	0	0	4	0.00
	Wild Steelhead/Rainbow	103	2	99	0	0	99	0.00
	Hatchery Steelhead/Rainbow	67	3	64	0	0	64	0.00
	Wild Coho	0	0	0	0	0	0	--
	Total	**748**	**17**	**699**	**0**	**1**	**698**	**0.00**
Upper Wenatchee Trap	Wild Subyearling Chinook	3	0	3	0	0	3	0.00
	Wild Yearling Chinook	524	13	491	5	0	486	0.95
	Wild Steelhead/Rainbow	72	2	69	0	0	69	0.00
	Hatchery Steelhead/Rainbow	0	0	0	0	0	0	--
	Wild Coho	0	0	0	0	0	0	--
	Wild Sockeye	11,103	7	10,082	76	0	10,006	0.68
	Total	**11,702**	**22**	**10,645**	**81**	**0**	**10,564**	**0.69**
Nason Creek Remote	Wild Subyearling Chinook	600	2	595	0	0	595	0.00
	Wild Yearling Chinook	3	0	3	0	0	3	0.00
	Wild Steelhead/Rainbow	328	8	318	0	0	318	0.00
	Hatchery Steelhead/Rainbow	37	5	32	0	0	32	0.00
	Wild Coho	109	0	12	0	0	12	0.00
	Total	**1,077**	**15**	**960**	**0**	**0**	**960**	**0.00**
Upper Wenatchee Remote	Wild Subyearling Chinook	2	0	2	0	0	2	0.00
	Wild Yearling Chinook	0	0	0	0	0	0	--
	Wild Steelhead/Rainbow	30	0	30	0	0	30	0.00
	Hatchery Steelhead/Rainbow	9	0	9	0	0	9	0.00
	Wild Coho	0	0	0	0	0	0	--
	Total	**41**	**0**	**41**	**0**	**0**	**41**	**0.00**
Middle Wenatchee Remote	Wild Subyearling Chinook	245	4	234	1	0	233	0.41
	Wild Yearling Chinook	0	0	0	0	0	0	--
	Wild Steelhead/Rainbow	1,608	84	1,518	1	0	1,517	0.06
	Hatchery Steelhead/Rainbow	67	10	57	0	0	57	0.00
	Wild Coho	0	0	0	0	0	0	--

Sampling Location	Species and Life Stage	Number held	Number of recaptures	Number tagged	Number died	Shed Tags	Total released	Percent mortality
	Total	**1,920**	**98**	**1,809**	**2**	**0**	**1,807**	**0.10**
Peshastin Creek Remote	Wild Subyearling Chinook	1	0	1	0	0	1	0.00
	Wild Yearling Chinook	0	0	0	0	0	0	--
	Wild Steelhead/Rainbow	312	5	307	0	0	307	0.00
	Hatchery Steelhead/Rainbow	0	0	0	0	0	0	--
	Wild Coho	0	0	0	0	0	0	--
	Total	**313**	**5**	**308**	**0**	**0**	**308**	**0.00**
Lower Wenatchee Trap	Wild Subyearling Chinook	0	0	0	0	0	0	--
	Wild Yearling Chinook	1,051	81	928	11	0	917	1.05
	Wild Steelhead/Rainbow	483	9	465	0	0	465	0.00
	Hatchery Steelhead/Rainbow	4	2	0	0	0	0	0.00
	Wild Coho	6	0	6	0	0	6	0.00
	Wild Sockeye	0	0	0	0	0	0	--
	Total	**1,544**	**92**	**1,399**	**11**	**0**	**1,388**	**0.71**
Total:	**Wild Subyearling Chinook**	**5,062**	**145**	**4,693**	**3**	**1**	**4,689**	**0.06**
	Wild Yearling Chinook	**8,323**	**386**	**7,711**	**20**	**0**	**7,691**	**0.24**
	Wild Steelhead/Rainbow	**3,924**	**117**	**3,737**	**2**	**0**	**3,735**	**0.05**
	Hatchery Steelhead/Rainbow	**187**	**20**	**164**	**0**	**0**	**164**	**0.00**
	Wild Coho	**115**	**0**	**18**	**0**	**0**	**18**	**0.00**
	Wild Sockeye	**11,103**	**7**	**10,082**	**76**	**0**	**10,006**	**0.68**
Grand Total:		**28,714**	**675**	**26,405**	**101**	**1**	**26,303**	

APPENDIX D

Wenatchee Steelhead Spawning Ground Surveys, 2010

STATE OF WASHINGTON
DEPARTMENT OF FISH AND WILDLIFE
FISH PROGRAM – SCIENCE DIVISION
SUPPLEMENTATION RESEARCH TEAM

3515 Chelan HWY, Wenatchee, WA 98801
Voice (509) 663-9678 FAX (509) 662-6606

1 March 2011

To: Distribution List

From: Andrew Murdoch and Chad Herring

Subject: 2010 Wenatchee River Basin Steelhead Spawning Ground Surveys

Summer steelhead migrate to their spawning grounds as early as nine months prior to spawning. Run escapement estimates of summer steelhead counted at Columbia River dams or at Tumwater Dam in the Wenatchee River may not accurately reflect the size of the spawning population because of fallback and prespawn mortality that may occur prior to spawning. English et al. (2003) reported fallback rates for Rock Island (4.9%) and Rocky Reach (6.5%) dams were similar, but no information regarding Tumwater Dam was reported. In the same study, survival to spawning was not explicitly calculated, but kelting rates for the Wenatchee River ranged between 68% and 77% and may serve as a minimum survival rate. Keefer et al. (2008) conducted a more comprehensive study throughout the Columbia Basin and reported mortality rates of summer steelhead that overwintered in the Columbia River or tributaries was 14.5% and 18.9%, respectively.

Redd counts may be used to calculate a more accurate estimate of the spawning population, but requires knowledge concerning the number of redds constructed per female and the number of fish per redd. Female steelhead have been reported to construct multiple redds, ranging between 1.02 and 6.91 redds (Reingold 1965; Gallagher and Gallagher 2005; Kuligowski et al. 2005). Large variation in the reported number of redds per female within and across populations may be natural or more simply a lack of precision in the methodology used (e.g., errors in redd counts or the number of female spawners). While the sex ratio may be an appropriate surrogate for the number of fish per redd under the assumption females construct a single redd. However, if female steelhead construct multiple redds, it is also likely male steelhead spawn at multiple redd locations with either the same or different females resulting in an overestimate of the spawning population. An estimate of the spawning population coupled with other population specific information (i.e., ratio of hatchery and wild spawners and age composition) are critical data needed to assess the productivity of the population (i.e., recruits per spawner).

Our objectives in conducting steelhead spawning ground surveys were to 1) determine spawn timing of naturally spawning steelhead (both hatchery and wild origin) and 2) estimate the abundance of redds constructed within selected tributaries and 3) calculate error rates in redd detection and determine what factors (e.g., environmental or habitat variables) affect observer efficiency. We also examined the relationship between run escapement upstream of Tumwater Dam (i.e., female and total) and redd counts as a method of assessing the precision of our estimates.

Methods

Run Escapement

Steelhead migrating upstream of Tumwater Dam were captured, sampled (sex, length, weight, scales), and PIT tagged as part of a separate study.   Gender was determined using ultrasonography and secondary sexual characteristics (i.e., kype, coloration, body shape). Origin was determined using hatchery marks (i.e., fin clip, VIE, CWT, or eroded fins) or scale pattern analysis if no marks were identified.

Spawning Ground Surveys

Spawning grounds surveys were primarily concentrated in the upper Wenatchee Basin because all hatchery fish were released upstream of Tumwater Dam. Peshastin Creek was included in our surveys because it was identified as a potential reference stream (i.e., no hatchery releases since 1998) for the Wenatchee Basin. Survey methodology involved surveying non-random index areas, defined as major spawning area(s) for each stream. Index areas included in the redd observer efficiency study were surveyed every third day, with the remaining index areas surveyed as frequently as once a week. Redds were either individually flagged or in the case of large aggregates of localized spawning, mapped and numbered sequentially. All redds were also geo-referenced using handheld global positioning devices. Between 2000 and 2003, the number of index areas has increased as more information became available. Beginning in 2004, survey methodology has remained similar. Hence, direct comparisons of redd counts to years before 2004 may not be appropriate.

Index area spawning ground surveys were conducted by foot or raft on the Wenatchee River and most major tributaries (Appendix A). For each index area, the same surveyor(s) conducted all weekly surveys. However, when the end of spawning within an index area was thought to be nearly complete, a different observer (i.e., naïve) surveyed the index area to determine the number of redds still visible at the end of spawning. At approximately the same time, non-index areas within a reach or stream were also surveyed. The total number of redds in non-index areas was estimated by dividing the number of redds found in non-index areas by the proportion of redds still visible inside the index area. The reach total redd count was calculated by combining the number of redds in the index area and the estimated number of redds in the non-index areas. Murdoch and Peven (2005) provide a more detailed description of the methodology (Appendix F, Task 7-3).

The sex ratio of the entire population upstream of Tumwater Dam was used as the redd expansion factor (i.e., number fish per redd). The sex ratio was calculated using the number of female and male steelhead passed upstream of Tumwater Dam during trapping and video count operations. Spawning escapement was estimated by multiplying the estimated total number of redds by the number of fish per redd. Linear regression analysis was used to examine the relationship between run escapement estimates, index area redd counts, and total redd counts upstream of Tumwater Dam. Fallback rates at Tumwater Dam were calculated based on the number of PIT tagged steelhead recaptured or tagged at Tumwater Dam that were detected downstream of Tumwater Dam prior to spawning divided by the total number of PIT tagged steelhead.

Observer Efficiency Study

In 2010, a three year study was initiated to estimate redd observer variability generally following the methods described in Thurow and McGrath (2010). A total of six index areas within the Wenatchee River Basin were selected for the observer efficiency study based on several biological, environmental, and habitat related variables that were thought to potentially influence redd detection (Table 1). For each study reach, hereafter referred as the census reach, the same surveyor(s) was used to conduct surveys every three days.

Table 1. Proposed study reaches and relevant data for Wenatchee Basin steelhead

Parameter	Pesh. 1	Icicle 1	Nason 1	Nason 3	Wen. 9	Wen. 10
Elevation (m)	893	1008	1720	1962	1526	1698
Stream Order	5	5	4	4	6	6
Gradient (%)	2.50	0.14	0.45	0.34	0.32	0.10
Stream width (m)	16	33	18	19	47	48
Survey method	Raft	Raft	Raft	Raft	Raft	Raft
Survey effort	1	2	1	1	2	2
Habitat type	Plane bed	Pool riffle	Pool riffle	Pool riffle	Plane bed	Pool riffle
Spawner abundance	Moderate	Moderate	Low	High	High	High
Spawner density (redds/m^2)	Moderate (0.0007)	Moderate (0.0007)	Low (0.0003)	High (0.0014)	Low (0.0001)	Low (0.0004)
Spawner distribution	Uniform	Clumped	Uniform	Uniform	Uniform	Clumped
Water clarity	Good	Excellent	Good	Good	Good	Excellent
Water source	Glacial/snow	Snow	Snow	Snow	Lake/Glacial	Lake
Contrast	Average	Excellent	Excellent	Good	Good	Average
Channel complexity	Simple	Simple	Complex	Complex	Simple	Simple

All census reaches had ten equidistant habitat transects to quantify habitat variables that may affect observer efficiency. Habitat transect data was collected during the first survey of each census reach. At each habitat transect a waypoint was taken using a hand held GPS unit. Measurements at each transect include wetted channel width, stream depth at ¼, ½ and ¾ of the wetted channel width, and proportion of substrate type. In between each habitat transect a count was made of large woody debris, gravel bars, islands and the percentage of substrate with overhead cover. During a census survey all features were georeferenced using a hand-held GPS unit and denoted on aerial photographs. Features were then classified as either redds, old redds, test or incomplete redds, or a hydrologic feature. During or after peak spawning for each census reach, multiple independent (naïve) observers conducted surveys and counted all redds observed. Independent observers georeferenced and denoted on aerial photographs all features that were believed to be steelhead redds. ArcGIS and aerial photographs were used to compare features believed to be redds identified by independent surveys to census survey features that were visible during the time the independent survey was conducted. Redds identified by the independent surveyors were then classified as true redd, a visible redd that was omitted, or a false identification.

Steelhead Redd Life

Because surveys were not conducted past the end of the spawning period, redd life for many redds could not be fully determined (i.e., redds were still visible on the last survey day). Hence, estimates of mean redd life for a specific reach would be biased if only redds with a complete redd life were included. High escapement in 2010 also influenced redd life via redd superimposition. We attempted to address both of these factors by calculating redd life using two different approaches. Standard redd life was defined as the number of days a redd was visible and were not affected by redd superimposition or a freshet. Standard redd life includes those redds that were still visible before the first major freshet of the season. Operational redd life is the number of days a redd is visible throughout the spawning period regardless of cause (i.e.., natural periphyton growth, redd superimposition or freshet).

Steelhead Spawning Location and Timing

The spawning distribution and timing of hatchery and naturally produced steelhead was assessed using colored anchor tags (origin specific) inserted at trapping locations (Priest Rapids, Dryden and Tumwater Dams). During spawning ground surveys, observations of tagged females were correlated with redd location and date. Comparisons of spawning location were made by stream (t-test) and by reach (ANOVA) using georeferenced redd locations converted to the distance (km) upstream from the mouth of the tributary. Because spawn timing is influenced by water temperature, an analysis of covariance was used to determine the influence of elevation on spawn timing. In cases where elevation did not significantly influence spawn timing, comparison of spawn date were compared using t-tests.

Results

Run Escapement

The estimated steelhead run escapement upstream of Tumwater Dam was 2,270 fish that included 7 fish detected on videotape, 13 surplus broodstock, and 2,250 trapped and released upstream. Run escapement in 2010 was 27% greater than in 2009, and was 53% greater than the previous 5-year average of 1,484 fish (Table 1). A greater proportion of male than female steelhead were observed at Tumwater Dam resulting in a fish per redd value of 2.33, assuming each female constructed a single redd. Of those steelhead released upstream of Tumwater Dam 35% (*N* = 787) were determined to be naturally produced.

Spawning Ground Surveys

A below average snow pack coupled with cool air temperatures led to below average stream flows for most of the survey season. During the third week of April an increase in air temperature resulted in a temporary increase in stream flow resulting in poor survey conditions for approximately 4 days. After the second week of May, air temperatures increased such that snowmelt resulted in elevated water conditions for the remainder of the spawning period. Overall, survey conditions in 2010 were less than optimal compared to previous years. Poor environmental conditions (i.e., snow, rain, wind and clouds) were more common in 2010 and likely had a negative impact on redd detection rates.

Steelhead began spawning during the first week of March in Peshastin Creek, the second week of March in the Wenatchee River and Icicle River and third week of March in Nason Creek. Spawning progressed upstream as water temperatures increased. Spawning activity appeared to begin once the mean daily stream temperature reached ~4.4^{o}C and was observed in water temperatures ranging from 3.1 - 9.0 ^{o}C. Steelhead spawning peaked in Peshastin Creek the second week of April. Peak spawning occurred the third week in April and the fourth week in April for the Wenatchee River and Nason Creek, respectively (Appendix B).

The estimated number of redds in the Wenatchee Basin increased 46% between 2009 (*N* = 662) and 2010 (*N* = 969) and was 149% greater the 5-year average of 389 redds (Table 2). In 2010, the proportion of redds in Nason Creek (27.9%) was less than the 5-year mean (31.5%; Table 2). Redd distribution in Nason Creek continues to primarily be occurring in the middle two reaches (77%; Appendix D1). Steelhead redds observed in the Chiwawa River were also found in locations consistent with previous years (Appendix D2). The proportion of redds found in all streams upstream of Tumwater Dam decreased from a high of 96% in 2006 to 75% in 2010 (Appendix D3). The number of redds in Peshastin Creek increased 269% between 2009 and 2010 (Appendix D4). The number of steelhead redds in Icicle Creek, another major spawning tributary downstream of Tumwater Dam, increased in 2010 and was 18% greater than the number of redds observed in 2009. While the overall number of redds in the Wenatchee River increased from 327 in 2009 to 380 in 2010, the proportion of all redds in the Wenatchee River decreased from 49.4% in 2009 to 39.2% in 2010. However, the proportion of redds found within index and non-index areas upstream of Tumwater Dam in 2010 (84%) was higher than the 9 year average (78%), but within the observed range (Table 3).

Table 1. Total number, gender, and sex ratio of steelhead migrating upstream of Tumwater Dam between 2001 and 2010. Sex ratio in 2001 was determined by the number of fish passed and collected during broodstock collection at Tumwater and Dryden dams. For 2002-2008, gender was determined visually at Tumwater Dam. For 2009 and 2010, gender was determined visually and/or by ultrasound.

Year	Number of steelhead to Tumwater Dam			Male to female ratio	Number of fish per redd
	Total	Female	Male		
2001	820	394	426	1.08	2.08
2002	1,720	641	1,079	1.68	2.68
2003	1,813	1,137	676	0.59	1.59
2004	1,918	869	1,049	1.21	2.21
2005	2,598	1,620	978	0.60	1.60
2006	1,057	505	552	1.09	2.09
2007	657	339	318	0.94	1.94
2008	1,328	473	855	1.81	2.81
2009	1,781	973	808	0.83	1.83
2010	2,270	973	1,297	1.33	2.33

Table 2. Comparison of the number and distribution of steelhead redds in 2010 and the five year geometric mean (2005-2009).

Stream	2010		Geo. mean (2005-2009)	
	Number of redds	Distribution (%)	Number of redds	Distribution (%)
Nason Creek	270	27.9	122	31.5
Chiwawa River	74	7.6	31	7.9
White River	3	0.3	<1	0.0
L. Wenatchee River	4	0.4	0	0.0
Peshastin Creek	118	12.2	44	11.4
Icicle Creek	120	12.4	24	6.1
Wenatchee River	380	39.2	168	43.1
Above Tumwater	287	75.5	124	78.2
Below Tumwater	93	24.5	34	21.8
Total	969	100.0	389	100.0

Table 3. Comparison of the number of redds found within index areas and the estimated number of redds in non-index areas upstream of Tumwater Dam between 2001 and 2010.

Year	Index area	Non-index area	Estimated total	Within index area (%)
2001	118	19	137	86
2002	296	179	475	62
2003	353	88	441	80
2004	277	92	369	75
2005	828	136	964	86
2006	192	34	226	85
2007	105	29	134	78
2008	124	35	159	78
2009	284	107	391	73
2010	517	95	612	84

Female and total escapement explained a similar proportion of the variation in the estimated total number of redds (Figure 1). Given the variation in sex ratios and that only female steelhead construct redds, we would expect female escapement to explain a greater proportion of the variation in number of redds. This would suggest that the mean number of redds constructed by a female is relatively constant.

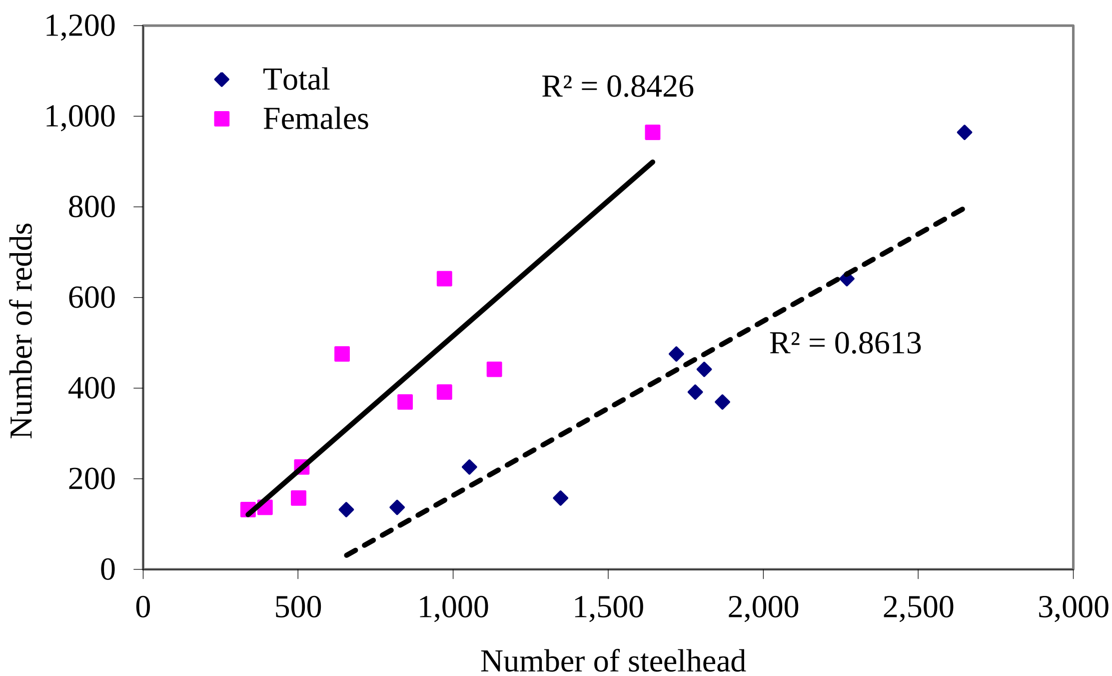


Figure 1. Relationship between steelhead run escapement (total and female) upstream of Tumwater Dam and total redd counts.

However, total run escapement explained a lesser proportion of the variation in index redd counts than total redd counts (Figure 2). As run escapement increases, habitat within the index areas may be near capacity and subsequently a greater proportion of redds are found outside index areas.

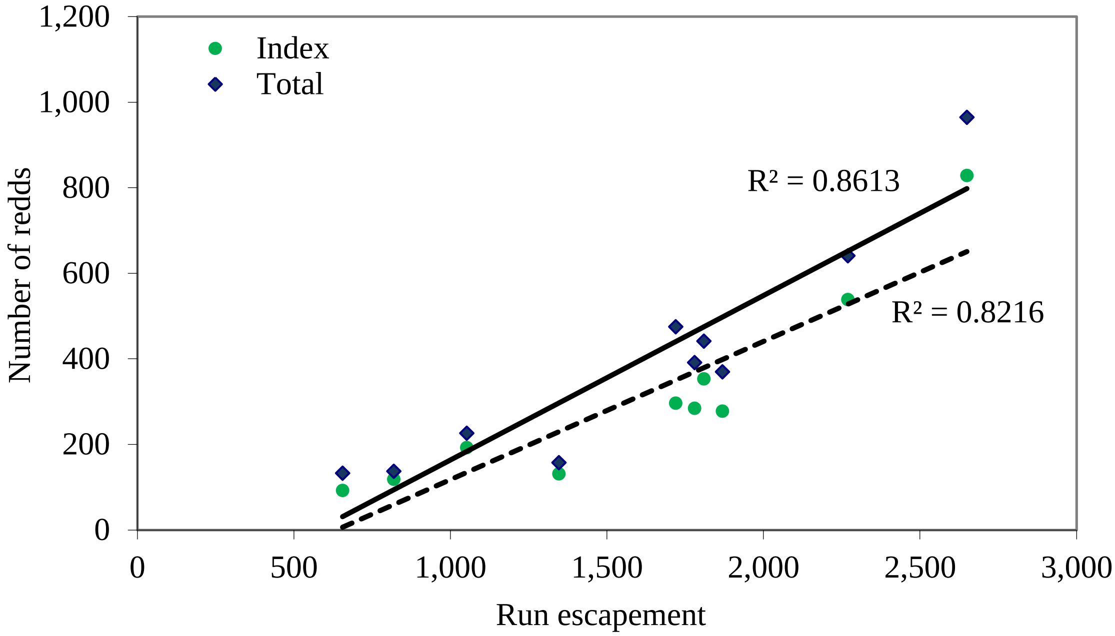


Figure 2. Relationship between steelhead run escapement upstream of Tumwater Dam and total and index area redd counts.

Spawning Escapement

In 2010, 66% of the steelhead migrating above Tumwater Dam were accounted for on spawning grounds compared to the 5-year average (2005-2009) of 44% (Table 4). While environmental conditions do affect the accuracy of our estimates, other factors also contribute to the differences observed between run and spawning escapement estimates that can be estimated or quantified (i.e., prespawn mortality and fallback). Because no estimate of survival to spawning is available for steelhead in the Wenatchee Basin, we assumed that survival to spawning was at a minimum similar to that of steelhead overwintering in lower Columbia River tributaries (i.e., Deschutes and John Day) reported by Keefer et al (2008). Actual survival in the Wenatchee River may be considerably lower than that reported by Keefer et al. (2008) as a result of colder water temperatures and depleted energy reserves attributed to a greater migration distance.

While direct enumeration of steelhead upstream of Tumwater Dam is possible, it may not be appropriate to assume that all steelhead that migrate upstream of Tumwater Dam spawn upstream of Tumwater Dam (i.e., fallback). Using PIT tag recapture data, we were able to calculate a minimum fallback rate of steelhead at Tumwater Dam in 2010. Nearly all the steelhead (99.7%) that migrated past Tumwater Dam were implanted with a PIT tag in the pelvic girdle. PIT tag detection at all Columbia and Snake River hydroelectric projects and some major spawning tributaries downstream of Tumwater

Dam (e.g., Peshastin Creek, Prosser Dam in the Yakima Basin) provided recapture data. Because some steelhead may have spawned in areas downstream of Tumwater Dam with no PIT tag antenna array (e.g., lower Wenatchee, Icicle, Mission, and Chumstick) or simply lost their tag, fallback rates were considered minimum values. Of the PIT tagged steelhead that were passed upstream of Tumwater Dam (N = 2,263), 1.3% (N = 29) were detected prior to spawning downstream of Tumwater Dam. While most fallback steelhead (86%, N = 25) were detected at hydroelectric dams in the Columbia River upstream of the Wenatchee River, a small number of fish were also detected in Peshastin Creek (N = 4). We used estimates of prespawn mortality and observed fallback rates to adjust run escapement estimates upstream of Tumwater Dam that may better represent the actual size of the spawning population. After adjustment, the proportion of the run escapement accounted for on the spawning grounds increased from 66% to 82% (Table 5).

Table 4. Comparison of run and estimated spawning escapement for steelhead upstream of Tumwater Dam between 2001 and 2010.

Year	Run escapement (A)	Number of redds (B)	Number of fish per redd (C)	Estimated spawning escapement (D = B x C)	Proportion of run escapement (E = D/A)
2001	820	137	2.08	285	0.35
2002	1,720	475	2.68	1,273	0.74
2003	1,813	441	1.59	701	0.39
2004	1,918	369	2.21	815	0.42
2005	2,598	964	1.60	1,542	0.59
2006	1,057	226	2.09	472	0.45
2007	657	134	1.94	260	0.40
2008	1,328	159	2.81	447	0.34
2009	1,781	391	1.83	716	0.40
2010	2,270	641	2.33	1,494	0.66

Table 5. Comparison of steelhead run escapement estimates at Tumwater Dam to the estimate spawning escapement derived from redd counts after adjusting for fallback and prespawn mortality.

Year	Tumwater Dam count	Adjusted Tumwater Dam counts		Number of redds	Number of fish per redd	Estimated spawning escapement	Proportion of run escapement
		Fallback	Prespawn mortality				
	(A)	(B = A - 3.0%)	(C = B - 18.9%)	(D)	(E)	(F = D x E)	(G = F/C)
2001	820	795	645	137	2.08	285	0.44
2002	1,720	1,668	1,353	475	2.68	1,273	0.94
2003	1,810	1,756	1,424	441	1.60	706	0.50
2004	1,869	1,813	1,470	369	2.21	815	0.55
2005	2,650	2,571	2,085	964	1.61	1,552	0.74
2006	1,053	1,021	828	226	2.05	463	0.56
2007	657	637	517	134	1.94	260	0.50
2008	1,358	1,317	1,068	159	2.81	447	0.42
2009	1,781	1,639[a]	1,329	391	1.83	716	0.54
2010	2,270	2,240[b]	1,817	641	2.33	1,494	0.82

[a] Adjusted for a fallback rate of 8.0% as determined by PIT tag detections for the 2009 brood.
[b] Adjusted for a fallback rate of 1.3% as determined by PIT tag detections for the 2010 brood.

Steelhead Redd Life

Standard redd life averaged 27 d in the 2010, but exhibited similar high variation within each reach (CV 37 – 43; Table 6). In all reaches, operational redd life (mean = 18 d) was shorter than standard redd life ranging between 53 – 87% of the standard redd life. Standard redd life was significantly correlated with reach elevation (r = 0.91, P < 0.02), but not operational redd life (r = 0.19, P = 0.72). Potential factors that influenced redd life (e.g., environmental and habitat) will be evaluated at a later date.

Table 6. Summary results of steelhead redd life variability in the Wenatchee Basin in 2010.

Reach	Mean	*N*	SD	CV	Range	
					Min	Max
			Standard redd life			
P1	20.3	26	8.8	43.3	9	41
I1	22.4	56	8.3	37.1	8	45
W9	24.8	44	9.9	39.9	6	49
W10	28.3	56	11.7	41.3	11	65
N1	28.3	7	10.4	36.7	17	47
N3	37.1	21	14.1	38.0	17	60
			Operational redd life			
P1	16.2	44	8.7	53.5	3	41
I1	19.5	47	6.7	34.4	8	32
W9	18.2	38	9	49.5	3	45
W10	18.0	50	9.1	50.6	3	45
N1	15.1	10	8.1	53.6	5	28
N3	20.4	13	5	24.5	14	33

Observer Efficiency Study

Of the six census reaches identified before spawning, one reach was not included in the analysis (Nason 1) because of low redd abundance. The redd abundance in Nason 1 reach was only 28 redds and well below the minimum sample size of 50 redds. Of those redds identified in Nason 1 reach, most were already not visible when independent surveys were to be conducted further reducing our sample size. Variation in the number of redds independent observers found within a census reach was large (CV range 29 - 77%; Table 7). The mean proportion of visible redds correctly indentified within a reach was positively correlated with density (r = 0.98; P < 0.005) and negatively correlated with stream width (r = - 0.80; P = 0.10).

Table 7. Summary results of single pass steelhead redd observer variability surveys in the Wenatchee Basin in 2010.

Census reach	*N*	Redd statistics			Redds		Omission		False ID	
		Mean	CV	Range	%	SD	%	SD	%	SD
P1	9	16	38	3 - 24	48.8	18.3	51.2	18.3	17.2	17.6
N3	10	34	45	17 - 54	61.2	16.2	38.8	16.2	14.0	11.3
I1	10	24	29	12 - 36	49.8	14.3	50.2	14.3	22.5	9.0
W9	8	21	77	9 - 52	30.9	22.3	69.1	22.3	40.6	11.7
W10	11	34	40	18 - 61	41.2	13.1	58.8	13.1	20.7	13.2

Individual surveyor observer efficiencies showed wide variation in correctly identifying steelhead redds with a range of 9.1% to 66% and a mean of 44.9% (Table 8). The proportion of features that were incorrectly classified as steelhead redds (i.e., False ID) was also highly variable with a range of 0% to 45.1% and a mean of 22.3%. The proportion of redds correctly identified by an independent observer among reaches was slightly lower and more variable (mean = 0.43; CV = 41%) than the variation within a reach (mean = 0.46; CV = 39%).

Table 8. Summary of individual redd observer variability conducted during steelhead spawning ground surveys in the Wenatchee Basin.

Surveyor Aliases	*N*	Redds		Omission		False ID	
		%	SD	%	SD	%	SD
A	5	52.6	19.3	47.4	19.3	20.6	14.4
B	4	37.0	15.5	63.0	15.5	22.8	16.2
C	4	50.5	18.0	49.5	18.0	5.6	8.1
D	5	66.0	11.8	34.0	11.8	32.8	7.6
E	2	59.7	33.1	40.3	33.1	15.1	6.1
F	2	54.0	31.3	46.0	31.3	33.8	15.9
G	3	47.1	2.6	52.9	2.6	14.3	5.4
H	4	33.8	17.2	66.2	17.2	29.5	14.4
I	4	44.4	10.8	55.6	10.8	14.1	11.8
J	2	35.3	14.6	64.7	14.6	27.4	3.4
K	3	46.6	17.2	53.4	17.2	27.0	10.4
M	3	52.4	32.2	47.6	32.2	17.3	19.7
N	2	26.7	12.4	73.3	12.4	45.1	31.7
O	1	45.5	-	54.5	-	0.0	-
P	1	9.1	-	90.9	-	40.0	-
Q	1	35.4	-	64.6	-	19.0	-
R	1	51.2	-	48.8	-	4.3	-
S	1	61.9	-	38.1	-	32.8	-
Mean		44.9	13.1	55.1	13.1	22.3	9.2

No relationship between experience conducting salmonid spawning ground surveys and the proportion of redds correctly (r = 0.06, P = 0.66) or the falsely identified (r = - 0.05, P = 0.73) was found. When restricted to only steelhead spawning ground surveys, relationships improved slightly for both correct redds (r = 0.19, P = 0.19) and false redds (r = - 0.06, P = 0.68) but not statistically significant. However, prior experience conducting steelhead spawning ground surveys on a specific reach was significantly related to the proportion of correctly identified redds (r = 32, P < 0.03; Figure 3), but not the proportion of redds falsely identified (r = - 0.22, P = 0.13). We also found that as the proportion of redds correctly identified increased, the proportion of false redds decreased (r = - 0.35, P < 0.02).

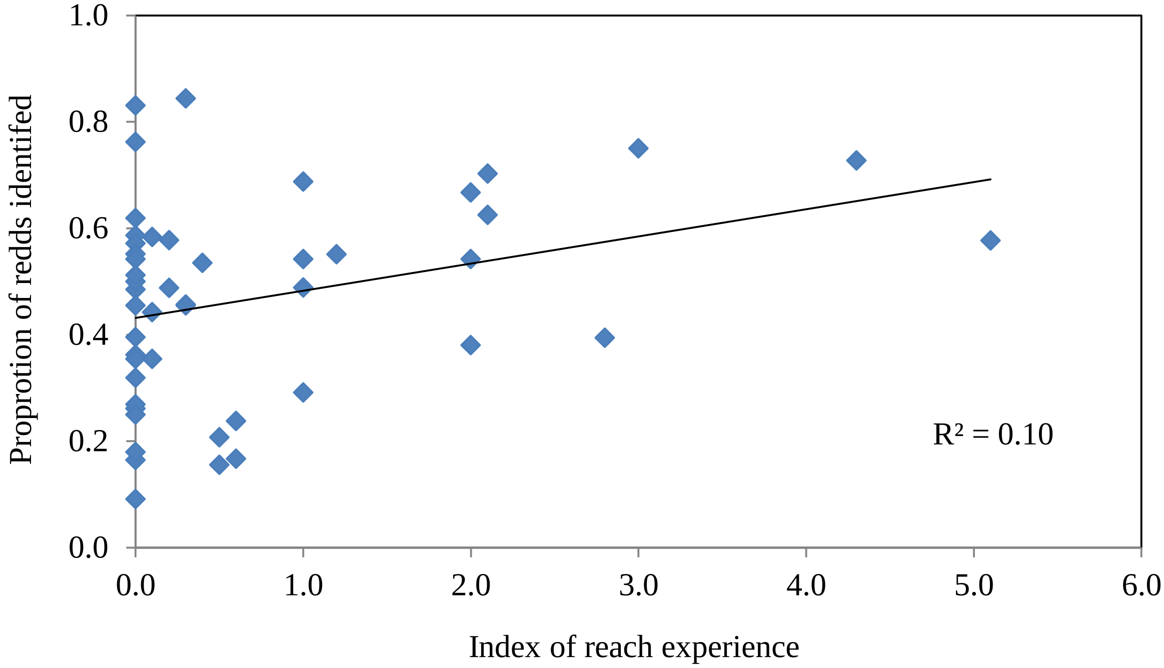


Figure 3. The relationship between the proportion of steelhead redds correctly identified and the surveyor's prior experience conducting steelhead surveys on a specific reach.

Because redd life is shorter than the spawning period, estimates of observer efficiency included only visible redds. Mean total error for redd observer efficiencies for visible redds was 67.1% (CV = 29.7) of all features identified (Figure 4). While net error was only 39.9% (CV = 58.2), but more variable than total error (Figure 5). Total and net error rates based on the total number redds were 36.8% (CV = 35.9) and 21.6% (CV = 63.1), respectively (Figure 6 and 7). While error rates based on the total number of redds were lower than those based only on visible redds, in nearly all cases (92%) redd abundance was underestimated (Figure 8 and 9). Interestingly, no relationship between total error rates (Figure 10) or net error rates (Figure 11) and the number of visible redds was detected.

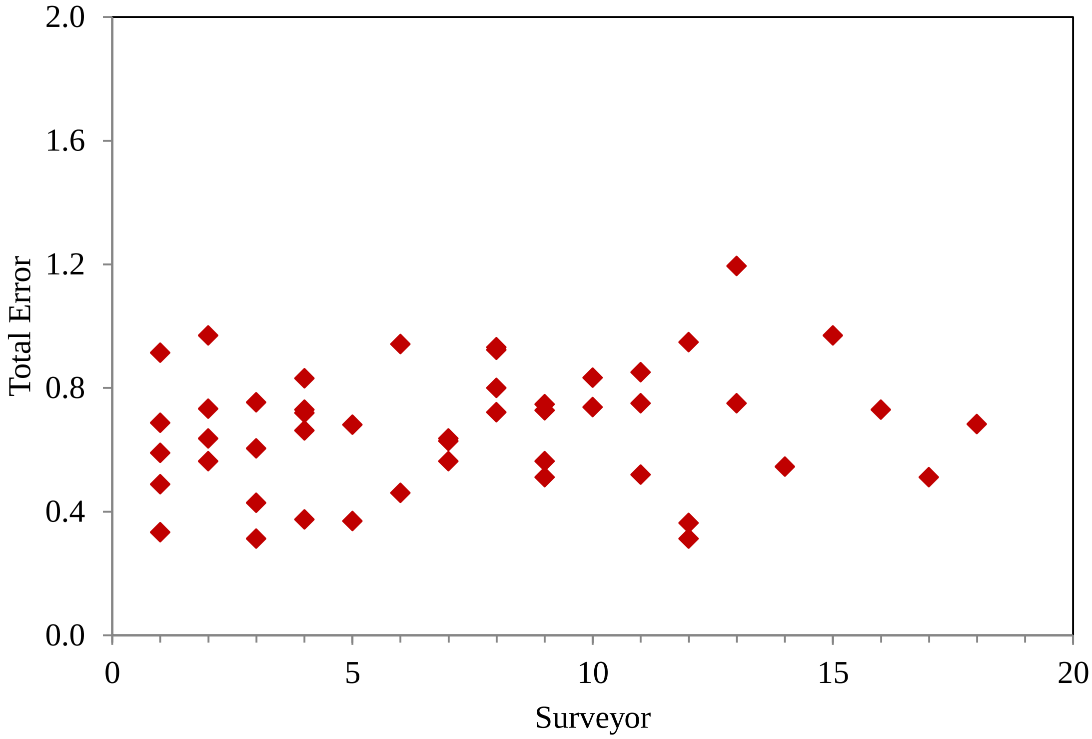


Figure 4. Total error (# of false redds + # of redds omitted/# of visible redds) by surveyor for Wenatchee steelhead spawning ground surveys in 2010.

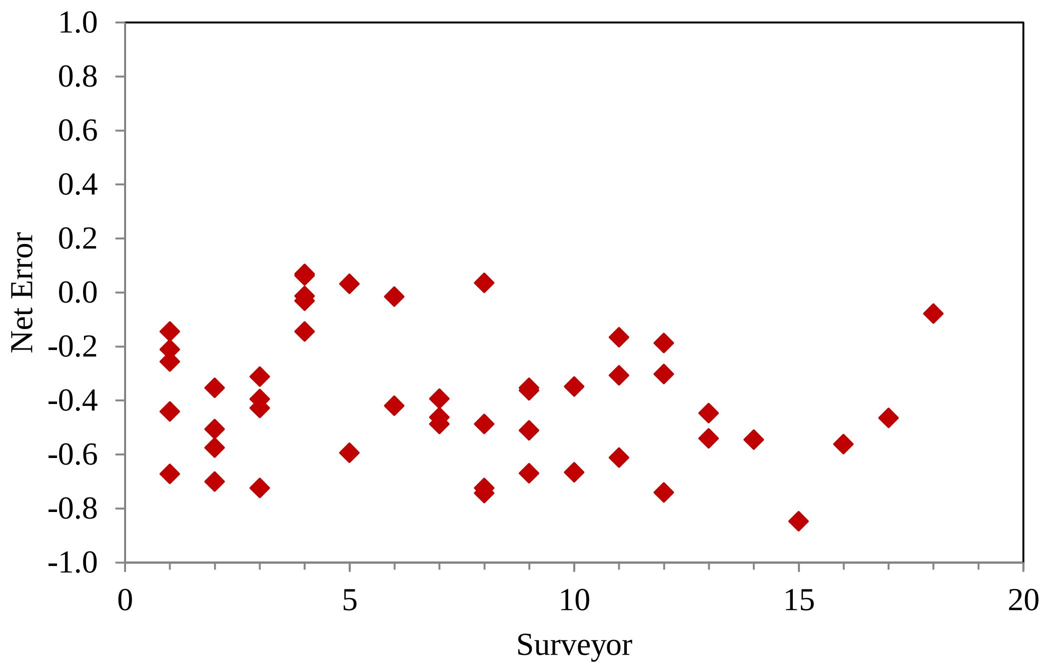


Figure 5. Net error (# of false redds - # of redd omitted/# of visible redds) by surveyor for Wenatchee steelhead spawning ground surveys in 2010.

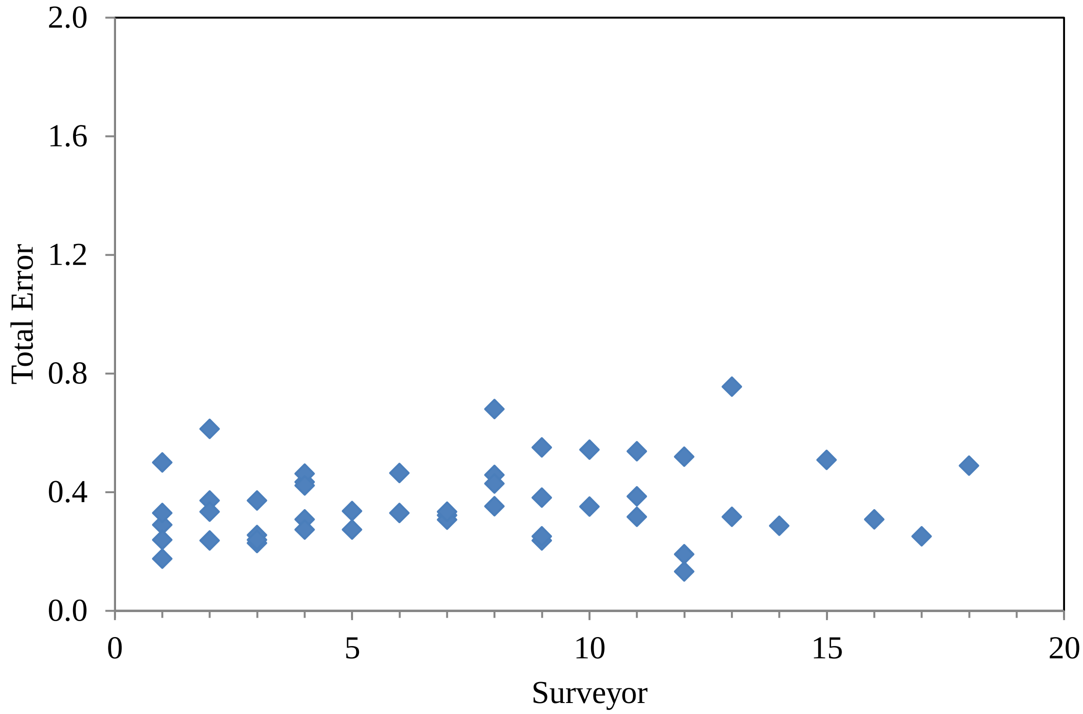


Figure 6. Total error (# of false redds + # of redds omitted/# of total redds) by surveyor for Wenatchee steelhead spawning ground surveys in 2010.

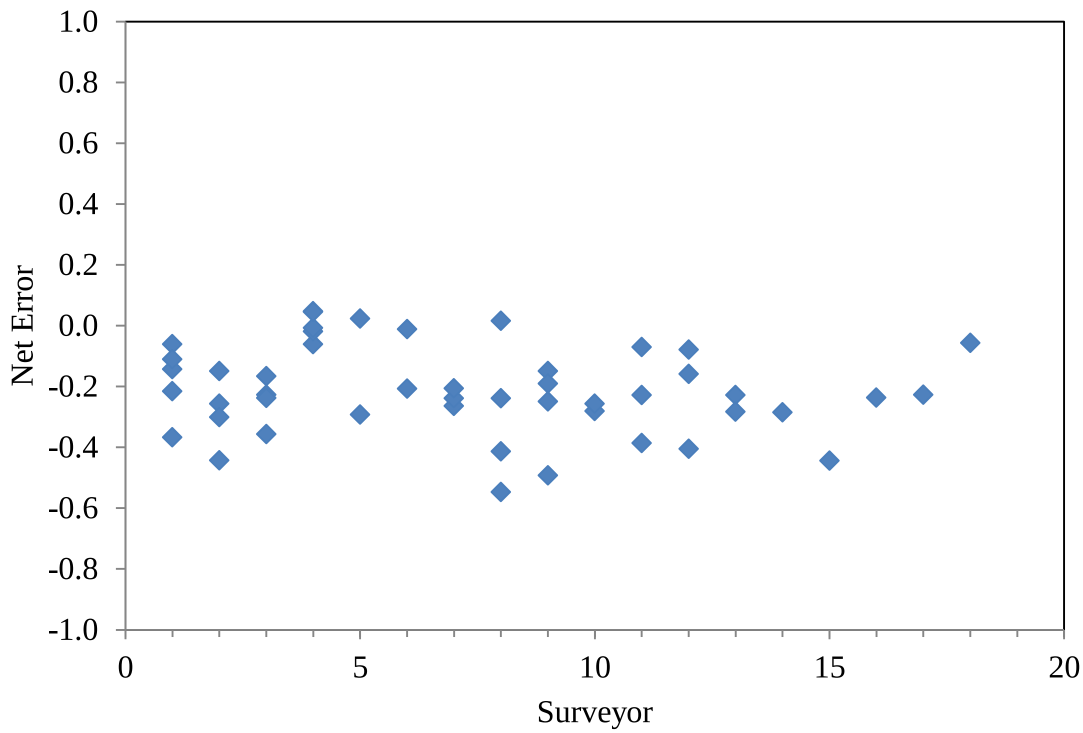


Figure 7. Net error (# of false redds - # of redd omitted/# of total redds) by surveyor for Wenatchee steelhead spawning ground surveys in 2010.

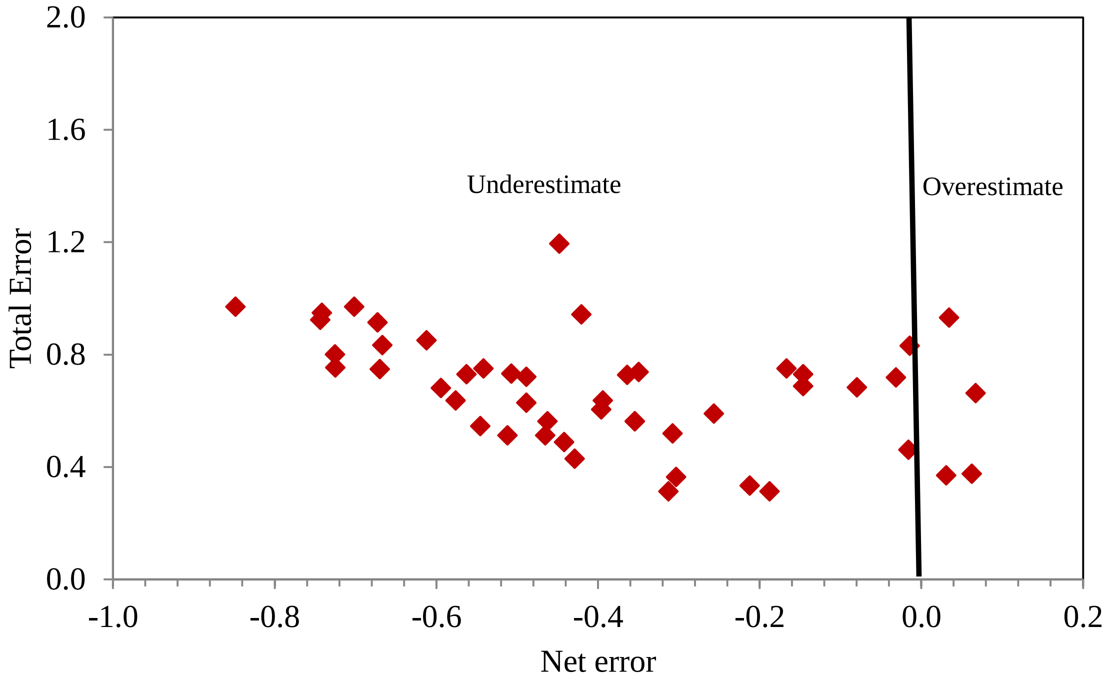


Figure 8. Total error rates compared to net error rates of visible redds for ground based redd counts in census reaches for Wenatchee steelhead in 2010.

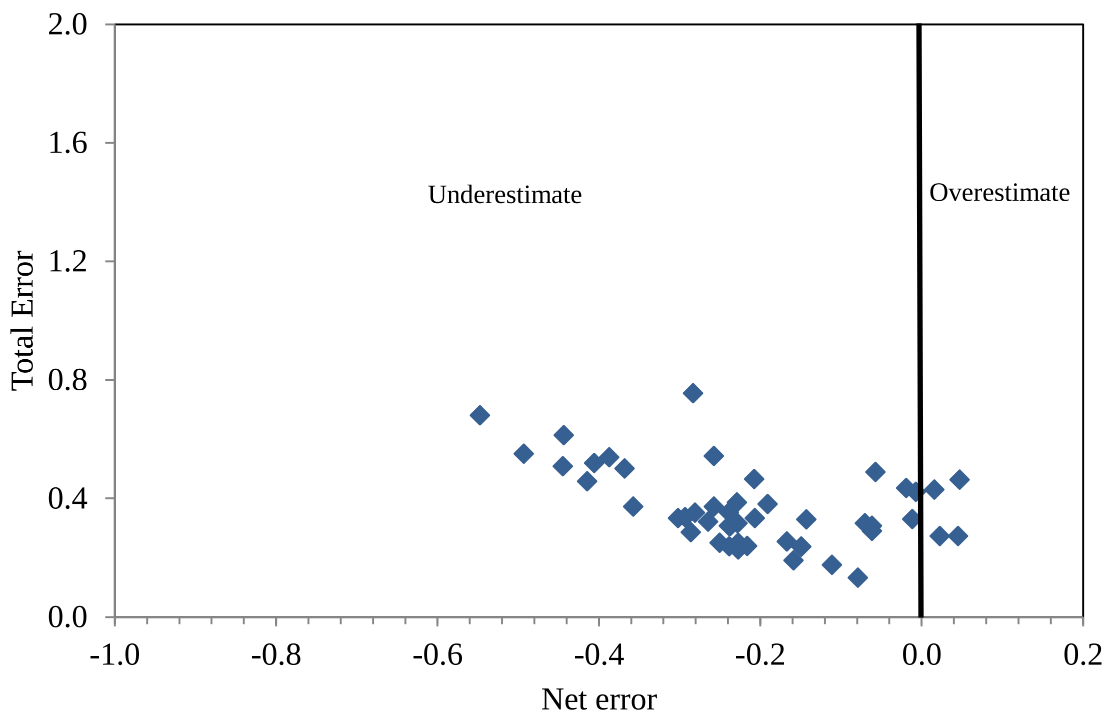


Figure 9. Total error rates compared to net error rates of the total number of redds for ground based redd counts in census reaches for Wenatchee steelhead in 2010.

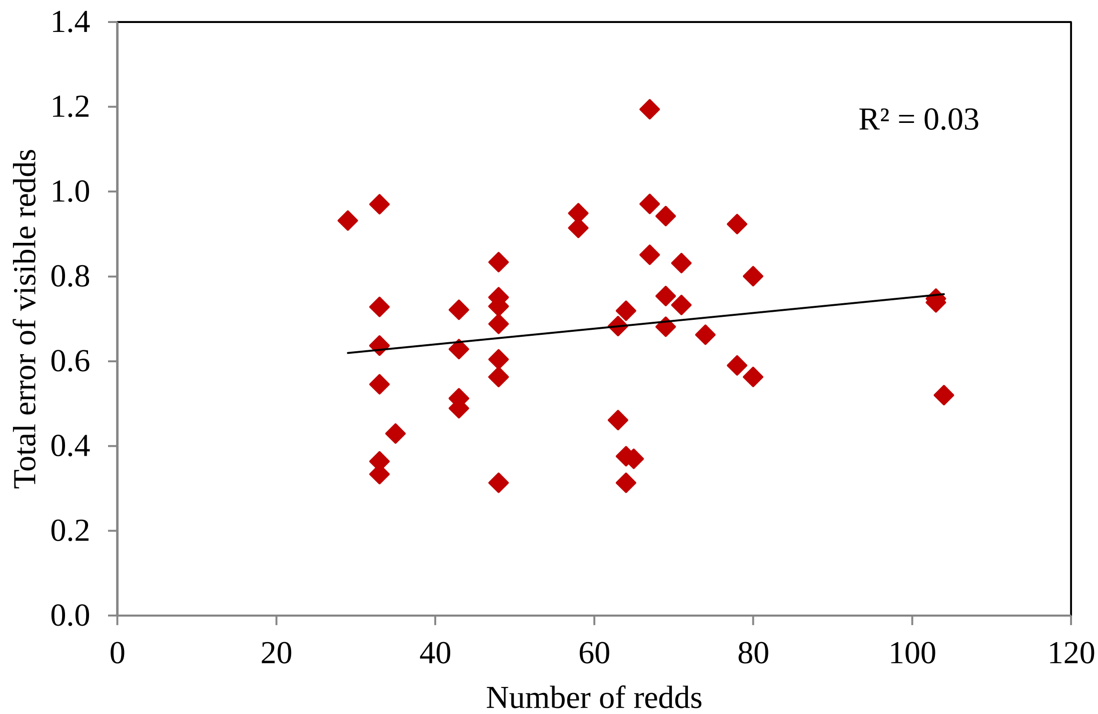


Figure 10. Total error rates compared to the number of visible redds based on ground based redd counts in census reaches for Wenatchee steelhead in 2010.

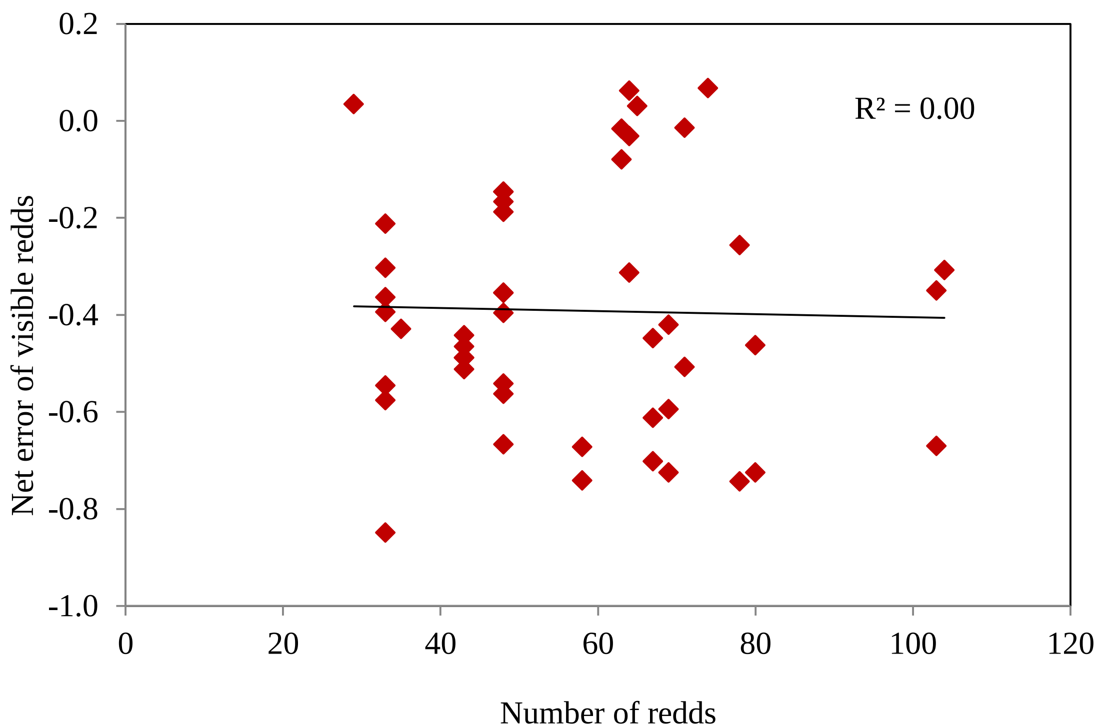


Figure 11. Net error rates compared to the number of visible redds based on ground based redd counts in census reaches for Wenatchee steelhead in 2010.

At the reach scale, mean error rates were highly variable within a reach (Table 9). However, mean error rates for tributaries were more similar than rates for Wenatchee River reaches. Mean error rates for tributaries were smaller but more variable than those for the Wenatchee River. Discharge was positively correlated with error rates (Figure 12). While redd density was negatively correlated (Figure 13). Error rates for visible redds was also significantly related to the error rates for all redds (Figure 14).

Table 9. Mean redd observer error rates for steelhead census reaches in Wenatchee Basin in 2010.

Reach	Error rates for all redds				Error rates for visible redds			
	Total	CV	Net	CV	Total	CV	Net	CV
I1	0.27	22.79	0.15	54.19	0.65	22.79	0.35	54.19
N3	0.30	26.10	0.15	67.64	0.51	27.00	0.29	74.63
P1	0.32	34.49	0.22	56.44	0.62	37.06	0.41	56.47
W10	0.41	19.64	0.27	49.05	0.72	17.28	0.46	47.99
W9	0.56	19.72	0.31	60.11	0.90	18.17	0.50	58.78

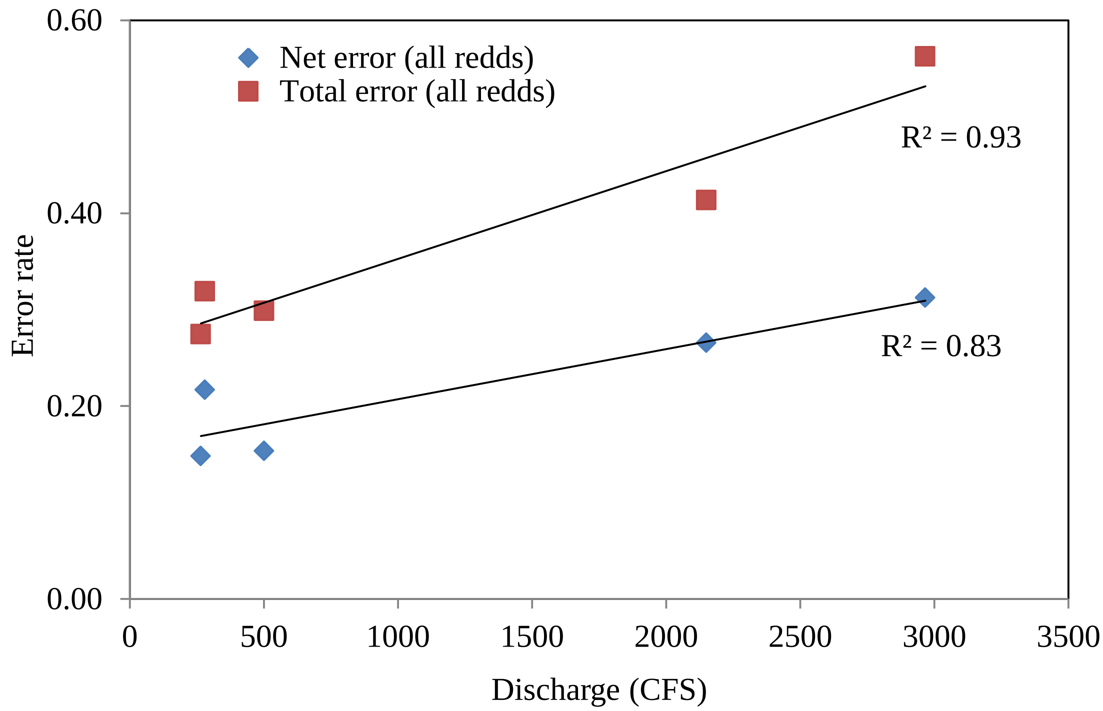


Figure 12. Relationship of mean error rates and discharge for steelhead census reaches in the Wenatchee River Basin in 2010.

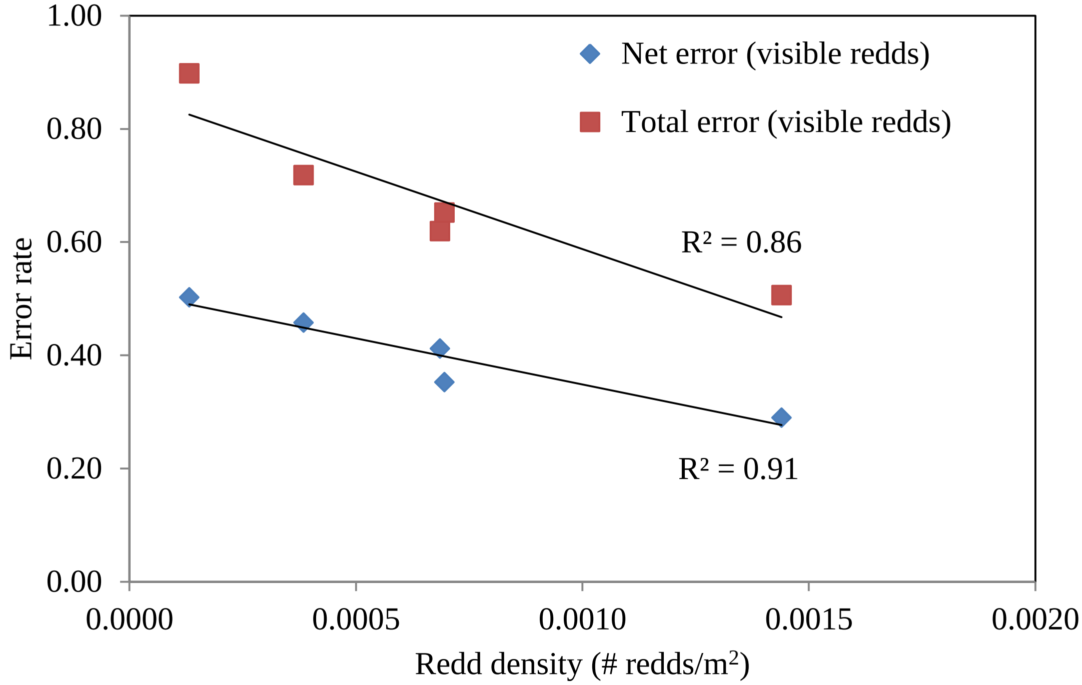


Figure 13. Relationship of mean error rates and redd density for steelhead census reaches in the Wenatchee River Basin in 2010.

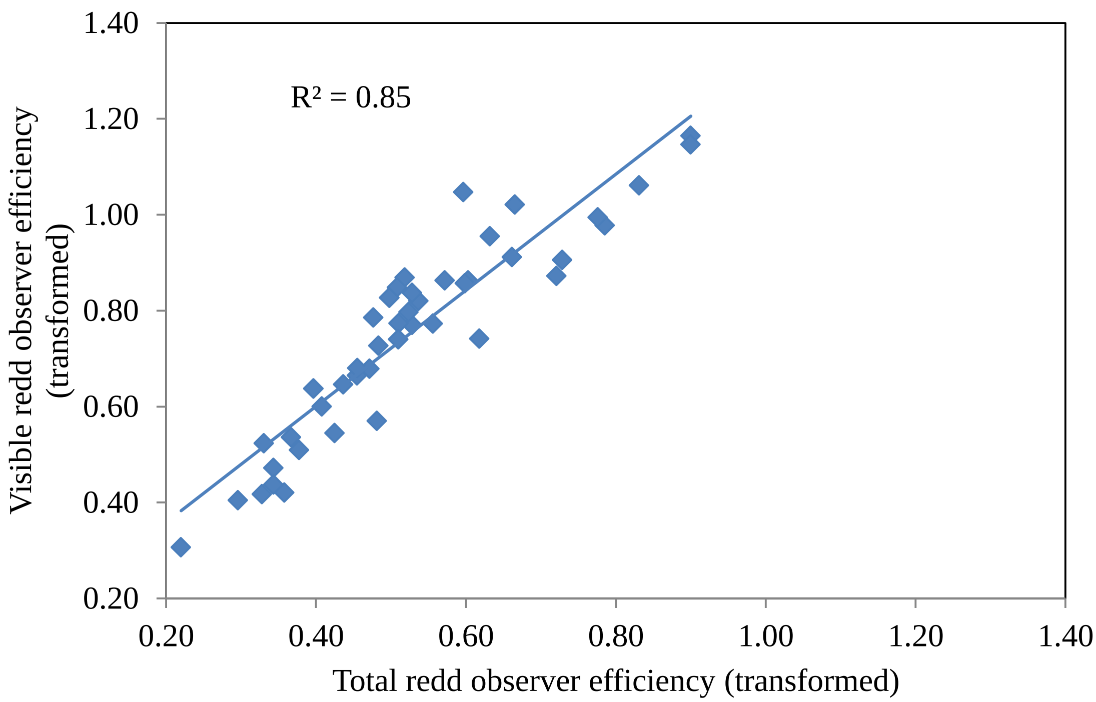


Figure 14. Relationship between visible and total error rates for steelhead census surveys in the Wenatchee River Basin in 2010.

Steelhead Spawning Distribution and Timing

Of the 935 redds identified in 2010, females were observed on 232 (25%). Of those, anchor tags were identified on 113 (49%) females comprised of 42 wild and 71 hatchery steelhead. The majority of the anchor tag observations were on the upper Wenatchee River (55%) and Nason Creek (40%). Hence, the analysis of hatchery and wild spawning distribution and timing was limited to the specific reaches were the majority of the observations were made.

In the Wenatchee River, steelhead redds were observed throughout the entire river, but exhibited a clumped distribution skewed heavily to the upper reaches (Figure 15). Tagged female steelhead were observed in the upper most reaches (W9 and W10) of the Wenatchee River (rkm 59-87), a section that contained 74% of all redds found in the Wenatchee River (Figure 16). No difference in spawning distribution of hatchery and naturally produced steelhead was detected in the upper Wenatchee River (t-test: $P = 0.24$) or in any reach of the upper Wenatchee River (ANOVA: $P = 0.40$). Spawn timing in the upper Wenatchee River was significantly influenced by elevation (Homogeneity of slopes model: elevation effect, $P < 0.02$). However, after accounting for elevation, no differences were found between hatchery and naturally produced steelhead (ANCOVA: Origin effect, $P = 0.76$; Figure 17).

The spawning distribution in Nason Creek was more uniform than in the Wenatchee River, but was still heavily skewed to the upper reaches (N2 and N3) of the survey area (Figure 18). No difference in spawning distribution of hatchery and naturally produced fish was detected (t-test: $P = 0.10$). Comparison by reach and parental origin (wild and hatchery [W x W and unknown]) also resulted in no significant difference (ANOVA: origin x reach effect, $P = 0.83$; Figure 19). Because no other known hatchery fish (H x W parental cross = green anchor tag) were observed in Nason Creek, we assumed that unknown hatchery fish were likely W x W fish that had lost their elastomer tag after release. Elevation did not significantly influence spawn timing in Nason Creek ($P = 0.67$) presumably due to relatively low gradient of the survey reaches. Pooling data across reaches, no difference in spawn timing was detected (t-test: $P = 0.90$).

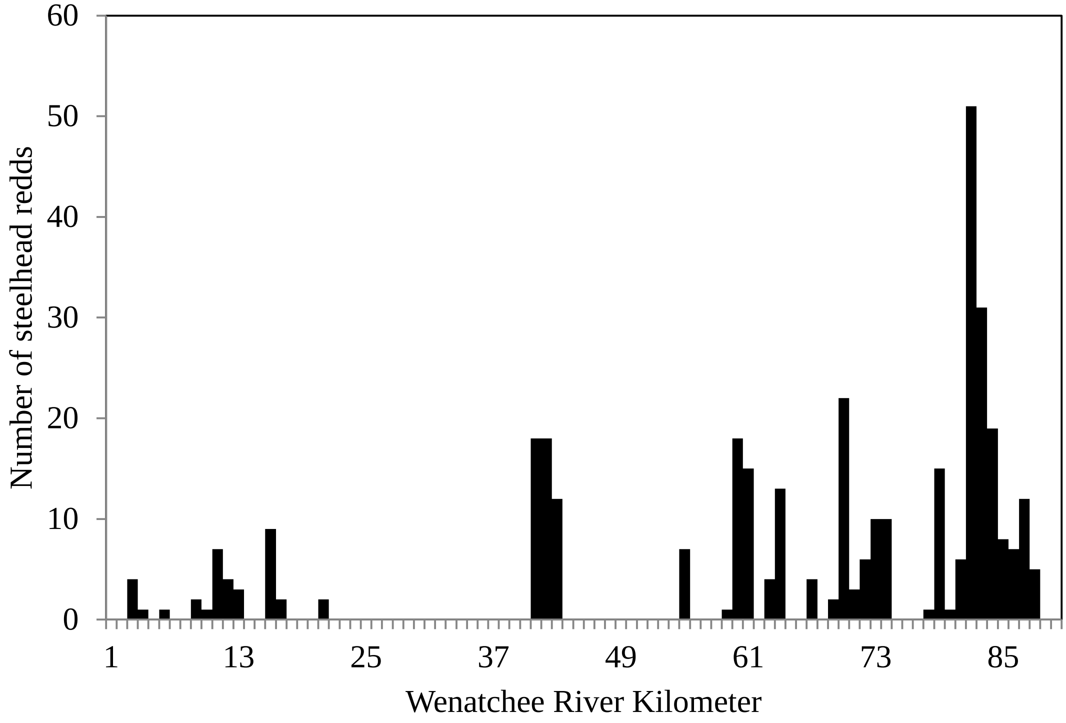


Figure 15. Distribution of steelhead redds in the Wenatchee River in 2010.

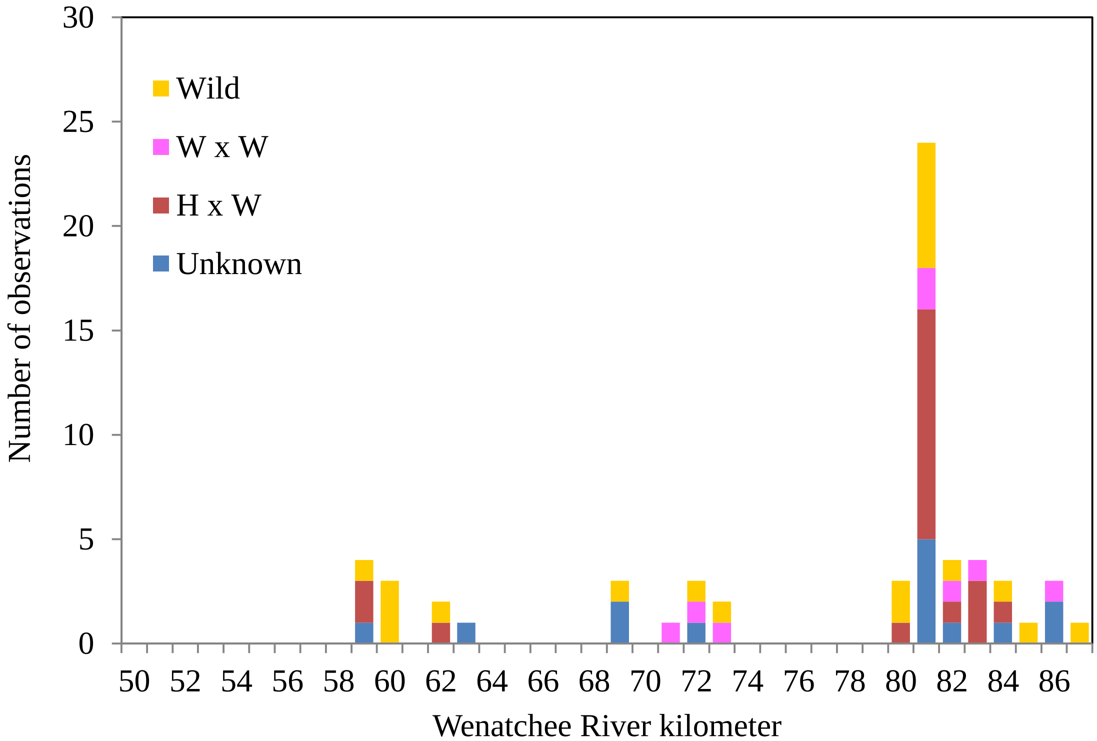


Figure 16. Distribution of anchor tagged female steelhead in the upper Wenatchee River.

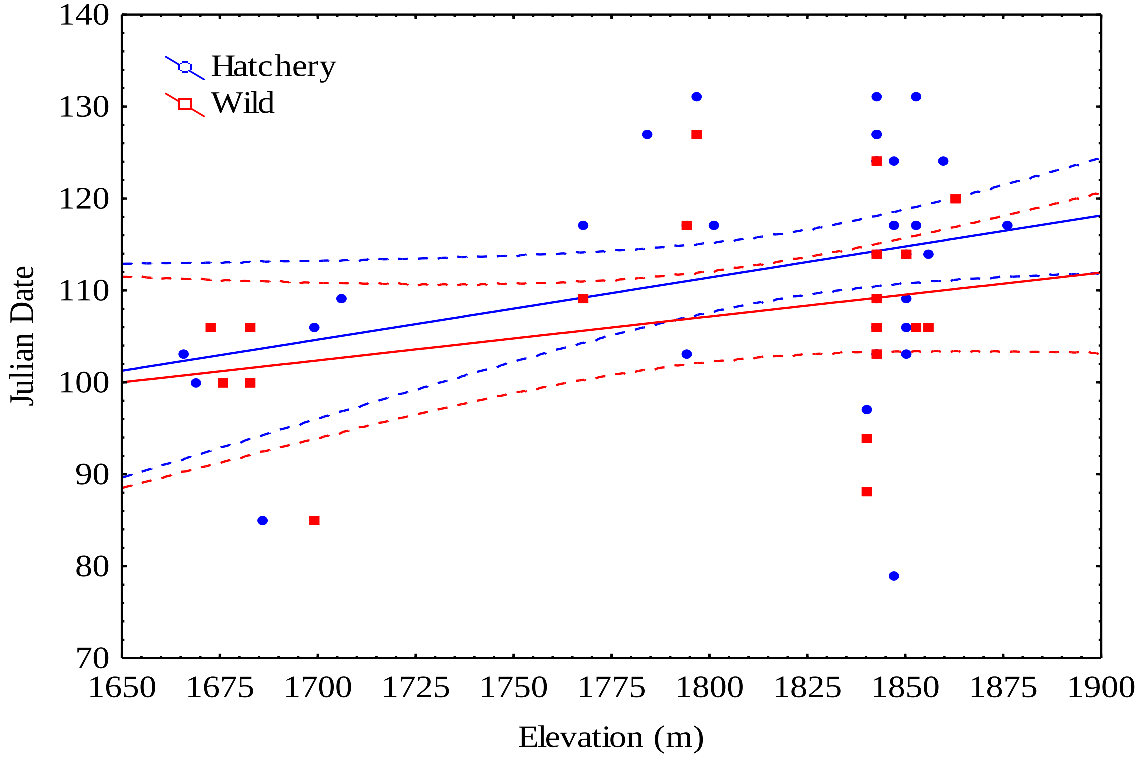


Figure 17. Relationship between day of the year (Julian Date) and elevation of hatchery and naturally produced steelhead in the upper Wenatchee River in 2010.

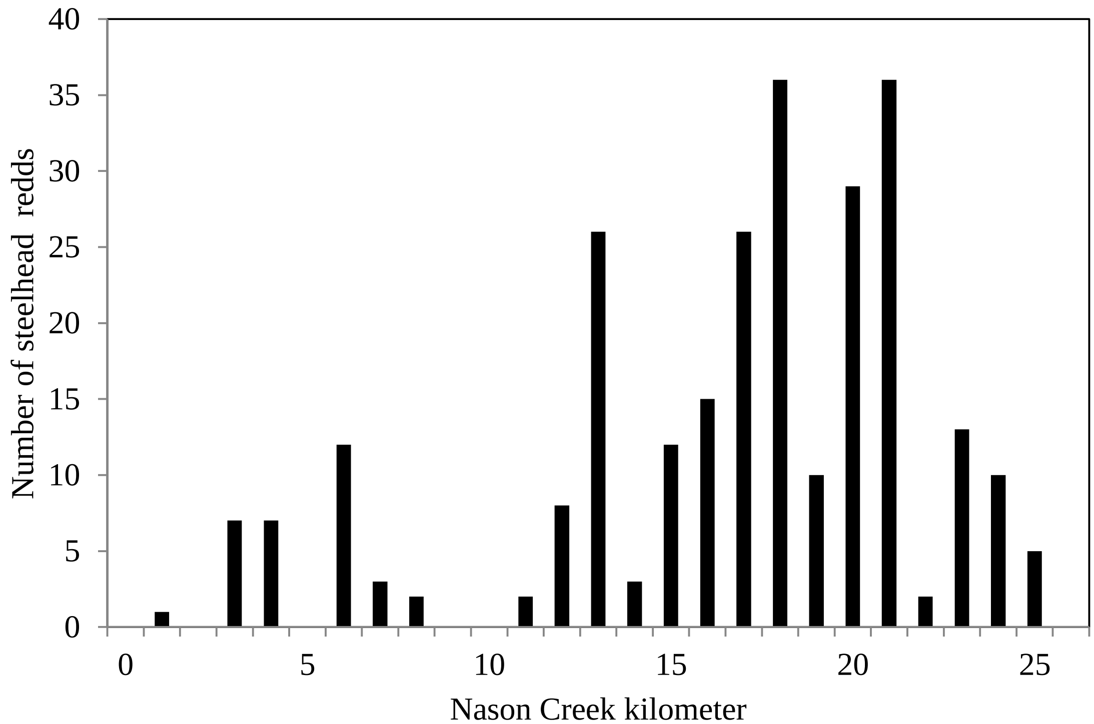


Figure 18. Distribution of steelhead redds in Nason Creek in 2010.

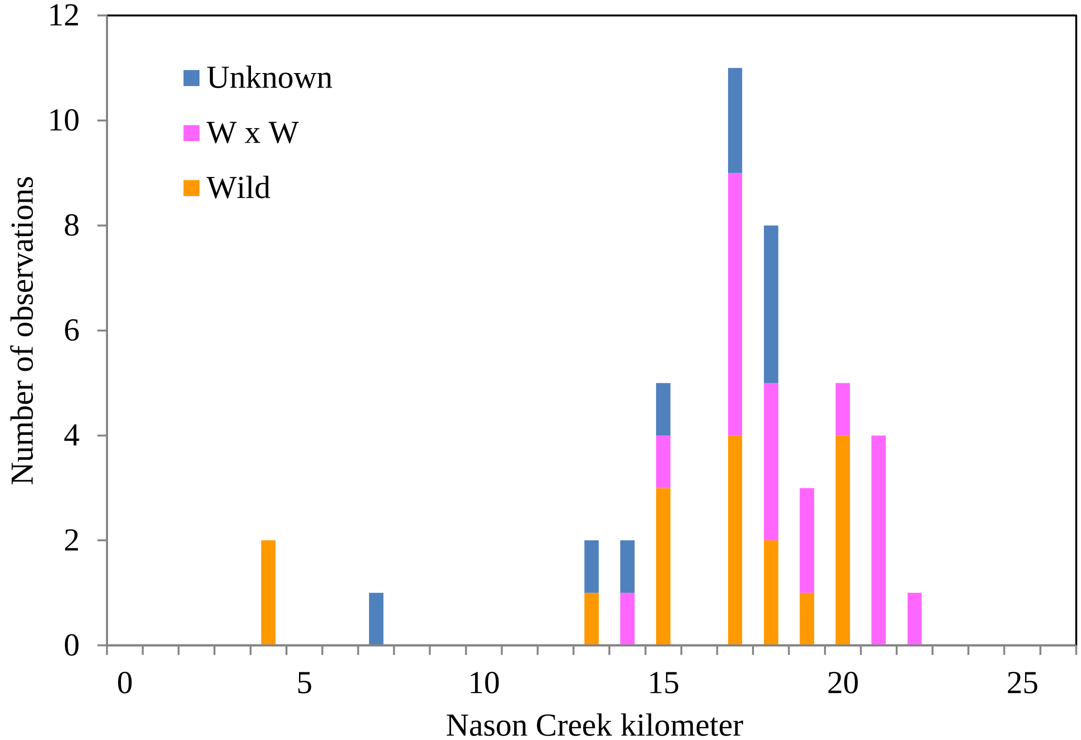


Figure 19. Distribution of anchor tagged female steelhead in the Nason Creek.

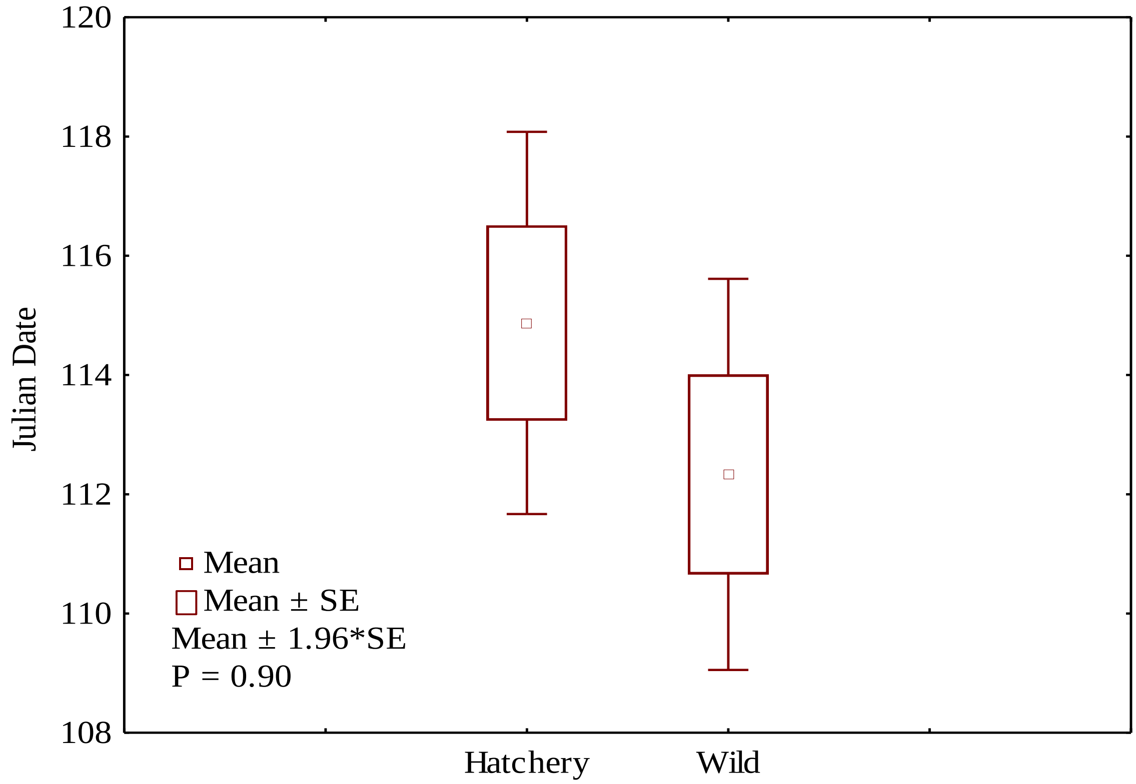


Figure 20. Mean spawn time of hatchery and natural origin steelhead in Nason Creek in 2010.

Discussion

Suboptimal survey conditions as a result of above normal river discharge during and following the peak of spawning likely decreased observer efficiency compared to previous years and may have resulted in an underestimate of redd abundance. Despite these factors, the proportion of the run escapement accounted for on the spawning grounds was much greater than expected. We attributed this increase to the increase in survey frequency. In previous years, index areas were surveyed approximately once a week. Female steelhead appear to have a relatively short redd residence time (1-3 d) compared to Chinook salmon (4-16 d). Hence, the probability of detecting a steelhead redd is likely greater when the redd is newly constructed and the female steelhead is still present on the redd. However, redd density was correlated to observer efficiency and may have contributed to a greater proportion of run escapement accounted for. In 2011, redd densities will be approximately 50% of 2010 and should provide more information on the influence of survey frequency.

High correlation between the expanded total redd counts and run escapement ($r = 0.93$) suggest that the methodology used to estimate spawner abundance can be very robust. It also suggests that factors responsible for the observed difference in run and estimated spawning escapement are relatively constant with respect to escapement levels across years. Given the large differences between run and spawn escapement upstream of Tumwater Dam, it is evident that multiple factors are contributing to the difference in the escapement estimates.

Tumwater Dam offers a unique opportunity to examine all the possible factors that may influence the size of the spawning population. Furthermore, it is not unreasonable to apply results of studies designed to answer these critical uncertainties to all populations in the upper Columbia River Basin. In the following section, we discuss these factors in more detail.

Estimates of the Number of Redds

The current methodology does not involve conducting weekly surveys of the entire available spawning habitat (e.g., spring Chinook, summer Chinook, and sockeye). Steelhead are thought to have a greater range of spawning habitats than other anadromous species making a total redd census logistically impractical and costly. In the Wenatchee Basin, the Integrated Status and Effectiveness Monitoring Program (ISEMP) has been conducting probabilistic sampling (e.g., GRTS) of those areas not covered under the current methodology. When available, annual estimates of redd abundance outside of the current survey area should provide some indication regarding the extent of steelhead spawning habitat. Within the current survey area, while a majority of the steelhead redds are consistently found within index areas, this may simply be a result of an artifact in the methodology and river reaches surveyed. Furthermore, observer efficiency is potentially a large source of error in conducting redd counts (Dunham et al. 2001; Muhlfeld et al. 2006). Studies were conducted in 2010 to estimate observer efficiency and not only identify, but also quantify sources of error (redd omission or false identification). Other studies are planned (i.e., 2011 and beyond) that are designed to evaluate the accuracy of the current spawning ground protocol.

Spawning Escapement Estimates

Monitoring and evaluation plans require estimates of the spawning population in order to evaluate hatchery program effectiveness (e.g, wild and hatchery abundance and productivity) and determine appropriate escapement levels (i.e., carrying capacity). Steelhead exhibit a diverse life history and complex migration patterns thereby reducing the reliability that run escapement estimates (i.e., dam counts) accurately reflect the size of the spawning population. Steelhead spawning ground surveys are currently conducted in every major steelhead population in the Upper Columbia Basin. However, uncertainty in using these data to estimate the size of the spawning population lies in some factors previously discussed (i.e., observer efficiency and sampling design), but also in the manner in which redd counts are expanded to estimate the population.

The conversion of redd counts to an estimate of the spawning population requires knowledge of the average number of redds constructed per female and the number of fish per redd (Gallagher et al. 2007). In some populations, female steelhead were reported to construct multiple redds. If steelhead in the Wenatchee Basin do construct multiple redds, differences in run and escapement estimates would increase as a result of a lower spawning escapement estimate. For example, if female steelhead construct an average of 1.5 redds, the difference in run and spawning escapement estimates would increase 9%. Redd abundance estimates are used to estimate the female escapement, which are then expanded by the sex ratio to estimate the male population on the spawning grounds. The number of fish per redd is based on the sex ratio of the population. Error associated with observer accuracy (i.e., gender misassignments) could be corrected using portable ultrasound devices. This approach assumes 1) equal survival to spawning and 2) every male spawns on average at one redd location. A tagging study is needed and planned in the next few years to test these assumptions.

Observer Efficiency

The correct identification of steelhead redds in the Wenatchee Basin was higher in the tributaries of the Wenatchee River than the main stem itself. This could be directly related with the attributes of the tributaries versus the main stem Wenatchee River (i.e. redd density, stream depth, width and channel complexity). In addition, other factors that may contribute to observer efficiency include surveyor experience and environmental conditions (i.e. discharge, cloud cover, precipitation and turbidity). Given the wide range of individual observer efficiencies an attempt to quantify surveyor experience and channel complexity should be made. Observer efficiencies rates calculated using this method represent instantaneous observer efficiency rather than the efficiency of weekly or semi-weekly surveys to estimate redd abundance. Methods are being developed to estimate the variance of redd counts and should be finalized in 2012.

Spawning Distribution and Timing

Differences in spawn timing have been observed in Wenatchee summer steelhead broodstock, but fish are held in a controlled environment on well water. Based on the differences observed in the hatchery, it is possible that a considerable portion of hatchery origin steelhead spawn prior to initiation of spawning ground surveys. Spawning ground surveys start in early March with redds typically being found during April suggesting that hatchery steelhead are spawning within the current survey period.

Results from 2010 suggest that hatchery and naturally produced fish do have similar spawning distributions, both spatially and temporally. Although the analysis was restricted to the upper Wenatchee River and Nason Creek, these areas comprise the majority of redds found upstream of Tumwater Dam. Similar studies planned for 2011 will provide an additional year of data.

Recommendations

Of all the factors that are contributing to the difference between run and spawning escapement estimates, redds constructed in streams not included in the survey area have the potential to account for a significant portion of the observed difference. The reported number of redds upstream of Tumwater Dam underestimate the total number of redds because all available spawning habitat (i.e., low order streams) is not surveyed. Studies have been ongoing in the Wenatchee Basin designed to estimate the number of redds in areas not covered under the current survey design. Data from these studies (i.e., ISEMP) must be analyzed and incorporated into spawning escapement estimates.

The accuracy and precision of the current methodology used in estimating the redd abundance and observer efficiency are currently ongoing. Studies focused on testing assumptions used in estimating the size of the spawning population (number of redds per female and number of fish per redd) should incorporate an assessment of 1) fallback 2) survival to spawning 3) the spawning distribution of the hatchery and wild steelhead. Information from these studies is required to ensure spawning escapement estimates have sufficient accuracy and precision, such that inferences regarding the efficacy of naturally spawning hatchery steelhead can be made in a timely manner.

Spawning distributions of hatchery and wild steelhead in the Wenatchee Basin can be assessed at the tributary level using PIT tags. All major and minor spawning areas will eventually have instream PIT tag antenna arrays. However, this methodology requires that an adequate and representative sample of adults is tagged every year. Spawning distribution within tributaries at a reach level can also be assessed using instream arrays if desired. However, assessment of spawn timing in the natural environment is problematic and will require a periodic assessment of individuals on the spawning grounds.

References

Dunham, J. B. Rieman, and K. Davis. 2001. Sources and magnitude of sampling error in redd counts for bull trout. North American Journal of Fisheries Management 21:343-352.

English, K. K., C. Sliwinski, B. Nass, and J. R. Stevenson. 2001. Assessment of adult steelhead migration through the Mid-Columbia River using radio-telemetry techniques, 1999-2000. Report prepared by LGL Limited for Public Utility District No.2 of Grant County, Public Utility District No. 1 of Chelan County, and Public Utility District No. 1 of Douglas County.

English, K. K., C. Sliwinski, B. Nass, and J. R. Stevenson. 2003. Assessment of adult steelhead migration through the Mid-Columbia River using radio-telemetry techniques, 2001-2002. Report prepared by LGL Limited for Public Utility District No.2 of Grant County, Public Utility District No. 1 of Chelan County, and Public Utility District No. 1 of Douglas County.

Gallagher, S.P., and C.M. Gallagher. 2005. Discrimination of Chinook salmon, coho salmon, and steelhead redds and evaluation of the use of redd data for estimating escapement in several unregulated streams in northern California. North American Journal of Fisheries Management 25:284-300.

Gallagher, S.P., P.K.J. Hahn, and D. H. Johnson. 2007. Redd counts. Pages 197 - 234 *in* Johnson, D.H., B.M. Shier, J.S. O'Neal, J.A. Knutzen, X. Augerot, T.A. O'Neil, T.N. Pearsons plus 37 contributing authors. Salmonid field protocols handbook: techniques for assessing status and trends in salmon and trout populations. American Fisheries Society, Bethesda, Maryland.

Keefer, M.L., C.T. Boggs, C.A. Perry, and C.C. Caudill. 2008. Overwintering distribution, behavior, and survival of adult summer steelhead: variability among Columbia River populations. North American Journal of Fisheries Management 28:81-96.

Kuligowski, D. R., M. J. Ford, and B. A. Berejikian. 2005. Breeding structure of steelhead inferred from patterns of genetic relatedness among nests. Transactions of the American Fisheries Society 134:1202–1212.

Muhlfeld, C.C., M.L. Taper, D.F. Staples, and B.B. Shepard. 2006. Observer error structure in bull trout redd counts in Montana streams: Implications for inference on true redd numbers. Transactions of the American Fisheries Society 135:643-654.

Murdoch, A.R., T.N. Pearsons, T.W. Maitland, M.J. Ford, and K. Williamson. 2008. Monitoring the reproductive success of naturally spawning hatchery and natural spring Chinook salmon in the Wenatchee River. Project No. 2003-039-00, Contract No. 00032138. Bonneville Power Administration, Portland, Oregon.

Murdoch, A. R. and C. M. Peven. 2005. Conceptual approach to monitoring and evaluating the Chelan county Public Utility District hatchery programs. Chelan County PUD, Wenatchee, WA.

Reingold, M. 1965. A steelhead spawning study. Idaho Wildlife Review 17:8-10.

Appendix A. Wenatchee River Basin survey reach and index/reference areas – surveys conducted weekly from March through June.

Reach	Index/reference area
Wenatchee River	
Sleepy Hollow Br. to Lower Cashmere Br. (W2)	Monitor boat ramp to Cashmere boat ramp
Leavenworth Bridge to Icicle Road Bridge (W6)	Leavenworth boat ramp to Icicle River
Tumwater Dam to Tumwater Bridge (W8)	Swiftwater boat ramp to Tumwater Bridge
Tumwater Bridge to Plain (W9)	Tumwater Bridge to Plain
Plain to Lake Wenatchee (W10)	Chiwawa pump station to Lake Wenatchee
Peshastin Creek	
Mouth to Camas Creek (P1)	Kings Bridge to Camas Creek
Camas Creek to mouth of Scotty Creek (P2A)	Ingalls Creek to Ruby Creek
Camas Creek to mouth of Scotty Creek (P2)	FR7320 to mouth of Shaser Cr.
Ingalls Creek	
Mouth to Trailhead rm 1.0 (D1)	Mouth to Trailhead rm 1.0
Trailhead to Wilderness Boundary rm 1.5 (D2)	Trailhead to Wilderness Boundary rm 1.5
Chiwawa River	
Mouth to Grouse Creek (C1)	Mouth to Road 62 Bridge rm 6.4
Grouse Creek to Rock Creek (C2)	Chikamin Creek to Log jam
Clear Creek	
Mouth to HWY 22 (V1)	Mouth to HWY 22
HWY 22 to Lower culvert rm 2.0 (V2)	HWY 22 to Lower culvert
Nason Creek	
Mouth to Kahler Creek Bridge (N1)	Mouth to Swamp Creek
HWY 2 Bridge to Lower R.R. Bridge (N3)	Highway 2 Bridge to Merrit Bridge
Lower R.R. Bridge to Whitepine Creek (N4)	Rayrock to Church camp
Icicle River	
Mouth to Hatchery (I1)	Mouth to Hatchery
Little Wenatchee River	
Mouth to Lost Creek (L2)	Fish Weir to Lost Creek
Lost Creek to Rainy Creek Bridge (L3)	Lost Creek to Rainy Creek Bridge
White River	
Sears Cr. Bridge to Napeequa River (H2)	Riprap bank to Napeequa River
Napeequa River to mouth of Panther Creek (H3)	Napeequa River to Grasshopper Meadows.
Napeequa River	
Mouth to rm 1.0 (Q1)	Mouth to rm 1.0

Appendix B. Summary of steelhead spawning ground index surveys in the Wenatchee River basin in 2010.

Reach	Survey Week of index Area														Index Total	Reach Total	Expanded # of redds
	28 Feb	7 Mar	14 Mar	21 Mar	28 Mar	4 Apr	11 Apr	18 Apr	25 Apr	2 May	9 May	16 May	23 May	30 May			
Wenatchee River																	
W1																6	8
W2		0	1	1	1	1	4		0	0	15				23	26	27
W3																4	6
W4																0	0
W5																0	0
W6	0	0	0	3	3	2	11	0	6	2	9				36	48	52
W7																0	0
W8		0	1	2	0	1	0	0	0		3				7	7	7
W9	0	0	2	4	2	22	32	15	18	11	2				108	113	117
W10	0	1	3	2	1	5	19	47	12	45	4		0		139	151	160
Total	0	1	7	12	7	31	66	62	36	58	33		0		313	355	377
Peshastin Creek																	
P1	0	2	3	4	11	7	14		13	9					63	67	69
P2			0	0	0	0	0	0	0		11				11	46	46
Total	0	2	3	4	11	7	14	0	13	9	11				74	113	115
Chiwawa River																	
C1		0	0	1	4	4	4	1	3	4	2				23	36	36
C2				1	0	0	0		0		0		0		1	3	4
Total		0	0	2	4	4	4	1	3	4	2		0		24	39	40

Appendix B. Continued.

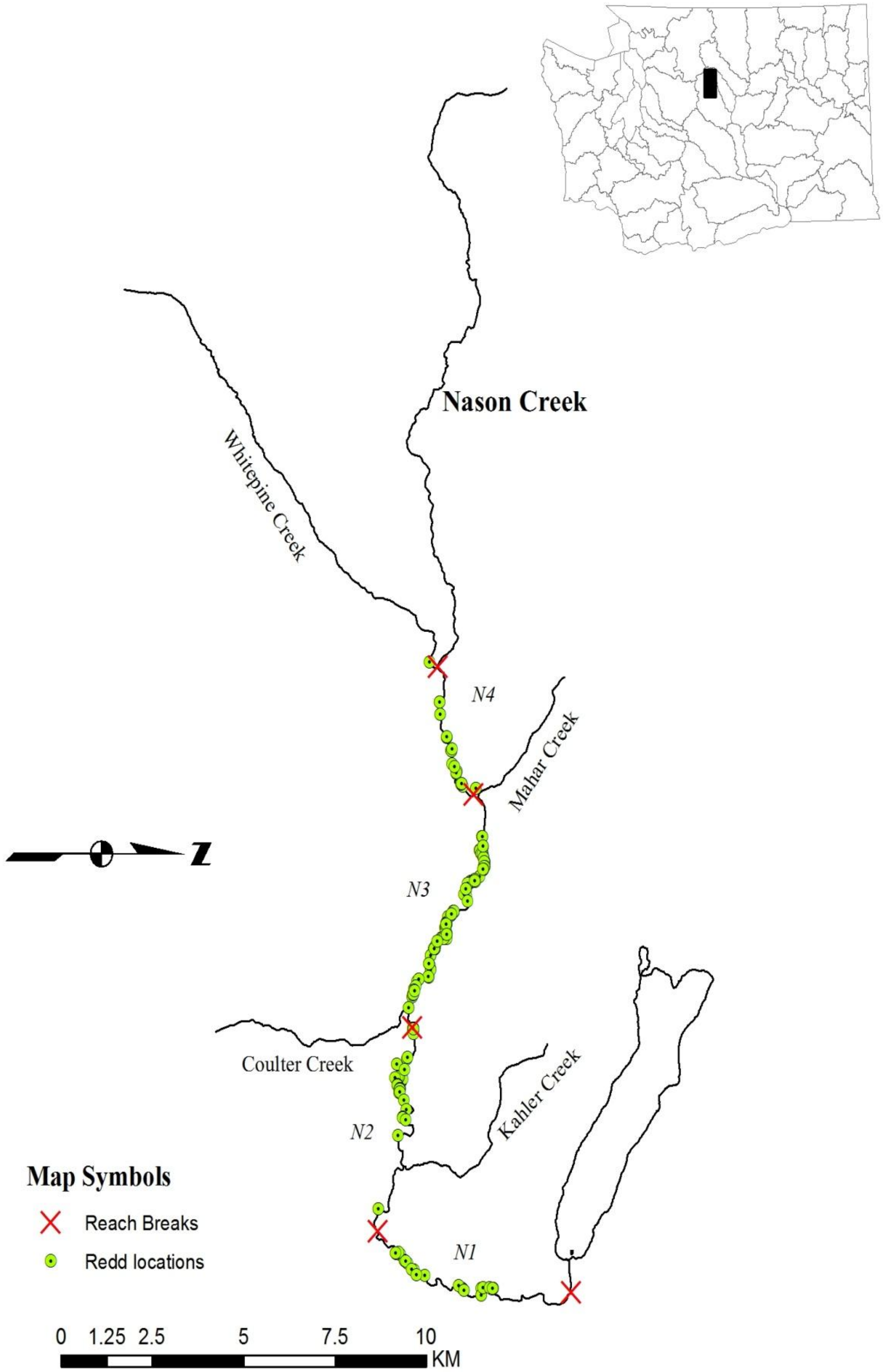
Reach	Survey Week of index Area														Index Total	Reach Total	Expanded # of redds
	28 Feb	7 Mar	14 Mar	21 Mar	28 Mar	4 Apr	11 Apr	18 Apr	25 Apr	2 May	9 May	16 May	23 May	30 May			
Clear Creek																	
V1		0	0	0	0	0	0	2	2	0	6		1		11	11	11
V2																1	1
Total		0	0	0	0	0	0	2	2	0	6		1		11	12	12
Nason Creek																	
N1	0	0	0	1	3	3	5	2	9	4	1		0		28	30	30
N2	0	0	0	0	2	1	2	1	5	3	2		0	0	16	53	53
N3	0	0	0	0	1	6	9	4	47	41	32		8	6	154	154	154
N4		0	0	0	0	0	3	0	5	9	3		2	1	23	28	32
Total	0	0	0	1	6	10	19	7	66	57	38		10	7	221	265	269
Icicle River																	
Total	0	0	1	8	4	14	40	0	36	11					114	118	120
White River																	
H2		0	0	0	0	0			1		2		0		3	3	3
H3		0	0	0	0	0			0		0		0		0	0	0
Total		0	0	0	0	0			1		2		0		3	3	3
Little Wenatchee River																	
L2					0						2				2	2	2
L3					0						2		0		2	2	2
Total					0						4		0		4	4	4
Wenatchee River Basin																	
Total	0	3	11	27	32	66	143	72	157	139	96		11	7	764	909	940

Appendix C. Steelhead spawning surveys in the Wenatchee River basin, 2001 – 2009. Redd counts are expanded values derived from sample rates within index areas.

Basin/subbasin	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010
Chiwawa River Basin										
Chiwawa River	25	27	26	17	118	8	3	9	68	40
Rock Creek	--	1	0	0	0	0	--	--	0	0
Chikamin creek	--	0	0	1	2	1	0	--	2	11
Meadow Creek	--	5	1	5	16	3	0	0	3	3
Twin Creek	--	4	0	--	0	--	--	--	--	0
Goose Creek	--	0	--	--	--	--	--	--	--	--
Alder Creek	--	0	5	2	14	0	0	0	0	8
Deep Creek	--	0	--	--	--	--	--	--	--	--
Clear Creek	--	43	32	37	12	7	8	2	2	12
Subtotal	25	80	64	62	162	19	11	11	75	74
Nason Creek Basin										
Nason Creek	27	80	121	124	410	74	78	87	126	269
White Pine Creek	--	--	--	0	0	0	0	--	0	1
Un-named Creek	--	--	--	3	0	3	0	1	0	0
Roaring Creek	--	--	--	--	2	0	0	0	0	0
Subtotal	27	80	121	127	412	77	78	88	126	270
White River Basin										
White River	--	0	1	0	2	0	1	0	0	3
Panther Creek	--	--	0	0	0	0	0	0	0	--
Napeequa River	--	0	2	0	0	0	0	1	0	0
Subtotal		0	3	0	2	0	1	1	0	3
Little Wenatchee River										
Mainstem	--	1	5	0	0	--	0	--	0	4
Icicle Creek										
Mainstem	19	27	16	23	8	41	6	37	102	120
Peshastin Creek Basin										
Peshastin Creek	--	--	15	32	91	67	17	48	32	115
Mill Creek	--	--	--	--	1	0	0	1	0	0
Ingalls Creek	--	--	0	0	0	0	--	--	--	--
Ruby Creek	--	--	0	0	0	--	--	--	0	0
Tronsen Creek	--	--	0	2	5	0	0	0	0	3
Scotty Creek	--	--	0	0	0	0	0	0	0	0
Shaser Creek	--	--	0	0	0	0	0	0	0	0
Schafer Creek	--	--	--	0	0	0	0	0	0	0

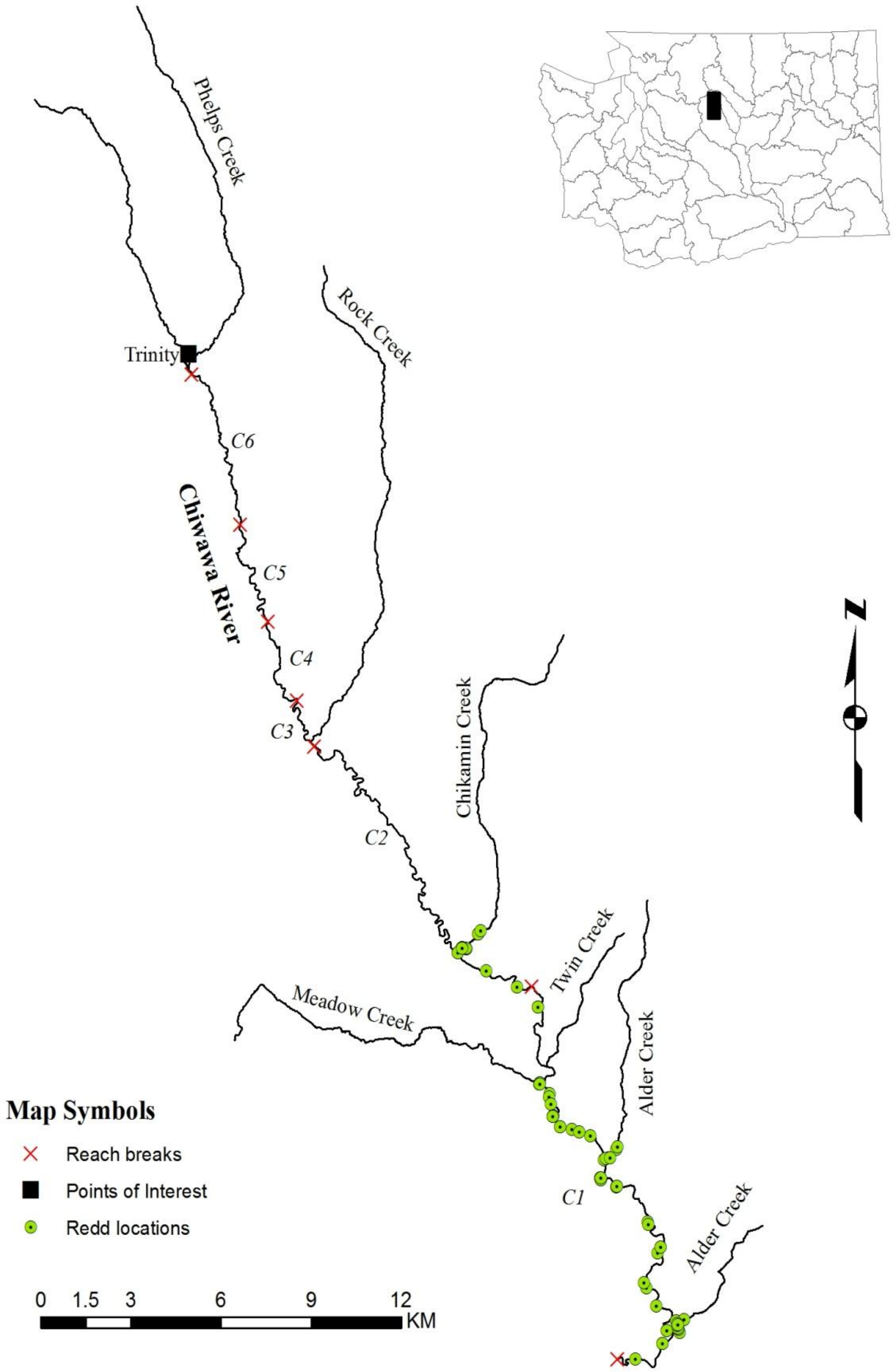
Subtotal	--	--	15	34	97	67	17	49	32	118
				Wenatchee River						
Mainstem	116	315	248	136	456	191	46	100	327	377
Beaver Creek	--	0	0	* 15	3	0	0	0	0	2
Chiwaukum Creek	--	--	0	--	0	0	--	0	0	1
Subtotal	116	315	248	151	459	191	46	100	327	3
Wenatchee Basin Total	**187**	**503**	**472**	**397**	**1,140**	**395**	**159**	**286**	**662**	**969**

***Redds were enumerated by USFS**

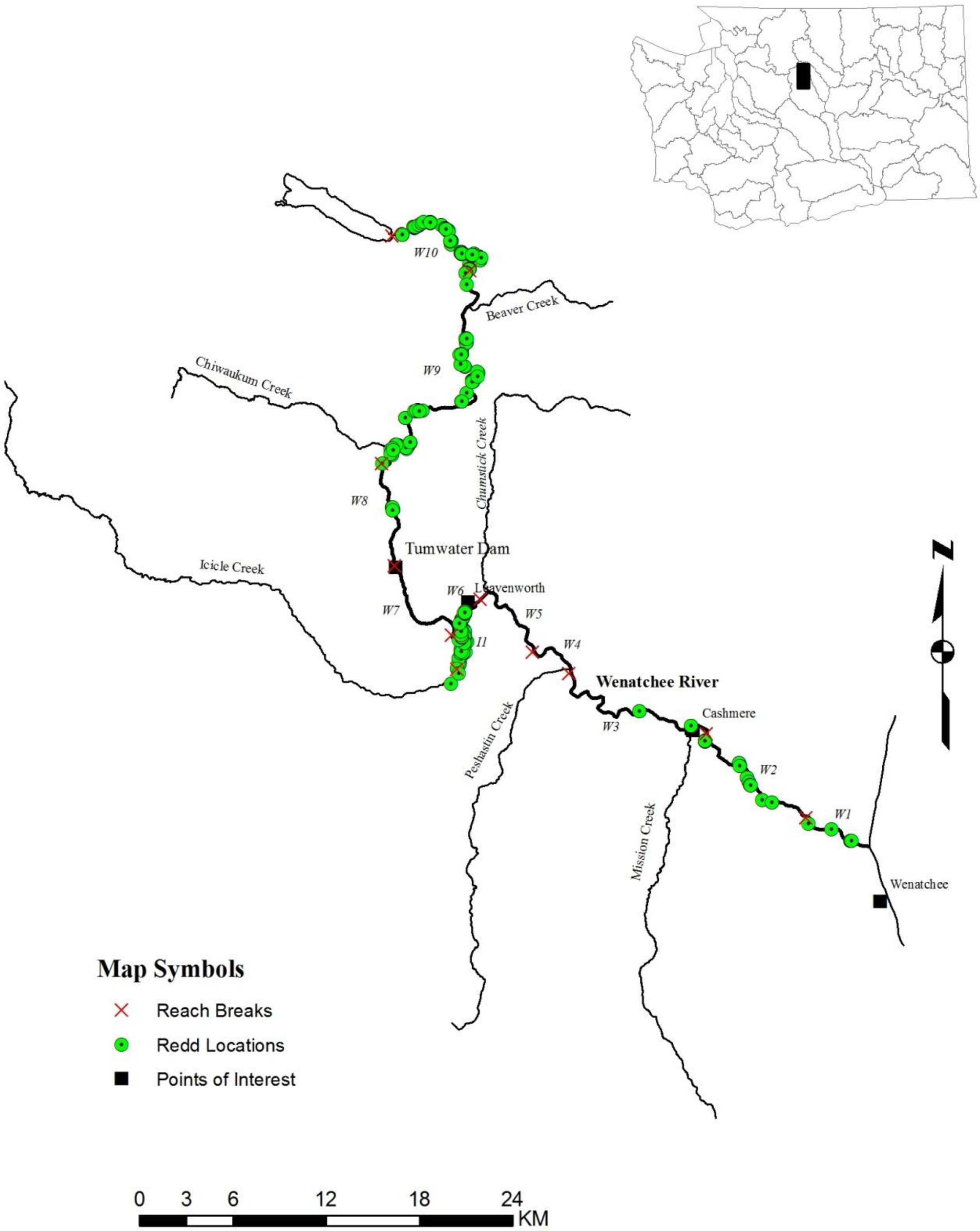


Nason Creek
Whitepine Creek
N4
Mahar Creek
N
N3
Coulter Creek
Kahler Creek
N2
N1
Map Symbols
Reach Breaks
Redd locations
0 1.25 2.5 5 7.5 10
KM

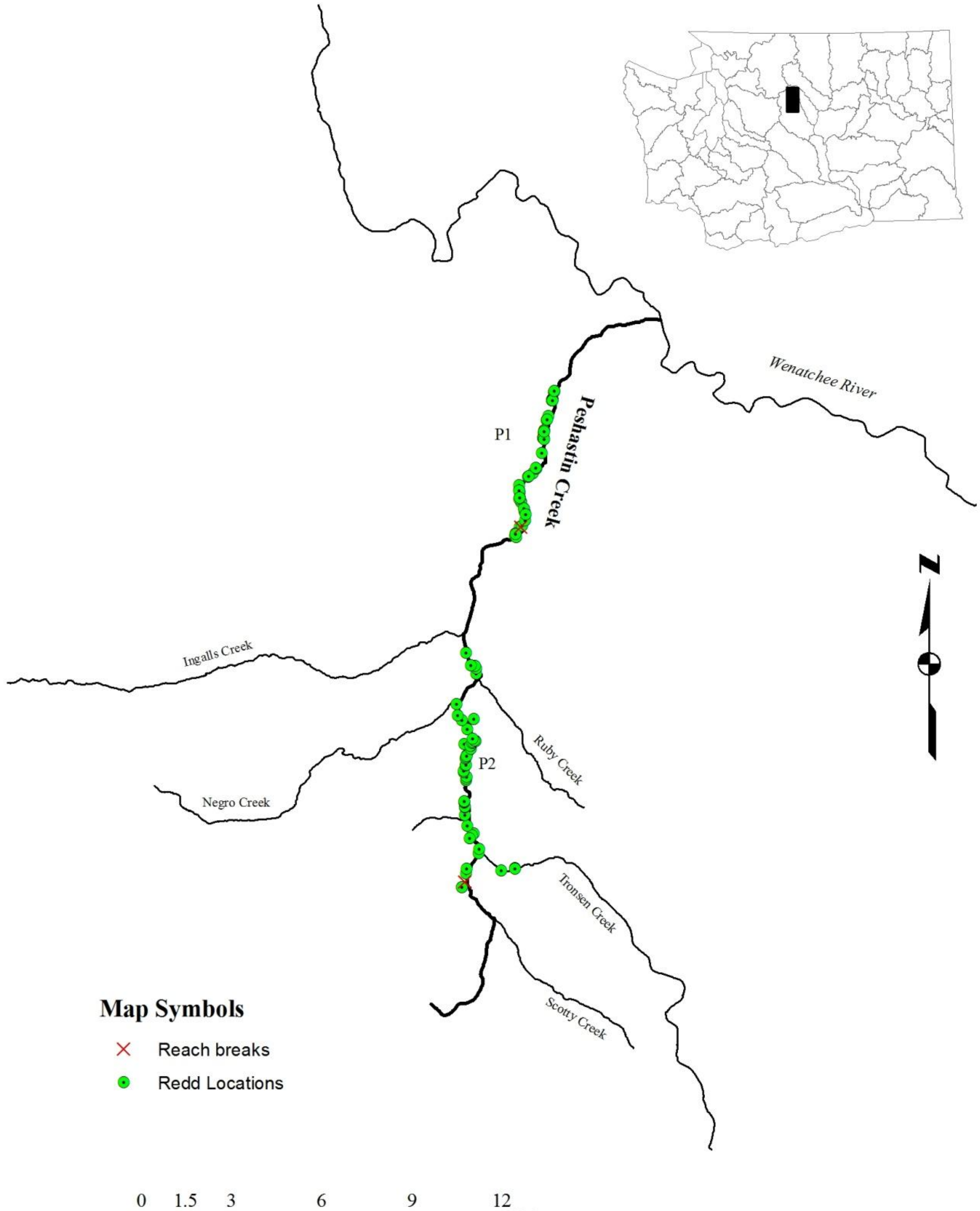
Appendix D1. Steelhead spawning distribution in the Nason Creek Basin in 2010.



Appendix D2. Steelhead spawning distribution in the Chiwawa River Basin in 2010.



Appendix D3. Steelhead spawning distribution in the Wenatchee River and Icicle Creek in 2010.



Appendix D4. Steelhead spawning distribution in the Peshastin Creek Basin in 2010.

APPENDIX E

NPDES Hatchery Effluent Monitoring, 2010

NPDES MONITORING FOR WDFW FACILITIES.

All WDFW hatcheries monitor their discharge in accordance with the National Pollutant Discharge Elimination System (NPDES) permit. This permit is administered in Washington by the Washington Department of Ecology under agreement with the United States Environmental Protection Agency. The permit was renewed effective June 1, 2005 and will expire June 1, 2010.

Facilities are exempted from sampling during any month that pounds of fish on hand fall below 20,000 lbs and pounds of feed used fall below 5,000 lbs, with the exception of offline settling basin discharges which are to be monitored once per month when ponds are in use and discharging to receiving waters.

Sampling at permitted facilities includes the following parameters:

<FLOW Measured in millions of gallons per day (MGD) discharge.

<SS EFF Average net settleable solids in the hatchery effluent, measured in ml/L.

<TSS COMP Average net total suspended solids, composite sample (6 x/day) of the hatchery effluent, measured in mg/L.

<TSS MAX Maximum daily net total suspended solids, composite sample (6 x/day) of the hatchery effluent, measured in mg/L.

<SS PA Maximum settleable solids discharge from the pollution abatement pond, measured in ml/L.

<SS % Removal of settleable solids within the pollution abatement pond from inlet to outlet, measured as a percent. No longer required under permit effective June 1, 2000.

<TSS PA Maximum total suspended solids effluent grab from the pollution abatement pond discharge, measured in mg/L.

<TSS % Removal of suspended solids within the pollution abatement pond from inlet to outlet, measured as a percent. No longer required under permit effective June 1, 2000.

<SS DD Settleable solids discharged during drawdown for fish release. One sample per pond drawdown, measured in ml/L.

<TRC Total residual chlorine discharge after rearing vessel disinfection and after neutralization with sodium thiosulfate. One sample per disinfection, measured in ug/L.

In addition, at Similkameen Hatchery only, the following sampling was conducted at the request of WA Dept of Ecology, but is not required under NPDES permit:

<SS IW Settleable solids influent grab taken as wastes are pumped into the pollution abatement pond, measured in mg/L.

<TSS IW Total suspended solids influent grab as wastes are pumped into the pollution abatement pond, measured in mg/L.

National Pollutant Discharge Elimination System (NPDES) Effluent Summary
for the period of January 1, 2010 through December 31, 2010
as reported on the Discharge Monitoring Reports (DMRs)
submitted to the Washington State Department of Ecology

Eastbank Hatchery
NPDES Permit Number WAG13-5011

YEAR	MONTH	FLOW	SS EFF	TSS COMP	TSS MAX	FLOW PA	SS PA	SS %	TSS PA	TSS %	Lbs of Fish	Lbs of Feed
2010	JAN	29.67	0	0.2	0.2	15000	0.01		26		109930	27166
	FEB	30.4	0	0.4	0.4	12500	0.01		21.3		124377	22608
	MAR	22.8	0	0.0	0.0	12000	0.01		11.8		65566	8416
	APR	18.11	0	0.2	0.2	7600	0.01		21.2		18606	8069
	MAY	11.1	0			5450	0.01		12.4		16334	4760
	JUN	18.24	0	0.0	0.0	7200	0.01		14.4		21099	8729
	JUL	28.45	0	0.2	0.2	3500	0.01		8.4		28880	11952
	AUG	28.77	0	0.8	1.6	5000	0.01		9.2		40785	16270
	SEP	29.09	0	0.0	0.0	7500	0.01		41.2		46753	14753
	OCT	20.82	0	0.0	0.0	5000	0.01		29.8		46574	16872
	NOV	19.43	0	0.0	0.0	4500	0.01		33.3		47541	13825
	DEC	19.44	0	0.0	0.0	3500	0.01		21.2		56290	16896

Turtle Rock
NPDES Permit Number WAG13-5004

YEAR	MONTH	FLOW	SS EFF	TSS COMP	TSS MAX	Lbs of Fish	Lbs of Feed	SS DD	TSS DD
2010	JAN	18	0	-0.2	-0.2	29099	4730		
	FEB	18	0	0.8	0.8	59643	7214		
	MAR	18	0	0.8	0.8	84888	9146		
	APR	14.4	0	0.4	0.4	91476	9174		
	MAY	7.2	0	0.4	0.4	29419	0	0.1	1.1
	JUN	No Monitoring				0	0		
	JUL	No Monitoring				0	0		
	AUG	No Monitoring				0	0		
	SEP	No Monitoring				0	0		
	OCT	7.2	0	-0.4	-0.4	10648	1848		
	NOV	7.2	0	1.8	1.8	18650	9864		
	DEC	10.8	0	0.8	1.2	38740	10747		

Wells Hatchery
NPDES Permit Number WAG13-5009

YEAR	MONTH	FLOW	SS EFF	TSS COMP	TSS MAX	FLOW PA	SS PA	SS %	TSS PA	TSS %	Lbs of Fish	Lbs of Feed	SS DD	TSS DD
2010	JAN	23.1	0	0.2	0.2	495	0		1.8		71577	19705		
	FEB	27.3	0	0.2	0.2	495	0		1.2		72321	16129		
	MAR	26.3	0	0.4	0.4	495	0		0.8		107441	29959		
	APR	19.2	0	0.2	0.2	495	0		1.2		63378	16114		
	MAY	34.4	0	-0.2	-0.2	495	0		1.2		5279	4370	0	3.25
	JUN	3.6	0	0.4	0.4	495	0		8		7876	3390		
	JUL	6.5	0	0	0	495	0		3.2		13325	5070		
	AUG	6.7	0	0.6	0.6	495	0		1.4		20415	7998		
	SEP	7.3	0	-1	-1	495	0		4.2		30161	10834		
	OCT	7.8	0	0.6	0.6	495	0		1.8		53419	14818		
	NOV	6.8	0	0.6	0.6	*	*		*		71842	19027		
	DEC	13.7	0	1.8	2.2	*	*		*		83800	19027		

Chiwawa Ponds
NPDES Permit Number WAG13-5015

YEAR	MONTH	FLOW	SS EFF	TSS COMP	TSS MAX	Lbs of Fish	Lbs of Feed	SS DD	TSS DD
2010	JAN	8.45	0	-0.4	-0.4	39430	704		
	FEB	8	0	-0.6	-0.6	37050	1230		
	MAR	8.5	0	-1.5	-0.8	51210	6194		
	APR	9.05	0.05	0.2	0.2	63003	5180		
	MAY	9.6	0			15204	0	0.03	18.4
	JUN	No Monitoring				0	0		
	JUL	No Monitoring				0	0		
	AUG	No Monitoring				0	0		
	SEP	9.43	0	3.7	5.8	28052	3488		
	OCT	8.25	0	-0.6	-0.6	27750	6253		
	NOV	8.55	0	-1.8	-1.8	43620	1870		
	DEC	8.18	0	0.2	0.2	40733	1628		

Carlton Acclimation Pond
NPDES Permit Number WAG13-5013

YEAR	MONTH	FLOW	SS EFF	TSS COMP	TSS MAX	Lbs of Fish	Lbs of Feed	SS DD	TSS DD
2010	JAN	No Monitoring				0	0		
	FEB	No Monitoring				0	0		
	MAR	10.08	0.01	0.2	0.2	28429	1100		
	APR	10.08	0.02	-0.2	0.4	27000	5300	0.5	30.6
	MAY	No Monitoring				0	0		
	JUN	No Monitoring				0	0		
	JUL	No Monitoring				0	0		
	AUG	No Monitoring				0	0		
	SEP	No Monitoring				0	0		
	OCT	No Monitoring				0	0		
	NOV	No Monitoring				0	0		
	DEC	No Monitoring				0	0		

Methow Hatchery
NPDES Permit Number WAG13-5000

YEAR	MONTH	FLOW	SS EFF	TSS COMP	TSS MAX	FLOW PA	SS PA	SS %	TSS PA	TSS %	Lbs of Fish	Lbs of Feed	SS DD	TSS DD
2010	JAN	10.76	0	3.2	3.2	14400	0.1		0		23422	667		
	FEB	10.49	0	0	0	14400	0.1		10.8		28500	1100		
	MAR	8.65	0	-1	-1	14400	0.1		1		28458	1200		
	APR	2.88	0.05	-0.8	-0.8	14400	0.1		0.2		2700	570	0.1	6.8
	MAY	4.03	0.013			14400	0.1		0.8		4400	750		
	JUN	6.29	0			14400	0.1		0		6425	516		
	JUL	6.48				14400	0		0		7700	2320		
	AUG	6.48				14400	0.1		0.6		10700	2900		
	SEP	6.48				14400	0.1		0.4		13700	3500		
	OCT	10.02	0	0	0	14400	0		0.4		14800	2920		
	NOV	10.02	0	-0.2	-0.2	14400	0		3		16000	3100		
	DEC	15.76	0	-1	-1	14400	0.1		1.8		18800	2600		

Similkameen Hatchery
NPDES Permit Number WAG13-5007

YEAR	MONTH	FLOW	SS EFF	TSS COMP	TSS MAX	FLOW PA	SS IW*	TSS IW*	Lbs of Fish	Lbs of Feed	SS DD	TSS DD
2010	JAN	5.9	0	0.4	0.4				12350	0		
	FEB	5.9	0	0.4	0.8				14319	1760		
	MAR	11.5	0	-0.6	-0.6				19087	5368		
	APR	11.5	0	0.2	0.2				18029	8052		
	MAY	11.5	0						13319	0	0.06	13.4
	JUN	No Monitoring							0	0		
	JUL	No Monitoring							0	0		
	AUG	No Monitoring							0	0		
	SEP	No Monitoring							0	0		
	OCT	11.7	0	-1	-1				21271	1144		
	NOV	11.7	0	0.1	0.2				14465	616		
	DEC	5.9	0	0.4	0.4				21913	0		

* IW- influent waste

Chelan Hatchery
NPDES Permit Number WAG13-5006

YEAR	MONTH	FLOW	SS EFF	TSS COMP	TSS MAX	FLOW FA	SS FA	SS %	TSS EF	TSS %	Lbs of Fish	Lbs of Feed
2010	JAN	9.8	0	4.2	4.2	9771840	0		0		25950	9476
	FEB	9.8	0	0.8	0.8	9771840	0		7.2		28582	11247
	MAR	9.8	0	1.8	1.8	9771840	0.2		2.8		33366	20801
	APR	9.9	0	1.8	1.8	7512748	0		2.6		26140	18024
	MAY	6.87	0	2.6	2.8	5512320	0.2		4.6		7248	6917
	JUN	6.87	0	1.8	1.8	*	*		*		8847	5261
	JUL	13.9	0	2.8	2.8	9011520	0.1		5.4		9247	4937
	AUG	15.3	0	4	4	9911520	0.1		3.4		14691	7307
	SEP	24.7	0	2.2	2.2	16021440	0.1		7.4		20209	9045
	OCT	6.97	0.05	1.6	1.6	68000	0.05		1.6		15418	8993
	NOV	7.3	0.05	2.8	2.8	68000	0.05		1.4		22749	12530
	DEC	4.38	0.05	3.4	3.4	68000	0.05		3.4		15458	8355

* PA pond-No discharge this month

Dryden Acclimation Pond
NPDES Permit Number WAG13-5014

YEAR	MONTH	FLOW	SS EFF	TSS COMP	TSS MAX	Lbs of Fish	Lbs of Feed	SS DD	TSS DD
2010	JAN	No Monitoring				0	0		
	FEB	No Monitoring				0	0		
	MAR	14.9	-0.03	0.6	0.6	98106	8356		
	APR	14.83	-0.01	1.8	2.6	83774	10604	0.02	1.6
	MAY	No Monitoring				0	0		
	JUN	No Monitoring				0	0		
	JUL	No Monitoring				0	0		
	AUG	No Monitoring				0	0		
	SEP	No Monitoring				0	0		
	OCT	No Monitoring				0	0		
	NOV	No Monitoring				0	0		
	DEC	No Monitoring				0	0		

Priest Rapids
NPDES Permit Number WAG13-7013

YEAR	MONTH	FLOW	SS EFF	TSS COMP	TSS MAX	Lbs of Fish	Lbs of Feed	SS DD	TSS DD
2010	JAN	31.9	0			0	0		
	FEB	34.9	0	1	1	7477	2324		
	MAR	33	0	0.1	0.2	28677	8936		
	APR	41.3	0	0.6	0.6	58818	22354		
	MAY	41.3	0	0	0	107427	15048		
	JUN	28.9	0	1	1	129166	16337	0	4.6
	JUL	No Monitoring				0	0		
	AUG	No Monitoring				0	0		
	SEP	58.2	0	2.8	2.8	15375	0		
	OCT	55.6	0	4	4.2	40860	0		
	NOV	55.6	0	1.4	1	30950	0		
	DEC	45.2				0	0		

APPENDIX F

Steelhead Stock Assessment at Priest Rapids Dam, 2008-2009

Priest Rapids Dam 2008-2009 Adult Upper Columbia River Steelhead Run-Cycle Stock Assessment Report

Introduction

Upper Columbia River (UCR) steelhead stock assessment sampling at Priest Rapids Dam (PRD) is authorized through the Endangered Species Act (ESA) Section 10 Permit 1395 (NMFS 2003). Permit authorizations include interception and biological sampling of up to 10 percent of the UCR steelhead passing PRD to determine upriver population size, estimate hatchery to wild ratios, determine age class contribution and evaluate the need for managing hatchery steelhead consistent with ESA recovery objectives which include fully seeding spawning habitat with naturally produced UCR steelhead supplemented with artificially propagated enhancement steelhead (NMFS 2003).

Stock Assessment

The 2008 steelhead sampling at Priest Rapids Dam began 10 July and concluded 16 October. Sampling consisted of operating the Priest Rapids Off Ladder Trap (OLAFT), located on the left bank Priest Rapids Dam, 8 hours per day, on Tuesdays and Thursdays, for a total of 32 sampling days. Steelhead were trapped, handled and released in accordance with Section 2.1 and 2.2.1 of the National Marine Fisheries Service (NMFS) Biological Opinion for ESA Permits 1395, 1396 and 1423 (NMFS 2003a). The cumulative sample rate attained during 2008 totaled 8.9% and no steelhead mortalities were observed.

The Washington Department of Fish and Wildlife (WDFW) sampled 1,454 steelhead of the 2008/2009 run-cycle passing PRD, totaling 16,558 steelhead, for an overall sampling rate of 8.9%. Of the 1,454 steelhead sampled, 1,188 (81.7%) were hatchery origin and 266 (18.3%) were wild origin. The estimated 2008-2009 run- cycle total wild steelhead return was 3,030 representing 135.5% of the 1986-2007 average, 110.3% of the recent 5-year average (Table 1).

Based on external marks, external and internal tags, 1,188 hatchery origin steelhead sampled at Priest Rapids Dam during the 2008 return cycle included, 24.7% Wenatchee hatchery-origin steelhead and 64.4% "above Wells Dam" hatchery origin steelhead [1/] (Table 2)., while 8.9% of the hatchery origin steelhead sampled could not be assigned to a specific hatchery program. Ringold FH origin steelhead were not represented in the sample (Table 2).

1/- Defined as "above Wells Dam" because hatchery origin, adipose-clipped steelhead release into the Methow River from the Wells FH and Winthrop NFH have the same marks and are indistinguishable for one another.

Table 1. Priest Rapids Dam adult steelhead returns and stock composition, 1974-2008

Run-cycle[1/]	Hatchery	Wild	Wild percent	Total run
1974				2,950
1975				2,560
1976				9,490
1977				9,630
1978				4,510
1979				8,710
1980				8,290
1981				9,110
1982				10,770
1983				32,000
1984				26,200
1985				34,010
1986	20,022	2,342	10.5	22,364
1987	9,955	4,058	29.0	14,013
1988	7,530	2,670	26.2	10,200
1989	8,033	2,685	25.1	10,718
1990	6,252	1,585	20.2	7,837
1991	11,169	2,799	20.0	13,968
1992	12,102	1,618	11.8	13,720
1993	4,538	890	16.4	5,428
1994	5,880	855	12.7	6,735
1995	3,377	993	22.7	4,370
1996	7,757	843	9.8	8,600
1997	8,157	785	8.8	8,942
1998	4,919	928	15.9	5,847
1999	6,903	1,374	16.6	8,277
2000	9,023	2,341	20.6	11,364
2001	24,362	5,715	19.0	30,077
2002	12,884	2,983	18.8	15,867
2003	14,890	2,837	16.0	17,729
2004	15,670	2,985	16.0	18,655
2005	10,352	3,127	23.2	13,479
2006	8,738	1,677	16.1	10,415
2007	12,160	3,097	20.3	15,257
2008	13,528	3,030	18.3	16,558
1986-2008 average	**10,357**	**2,270**	**18.0**	**12,627**
2003-2008 average	**12,603**	**2,819**	**18.4**	**15,423**

[1/] A return cycle is the combined total of steelhead passing PRD from 1 June – 30 November during year (x), plus steelhead passing PRD between 15 April and 31 May on year (x+1).

Table 2. Origin classification of steelhead sampled at Priest Rapids Dam, 10 July – 16 October 2008.

Steelhead origin																					
Wild			Hatchery																		
Wild			Wenatchee						Above Wells				Ringold FH			Unk. Hat.					
Criteria			VIE						Criteria				Criteria			Criteria			Total	Total	Total
NS	NM	Total	LTGR	RTGR	RTOR	RTPK	LTRD	Total	AD	LTYL	RTYL	Total	AD	RV	Total	SD	NM	Total	Wild	Hatchery	Total
x	x	266	x					138	x			777	x	x	0	x	x	106	266	1,188	1,454
				x				36		x		11									
					x			0			x	1									
						x		34													
							x	85													
Total		**266**						**293**				**789**			**0**			**106**	**266**	**1,188**	**1,454**
% Hatchery								**24.7**				**66.4**			**0.0**			**8.9**		**100.0**	
% Total		**18.3%**						**20.2**				**54.2**			**0.0**			**7.3**	**18.3**	**81.7**	**100.0**

Reconciliation of salt water age of wild and hatchery steelhead sampled at Priest Rapids Dam during 2008 was accomplished through scale sample analysis. Salt-age analysis of the 2008 UCR steelhead run-cycle provides an estimated hatchery-origin 1- salt and 2-salt age composition of 48.3%, 51.7%, respectively (Table 3). Natural origin steelhead salt ages were 62.0% and 38.0% for salt ages 1 and 2, respectively (Table 3).

Table 3. Salt-water age composition of 2008 - 2009 return cycle Upper Columbia River steelhead sampled at Priest Rapids Dam, corrected by scale age/origin determination.

	Origin					
	Hatchery		Wild		Combined	
Salt-age	*N*	%	*N*	%	*N*	%
1-salt	351	48.3	168	62.0	519	52.3
2-salt	376	51.7	97	38.0	473	47.7
3-salt	-	-	-	-	-	-
4-salt	-	-	-	-	-	-
Total	**727**	**100**	**271**	**100**	**992**	**100**

Freshwater residency of naturally produced Upper Columbia River steelhead present in the 2008-2009 run cycle were dominated by age-2 freshwater fish (71.4%), and was marginally lower than the 1986-2007 average of 75.7% (Table 4).

Table 4. 2008 return year freshwater age of wild Upper Columbia River steelhead sampled at Priest Rapids Dam during steelhead stock assessment activities, compared to July – October 1986-2007 average.

Freshwater age	2007-2008 run cycle		1986-2007 average	
	N	%	*N*	%
1.x	29	11.5	186	6.6
2.x	180	71.4	2,126	75.7
3.x	42	16.7	475	17.0
4.x	1	0.4	18	0.6
5.x	-	-	2	0.1
Total	**252**	**100**	**2,807**	**100**

Wild and hatchery origin steelhead exhibited similar saltwater growth in the 2008 run-cycle. Wild 1and 2-salt adults were slightly larger than their hatchery cohorts (Table 5). Age 1-salt hatchery and age 1 and 2-salt wild steelhead observed in the 2008-2009 adult run-cycle return past PRD were comparable in size to the 1986-2007 run-cycle average (Table 5).

Table 5. Average fork length of 1-salt and 2-salt, Upper Columbia River steelhead sampled at Priest Rapids Dam during July – October 2008 and the period between 1986-2007.

	Average fork length (cm)			
	2008-2009 run cycle		1986-2007 run cycle	
Salt age	Wild	Hatchery	Wild	Hatchery
x.1	60.5	58.8	60.2	59.1
x.2	73.5	73.0	73.0	71.9

APPENDIX G

Wenatchee Sockeye and Summer Chinook Spawning Ground Surveys, 2010

PUBLIC UTILITY DISTRICT NUMBER 1 OF CHELAN COUNTY
Natural Resource Division
Fish and Wildlife Department
327 N. Wenatchee Ave., Wenatchee WA 98801 (509) 663-8121

January 21, 2011

To: HCP Hatchery Committee

From: Joe Miller

Subject: 2010 Wenatchee River Basin Summer Chinook and Sockeye Salmon Spawning Ground Surveys

Introduction

The Chelan County Public Utility District (District) has conducted or funded others to conduct intensive spawning ground surveys of spring and summer/fall (late run)[1] Chinook salmon (*Oncorhyncus tshawytscha*) and sockeye salmon (*O. nerka*) in river basins of the Columbia River upstream of Rock Island Dam. Summer/fall Chinook spawn in the entire mainstem of the Wenatchee River, from the mouth to the lake (Figure 1; Table 1). Sockeye spawn in the White and Little Wenatchee River basins (Figure 2).

The spawning surveys are performed yearly to assist in evaluating the effectiveness of the District's hatchery program. The purpose of this document is to report the results of the 2010 Chinook and sockeye salmon spawning ground surveys in the Wenatchee River basin. Information included in this document describes abundance, distribution, and timing of spawning activity.

[1] The majority of Chinook that ascend the mid-Columbia River as adults after July spawn between October and November in the mainstem of the Columbia, Wenatchee, Methow, Similkameen and Okanogan rivers. These fish have been called "summer" and "fall" Chinook based on their migration timing past the dams. Their life histories are identical (Mullan 1987), and should be termed "late-run" to separate them from earlier running "spring" Chinook that have a different life history. For consistency with previous year's reports, only the earlier segment of the late-run (those that ascend Rock Island Dam between June 24 and September 1; "summers") will be focused on in this report.

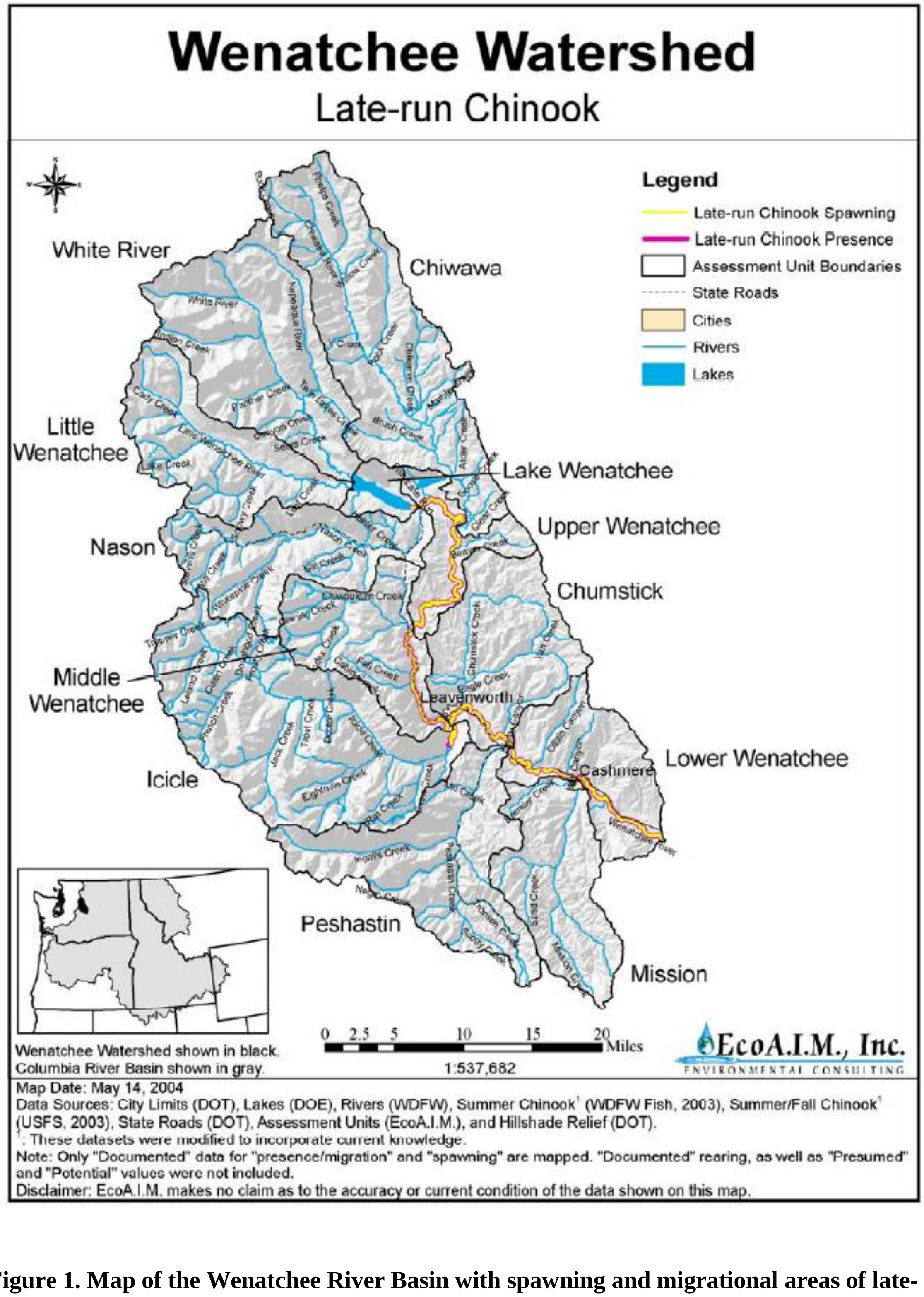


Figure 1. Map of the Wenatchee River Basin with spawning and migrational areas of late-run (summer/fall Chinook) areas highlighted (copied from the Wenatchee Sub basin Plan, NWPCC 2004).

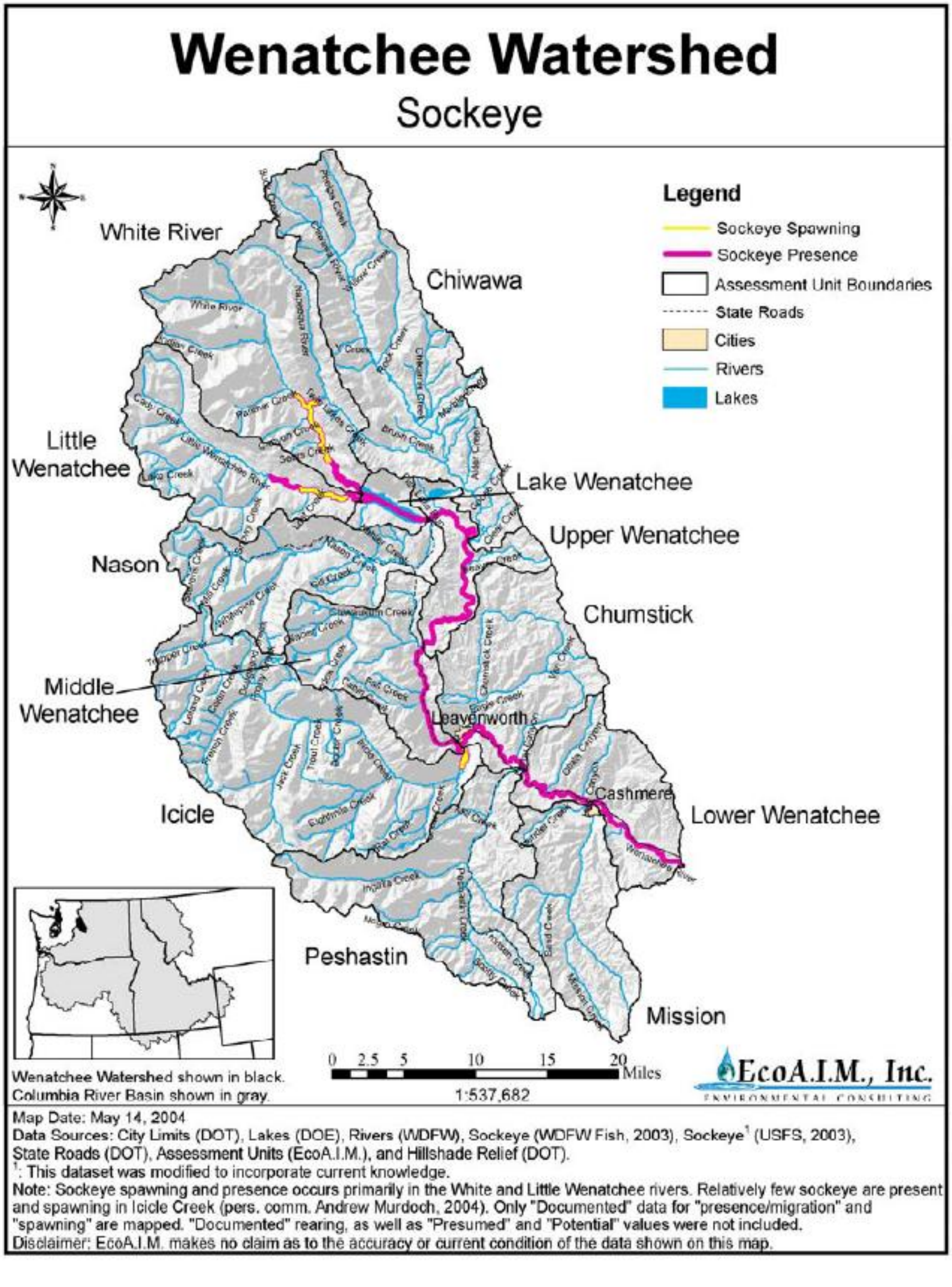


Figure 2. Map of the Wenatchee River Basin with spawning and migrational areas for sockeye highlighted (copied from the Wenatchee Sub basin Plan, NWPCC 2004).

Methods

In 2010, the study methodology was the same as used in 2009. In 2008, the summer Chinook spawning surveys were modified to incorporate additional mapping index areas in all ten river reach strata. Additionally, summer Chinook naïve counts were also performed in all river reach strata by the Washington State Department of Fish and Wildlife (WDFW) and the District. Previously, mapping index counts focused on six of the ten reaches and naïve counts were conducted solely by WDFW.

Chinook Spawning Ground Surveys

Chinook spawning ground surveys are conducted by foot, raft, or canoe. The most appropriate survey method is chosen for a given stream reach based on stream size, flow, and density of spawners. Because of the broad stream width and high spawner densities, individual summer Chinook redds are not flagged. Each reach is surveyed approximately once per week.

In 2010, summer Chinook spawning ground surveys occurred from September 20 to November 1.

Table 1: Designated survey reaches for spawning ground areas on the Wenatchee, Little Wenatchee, White, and Nepeequa rivers for all species.

Survey Section	River Mile
Wenatchee River-Summer Chinook	
Mouth to Sleepy Hollow Bridge	0 – 3.5
Sleepy Hollow Bridge to Lower Cashmere Bridge	3.5 – 9.5
Lower Cashmere Bridge to Dryden Dam	9.5 - 17.5
Dryden Dam to Peshastin Bridge	17.5 – 20.0
Peshastin Bridge to Leavenworth Bridge	20.0 – 23.9
Leavenworth Bridge to Icicle Road Bridge	23.9 – 26.4
Icicle Road Bridge to Tumwater Dam	26.4 – 30.9
Tumwater Dam to Tumwater Bridge	30.9 – 35.6
Tumwater Bridge to Chiwawa River	35.6 – 48.4
Chiwawa River to Lake Wenatchee	48.4 – 54.2
Little Wenatchee River-Sockeye	
Mouth to Old Fish Weir	0 – 2.7
Old Fish Weir to Lost Creek	2.7 – 5.2
Lost Creek to Rainey Creek	5.2 – 9.2
Rainey Creek to End	9.2 – End
White River-Sockeye	
Mouth to Sears Creek Bridge	0 – 6.4
Sears Creek Bridge to Napeequa River	6.4 – 11.0
Napeequa River to Grasshopper Meadows	11.0 – 12.9
Grasshopper Meadows to Falls	12.9 – 14.3
Napeequa River-Sockeye	
Mouth to End	0 - End

Peak and total redd count methodologies were used during the summer Chinook surveys in 2010 (see Appendix F of Murdoch and Peven (2005) for more detail). A peak count is conducted by counting all <u>visible</u> redds (new and old) observed within a reach on each survey. The objective of the peak redd count methodology is to capture the apex of spawning activity over an entire spawning season. This apex occurs at different times between reaches during the season, i.e. spawning begins sooner in the upstream reaches compared to the downstream reaches. The sum of all of the apex counts for the entire river is the peak redd count for the year. Peak counts provide an index of spawning and have been used historically (Attachment 1).

Two different approaches were used to estimate the total number of redds within the Wenatchee River. The first method used map counts to expand peak counts. Under this approach, a total redd count is conducted by counting or mapping only new or recently constructed redds within an area. Each new redd is mapped on aerial photos and enumerated. The objective of the total redd count methodology is to capture 1) "early" redds that may fade over time due to siltation or algae growth, and 2) redds that become disfigured by superimposition (when new redds are constructed on top of previously existing redds).

Since it is not feasible to map all new redds within the entire river, an expansion is used to estimate total count for the entire Wenatchee River. To account for the different spawning substrate types in the main stem Wenatchee River, the river was delineated into ten distinct reaches in consultation with WDFW (Table 2). Within each of these reaches, index areas have been identified as being representative areas of spawning activity. Peak counts are performed within each total reach (referred to as non-index areas), while mapping new redds only occurs within the index areas. An expansion is developed based on the ratio of mapped to peak counts for each reach (i.e., each reach has its own expansion factor), and the sum of the expanded counts is the estimate of the total redd counts. Additional details of how total redd counts are calculated are provided below.

a. Calculate an index peak expansion factor (*IP*) by dividing the peak number of redds in the index by the total number of redds (map count) in the index area.

$$IP = n_{peak} / n_{total}$$

b. Expand the non-index area peak redd counts by the *IP* to estimate the total number of redds in the entire reach (reach total; *RT*).

$$RT_{peak} = n_{peak} / IP$$

c. Estimate the total number of redds (total redds; *TR*) by summing the reach totals.

$$TR_{peak} = \sum RT$$

The second approach relied on a “naïve” count to expand redd numbers in reaches that did not have map counts. As noted above, the reaches with map counts are referred to as index reaches and those that were not mapped are called non-index reaches. Near the end of the spawning period (early November), one team of observers counts all visible redds within all non-index reaches. A separate, independent team counts all visible redds within the index reaches (these are the naïve counts). Surveys within the index and non-index areas should occur within one day of each other near the end of the spawning period. The naïve counts are divided by the total map count to estimate an index expansion factor. This factor is then applied to the total visible count in the non-index areas to estimate the total number of redds within each reach. The sum of the expanded counts is the estimate of the total redd count for the river. Additional details of how total numbers of redds are estimated using this approach are provided below.

a. Calculate an index expansion factor (*IF*) by dividing the number of visible redds in the index by the total number of redds (map counts) in the index area.

$$IF = {n_{visible}} / {n_{total}}$$

b. Expand the non-index area redd counts by the proportion of visible redds in the index to estimate the total number of redds in the entire reach (reach total; *RT*).

$$RT_{visible} = {n_{non-index}} / {IF}$$

c. Estimate the total number of redds (total redds; *TR*) by summing the reach totals.

$$TR_{visible} = \sum RT$$

The total redd count methods are believed to provide a more accurate indication of total spawning than the peak redd count methodology, because the peak count methodology only accounts for <u>visible</u> redds each week during the survey season. For example, summer Chinook redds that were visible during the first week of spawning may not be visible during the third week; those redds would be missed in the third and subsequent weeks’ redd counts. Using the total count methodology, the redds in the first week would be mapped and accounted for in subsequent weeks, even though they may fade at some point during the future surveys.

Table 2: Index (Mapping) Areas on the Wenatchee River for 2010.

Reach	Reach description	Distance (miles)	Mapping index area within reach
1	Sleepy Hollow Br to River Mouth	3.5	Sleepy Hollow Br to River Bend
2	Cashmere Br to Sleepy Hollow Br	6	Cashmere Br 2 to Old Monitor Br.
3	Dryden Dam to Cashmere Br	8	Dryden Dam to Williams Canyon
4	Peshastin Br to Dryden Dam	2.5	Peshastin Br to Dryden Dam
5	Leavenworth Br to Peshastin Br	3.9	Leavenworth Br to Irrigation Flume
6	Icicle Rd Br to Leavenworth Br	2.5	Icicle Mouth to Boat Takeout
7	Tumwater Dam to Icicle Rd Br	4.5	Penstock Br to Icicle Rd Br
8	Tumwater Br to Tumwater Dam	4.7	Tumwater Br to Swiftwater Campground
9	Old Plain Br to Tumwater Br	12.8	RR Tunnel to Swing Pool
10	Lake Wenatchee to Old Plain Br	5.8	Bridge to Swamp

Sockeye Spawning Abundance

In 2010, sockeye abundance was enumerated using two methods: (1) on-the-ground surveys utilizing an "area-under-the-curve" (AUC) approach, and (2) a PIT tag based mark recapture study.

AUC Method:

Sockeye spawning ground surveys began August 24 and ended October 19. Spawning areas in the Little Wenatchee, Napeequa, and White rivers (Table 1) were surveyed at least once per week. Both the Little Wenatchee and White rivers have blocking falls, and spawning is known to occur only within the first few miles of the Napeequa River, a tributary to the White River.

The AUC method is based on the number of live spawners counted. Using AUC, the number of fish observed in a survey is plotted against the day of the year and the number of fish-days is estimated using an algorithm. The number of fish spawning is then estimated by dividing the cumulative fish-days by the estimated mean number of days that the average spawner is alive in the survey area (survey- or stream-life). This is then multiplied by a correction factor for fish visibility (observer efficiency; Hillborn et al. 1999).

Hillborn et al. (1999) outlined what they termed as the most commonly used form of AUC, *trapezoidal approximation*:

$$AUC = \sum_{i=2}^{n} (t_i - t_{i-1}) \frac{(x_i + x_{i-1})}{2}$$

where t_i is the day of the year and x_i is the number of salmon observed for the *i*th survey. Attempts are often made to initiate surveys prior to the presence of fish; however, when the first or last survey is not zero, then the above algorithm is not valid and Hillborn et al. (1999) recommend using the “rules” that the Alaska Department of Fish and Game use:

$$AUC_{first} = \frac{x_i s}{2}$$

where s is the survey life. Attempts should also be made until all salmon die, but when this is not possible, then the final survey should be calculated:

$$AUC_{last} = \frac{x_{last} s}{2}$$

Then total escapement (E) is estimated:

$$\hat{E} = \frac{AUC}{s} v$$

where v is a correction for observer efficiency. Since survey life has not been empirically estimated for the Wenatchee system, we used 11 days based on Perrin and Irvine (1990) and Hyatt et al. (2006).

Mark Recapture Method:
Adult sockeye salmon were removed from the adult fishway at Tumwater Dam on the Wenatchee River, northwest of Leavenworth, Washington during the 2009 and 2010 migration. Fish were anesthetized, tagged with a PIT, and released into the forebay consistent with techniques used by the Washington Department of Fish and Wildlife. Resulting tag files were queried in PITAGIS (2010), providing detection histories for each study fish. Adult sockeye salmon were tagged at Bonneville Dam by another organization in 2009 and 2010; fish from this tag group that were detected at Tumwater Dam were also used in the analyses. Total passage of adult sockeye salmon through Tumwater Dam were obtained from Columbia River Data Access in Real Time (DART 2010).

Detection efficiency of in-stream arrays was calculated for the Little Wenatchee River in both 2009 and 2010; efficiency was calculated for the White River arrays after the 2010 migration since only a single array was available during 2009. The in-stream arrays include a series of upstream and downstream coils (i.e., Figure). Combined, these coils represented the upstream and downstream detection arrays, respectively. Overall detection efficiency P_{all} of the arrays was calculated based on observed detection probabilities of individual arrays:

$$P_{all} = 1 - (1 - P_{array\ 1})(1 - P_{array\ 2})$$

where the probability of missing a fish on both the upstream $P_{array\ 1}$ and downstream P_{array2} arrays are combined for an overall efficiency P_{all} (Connolly et al. 2008).

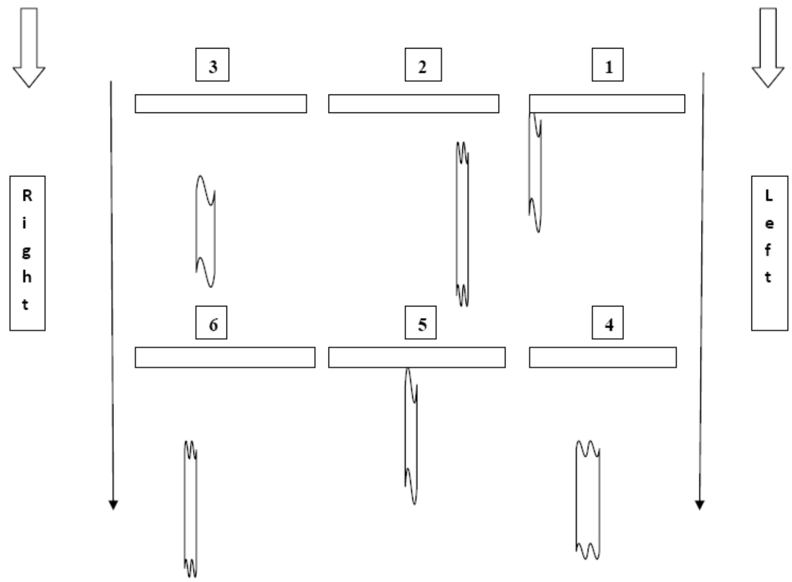


Figure 3. PIT array configuration on the Little Wenatchee River, 2009.

Resulting data from passage at Tumwater Dam, mark and recapture using PITs, and detection efficiency estimates can provide estimation of escapement to spawning tributaries. Basic assumptions include: (1) the study population is “closed,” i.e., no individuals die or emigrate between the initial mark and subsequent recaptures; (2) tags are not lost and detections are correctly identified; (3) all individuals have the same probability of being detected, and (4) the number of recapture events are proportional to the total population. Lastly, it is assumed that PIT-tagging efforts at Tumwater have negligible influence on fish behavior and tagged individuals behave similarly to untagged individuals. The resulting escapement rate, adjusted for detection efficiency, can then be applied to the total population as such:

$$Escapement = \left(\frac{\left(\frac{Obs_{LWN}}{Eff_{LWN}} + \frac{Obs_{WTL}}{Eff_{WTL}} \right)}{PITs_{TUM}} \right) \times Counts_{TUM}$$

where the PIT detections (*Obs*) at the Little Wenatchee (*LWN*) and lower White River (*WTL*) are adjusted for detection efficiency (*Eff*) at both sites, compared to the number released (*PITs*) at Tumwater Dam (*TUM*), and the resulting proportion is applied to the population observed (*Counts*) passing Tumwater Dam.

Results

Summer Chinook

Peak Counts

The cumulative peak summer Chinook redd count was 2,553 in 2010, based on District ground surveys along the Wenatchee River (Table 3). Spawning activity began the last week of September and peaked during middle of October.

Table 3. Summary of summer Chinook redd peak counts, total redd estimates (TR) and spawner densities by reach in the Wenatchee River, 2010. Expansion factors were rounded to two decimal places (0.00) prior to calculating reach totals.

Reach	Peak Count	CCPUD Estimates		WDFW Estimates	
		RT_{Peak}	$Density_{Peak}$ (redds/mile)	$RT_{Visible}$	$Density_{Visible}$ (redds/mile)
1	12	18	5	18	5
2	129	183	30	111	18
3	184	230	29	463	58
4	58	77	31	153	61
5	76	111	28	87	22
6	1047	1426	570	1394	558
7	249	268	60	221	49
8	86	101	21	100	21
9	341	431	34	562	44
10	371	397	68	610	105
Total	***2,553***	***3,242***	***60***	***3,719***	***69***

Total Counts

The total number of redds in the Wenatchee River was 3,242 (RT_{peak}), using data from District surveys and the peak expansion factor. WDFW estimated 3,719 redds ($RT_{visible}$) based on their naïve surveys (Table 3). All survey methods (peak and visible) indicated that redd densities were highest in Reach 6 and lowest in Reach 1 (Table 3; Figure 4), consistent with the previous three years. The historical summer Chinook peak counts (1996-2010) for the Wenatchee River basin are summarized in Attachment 1.

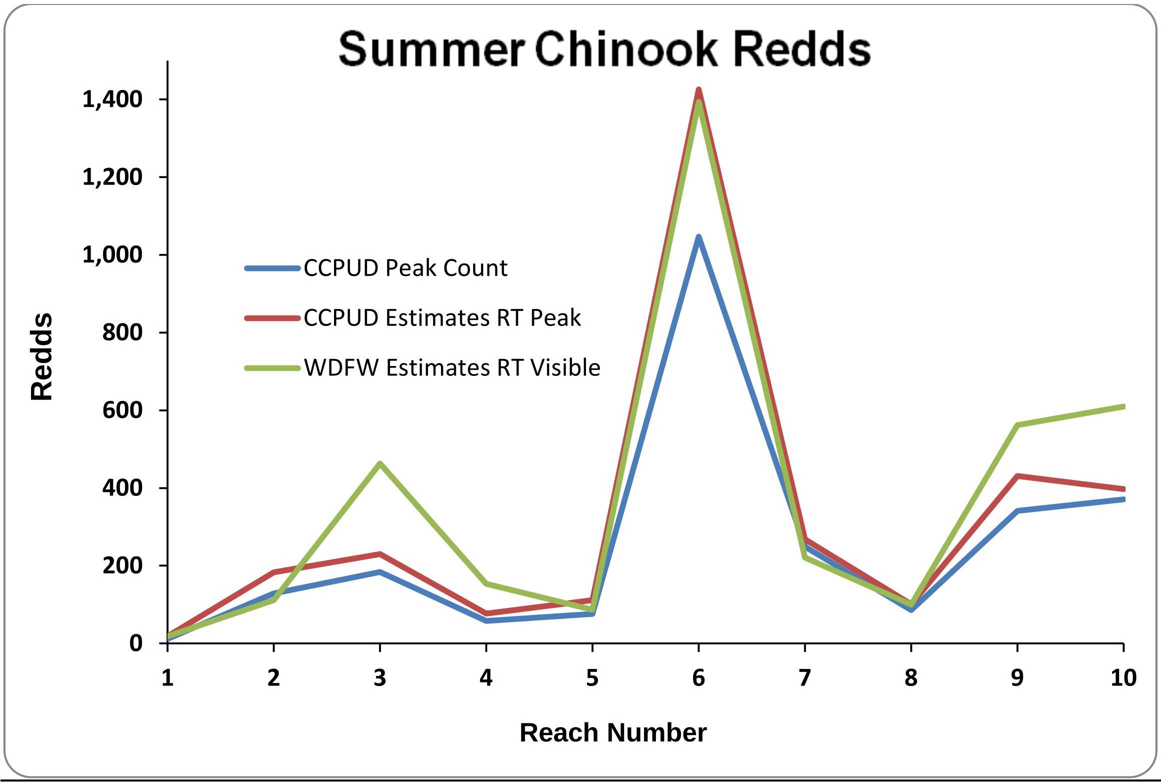


Figure 4. Alternative estimates of reach totals (RT) for summer Chinook redds in the Wenatchee River in 2010 [RT_{peak}=District peak counts expanded by peak expansion method and $RT_{visible}$ (WDFW)=WDFW naïve counts expanded by naïve expansion factor].

Sockeye AUC Method

Live fish counts
Fish counts were conducted for sockeye from August 24 through October 19. Peak spawning occurred in the Little Wenatchee (1,762); Napeequa River (321); and White River (11,059) during the middle of September (Figure 5; Table 4).

Escapement
The total estimated spawning escapement of sockeye to the Wenatchee tributaries was 21,700 in 2010 (Table 4). The escapement estimate is based solely on tributary observations and does not include fish harvested in the Lake Wenatchee sockeye fishery.

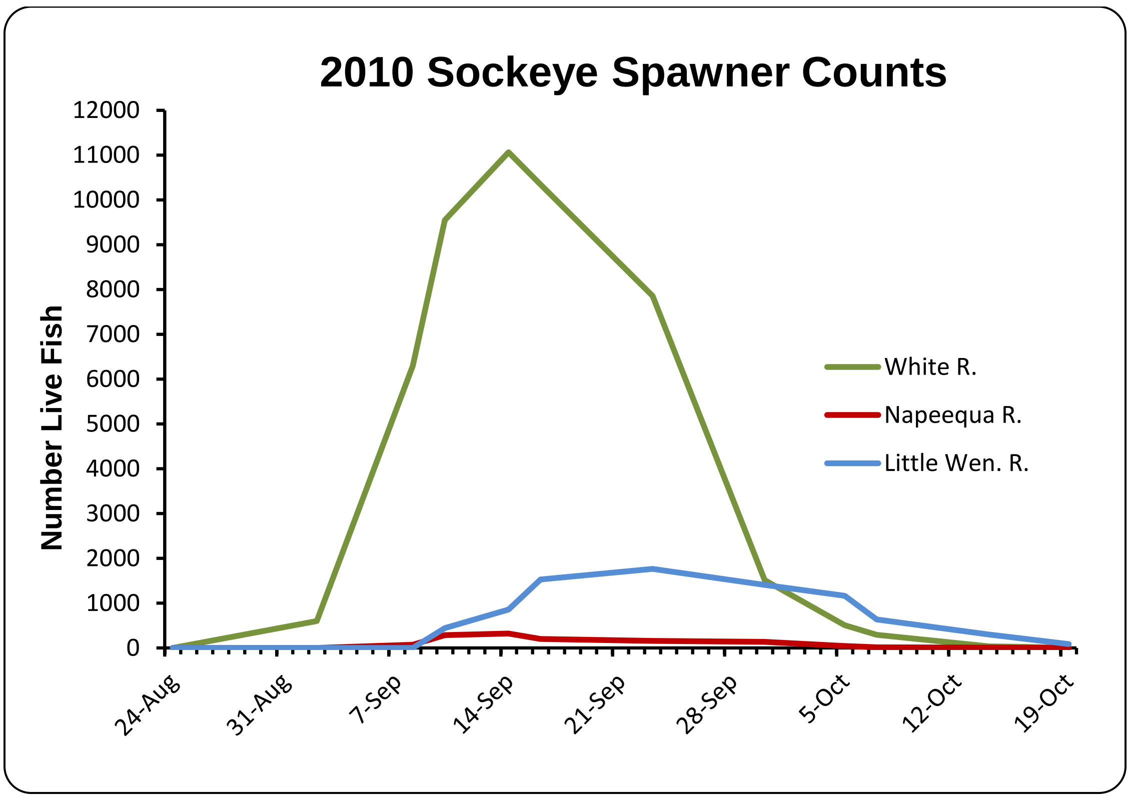


Figure 5. Approximate live counts and survey dates for sockeye salmon in the Wenatchee River Basin, 2010.

Table 4. Number of live fish and total spawning escapement estimates for sockeye salmon in the Wenatchee Basin, August through October, 2010.

River	Peak number of live fish	Escapement
Little Wenatchee	**1,762**	**2,543**
Napeequa	**321**	**470**
White	**11,059**	**18,687**
Total	***13,142***	***21,700***

Sockeye Mark Recapture Method

Fishway enumeration at Tumwater Dam indicated that 16,034 and 35,821 adult sockeye salmon passed the facility during the 2009 and 2010 migrations, respectively. The recreational harvest removed an estimated 2,229 and 4,129 fish during the two years, respectively, although anglers were requested to released marked fish. PIT tags were implanted in 1,085 and 1,164 (Table 5) of these fish prior to subsequent detections in nearby tributaries. Based on the recapture of PIT-tagged adult sockeye and assigned detection efficiencies, total estimated escapement from Tumwater Dam to the White and Little Wenatchee rivers was 14,452 in 2009, including 13,876 fish in the White River and 576 fish in the Little Wenatchee River (Table 6). Estimated escapement in 2010 totaled 21,604, including 19,542 fish in the White River and 2,062 fish in the Little Wenatchee River (Table 6). Combined escapement rates represented 0.901 of the population in 2009, and 0.603 in 2010 (Table 6).

Table 5. Number of adult sockeye salmon PIT-tagged, released, and detected upstream of Tumwater Dam in 2009 and 2010, including escapement estimates of PIT-tagged fish based on array detection probabilities.

Release Location	Number Released	White River [3]		L. Wenatchee River [4]		Chiwawa R.	Nason Creek
		Observed	*Estimated*	Observed	*Estimated*	Observed	Observed
Tumwater (2009) [1]	998	347	*855*	34	*35*	35	7
Bonneville (2009) [2]	87	34	*84*	4	*4*	2	0
Tumwater (2010) [1]	1,054	530	*589*	61	*61*	3	1
Bonneville (2010) [2]	110	41	*46*	6	*6*	0	0
Combined (2009)	1,085	381	*939*	38	*39*	37	7
Combined (2010)	1,164	571	*635*	67	*67*	3	1

[1] Also includes fish detected downstream of release point (fallbacks).
[2] Number of fish released at Bonneville and subsequently detected at Tumwater Dam.
[3] Based on a detection efficiency p_{all} = 0.406 in 2009 (assigned from 2010 data) and p_{all} = 0.900 in 2010.
[4] Based on a detection efficiency p_{all} = 0.971 in 2009 and p_{all} = 1.000 in 2010.

Table 6. Estimated escapement of adult sockeye salmon to Little Wenatchee and White rivers based on mark-recapture events, in-stream detection efficiency, and adult enumeration at Tumwater Dam, 2009-2010.

Year	Tumwater count	Recreational harvest	Little Wenatchee	White River	Combined	Escapement
2009	16,034	2,229	576	13,876	14,452	0.901
2010	35,821	4,129	2,062	19,542	21,604	0.603
Total	*51,855*	*6,358*	*2,638*	*33,418*	*36,056*	*0.695*

References

Hillborn, R. B.G. Bue, and S. Sharr. 1999. Estimating spawning escapements from periodic counts: a comparison of methods. Can. J. Fish. Aquat. Sci. 56: 888-896.

Hyatt, K.D., M.M. Stockwell, H. Wright, K. Long, J. Tamblyn, and M. Walsh. 2006. Fish and Water Management Tool Project Assessments: Okanogan Adult Sockeye Salmon (*Oncorhynchus nerka*) Abundance and Biological Traits in 2005. DRAFT Report to file: JSID-SRe 3-05. Salmon and Freshwater Ecolsystems Division, Fisheries and Oceans Canada, Nanaimo, B.C. V9T 6N7.

Mullan, J. W. 1987. Status and propagation of Chinook salmon in the mid-Columbia River through 1985. U.S. Fish and Wildlife Serv. Biol. Rep. 87(3) 111 pp.

Murdoch, A. and C. Peven. 2005. Conceptual Approach to Monitoring and Evaluating the Chelan County Public Utility District Hatchery Programs. *Prepared for:* Chelan PUD Habitat Conservation Plan’s Hatchery Committee. Chelan PUD, Wenatchee, WA

Perrin, C.J. and J.R. Irvine. 1990. A review of survey life estimates as they apply to the area-under-the-curve method for estimating the spawning escapement of Pacific salmon. Canadian Tech. Rep. of Fisheries and Aquatic Sciences No. 1733. Department of Fisheries and Oceans, Nanaimo, B.C. V9R 5K6.

Peven, C. M. 1990. The life history of naturally produced steelhead trout from the Mid-Columbia River Basin. MS Thesis, University of Washington, Seattle.

Attachment 1.

Historic peak redd counts in the Wenatchee River for summer/fall Chinook salmon. Prior to 1995, all counts based on highest count of multiple agencies surveys, which were usually aerial counts from fixed-wing aircraft. Since 1995, counts are ground counts based on Chelan PUD surveys.

Year	Highest Count	Year	Highest Count	Year	Highest Count
1960	502	1970	1333	1980	2024
1961	872	1971	1419	1981	1469
1962	1035	1972	1364	1982	1140
1963	1223	1973	1119	1983	723
1964	1300	1974	1155	1984	1332
1965	706	1975	925	1985	1058
1966	1260	1976	1106	1986	1322
1967	1593	1977	1365	1987	2955
1968	1776	1978	1956	1988	2102
1969	1354	1979	1698	1989	3331
1990	2479	2000	2022	2010	2553
1991	2180	2001	2857		
1992	2328	2002	5419		
1993	2334	2003	4281		
1994	2426	2004	3764		
1995	1872	2005	3327		
1996	1435	2006	7165		
1997	1388	2007	1857		
1998	1660	2008	2338		
1999	2188	2009	2667		

APPENDIX H

Genetic Diversity of Wenatchee Sockeye Salmon.

Assessing the Genetic Diversity of Lake Wenatchee Sockeye Salmon And Evaluating The Effectiveness Of Its Supportive Hatchery Supplementation Program

Developed for

Chelan County PUD

and the

Habitat Conservation Plan's Hatchery Committee

Developed by
Scott M. Blankenship, Cheryl A. Dean, Jennifer Von Bargen
WDFW Molecular Genetics Laboratory
Olympia, WA

and

Andrew Murdoch
Supplementation Research Team
Wenatchee, WA

March 2008

Executive Summary

Nine spawning populations of sockeye (*Oncorhynchus nerka*) salmon have been identified in Washington, including stocks in the Lake Wenatchee basin (SaSI 5800) (Washington Department of Fisheries et al. 1993). Lake Wenatchee sockeye are classified as an Evolutionary Significant Unit (ESU), and consists of sockeye salmon that spawn primarily in tributaries above Lake Wenatchee (the White River, Napeequa River, and Little Wenatchee Rivers). Since 1990, the Wenatchee Sockeye Program has released juveniles into Lake Wenatchee to supplement natural production of sockeye salmon in the basin. The program's broodstock are predominantly natural-origin sockeye adults returning to the Wenatchee River captured at Tumwater Dam (Rkm 52.0), where a net-pen system is used to house both maturing adults and juveniles prior to release into Lake Wenatchee to over-winter.

Previous genetic studies have generally found a lack of concordance between population genetic relationships and their geographic distributions. These studies indicate that the nearest geographic neighbors of sockeye salmon populations are not necessarily the most genetically similar. Specifically for the Columbia River Basin, sockeye from Lake Wenatchee, Okanogan River, and Redfish Lake may be more closely related to a population from outside the Columbia River (depending on marker used) then to each other.

In this study we investigated the temporal and spatial genetic structure of Lake Wenatchee sockeye collections, without regard to sockeye populations outside of the Lake Wenatchee area. Our primary objective here was to determine if the Wenatchee Sockeye Program affected the natural Lake Wenatchee sockeye population. More specifically, we were tasked to determine if the genetic composition of Lake Wenatchee sockeye population had been altered by a supplementation program that was based on the artificial propagation of a small subset of that population. Using microsatellite DNA allele frequencies, we investigated population differentiation between temporally replicated collections of natural-origin Lake Wenatchee sockeye and program broodstock. We analyzed thirteen collections of Lake Wenatchee sockeye (Table 1), eight temporally replicated collections of natural-origin Lake Wenatchee sockeye (N=786) and five temporally replicated collections of Wenatchee Sockeye Program broodstock (N=248). Paired natural – broodstock collections were available from years 2000, 2001, 2004, 2006, and 2007.

Conclusions

We observed that allele frequency distributions were consistent over time, irrespective of collection origin, resulting in small and statistically insignificant measures of genetic differentiation among collections. We interpreted these results to indicate no year-to-year differences in allele frequencies among natural-origin or broodstock collections. Furthermore, there were no observed difference between pre- and post-supplementation collections. Therefore, we accepted our null hypothesis that the allele frequencies of the broodstock collections equaled the allele frequencies of the natural collections, which

equaled the allele frequency of the donor population. Given the small differences in genetic composition among collections, the genetic model for estimating N_e produced estimates with extremely large variances, preventing the observation of any trend in N_e.

Introduction

A report titled "Conceptual Approach to Monitoring and Evaluating the Chelan County Public Utility District Hatchery Programs" was prepared July 2005 by Andrew Murdoch and Chuck Peven for the Chelan PUD Habitat Conservation Plan's Hatchery Committee. This report outlined 10 objectives to be applied to various species assessing the impact (positive or negative) of hatchery operations mitigating the operation of Rock Island Dam. This current study pertains only to Lake Wenatchee sockeye and objective 3:

> *Determine if genetic diversity, population structure, and effective population size have changed in natural spawning populations as a result of the hatchery program. Additionally, determine if hatchery programs have caused changes in phenotypic characteristics of natural populations.*

In order to evaluate cause and effect of hatchery supplementation, WDFW Molecular Genetics Lab surveyed genetic variation of Lake Wenatchee sockeye. The conceptual approach for this project follows that of a parallel study regarding the Wenatchee River spring Chinook supplementation program (Blankenship et al. 2007). We determined the genetic diversity present in the Lake Wenatchee sockeye population by analyzing temporally replicated collections spanning 1989 – 2007, which included collections from before and following the inception of the Wenatchee Sockeye Program. Documenting the genetic composition of the Lake Wenatchee sockeye population is necessary to assess the effect of the hatchery program on the Lake Wenatchee population. In addition, this work provides a genetic baseline for future projects requiring genetic data. See study objectives below for specific details about how this project addresses Murdoch and Peven (2005) objective 3.

Lake Wenatchee Sockeye Salmon

Nine spawning populations of sockeye (*Oncorhynchus nerka*) salmon have been identified in Washington (Washington Department of Fisheries et al. 1993): 1) Baker

River, 2) Ozette Lake, 3) Lake Pleasant, 4) Quinault Lake, and 5) Okanogan River (classified as native stock); 6) Cedar River (classified as non-native stock); 7) Lake Wenatchee, classified as mixed stock); 8) Lake Washington/Lake Sammamish tributaries; and 9) Lake Washington beach spawners (classified as unknown origin). Chapman et al. (1995) listed four additional spawning aggregations of sockeye salmon that appear consistently in Columbia River tributaries: the Methow, Entiat, and Similkameen Rivers; and Icicle Creek in the Wenatchee River drainage.

Located in north central Washington, the Wenatchee River basin drains a portion of the eastern slope of the Cascade Mountains, including high mountainous regions of the Cascade crest. The headwater area of the Wenatchee River is Lake Wenatchee, a typical low productivity oligotrophic or ultra-oligotrophic sockeye salmon nursery lake (Allen and Meekin 1980, Mullan 1986, Chapman et al. 1995). Sockeye salmon bound for Lake Wenatchee enter the Columbia River in April and May and arrive at Lake Wenatchee in late July to early August (Chapman et al. 1995; Washington Department of Fisheries et al. 1993). The run timing of Lake Wenatchee sockeye salmon, classified as an Evolutionary Significant Unit (ESU), appears to have become earlier by 6 - 30 days during the past 70 years (Chapman et al. 1995; Quinn and Adams 1996). Additionally, scale pattern analysis suggests Wenatchee sockeye migrate past Bonneville Dam earlier than the sockeye bound for the Okanogan River (Fryer and Schwartzberg 1994). The Wenatchee population spawns from mid-September through October in the Little Wenatchee, White, and Napeequa Rivers above Lake Wenatchee (Washington Department of Fisheries et al. 1993), peaking in late September (Chapman et al. 1995). Limited beach spawning is believed to occur in Lake Wenatchee (L. Lavoy pers. com.; Mullan 1986), although Gangmark and Fulton (1952) reported two lakeshore seepage areas in Lake Wenatchee that were used by spawning sockeye salmon. Sockeye salmon fry enter Lake Wenatchee between March and May (Dawson et al. 1973), and typically rear in the lake for one year before leaving as smolts (Gustafson et al. 1997; Peven 1987).

Both the physical properties of the habitat and ecological/biological factors of the sockeye populations differ between the Lake Wenatchee ESU and the geographically proximate Okanogan ESU. For example: 1) Different limnology is encountered by sockeye salmon in Lakes Wenatchee and Osoyoos; 2) Lake Wenatchee sockeye predominantly return at ages four and five (a near absence of 3-year-olds), where a large percentage of 3-year-olds return to the Okanogan population; and 3) the apparent one month separation in juvenile outmigration-timing between Okanogan- and Wenatchee-origin fish (Gustafson et al. 1997 and references therein).

Sockeye Artificial Propagation In Lake Wenatchee

The construction of Grand Coulee Dam completely blocked fish passage to the upper Columbia River, and 85% of sockeye salmon passing Rock Island Dam between 1935 and 1936 were estimated to be from natural stocks bound for areas up-river to Grand Coulee Dam (Mullan 1986; Washington Department of Fisheries et al. 1938). To compensate for loss of habitat resulting from Grand Coulee Dam, the federal government initiated the Grand Coulee Fish-Maintenance Project (GCFMP) in 1939 to maintain fish runs in the Columbia River above Rock Island Dam. Between 1939 and 1943, all sockeye salmon entering the mid-Columbia River were trapped at Rock Island Dam, and over 32,000 mixed Lake Wenatchee, Okanogan River, and Arrow Lake adult sockeye salmon were released into Lake Wenatchee (Gustafson et al. 1997 Appendix Table D-2). In addition to adult relocation, between 1941 and 1969 over 52.8 million fry descended from original spawners collected at Rock Island and Bonneville Dams, were released into Lake Wenatchee (Gustafson et al. 1997 Appendix Table D-2).

No releases of artificially-reared sockeye salmon occurred in the Wenatchee watershed during the years 1970 to 1989 (Gustafson et al. 1997 Appendix Table D-2). Since 1990, the Wenatchee Sockeye Program has released juveniles into Lake Wenatchee to supplement natural production of sockeye salmon in the basin. Sockeye adults returning to the Wenatchee River are captured at Tumwater Dam (Rkm 52.0) and transferred to Lake Wenatchee net pens until mature. The Wenatchee Sockeye Program goals are 260 adults with an equal sex ratio, <10% hatchery-origin returns (identified by coded wire tags), and the adults removed for broodstock account for <10% of the run size. Fish are spawned at Lake Wenatchee and their gametes are taken to Rock Island Fish Hatchery

Complex (i.e., Eastbank) for fertilization and incubation. Fry are returned to the Lake Wenatchee net -pens after they are large enough to be coded wire tagged, and are housed in the pens until fall (one year after spawning), when they are liberated into the lake to over-winter. For brood years 1991 – 2004 an average of 218,683 (std. dev. = 71,090) pen-reared Lake Wenatchee-origin juvenile sockeye salmon have been released yearly into Lake Wenatchee.

Previous Genetic Studies

Protein (allozyme) variation – Surveying genetic variation at 12 allozyme loci, Utter et al. (1984) reported moderate population structure among 16 sockeye collections from southeast Alaska through the Columbia River Basin, including Okanogan and Wenatchee stocks, with an apparent genetic association between upper Fraser River and Columbia River sockeye salmon. Winans et al. (1996) surveyed variation at 55 allozyme loci for 25 sockeye salmon and two kokanee collections from 21 sites in Washington, Idaho, and British Columbia, and reported the lowest level of allozyme variability of any species of Pacific salmon and a highest level of inter-population differentiation. Furthermore, these authors reported that there was no clear relationship between geographic and genetic differentiation among the populations within there study. Other studies corroborate the results of Winans et al. (1996), finding a lack of discernible geographic patterning for sockeye salmon populations in British Columbia, Alaska, and Kamchatka (Varnavskaya et al. 1994, Wood et al. 1994, Wood 1995). These studies indicate that the nearest geographic neighbors of sockeye salmon populations are not necessarily the most genetically similar, which contrasts with the other Pacific salmon species that exhibit concordance between geographic and genetic differentiation (Utter et al. 1989, Winans et al. 1994, Shaklee et al. 1991). As part of the comprehensive status review of west coast sockeye salmon (Gustafson et al. 1997), NMFS biologists collected new allozyme genetic information for 17 sockeye salmon populations and one kokanee population in Washington and combined these data for analysis with the existing Pacific Northwest sockeye salmon and kokanee data from Winans et al. (1996). Results of the updated study were consistent with Winans et al. (1996), with no clear concordance between geographic and genetic distances. Sockeye salmon from Lake Wenatchee, Redfish Lake, Ozette Lake, and Lake Pleasant are very distinct from other collections in the study, and Columbia River populations were not necessarily most closely related to each other. Gustafson et al. (1997) also examined between-year variability within a collection location and found low levels of statistical significance among the five Lake Wenatchee collections included in the study (For 10 pair-wise comparisons using sum-G test, five were statistically significant). Lake Wenatchee brood year 1987 accounted for three of the significant comparisons, which were driven by unusually high frequencies of two allozyme alleles (ALAT*95 and ALAT*108) (Winans et al. 1996). Nevertheless, Gustafson et al. (1997) conclude that, in general, temporal variation at a locale was considerably less than between-locale variation.

Nucleic acid variation - Beacham et al. (1995) reported levels of variation in nuclear DNA of *O. nerka* using minisatellite probes. They analyzed 10 collections, including a sample from Lake Wenatchee. Cluster analysis showed the Lake Wenatchee sample was different from all the other collections, including those from the Columbia River. Using a similar molecular technique, Thorgaard et al. (1995) examined the use of multi-locus DNA fingerprinting (i.e., banding patterns) to discriminate among 14 sockeye salmon and kokanee populations. Dendrograms based on analysis of banding patterns produced different genetic affinity groups depending on the probes used. While none of the five DNA probes showed a close relationship between Lake Wenatchee and Okanogan River sockeye salmon, if information from all probes were combined, *O. nerka* from Redfish Lake, Wenatchee, and Okanogan were separate from kokanee of Oregon and Idaho and a sockeye salmon sample from the mid-Fraser River.

Study Objective

We documented temporal variation in genetic diversity (i.e., heterozygosity and allelic diversity), and investigated population differentiation between temporally replicated collections of natural-origin Lake Wenatchee sockeye and program broodstock, using microsatellite DNA allele frequencies. Temporally replicated collections from the same location can also be used to estimate effective population size (N_e). If populations are "ideal", the census size of a population is equal to the "genetic size" of the population.

Yet, numerous factors lower the "genetic size" below census, such as, non-equal sex ratios, changes in population size, and variance in the numbers of offspring produced from parent pairs. N_e is thought to be between 0.10 and 0.33 of the estimated census size (Bartley et al. 1992; RS Waples pers. comm.), although numerous observations differ from this general rule. N_e can be calculated directly from demographic data, or inferred from observed differences in genetic variance over time. Essentially, when calculated from genetic data, N_e is the estimated size of an "ideal" population that accounts for the genetic diversity changes observed, irrespective of abundance.

We will address the hypotheses associated with Objective 3 in Murdock and Peven (2005) using the following four specific tasks:

Task 1 - Document the observed genetic diversity.

Task 2 - Test for population differentiation among Lake Wenatchee collections and the associated supplementation program.

Task 2 was designed to address two hypotheses listed as part of Objective 3 in Murdoch and Peven (2005):

- Ho: Allele frequency $_{\text{Hatchery}}$ = Allele frequency $_{\text{Naturally produced}}$ = Allele frequency $_{\text{Donor pop}}$.
- Ho: Genetic distance between subpopulations $_{\text{Year x}}$ = Genetic distance between subpopulations $_{\text{Year y}}$

Murdoch and Peven (2005) proposed these two hypotheses to help evaluate supplementation programs through a "Conceptual Process" (Figure 5 in Murdoch and Peven 2005). There are two components to the first hypothesis, which must be considered separately for Lake Wenatchee sockeye. The first component involves comparisons between natural-origin populations from Lake Wenatchee to determine if there have been changes in allele frequencies through time starting with the donor population. Documenting a change does not necessarily indicate that the supplementation program has directly affected the natural-origin fish, as additional tests would be necessary to support that hypothesis. The intent of the second component is to determine if the hatchery produced populations have the same genetic composition as the naturally produced populations.

Task 3 - Calculate N_e using the temporal method for multiple samples from the same location to document trend.

Task 4 - Compare N_e estimates with trend in census size for Lake Wenatchee sockeye.

Methods and Materials

Sampling

Thirteen collections of Lake Wenatchee sockeye were analyzed, eight temporally replicated collections of natural Lake Wenatchee sockeye (N=786) and five temporally replicated collections of Wenatchee Sockeye Program broodstock (N=248) (Table 1). Paired natural – broodstock collections were available from years 2000, 2001, 2004, 2006, and 2007 (Table 1). All collections were made at Tumwater Dam on the Wenatchee River. Note that collections classified as broodstock were predominantly natural-origin sockeye. A majority of the genetic samples were from dried scales. The tissue collections from 2006 and 2007 were fin clips stored immediately in ethanol after collection. DNA was extracted from stored tissue using Nucleospin 96 Tissue following the manufacturer's standard protocol (Macherey-Nagel, Easton, PA, U.S.A.).

Laboratory Analysis

Polymerase chain reaction (PCR) amplification was performed using 17 fluorescently end-labeled microsatellite marker loci, *One* 2 (Scribner et al 1996) *One* 100, 101, 102, 105, 108, 110, 114, and 115 (Olsen et al. 2000), *Omm* 1130, 1135, 1139, 1142, 1070, and 1085 (Rexroad et al. 2001), *Ots* 3M (Banks et al. 1999) and *Ots* 103 (Small et al. 1998). PCR reaction volumes were 10 μL, with the reaction variables being 2 μL 5x PCR buffer (Promega), 0.6 μL $MgCl_2$ (1.5 mM) (Promega), 0.2 μL 10 mM dNTP mix (Promega), and 0.1 μL *Go Taq* DNA polymerase (Promega). Loci were amplified as part of multiplexed sets, so primer molarities and annealing temperatures varied. Multiplex one had an annealing temperature of 55°C, and used 0.09 Molar (M) *One* 108, 0.06 M *One* 110, and 0.11 M *One* 100. Multiplex two had an annealing temperature of 53°C, and used 0.08 M *One* 102, 0.1 M *One* 114, and 0.05 M *One* 115. Multiplex three had an annealing temperature of 55°C, and used 0.08 M *One* 105 and 0.07 M *Ots* 103. Multiplex four had an annealing temperature of 53°C, and used 0.09 M *Omm* 1135 and 0.08 M *Omm* 1139. Multiplex five had an annealing temperature of 60°C, and used 0.2 M *Omm* 1085, 0.09 M *Omm* 1070, and 0.05 M *Ots* 3M. Multiplex six had an annealing temperature of 48°C, and used 0.06 M *One* 2, 0.08 M *Omm* 1142, and 0.08 M *Omm* 1130. *One* 101 was run in isolation with a primer molarity of 0.06. Thermal cycling was conducted on either PTC200 (MJ Research) or GeneAmp 9700 thermal cyclers as follows: 94°C (2 min); 30 cycles of 94°C for 15 sec., 30 sec. annealing, and 72°C for 1 min.; a final 72°C extension and then a 10°C hold. PCR products were visualized by denaturing polyacrylamide gel electrophoresis on an ABI 3730 automated capillary analyzer (Applied Biosystems). Fragment analysis was completed using GeneMapper 3.7 (Applied Biosystems).

Genetic data analysis

Assessing within collection genetic diversity - Heterozygosity measurements were reported using Nei's (1987) unbiased gene diversity formula (i.e., expected heterozygosity) and Hedrick's (1983) formula for observed heterozygosity. Both tests were implemented using the microsatellite toolkit (Park 2001). For each locus and collection FSTAT version 2.9.3.2 (Goudet 1995) was used to assess Hardy-Weinberg equilibrium, where deviations from the neutral expectation of random associations among alleles were calculated using a randomization procedure. Alleles were randomized among individuals within collections (4160 randomizations for this dataset) and the F_{IS} (Weir and Cockerham 1984) calculated for the randomized datasets were compared to the observed F_{IS} to obtain an unbiased estimation of the probability that the null hypothesis was true. The 5% nominal level of statistical significance was adjusted for multiple tests (Rice 1989). Genotypic linkage disequilibrium was calculated following Weir (1979) using GENETIX version 4.05 (Belkhir et al. 1996). Statistical significance of linkage disequilibrium results was assessed using a permutation procedure implemented in GENETIX for each locus by locus combination within each collection.

Assessing among collection genetic differentiation - The temporal stability of allele frequencies was assessed by the randomization chi-square test implemented in FSTAT version 2.9.3.2 (Goudet 1995). Multi-locus genotypes were randomized between collections. The G-statistic for observed data was compared to G-statistic distributions from randomized datasets (i.e., null distribution of no differentiation between collections). Population differentiation was also investigated using pairwise estimates of F_{ST}. Multi-locus estimates of pairwise F_{ST}, estimated by a “weighted” analysis of variance (Weir and Cockerham, 1984), were calculated using GENETIX version 4.05 (Belkhir et al.1996). F_{ST} was used to quantify population structure, the deviation from statistical expectations (i.e., excess homozygosity) due to non-random mating between populations. To determine if the observed F_{ST} estimate was consistent with statistically expectations of no population structure, a permutation test was implemented in GENETIX (1000 permutations).

Effective population size (N_e) – Estimates of the effective population size were obtained using a multi-collection temporal method (Waples 1990a). The temporal method assumes that cohorts are used, but we did not decompose the collection year samples into their respective cohorts using age data. Therefore, N_e estimates that pertain to individual year classes of breeders are not valid; however the harmonic mean over all samples will estimate an N_e that pertains to the time period from which the collections are derived. Comparing samples from years *i* and *j*, Waples’ (1990a) temporal method estimates the effective number of breeders ($\hat{N}_{b(i,j)}$) according to:

$$\hat{N}_{b(i,j)} = \frac{b}{2(\hat{F} - 1/\tilde{S}_{i,j})}$$

The standardized variance in allele frequency ($\hat{F}$) is calculated according to Pollack (1983). The parameter b is calculated analytically from age structure information and the number of years between samples (Tajima 1992). The age-at-maturity information required to calculate b was obtained from ecological data (Hillman et al. 2007). The harmonic mean of sample sizes from years *i* and *j* is $\tilde{S}_{i,j}$. The harmonic mean over all pairwise estimates of $\hat{N}_{b(i,j)}$ is $\tilde{N}_b$. SALMONNb (Waples et al. 2007) was used to calculate $\tilde{N}_b$.

Results and Discussion

In this section we combine our presentation and interpretations of the genetic analyses. Additionally, this section is organized based on the task list presented in the study plan.

Task 1 - Document the observed genetic diversity.

Substantial genetic diversity was observed over all Lake Wenatchee sockeye collections analyzed (Table 1), with heterozygosity estimates over all loci having a mean of 0.79. Genetic diversity was consistent with expected Hardy-Weinberg random mating genotypic proportions for all collections. The F_{IS} observed for each collection was not statistically significant given the distribution of F_{IS} generated using a randomization procedure. Additionally, there were no statistically significant associations observed between alleles across loci (i.e., linkage equilibrium) (data not shown). We concluded from these results that the genetic data from each collection was consistent with statistical expectations for random association of alleles within and between loci. In other words, each collection represents samples from a single gene pool (i.e., populations), and the genetic diversity observed has no detectable technical artifacts or evidence of natural selection.

Task 2 - Test for differentiation among Lake Wenatchee collections and the associated supplementation program.

We explicitly tested the hypothesis of no significant differentiation within natural-origin or broodstock collections from Lake Wenatchee using a randomization chi-square test. The null hypothesis for these tests was that the allele frequencies from two different populations were drawn from the same underlying distribution. We show the results for the pairwise comparisons among eight temporally replicated natural-origin collections from Lake Wenatchee (28 pairwise tests), and report all tests were non-significant (Table 2A). Similarly, for five temporally replicated broodstock collections, 10 of 10 pairwise tests were non-significant (Table 2B). We also tested if natural-origin and broodstock collections were differentiated from each other over time, and report that 40 of 40 tests were non-significant (Table 2C). The nominal level of statistical significance ($\alpha = 0.05$) was adjusted for multiple comparisons using strict Bonferroni correction (Rice 1989). Yet, there are perhaps slight differences between paired natural-broodstock collections. Note that the p-values for comparisons regarding 2006 and 2007 paired collections are lower than for comparisons regarding 2000, 2001, and 2004. The small sample sizes for broodstock collections in 2006 and 2007 may not have been random samples from the Lake Wenatchee sockeye population.

Given the consistencies observed for allele frequency distributions over time, metrics of population structure were expected to be small. This was the case, as the estimated F_{ST} over all thirteen collections was 0.0003. This observed value fell within the distribution of F_{ST} values expected if there were no population structure present (permutation test p-value 0.12). Analysis of the paired natural-broodstock collections corroborated this result. Pairwise estimates of F_{ST} were 0.000 for years 2000, 2001, 2004, and 2007, and 0.002 for 2006. All five estimates were non-significant. Essentially, all 13 sockeye collections could be considered samples from the same population. Given these results, it is valid to combine all collections for statistical analysis. Therefore, we did not calculate genetic distances among any collections, as it is inappropriate to estimate distances that are effectively zero.

Conclusions

We interpret these data to indicate that there appears to be no significant year-to-year differences in allele frequencies among natural-origin or broodstock collections, nor are there observed differences between collections pre- and post-supplementation. As a result, we accept the null hypothesis that the allele frequencies of the broodstock collections equal the allele frequencies of the natural collections, which equals the allele frequency of the donor population. Furthermore, the observed genetic variance that can be attributed to among collection differences was negligible.

Task 3 - Calculate N_e using the temporal method for multiple samples from the same location to document trend.

The fundamental parameter for inferring N_e using genetic data is the standardized variance in allele frequency ($\hat{F}$) (Pollack 1983). Methods estimate N_e from observed changes in $\hat{F}$ over temporally replicated collections from the same location. Yet, as previously shown, there were no statistically significant differences detected in allele frequencies. The underlying model for estimating N_e produced estimates with extremely large variances, given small temporal differences in $\hat{F}$, which rendered any trend in N_e unobservable. Table 3 shows N_e estimates calculated using temporally replicated natural collections.

Task 4 - Compare N_e estimates with trend in census size for Lake Wenatchee sockeye.

See Task 3

Acknowledgements

We would like to thank Jeff Fryer (CRITFC) for providing critical collections of natural-origin sockeye from Lake Wenatchee. We would like to thank Norm Switzler for collection curation and Ken Warheit and Denise Hawkins for helpful comments regarding this project. This project was funded by Chelan County PUD and the Washington State General Fund.

Literature Cited

Allen RL and Meekin TK (1980) Columbia River sockeye salmon study, 1971-1974. Wash. Dep. Fish. Prog. Rep. 120, 75 p.

Banks MA, Blouin MS, Baldwin BA, Rashbrook VK, Fitzgerald HA, Blankenship SM, Hedgecock D (1999) Isolation and inheritance of novel microsatellites in chinook salmon (Oncorhynchus tschawytscha). *Journal of Heredity*, 90:281-288.

Bartley D, Bentley B, Brodziak J, Gomulkiewicz R, Mangel M, and Gall GAE (1992) Geographic variation in population genetic structure of chinook salmon from California and Oregon. Fish. Bull., U.S. 90:77-100.

Blankenship SM, Von Bargen J, Warheit KI, and Murdoch AR (2007) Assessing the Genetic Diversity of Natural Chiwawa River Spring Chinook Salmon and Evaluating the Effectiveness of its Supportive Hatchery Supplementation Program. WDFW report to Chelan County PUD, March 2007.

Belkhir K, Borsa P, Chikhi L et al (1996) GENETIX, logiciel sous Windows TM pour la Génétique des populations. Laboratoire Génome, Populations, Interactions, CNRS UMR 5000, Université de Montpellier II, Montpellier (France).

Chapman D, Peven C, Giorgi A, Hillman T, and Utter F (1995) Status of spring chinook salmon in the mid-Columbia River. Don Chapman Consultants, Inc., 477 p. (Available from Don Chapman Consultants, 3653 Rickenbacker, Ste. 200, Boise, ID 83705.)

Crawford BA (1979) The origin and history of trout brood stocks of the Washington Department of Game. Wash. State Game Dep., Fish. Res. Rep. 76 p.

Dawson JJ, Thorne RE, and Traynor JJ (1973) Acoustic surveys of Lake Wenatchee and Lake Osoyoos in 1973. Final Report, Service Contr. 526, to Wash. Dep. Fish., by Fish. Res. Inst., Coll. of Fish., Univ. Washington, Seattle, WA, 18 p.

Fryer JK and Schwartzberg M (1994) Identification of Columbia Basin sockeye salmon stocks using scale pattern analyses in 1993. Columbia River Inter-Tribal Fish Commission, Tech. Rep. 94-2, 39 p.

Gangmark HA and Fulton LA (1952) Status of Columbia blueback salmon runs, 1951. U. S. Fish Wildl. Serv. Spec. Sci. Rep. 74, 29 p.

Goudet J (1995) FSTAT (Version 1.2): A computer program to calculate F-statistics. Journal of Heredity 86: 485-486.

Gustafson RG, Wainwright TC, Winans GA, Waknitz FW, Parker LT, and Waples RS (1997) Status review of sockeye salmon from Washington and Oregon. U.S. Dept. Commer., NOAA Tech. Memo. NMFS-NWFSC-33, 282 p.

Hedrick PW (1983) Genetics of Populations, Science Books International, Boston

Hillman T, Miller M, Peven C, Tonseth M, Miller T, Truscott K, and Murdoch A (2007) Monitoring and Evaluation of the Chelan County PUD Hatchery Programs: 2007 Annual Report.

Knutzen D (1995) Letter to R. Gustafson, NMFS, from D. Knutzen, WDFW, re. Historical kokanee planting records for Lake Wenatchee, Lake Pleasant, Lake Ozette, Lake Shannon, and Baker Lake from 1981-1994, dated 17 July 1995. 1 p. plus attachment. (Available from West Coast Sockeye Salmon Administrative Record, Environmental and Technical Services Division, Natl. Mar. Fish. Serv., 525 N. E. Oregon Street, Portland, OR 97232.)

Mullan JW (1986) Determinants of sockeye salmon abundance in the Columbia River, 1880's-1982: A review and synthesis. U.S. Fish Wildl. Serv. Biol. Rep. 86(12), 135 p.

Murdoch AR and Peven C (2005) Conceptual Approach to Monitoring and Evaluating the Chelan County Public Utility District Hatchery Programs, Final Report.

Nei M (1978) Estimation of average heterozygosity and genetic distance from a small number of individuals. Genetics 89:583-590.

Olsen JB, Wilson SL, Kretschmer EJ, Jones KC, Seeb JE (2000) Characterization of 14 tetranucleotide microsatellite loci derived from sockeye salmon. *Molecular Ecology* 9, 2185-2187.

Park SDE (2001) Trypanotolerance in West African Cattle and the Population Genetic Effects of Selection [Ph.D. thesis], University of Dublin

Peven CM (1987) Downstream migration timing of two stocks of sockeye salmon on the Mid-Columbia River. Northwest Sci. 61(3):186-190.

Pollak E (1983) A new method for estimating the effective population size from allele frequency changes. Genetics 104, 531-548.

Quinn TP and Adams DJ (1996) Environmental changes affecting the migratory timing of American shad and sockeye salmon. Ecology 77:1151-1162.

Rexroad CE, Coleman RL, Martin AM, Hershberger WK, Killefer J (2001) Thirty-five polymorphic microsatellite markers for rainbow trout (Oncorhynchus mykiss). *Animal Genetics*, 32:317-319.

Rice WR, (1989) Analyzing tables of statistical tests. Evolution. 43:223-225.

Scribner KT, Gust JR, Fields RL (1996) Isolation and characterization of novel salmon microsatellite loci: cross-species amplification and population genetic applications. *Candian Journal of Fisheries and Aquatic Sciences.* 53, 833-841.

Shaklee JB, Klaybor DC, Young S, and White BA (1991) Genetic stock structure of odd-year pink salmon, Oncorhynchus gorbuscha (Walbaum), from Washington and British Columbia and potential mixed-stock fisheries applications. J. Fish. Biol. 39(A):21-34.

Small MP, Beacham TD, Withler RE, and Nelson RJ (1998) Discriminating coho salmon (*Oncorhynchus kisutch*) populations within the Fraser River, British Columbia. *Molecular Ecology* 7: 141-155.

Tajima F (1992) Statistical Method for Estimating the Effective Population Size in Pacific Salmon. J Hered 83, 309-311.

Utter F, Aebersold P, Helle J, and Winans G (1984) Genetic characterization of populations in the southeastern range of sockeye salmon. In J. M. Walton and D. B. Houston (editors), Proceedings of the Olympic wild fish conference, p. 17-31. Fisheries Technology Program, Peninsula College, Port Angeles, WA.

Utter F, Milner G, Stahl G, and Teel D (1989) Genetic population structure of chinook salmon, *Oncorhynchus tshawytscha*, in the Pacific Northwest. Fish. Bull., U.S. 87:239-264.

Varnavskaya NV, Wood CC, and Everett RJ (1994) Genetic variation in sockeye salmon (Oncorhynchus nerka) populations of Asia and North America. Can. J. Fish. Aquat. Sci. 51(Suppl. 1):132-146.

Waples RS (1990a) Conservation genetics of Pacific salmon. III. Estimating effective population size. Journal of Heredity 81:277-289

Waples RS, Masuda M, Pella J (2007) SALMONNb: a program for computing cohort-specific effective population sizes (N_b) in Pacific salmon and other semelparous species using the temporal method. Molecular Ecology Notes 7, 21-24.

Washington Department of Fisheries (WDF), Washington Department of Game (WDG), and United States Bureau of Fisheries (USBF) (1938) A report on the preliminary investigations into the possible methods of preserving the Columbia River salmon and steelhead at the Grand Coulee Dam. Wash. Dep. Fish, Olympia, WA, 120 p.

Washington Department of Fisheries (WDF), Washington Department of Wildlife (WDW), and Western Washington Treaty Indian Tribes (WWTIT) (1993) 1992 Washington State salmon and steelhead stock inventory (SASSI). Wash. Dep. Fish Wildl., Olympia, WA, 212 p. plus 5 regional volumes.

Washington Department of Fish and Wildlife (WDFW) (1996) Letter to M. Schiewe, NMFS, from R. Lincoln, Assistant Director, Fish Management Program, Washington Department of Fish and Wildlife, dated 12 July 1996. 3 p. plus appendix. (Available from West Coast Sockeye Salmon Administrative Record, Environmental and Technical Services Division, Natl. Mar. Fish. Serv., 525 N. E. Oregon Street, Portland, OR 97232.)

Weir BS (1979) Inferences about linkage disequilibrium. Biometrics 35:235-254.

Weir BS, Cockerham CC (1984) Estimating F-Statistics for the Analysis of Population-Structure. Evolution 38:1358-1370.

Winans GA, Aebersold PB, Urawa S, and Varnavskaya NV (1994) Determining continent of origin of chum salmon (*Oncorhynchus keta*) using genetic stock identification techniques: status of allozyme baseline in Asia. Can. J. Fish. Aquat. Sci. 51 (Suppl. 1):95-113.

Winans GA, Aebersold PB, and Waples RS (1996) Allozyme variability of *Oncorhynchus nerka* in the Pacific Northwest, with special consideration to populations of Redfish Lake, Idaho. Trans. Am. Fish. Soc. 205:645-663.

Wood CC, Riddell BE, Rutherford DT, and Withler RE (1994) Biochemical genetic survey of sockeye salmon (*Oncorhynchus nerka*) in Canada. Can. J. Fish. Aquat. Sci. 51(Suppl. 1):114-131.

Wood CC (1995) Life history variation and population structure in sockeye salmon. *In* J. L. Nielsen (editor), Evolution and the aquatic ecosystem: defining unique units in population conservation. Am. Fish. Soc. Symp. 17:195-216.

Table 1 Lake Wenatchee sockeye collections analyzed. MNA is the mean number of alleles per locus, Hz is unbiased heterozygosity, Obs Hz is observed heterozygosity, and HW is the p-value of the null hypothesis of random association of alleles (i.e., Hardy – Weinberg equilibrium). For reference, the nominal level of statistical significance at $\alpha = 0.05$ is 0.0002 after correction for multiple tests.

Year	Collection Code	Tissue Type	Source	N	MNA	Hz	Obs Hz	HW
1989	89[1]	Scales	Natural	96	14.35	0.792	0.791	0.424
1990	90[1]	Scales	Natural	96	13.19	0.793	0.779	0.131
2000	00AAE	Scales	Broodstock	96	12.31	0.787	0.776	0.213
2000	00[1]	Scales	Natural	96	11.76	0.801	0.826	0.868
2001	01AAS	Scales	Broodstock	53	9.47	0.788	0.793	0.392
2001	01[1]	Scales	Natural	96	14.35	0.786	0.794	0.456
2002	02[1]	Scales	Natural	96	14.53	0.794	0.777	0.780
2004	04[1]	Scales	Natural	96	14.65	0.798	0.803	0.704
2004	04AAV	Scales	Broodstock	43	14.35	0.796	0.795	0.051
2006	06CN	Tissue	Broodstock	38	14.59	0.793	0.785	0.688
2006	06CO	Tissue	Natural	96	14.53	0.806	0.803	0.408
2007	07EE	Tissue	Broodstock	18	14.00	0.790	0.790	0.221
2007	07EF	Tissue	Natural	96	14.35	0.789	0.800	0.347

[1] Samples taken from scale cards provided by Jeff Fryer (CRITFC)

Table 2 Allelic differentiation for Lake Wenatchee sockeye collections. A single analysis tested (pairwise) the allelic differentiation between all thirteen collections; however p-values for G-statistics are partitioned in the table by A) natural-origin, B) broodstock, and C) natural versus broodstock. Underlined values are for paired natural-broodstock collections from the same year. For reference, the nominal level of statistical significance at $\alpha = 0.05$ is 0.0006 after correction for multiple tests. No significant values were observed.

A) Natural-Origin Collections

	89	90	00	01	02	04	06CO	07EF
89		0.257	0.359	0.531	0.331	0.127	0.031	0.263
90			0.953	0.148	0.753	0.903	0.077	0.283
00				0.328	0.527	0.607	0.604	0.400
01					0.209	0.081	0.127	0.093
02						0.085	0.707	0.235
04							0.312	0.577
06CO								0.435
07EF								

B) Broodstock Collections

	00AAE	01AAS	04AAV	06CN	07EE
00AAE		0.189	0.090	0.008	0.058
01AAS			0.122	0.020	0.116
04AAV				0.008	0.031
06CN					0.326
07EE					

C) Natural vs. Broodstock

	89	90	00	01	02	04	06CO	07EF
00AAE	0.027	0.309	<u>0.572</u>	0.018	0.041	0.012	0.093	0.040
01AAS	0.115	0.471	0.160	<u>0.219</u>	0.519	0.049	0.654	0.133
04AAV	0.136	0.219	0.210	0.423	0.208	<u>0.328</u>	0.037	0.153
06CN	0.029	0.004	0.053	0.007	0.022	0.004	<u>0.019</u>	0.001
07EE	0.099	0.229	0.053	0.015	0.093	0.178	0.090	<u>0.037</u>

Table 3 Estimation of N_e for temporally replicated natural-original sockeye collections. Above the diagonal are pairwise estimates of N_e, where negative values mean sampling variance can account for genetic variance observed (i.e., genetic drift unnecessary). Below the diagonal are variances for pairwise estimates of N_e. Absent variance values (denoted by **-**) were too large for SalmonNb to display.

Collection	89	90	00	01	02	04	06CO	07EF
89		-3936.6	-1414	-2636.3	671.4	1871.1	1066.1	1951.2
90	2.59E+09		-1490.3	3649.1	-31144	-6808.4	817.6	93190.2
00	1.40E+09	4.45E+09		-592.2	-6842.2	-667.1	-1736.9	-1350.1
01	1.21E+09	1.47E+09	2.33E+09		977.1	6160.4	387.8	2531.5
02	1.91E+09	1.33E+09	1.16E+09	2.29E+09		1495.6	-848.5	3213.6
04	2.21E+09	3.62E+09	4.08E+09	1.27E+09	1.14E+09		896.6	2155.3
06CO	1.34E+09	1.39E+09	1.73E+09	**-**	4.51E+09	1.2E+09		3278.6
07EF	2.15E+09	1.51E+09	1.18E+09	1.68E+09	**-**	1.36E+09	2.65E+09	

APPENDIX I

Genetic Diversity of Natural Chiwawa River Spring Chinook Salmon.

Assessing the Genetic Diversity of Natural Chiwawa River Spring Chinook Salmon and Evaluating the Effectiveness of its Supportive Hatchery Supplementation Program

Developed for

Chelan County PUD

and the

Habitat Conservation Plan's Hatchery Committee

Developed by
Scott M. Blankenship, Jennifer Von Bargen, and Kenneth I. Warheit
WDFW Molecular Genetics Laboratory
Olympia, WA

and

Andrew R. Murdoch
Supplementation Research Team
Wenatchee, WA

March 30, 2007

Table of Contents

Executive Summary

The main objective of this study was to determine the potential impacts of the Chiwawa River Supplementation Program on natural spring Chinook in the upper Wenatchee system. We did this by investigating population differentiation between temporally replicated Chiwawa River natural and hatchery samples from the Wenatchee River watershed using microsatellite DNA allele frequencies and the statistical assignment of individual fish to specific populations. Additionally, to assess the genetic effect of the hatchery program, we investigated the relationship between census and effective population sizes using collections obtained before and after the supplementation program. In this summary, we briefly describe the salient results contained within this report; however, each "Task" within the Results/Discussion section below contains extended coverage for each topic along with an expanded interpretation of each result.

Overall, we observed substantial genetic diversity within collections, with heterozygosities equal to roughly 80%, over thirteen microsatellite markers. Microsatellite allele frequencies among temporally replicated collections from the same population (i.e., location) were variable, resulting in significant genetic differentiation among these collections. However, these difference are likely the result of salmon life history in this area, as four-year-old Chinook comprise a majority of returns each year. That is, the genetic tests are detecting the differences of contributing parents from each cohort, rather than a hatchery effect.

Analysis of Chiwawa River Collections

To assess the multiple competing hypotheses regarding population differentiation within and among Chiwawa River collections, we found it necessary to organized the Chiwawa genetic data into three data sets: (1) fish origin (hatchery versus natural), (2) spawning location (hatchery broodstock versus in-river (natural) spawners), and (3) four "treatment" groups (1. hatchery-origin hatchery broodstock, 2. hatchery-origin natural spawner, 3. natural-origin natural spawner, and 4. natural-origin hatchery broodstock). We conducted separate analyses using each of the three data sets, with each analysis

touching on some aspect of the components necessary to move through the Conceptual Process outlined by Murdoch and Peven (2005).

Origin Dataset – We report that allele frequencies within and between natural- and hatchery-origin collections are significantly different, but there does not appear to be a robust signal indicating that the recent natural-origin collections have diverged greatly from the pre- or early post-supplementation collections. Genetic drift will occur in all populations, but does not appear to be a major factor affecting allele frequencies within the Chiwawa collections.

Spawning Location Dataset – There are significant allele frequency differences within and between hatchery broodstock and natural spawner collections. However, in recent years the allele frequency differences between the hatchery broodstock and natural spawner collections have declined. Furthermore, based on linkage disequilibrium, there is a genetic signal that is consistent with increasing homogenization of allele frequencies within hatchery broodstock collections, but a similar homogenization within the natural spawner collection is not apparent. These data suggest that there exists consistent year-to-year variation in allele frequencies among hatchery and natural spawning collections, but there is a trend toward homogenization of the allele frequencies of the natural- and hatchery-origin fish that compose the hatchery broodstock.

Four Treatment dataset – Although there are signals of allelic differentiation among Chiwawa River collections, there are no robust signs that these collections are substantially different from each other. We used two different analyses to measure the degree of genetic variation that exists among individuals and collections within the Chiwawa River. First, we conducted a principal component analysis using all Chiwawa samples with complete genotypes (i.e., no missing alleles from any locus). Although the first two principal component axes account for only 10.5% of the total molecular variance, a substantially greater portion of that variance is among individual fish, regardless of their identity, rather than among hatchery and natural collections. The variances in principal component scores among individuals are 11 and 13 times greater than the variance in scores among collections.

Secondly, using an Analysis of Molecular Variance (AMOVA), we were able to determine how best to group populations, with "best" being defined as that grouping that accounts for the greatest proportion of among group (i.e., population) variance. Furthermore, by partitioning molecular variance into different hierarchical components, we are able to determine what level accounts for the majority of the molecular variance. The AMOVA results clearly show that nearly all molecular variation, no matter how the data are organized, resides within a collection. The percentage of total molecular variance occurring within collections ranged from 99.68% to 99.74%. These results indicate that the significant differences among collections of Chiwawa fish account for less than one percent of the total molecular variance, and these differences cannot be attributed to fish origin or spawning location.

Effective Population Size (N_e)

The contemporary estimate of N_e calculated using genetic data combined for Chiwawa natural-origin spawners (NOS) and hatchery-origin spawners (HOS) Chinook is N_e=386.8, which is slightly larger than the pre-hatchery N_e we estimated using demographic data from 1989 – 1992. Additionally, the N_e /N ratio calculated using 386.8 for N_e and the arithmetic mean yearly census of NOS and HOS Chinook from 1989 – 2005 for N is 0.40. These results suggest the N_e has not declined during the period of Chiwawa Hatchery Supplementation Program operation.

Analysis Of Upper Wenatchee Tributary Collections

We compared genetic data for spring Chinook collected from the major spawning aggregates of the Wenatchee River. We observed significant differences in allele frequencies among temporally replicated collections within populations, and among populations within the upper Wenatchee. However, these differences account for a very small portion of the overall molecular variance, and these populations overall are very similar to each other. Of all the populations within the Wenatchee River, the White River appears to be the most distinct. Yet, this distinction is more a matter of detail than of large significance, as the median F_{ST} between White River collections and all other collections (except the Little Wenatchee collection; see Results/Discussion) is less than 1.5% among population variance. We consider the implications of these results in the Conclusion section that follows the Results/Discussion section. Additionally, there is no evidence that the Chiwawa River Supplementation Program has changed the allele frequencies in the Nason Creek and White River populations, despite the presence of hatchery-origin fish in both these systems.

Introduction

Murdoch and Peven (2005) outlined 10 objectives to assess the impact (positive or negative) of hatchery operations mitigating the operation of Rock Island Dam. Two objectives relate to monitoring the genetic integrity of populations:

Objective 3: Determine if genetic diversity, population structure, and effective population size have changed in natural spawning populations as a result of the hatchery program. Additionally, determine if hatchery programs have caused changes in phenotypic characteristics of natural populations.

Objective 5: Determine if the stray rate of hatchery fish is below the acceptable levels to maintain genetic variation between stocks.

This study addresses Objective 3 (above), and documents analyses and results WDFW completed for populations of spring Chinook (*Oncorhynchus tshawytscha*) in the Wenatchee River watershed. This study was not intended to specifically address Objective 5 (above); however, genetic data provide results relevant to Objective 5. The critical component of Objective 3 is to determine if hatchery supplementation has effected change. Furthermore, change in this context means altering census size and/or genetic marker allele frequencies; we did not attempt to measure changes in fitness. Perhaps a more meaningful rewording of Objective 3 is, “Did the hatchery supplementation program succeed at increasing the census size of a target population while leaving genetic integrity intact?” In order to evaluate cause and effect of hatchery supplementation, we surveyed and compared genetic variation in samples collected before and after potential effects from the Chiwawa Hatchery Supplementation Program. Samples were acquired from the primary spawning aggregates in the upper Wenatchee River watershed: Nason Creek, Little Wenatchee River, White River, and Chiwawa River. Hatchery samples were acquired from programs that could potentially affect genetic composition of Wenatchee stocks, the integrated Chiwawa River stock (local stock), Leavenworth National Fish Hatchery spring Chinook (Carson Stock – non local), and Entiat NFH (Carson Stock – non local). Additionally, the genetic markers used were the Genetic Analysis of Pacific Salmonids (GAPS) (Seeb et al. in review) standardized microsatellites, so all data from the Wenatchee study will be available for inclusion in the GAPS Chinook coastwide microsatellite baseline.

History of Artificial Propagation

Artificial propagation in the upper Columbia River began in 1899 when hatcheries were constructed on the Wenatchee and Methow rivers (Mullan 1987). These initial operations were small, with the Tumwater Hatchery on the Wenatchee River releasing several hundred thousand fry, and the Methow River hatchery producing few Chinook salmon before it was closed in 1913 (Craig and Suomela 1941, Nelson and Bodle 1990). The Leavenworth State Hatchery operated in the Wenatchee River Basin between 1913 and 1931 using eggs from non-native stocks (Willamette River spring-run and lower Columbia Chinook hatchery fall-run). These early attempts at hatchery production were largely unsuccessful for spring-run Chinook (WDF 1934). Between 1931 and 1939, no Chinook salmon hatcheries were in operation above Rock Island Dam (Rkm 730).

In 1938, the last salmon was allowed to pass upstream through the uncompleted Grand Coulee Dam (Rkm 959). To mitigate the loss of habitat, adult Chinook salmon were trapped, under the auspices of the Grand Coulee Fish Maintenance Project (GCFMP), at Rock Island Dam beginning in May 1939, and relocated into three of the remaining accessible tributaries to the upper Columbia River: the Wenatchee, Entiat, and Methow Rivers. GCFMP transfers continued through the autumn of 1943. Spring- and summer/fall-run fish were differentiated at Rock Island Dam based on a 9 July cutoff date for Chinook arrivals at Rock Island Dam (Fish and Hanavan 1948). Spring-run adults collected at Rock Island Dam (pre 9 July fish) were either transported to Nason Creek on the Wenatchee River to spawn naturally (1939-43), or to the newly constructed Leavenworth NFH (1940) for holding and subsequent spawning (1940-43). Eggs were incubated on site or transferred to the Entiat NFH (1941) and Winthrop NFH (1941). In 1944 spring-run adults were allowed to freely pass Rock Island Dam. The GCFMP did not differentiate among late-run stocks (post 9 July fish) passing Rock Island Dam. Late-run offspring reared at the Leavenworth NFH, Entiat NFH, and Winthrop NFHs were an amalgamation of summer and fall upper Columbia River populations (Fish and Hanavan 1948). Late-run fish were transplanted into the upper and lower Wenatchee, Methow, and Entiat Rivers.

After 1943, the Winthrop NFH continued to use local spring-run Chinook for hatchery production, while the other NFHs largely focused on summer-run Chinook salmon. Renewed emphasis on spring run production in the mid-1970s saw the inclusion of local and non-local eggs (Carson NFH stock, Klickitat River stock, and Cowlitz River stock) to the NFHs. In the early 1980s, imports of non-native eggs were reduced significantly, and thereafter the Leavenworth, Entiat, and Winthrop NFHs have relied on adults returning to their facilities for their egg needs (Chapman et al. 1995). Regarding late-run Chinook, due to the variety of methods employed to collect broodstock at dams, hatcheries, or the result of juvenile introductions into various areas, Chinook populations and runs (i.e., summer and fall) have been mixed considerably in the upper Columbia system over the past five decades (reviewed in Chapman et al. 1994).

Washington Department of Fish and Wildlife (WDFW) operates two facilities producing spring-run Chinook, the Methow Fish Hatchery (MFH) owned by Douglas County PUD that began operation in 1992 and Eastbank Fish Hatchery (EFH) owned by Chelan County PUD that began operation in 1989. Both programs were designed to implement supplementation (supportive breeding) programs for naturally spawning populations on the Methow and Wenatchee Rivers, respectively (Chapman et al. 1995). As part of the Rock Island Mitigation Agreement between Chelan County Public Utility District and the fishery management parties (RISPA 1989), a supplementation (supportive breeding) program was initiated in 1989 on the Chiwawa River to mitigate smolt mortality resulting from the operation of Rock Island Hydroelectric Project. EFH uses broodstock collected at a weir on the Chiwawa River, although in recent years hatchery fish have been collected at Tumwater Dam. Similarly, the MFHC uses returning adults collected at weirs on the Methow River and its tributaries, the Twisp and Chewuch Rivers (Chapman et al. 1995; Bugert 1998). Although low run size and trap efficiency has resulted in most broodstock being collected from the hatchery outfall or in some years Wells Dam, progeny produced from these programs are reared at and released from satellite sites on the tributaries where the adults were collected. Numerous other facilities have reared spring-run Chinook salmon on an intermittent basis.

Previous Genetic Studies – Population differentiation

Waples et al. (1991a) examined 21 polymorphic allozyme loci in samples from 44 populations of Chinook salmon in the Columbia River Basin. These authors reported three major clusters of Columbia River Basin Chinook salmon: 1) Snake River spring- and summer-run Chinook salmon, and mid and upper Columbia River spring-run Chinook salmon, 2) Willamette River spring-run Chinook salmon, 3) mid and upper Columbia River fall- and summer-run Chinook salmon, Snake River fall-run Chinook salmon, and lower Columbia River fall- and spring-run Chinook salmon. Utter et al. (1995) examined allele frequency variability at 36 allozyme loci in samples of 16 upper Columbia River Chinook populations. Utter et al. (1995) indicated that spring-run populations were distinct from summer- and fall-run populations, where the average genetic distance between spring-run and late-run Chinook were about eight times the average of genetic distances between samples within each group. Additionally, allele frequency differences among spring-run populations were considerably greater than that among summer- and fall-run populations in the upper Columbia River. Utter et al. (1995) also reported hatchery populations of spring-run Chinook salmon were genetically distinct from natural spring-run populations, but hatchery populations of fall-run Chinook salmon were not genetically distinct from natural fall-run populations.

As part of an evaluation of the relative reproductive success for the Chiwawa River supplementation program, Murdoch et al. (2006), used eleven microsatellite loci to assess population differentiation among spring Chinook salmon population samples in the upper Wenatchee River. Murdoch et al. (2006) reported a >99% accuracy of correctly identifying spring-run and fall-run Chinook from the Wenatchee River. They also reported slight, but significantly different genetic variation among wild spring populations and between wild and hatchery stocks. Yet, since the spring-run populations are genetically similar, identifying individuals genetically from the upper tributaries of the Wenatchee River was difficult. This result is exemplified in their individual assignment results, where < 8% of spring-run individuals, hatchery or wild, were correctly assigned using their criterion of an LOD (log of odds) score greater than 2. Murdoch et al. (2006) also reported contemporary natural spring Chinook show heterozygote deficit and low linkage disequilibrium (LD), while contemporary hatchery spring Chinook show heterozygote excess and high LD.

Williamson et al. (submitted) have continued the work of Murdoch et al. (2006) by analyzing Chiwawa River demographic data from 1989 – 2005 to estimate the proportions of recruits that were produced by Chinook with hatchery or wild origin. In an "ideal" population, the genetic size (i.e., effective size or N_e) and the census size are equal; however various demographic factors such as unequal sex ratios and variance in reproductive success among individuals reduces the genetic size below the census size. It is generally thought that the genetic size is approximately 10-33% the census size (Bartley et al. 1992; RS Waples pers. comm.), although values have been reported outside this range (Araki et al. 2007; Arden and Kapuscinski 2003; Heath et al. 2002). Despite being difficult to estimate, the effective population size in many respects is a more important parameter to know than census size, because N_e determines how genetic diversity is distributed within populations and how the forces of evolution (i.e., forces that change genetic diversity over time) will affect the genetic variation present.

Williamson et al. (submitted) used demographic data to 1) investigate the effect of unequal sex ratio on genetic diversity, 2) investigate the effect of variation in reproductive success on genetic diversity, 3) investigate the effect of fluctuations in population size on genetic diversity, and 4) estimate the effective population size, using the inbreeding method (Ryman and Laikre 1991). Most importantly, they use demographic data from 1989 – 2000 to assess the impact of the Chiwawa Hatchery Supplementation Program on the effective population size of natural-origin Chiwawa River spring Chinook. They estimate that the N_e of naturally spawning Chiwawa Chinook (i.e., both hatchery- and wild-origin fish on the spawning grounds) from 1989 –

1992 was N_e = 2683 and in 1997 – 2000 was N_e = 989. They compare spawning ground N_e to estimates calculated from combined broodstock and naturally spawning Chinook demographic data. The combined inbreeding N_e estimate from 1989 – 1992 was N_e = 147 and in 1997 – 2000 was N_e = 490. Williamson et al. (submitted) argue that since the combined N_e estimate is lower than the naturally spawning estimate, the supplementation program has had a negative impact on the Chiwawa River N_e.

Williamson et al. (submitted) also present genetic data for Chinook recovered on spawning grounds in upper Wenatchee River tributaries in 2004 and 2005. These genetic data are derived from the Murdoch et al. (2006) study. They compare samples collected from Chiwawa River (i.e., hatchery and wild), White River, Nason Creek, and Leavenworth Hatchery. Additionally, they include a 1994 Chiwawa River wild smolt sample for comparison with the 2004 brood year. Williamson et al. (submitted) report statistically significant genetic differentiation among Chiwawa River, White River and Nason Creek. Additionally, they report that the 1994 and 2004 Chiwawa River wild samples are not statistically different, but the 2004 Chiwawa wild and hatchery collections are statistically different.

Study Objectives

This study investigated within and among population genetic diversity to assess the effect of the Chiwawa Hatchery's supplemental program on the natural Chiwawa River spring Chinook population. Differences among temporal population samples, the census size, heterozygosity, and allelic diversity were documented. We investigated population differentiation between the Chiwawa River natural and hatchery samples, and among all temporally replicated samples from the Wenatchee River watershed using microsatellite DNA allele frequencies and the statistical assignment of individual fish to specific populations. To assess the genetic effect of the hatchery program, correlation between census and effective population sizes were investigated using temporally replicated samples obtained before and after the supplementation program operation. To address the hypotheses associated with Objective 3 in Murdock and Peven (2005) we developed eleven specific “Tasks” (Blankenship and Murdoch 2006), to which we analyzed specific genetic data. We present the results from these analyses specific to each individual Task.

Methods and Materials

Tissue collection and DNA extraction

We analyzed thirty-two population collections of adult spring Chinook salmon (*Oncorhynchus tshawytscha*) obtained from the Wenatchee River between 1989 and 2006 (Table 1). Nine collections of natural Chinook adults from the Chiwawa River (n=501), and nine collections of Chiwawa Hatchery Chinook (n=595) were collected at a weir located in the lower Chiwawa River. The 1993 and 1994 Chiwawa Hatchery samples are smolt samples from the 1991 and 1992 hatchery brood years, respectively. Additional samples were collected from upper Wenatchee River tributaries, White River, Little Wenatchee River, and Nason Creek. Six collections of natural White River Chinook (n=179), one collection from the Little Wenatchee (n=19), and six collections from Nason Creek (n=268) were obtained. Single collections were obtained for Chinook spawning in the mainstem Wenatchee River and Leavenworth National Fish Hatchery. An additional out-of-basin collection from Entiat River was also included in the analysis. Samples collected in 1992 or earlier are scale samples. All other samples were either fin clips or operculum punches, stored immediately in ethanol after collection. DNA was extracted from stored tissue using Nucleospin 96 Tissue following the manufacturer’s standard protocol (Macherey-Nagel, Easton, PA, U.S.A.).

Laboratory analysis

We performed polymerase chain reaction (PCR) amplification on each fish sample using the 13 fluorescently end-labeled microsatellite marker loci standardized as part of the GAPS project (Seeb et al. in review). GAPS genetic loci are: *Ogo*2, *Ogo*4 (Olsen et al. 1998); *Oki*100 (unpublished); *Omm*1080 (Rexroad et al. 2001); *Ots*201b (unpublished); *Ots*208b, *Ots*211, *Ots*212, and *Ots*213 (Grieg et al. 2003); *Ots*3M, *Ots*9 (Banks et al.

1999); *Ots*G474 (Williamson et al. 2002); *Ssa*408 (Cairney et al. 2000). PCR reaction volumes were 10 µL, and contained 1 µL 10x PCR buffer (Promega), 1.0 µL MgCl2 (1.5 mM final) (Promega), 0.2 µL 10 mM dNTP mix (Promega), and 0.1 units/mL Taq DNA polymerase (Promega). Loci were amplified as part of multiplexed sets, so primer molarities and annealing temperatures varied. Multiplex one had an annealing temperature of 50°C, and used 0.37 Molar (M) *Oki*100, 0.35 M *Ots*201b, and 0.20 M *Ots*208b, and 0.20 M *Ssa*408. Multiplex two had an annealing temperature of 63°C, and used 0.10 M *Ogo*2, and 0.25 M of a non-GAPS locus (*Ssa* 197). Multiplex three had an annealing temperature of 56°C, and used 0.18 M *Ogo*4, 0.18 M *Ots*213, and 0.16 M *Ots*G474. Multiplex four had an annealing temperature of 53°C, and used 0.26 M *Omm*1080, and 0.12 M *Ots*3M. Multiplex five had an annealing temperature of 60°C, and used 0.30 M *Ots*212, 0.20 M *Ots*211, and 0.10 M *Ots*9. Thermal cycling was conducted on either a PTC200 thermal cycler (MJ Research) or GeneAmp 9700 (Applied Biosystems) as follows: 95°C (2 min); 30 cycles of 95°C for 30 sec., 30 sec. annealing, and 72°C for 30 sec.; a final 72°C extension and then a 10°C hold. PCR products were visualized by electrophoresis on an ABI 3730 automated capillary analyzer (Applied Biosystems). Fragment analysis was completed using GeneMapper 3.7 (Applied Biosystems). Standardization of genetic data to GAPS allele standards was conducted following Seeb et al. (in review).

Genetic data analysis

Assessing within population genetic diversity - Heterozygosity measurements are reported using Nei's (1987) unbiased gene diversity formula (i.e., expected heterozygosity) and Hedrick's (1983) formula for observed heterozygosity. Both tests are implemented using the microsatellite toolkit (Park 2001). We used GENEPOP version 3.4 (Raymond and Rousset 1995) to assess Hardy-Weinberg equilibrium (HWE), where deviations from the neutral expectation of random associations among alleles are calculated using a Markov chain method (5000 iterations in this study) to obtain unbiased estimates of Fisher's exact test. Global estimates of F_{IS} according to Weir and Cockerham (1984) were calculated using GENEPOP version 3.4. Genotypic linkage disequilibrium was calculated following Weir (1979) using GENEPOP version 3.4.

Linkage results for population collections are reported as the proportion of pairwise (locus by locus) tests that are significant (alpha = 0.01). Linkage disequilibrium is considered statistically significant if more than 5% of the pairwise tests based on permutation are significant for a collection.

Within- and among-population genetic differentiation – The temporal stability of allele frequencies within populations, and pairwise differences in allele frequencies among populations were assessed using several different procedures. First, we tested for differences in allele frequencies among populations defined in Table 1 using a randomization chi-square test implemented in GENEPOP version 3.4 (Raymond and Rousset 1995). This procedure tests for differences between pairs of populations where alleles are randomized between the populations (i.e., genic test). The null hypothesis for this test is that the allele frequency distributions between two populations are the same. A low p-value should be interpreted as the allele frequency distributions being compared are unlikely to be samples drawn from the same underlying distribution.

Second, to graphically describe allele frequency differences among populations we conducted a nonmetric multidimensional scaling analysis using allele-sharing distance matrices from two different data sets. Pairwise allele-sharing distances are calculated as 1 – (mean over all loci of the sums of the minima of the relative frequencies of each allele common to a pair of populations). To calculate the allele-sharing distances for each pair of populations we used PowerMarker v3.25 (Liu and Muse 2005). Nonmetric multidimensional scaling is a technique designed to construct an n-dimensional “map” of populations, given a set of pairwise distances between populations (Manly 1986). The output from this analysis is a set of coordinates along n-axes, with the coordinates specific to the number of n-dimensions selected. To simplify our analysis we selected a 2-dimensional analysis to represent the relative positions of each population in a typical bivariate plot. The goodness of fit between the original allele-sharing distances and the pairwise distances between all populations along the 2-dimensional plot is measured by a “stress” statistic. Kruskal (in Rohlf 2002) developed a five-tier guide for evaluating stress levels, ranging from a perfect fit (stress=0) to a poor fit (stress=0.40). We conducted the nonmetric multidimensional scaling analysis for one data set containing Chiwawa natural- and hatchery-origin collections, and another data set containing Chiwawa broodstock and in-river spawner collections. We used the mdscale module in MATLAB R2006b (The Mathworks 2006) to generate the nonmetric multidimensional scaling coordinates.

We examined the geographic and temporal structure of populations in the upper Wenatchee (Chiwawa River, Nason Creek, and White River, only) using a series of analyses of molecular variance (AMOVAs). Here, we defined an AMOVA as an analysis of variance of allele frequencies, as originally designed by Cockerham (1969), but implemented in Arlequin v2.1 (Schneider et al. 2000). These analyses permit populations to be aggregated into groups, and molecular variance is then partitioned into within collections, among collections, but within groups, and among group components. With this approach, we were able to determine how best to group populations, with "best" being defined as that grouping that accounts for the greatest proportion of among group variance. Furthermore, by partitioning molecular variance into three different hierarchical components, we are able to determine what level accounts for the majority of the molecular variance.

Finally, we explored the partitioning of molecular variance between among-individuals and among-populations using a principal component analysis and multi-locus estimates of pairwise F_{ST}, estimated by a "weighted" analysis of variance (Weir and Cockerham, 1984). Principal component analysis is a data-reduction technique whereby the correlation structure among variables can be used to combine variables into a series of multivariate components, with each original variable receiving a weighted value for each component based on its correlation with that component. Here, we used a program written by Warheit in MATLAB R2006b (The Mathworks 2006) that treats each allele for each locus as a single variable (13 loci = 26 alleles or variables), and these 26 "variables" were arranged into 26 components, with each component accounting for a decreasing amount of molecular variance. Estimates of F_{ST} were calculated using GENETIX version 4.05 (Belkhir et al.1996). To determine if the F_{ST} estimates were statistically different from random (i.e., no structure), 1000 permutations were implemented in GENETIX version 4.05 (Belkhir et al.1996).

Effective population size (N_e) – Estimates of the effective population size were obtained using two methods, a multi-collection temporal method (Waples 1990), and a single-collection method (Waples 2006) using linkage disequilibrium data. The temporal method assumes that cohorts are used, but we did not decompose the collection year samples into their respective cohorts using age data. Therefore, N_e estimates that pertain to individual year classes of breeders are not valid; however the harmonic mean over all samples will estimate the contemporary N_e. Comparing samples from years *i* and *j*, Waples' (1990) temporal method estimates the effective number of breeders ($\hat{N}_{b(i,j)}$) according to:

$$\hat{N}_{b(i,j)} = \frac{b}{2(\hat{F} - 1/\hat{S}_{i,j})}$$

The standardized variance in allele frequency ($\hat{F}$) is calculated according to Pollack (1983). The parameter b is calculated analytically from age structure information and the number of years between samples (Tajima 1992). The age-at-maturity information required to calculate b was obtained from Murdoch et al. (2006) for this analysis. They observed for Chiwawa Hatchery Chinook that 8.6% matured at age 2, 4% at age 3, 87% at age 4, and 0.4% at age 5. For Chiwawa natural Chinook, Murdoch et al. (2006) observed that 1.8% matured at age 3, 81.6% at age 4, and 16.7% at age 5. The harmonic mean of sample sizes from years *i* and *j* is $\tilde{S}_{i,j}$. Over all pairwise comparisons the harmonic mean of all $\hat{N}_{b(i,j)}$ is $\tilde{N}_b$, the contemporary estimate of the effective population size (N_e). SALMONNb (Waples et al. 2007) was used to calculate $\tilde{N}_b$. As suggested by authors, alleles with a frequency below 0.05 were excluded from the analysis to reduce potential bias.

The method of Waples (2006) uses linkage disequilibrium (i.e., mean squared correlation of allele frequencies at different gene loci) as a means of estimating effective population size (N_e) from a single sample. While this method is biased in some cases where N_e /N ratio is less the 0.1 and the sample size is less than the true N_e, it has been shown to produce comparable results to the temporal method. Burrows' delta method is used to estimate LD, and a bias corrected estimate of N_e is calculated after eliminating alleles with frequency less than 0.05. This test was implemented using LDN_e (Do and Waples unpublished). In age-structured species, N_e estimates based on LD are best interpreted as the effective number of breeders (N_b) that produced the sample (Waples 2006). N_b should be multiplied by the mean generation length (i.e., 4 in this case) to obtain an overall estimate of N_e based on an N_b estimate. We analyzed collections categorized by spawning location (i.e., hatchery broodstock or in-river) and did not analyze collections categorized by origin (i.e., hatchery or natural). Waples' (2006) method estimates N_e from observed LD, therefore the corresponding N_e estimates for the hatchery collections would be low and the estimates for the natural collections would be high. Yet, since the supplementation program is integrated, and hatchery fish can spawn naturally, we feel it inappropriate to analyze the hatchery and natural samples as if they were separate, which would essentially partition all the LD into the hatchery samples.

Each collection has an N_b estimate and an associated confidence interval. If the confidence interval includes infinity, it means that sampling error accounts for all the LD observed (i.e., empirical LD is less than expected LD). The usual interpretation is that there is no evidence for any disequilibrium caused by genetic drift in a finite number of parents. Since the LD method estimates the number of breeders that contributed to the sample being analyzed, in order to calculate an N_e /N ratio, the appropriate census size must be used. The census size used to derive a ratio was the estimate four years prior to the collection analyzed using LD, which assumed a strict four-year-old lifecycle, although the observed proportion of four-year-olds was approximately 85% each year. The census numbers (Table 2) used to calculate the ratios for Chiwawa broodstock and in-river spawners were combined NOS (natural-origin spawners) and HOS (hatchery-origin spawners) census estimates.

Individual assignment – A population baseline file was constructed containing all 1704 individual Chinook from 34 population collections (Table 1; Chiwawa origin data set plus all samples from other populations). All individuals in the baseline had geneotypes that included nine or more loci. Individual Chinook were assigned to their most likely population of origin based on the partial Bayesian criteria of Rannala and Mountain (1997), using a "jack-knife" procedure, where each individual to be assigned was removed from the baseline prior to the calculation of population likelihoods. This procedure was implemented in a program written by Warheit in MATLAB R2006b (The Mathworks 2006). Two assignment criteria were used, 1) the population with the largest posterior probability for an individual was the "most-likely" population of origin (i.e., all individuals assigned to a collection), and 2) an assignment was consider valid only if the posterior probability was greater than or equal to 0.9. Please note that while the analysis used 34 population collections to assign Rannala and Mountain likelihoods for each individual, these likelihoods were aggregated based on "population" (i.e., Chiwawa, Nason, White, and so on) and posterior probabilities were calculated for population location, rather than individual collections.

Results and Discussion

In this section we combine our presentation and interpretations of the genetic analyses. Additionally, this section will be organized based on the task list presented in the study plan. Overall conclusions are provided following this section.

Task 1: Determine trend in census size for Chiwawa River spring Chinook.

Census data from 1989 – 2005 are provided in Table 2 for the Chiwawa Hatchery broodstock and spring Chinook present in the Chiwawa River. The demographic data for naturally spawning Chinook are based on redd sampling and carcass surveys, while broodstock data are based on Chiwawa hatchery records. As the supplementation program is integrated by design, we also present the proportion of natural-origin broodstock (pNOB) incorporated into the hatchery, in addition to the number of natural-origin (NOS) and hatchery-origin (HOS) spawners present in Chiwawa River. The census size fluctuated yearly, and a general reduction in census size was observed in the mid to late 1990's. This trend was apparent in both the broodstock and in the river. The arithmetic mean census size from 1989 – 2005 for the Chiwawa Hatchery (i.e., broodstock) was N=87.5 per year. The arithmetic mean census size from 1989 – 2005 for the Chiwawa River (i.e., NOS and HOS combined) was N=961.9 per year. For collection years when adult Chiwawa hatchery-origin fish would have been absent in the Chiwawa River (1989 – 1992), the arithmetic mean of natural Chiwawa Chinook census size is N=962.7. We will use this number as the baseline census size to assess if census size has changed. We used two different values for the contemporary census size in the Chiwawa River, NOS only and NOS + HOS. Additionally, we used collection years 2002 – 2005 for the contemporary NOS and HOS estimates, as these are the most recent data and the number of years included for estimation is the same as the pre-hatchery estimate above (i.e., four years). For NOS only, the arithmetic mean census size from 2002 – 2005 was N=536.0. For total census size (i.e., NOS and HOS combined), the arithmetic mean census size from 2002 – 2005 was N=1324.0. For the demographic data presented here, the contemporary census size is larger than the census estimate derived from the years prior to hatchery operation.

Task 2: Document the observed genetic diversity.

Genetic Diversity Categorized By Origin

For Chiwawa River collections categorized by origin (Table 1A), substantial genetic diversity was observed, with heterozygosity estimates over all loci, having a mean of 0.80. Genetic diversity was consistent with expected Hardy-Weinberg random mating genotypic proportions for ten of the eighteen collections. Eight of the nine Chiwawa natural collections were consistent with HWE, and two of nine Chiwawa Hatchery collections were consistent with HWE. F_{IS} is observed to be slight for all Chiwawa population collections, suggesting individuals within collections do not show excessive homozygosity.

The deviations from HWE observed were generally associated with hatchery collections. The two smolt collections (i.e., 1993 and 1994) showed significant deviations from HWE, which may be a function of non-random hatchery practices involving the contributing natural-origin parental broodstocks (i.e., 1991 and 1992 cohort). Deviations from HWE in the remaining hatchery collections may be the result of few individuals being represented in the broodstock (see below).

Additionally, linkage disequilibrium (LD) was also common for Chiwawa hatchery-origin collections and minimal for Chiwawa natural-origin collections. The random association of alleles between loci (i.e., linkage equilibrium) is expected under ideal conditions. LD is observed when particular genotypes are encountered more than expected by chance. Laboratory artifacts (e.g. null alleles) or physical linkage of loci on the same chromosome can cause LD, but the LD we observed was not associated with certain locus combinations, which you would expect if either artifacts or physical linkage were the cause of LD. LD was observed for seven of the nine hatchery-origin collections. As with the deviations from HWE, the high LD in the 1993 and 1994 hatchery-origin collections may be a result of non-random hatchery practices. The substantial LD observed in the hatchery-origin adult collections (collection years 2000, 2001, 2004, and 2006) might be the result of small parental broodstock sizes contributing to those returning adults. During the mid 1990's, the Chiwawa broodstock size was low, with zero individuals collected in 1995 and 1999; so fewer individuals would be contributing to the hatchery adult returns than the natural. This idea is corroborated by the lower LD observed for the 2005 hatchery-origin collection, which had a contributing parental broodstock size in 2001 (i.e., the major contributing parental generation) approximately eight times as large as the previous few collection years (Table 2). LD reappears in the 2006 Chiwawa hatchery-origin collection, which had a contributing parental broodstock size (i.e., for the most-part, the 2002 hatchery brood year) five times lower (Table 2) than that of the 2005 collection.

While seven of nine hatchery-origin collections showed significant LD, only one natural origin collection showed LD, and for this collection, only 10% of the loci-pairs were in disequilibrium (Table 1). The fact that LD predominated in the hatchery samples, suggests that variance in reproductive success (i.e., overrepresentation of particular parents) is higher in the hatchery-origin than in natural-origin collections.

Genetic Diversity Categorized By Spawning Location

For upper Wenatchee River collections categorized by spawning location (Table 1B), substantial genetic diversity was observed, with heterozygosity estimates over all loci, having a mean of 0.79 and ranging from a low of 0.69 (1993 White River) to 0.85 (1993 Little Wenatchee). Genetic diversity was consistent with HWE for nineteen of twenty-nine population collections. For the collections that departed from HWE, seven were from the Chiwawa River, one was from Leavenworth Hatchery, one was the Wenatchee mainstem collection of hatchery-origin – naturally spawning fish, and one was from the White River. F_{IS} is observed to be slight for all population collections except the 1993 White River collection (10% heterozygote deficit) (Table 1B). Collections deviating with HWE generally correlated with collections having high LD. Twelve population collections showed a proportion of pairwise linkage disequilibrium tests (across all loci) greater than 5% (Table 1B), eight of which were Chiwawa collections.

Starting in 1996, spawning location collections are composed of both natural- and hatchery-origin samples. The LD seen in the later spawning location collections may be caused by an admixing effect (i.e., mixing two populations), where random mating has not had the chance to freely associate alleles into genotypes. Interestingly, there appears to be a trend of reducing LD through time within the broodstock collections (Table 1B), which suggests that a “homogenizing” effect is taking place within the Chiwawa River. This observation is discussed more fully in Task 3 below.

Task 3: Test for population differentiation among collections within the Chiwawa River and associated supplementation program.

Introduction

Task 3 was designed to address two hypotheses listed as part of Objective 3 in Murdoch and Peven (2005):

- Ho: Allele frequency $_{\text{Hatchery}}$ = Allele frequency $_{\text{Naturally produced}}$ = Allele frequency $_{\text{Donor pop}}$.
- Ho: Genetic distance between subpopulations $_{\text{Year x}}$ = Genetic distance between subpopulations $_{\text{Year y}}$

Murdoch and Peven (2005) proposed these two hypotheses to help evaluate the Chiwawa supplementation program through the "Conceptual Process" (Figure 5 in Murdoch and Peven 2005; repeated here as Figure 1). There are two components to the first hypothesis, which must be considered separately. The first component involves comparisons between natural-origin populations in the Chiwawa to determine if there have been changes in allele frequencies or genetic distances, through time starting with the donor population. Documenting a change does not necessarily indicate that the supplementation program has directly affected the natural origin fish, as additional tests would be necessary to support that hypothesis. The intent of the second component is to determine if the hatchery produced populations have the same genetic composition as the naturally produced populations.

Although on the surface these two components and their associated comparisons may appear simple, from a hypothesis-testing perspective the analyses are complicated by the fact that natural-origin fish may have had hatchery-origin parents, and hatchery-origin fish may have had natural-origin parents. As such, we organized the Chiwawa genetic data into three data sets: (1) fish origin (hatchery versus natural), (2) spawning location (hatchery broodstock versus in-river (natural) spawners), and (3) four "treatment" groups (1. hatchery-origin hatchery broodstock, 2. hatchery-origin natural spawner, 3. natural-origin natural spawner, and 4. natural-origin hatchery broodstock). We conducted separate analyses using each of the three data sets, with each analysis touching on some aspect of the components necessary to move through the Conceptual Process (Figure 1).

Hatchery- Versus Natural-Origin

We address the following questions with the origin data set:

1. Are there changes in allele frequencies and allele sharing distances in the natural-origin collections from pre-supplementation to today?
2. Are there changes in allele frequencies and allele sharing distances in the hatchery-origin collections from early supplementation to today?
3. Are there significant differences in allele frequencies and large allele sharing distances between hatchery- and natural-origin adults from a collection year, and has this pattern changed through time?

Genic Differentiation Tests – We explicitly tested the hypothesis of no significant differentiation within natural- or hatchery-origin collections from the Chiwawa River using a randomization chi-square test. We show the results for the pairwise comparisons among natural-origin collections from the Chiwawa River populations in the first block of the second page of Table 3. Ten of the 36 (28%) pairwise comparisons have highly significant allele frequency differences, while only 12 of the 36 comparisons (33%) showed no significant differences. Eight of these 12 comparisons involved the 1996 collection, which included only eight samples and therefore provided little power to differentiate allele frequencies. If we exclude the 1996 collection, only 14% of the pairwise comparisons showed no significant differences, and here all but one of these comparisons involved the 1989 collection. The 1989 collection appeared to be the least differentiated collection in the natural-origin data set in that all pairwise comparisons were either not significant, or only mildly significant at the nominal critical value. No comparisons involving the 1989 collection were significant using a Bonferroni-corrected critical value, and 1989 is the only natural-origin collection in our data set that can be classified as "pre-supplementation."

We can interpret these results to indicate that although there appears to be significant year-to-year differences in allele frequencies among post-supplementation collections, the allele frequencies between each post-supplementation collection and the 1989 pre-supplementation collection are not greatly different. However, the level of differentiation does increase from the early post-supplementation years to the more recent years (2001, 2004-2006), although the statistical level of this significance never exceeds the Bonferroni-corrected critical value. Finally, sample sizes were also small for the 1989 collection (n = 36) and we cannot eliminate a reduction in power as a contributing factor for the lack of significance for these tests.

As with the hatchery-origin collections, most pairwise comparisons of allele frequencies between hatchery-origin samples were significant (Table 3, first page, upper block). Out of the 36 pairwise comparisons, all but three are significant at some level, and most comparisons are highly significant. Similar to the natural-origin analysis, the non-significant results were limited to comparisons involving the 1996, which included only eight samples.

As a result of this analysis *we reject the hypothesis that there was no significant differentiation among natural- or hatchery-origin collections from the Chiwawa River*. Furthermore, the allele frequencies of the hatchery-origin collections are significantly different from those of natural-origin collections (Table 3, first page, second block). For those fish collected in the same year, allele frequencies are significantly different between hatchery- and natural-origin collections, although in 2005 the level of significance was below the Bonferroni critical value (Table 3). The next step is to examine the pattern of allelic differentiation to discover first if there is a trend among the data, and second, if this trend suggests that the allele frequency differences among Chiwawa River natural-origin fish collections has been affected by the hatchery-origin fish.

Allele-sharing and Nonmetric Multidimensional Scaling – We constructed a pairwise allele-sharing distance matrix for all hatchery- and natural-origin collections from the Chiwawa River and subjected this matrix to a nonmetric multidimensional scaling analysis, restricting the analysis to two dimensions (Figure 2). The stress statistic for this analysis is 0.09, a value Kruskal (in Rohlf 2002) listed as a good to excellent fit between the actual allele-sharing distances and the Euclidean (straight-line) distances in the plot.

In other words, Figure 2 is a good visual representation of the allele sharing distance matrix; collections with a high percentage of alleles shared will be closer to each other than collections with a lower percentage of alleles shared.

With the exception of the two outlier years (1996 and 1998) the Chiwawa natural-origin collections form a tight cluster indicating an overall common set of shared alleles among these collections. Even if we ignore the 1996 and 1998 hatchery-origin collections, there appears to be a greater variance in shared alleles among the Chiwawa hatchery-origin collections than the natural-origin collections (Figure 2). In fact, the median percentage of alleles shared among the Chiwawa natural-origin collections is 76% compared with 69% alleles shared among the Chiwawa hatchery-origin collections.

Also, there appears to be a convergence in allele sharing distances (i.e., a decrease in allele frequency differences) between the hatchery- and natural-origin fish from the late 1980s/early 1990s to 2006. The series of red arrows in Figure 2 represent the progression of change in hatchery-origin allele sharing distances from 1996 (first adult hatchery origin fish in our analysis) to 2006 and this progression is decidedly in the direction of the natural-origin cluster. However, the most recent natural-origin collections (2001, 2004-2006) appear to have pulled closer to the hatchery-origin collections, compared with the 1989 natural-origin collection (note the close proximity of the 2000 and 1989 natural-origin collections). Nevertheless, the cluster of natural-origin collections adjacent to the hatchery-origin collections in Figure 2 also includes the 1993 natural-origin collection. Qualitatively, it appears that the initial hatchery-origin and natural-origin collections were more different from each other in terms of the percentage of shared alleles than are the most recent hatchery- and natural-origin collections. This may have been a result of a non-random sample of natural-origin fish that was used as broodstock in the initial years of the supplementation program (see discussion in Task 2 concerning deviations from HWE and linkage disequilibrium).

That being said, we do need to emphasize that Figure 2 is dominated by five outlier collections (two each from the 1996 and 1998 collections, and the 1994 smolt collection).

The 1996 and 1998 collections are characterized by small samples sizes, and the 1994 smolt collection has nearly all pairs of loci in linkage disequilibrium (Table 1). If we eliminate these five outlier groups, both the hatchery- and natural-origin collections form a relatively tight cluster. Excluding the five outliers, the median percentage of shared alleles among all pairwise combinations of Chiwawa hatchery versus Chiwawa natural collections is 76%. This compares with a median pairwise percentage of 79% among only Chiwawa natural-origin collections. That is, there are nearly as many alleles shared between the hatchery-origin and natural-origin collections as there are among the natural-origin collections themselves. There is also a narrowing of differences between natural- and hatchery-origin fish from the same collection years from 1993 (76% shared alleles) through 2006 (83% shared alleles).

If allelic differentiation among collections is a function of genetic drift, we would expect a positive correlation between the number of years between two collections and the allele sharing distance. That is, if genetic drift is the primary cause of allele frequency differences between two collections, the greater the number of years between the two collections the larger the allele-sharing distance. For both the natural- and hatchery-origin collections we examined the relationship between the number of years between a pair of collections and the collections' allele-sharing distance (Figure 3). Although the relationship between time interval and allele distance appears to be a positive function in the natural collections, the slope of the regression line is 0.0017, and is not significantly different from zero. Furthermore, the correlation coefficient (r^2) equals 0.1068, which means that the time interval between collections accounts for only 10% of the pairwise differences in allelic distance. The hatchery-origin collections do show a significantly positive slope (0.0037; $p = 0.0254$) and a regression coefficient nearly three times greater than that for the natural-origin collections. However, the correlation coefficient is still relatively small ($r^2 = 0.3290$), indicating that the time interval between collections accounts for one-third of the pairwise differences in allelic distance. The results suggest that if genetic drift is a factor in allelic differentiation between collections, it is only a minor factor, and appears to have affected the hatchery-origin collections more than the natural-origin collections.

If four-year-old fish dominate each collection year, we would expect a closer relationship among collections that are spaced at intervals of four years. The average percentage of alleles shared between two natural-origin collections that are separated by four years or a multiple of four years is 81%, compared with 78% for natural-origin collections separated by years that are not divisible by four. Likewise, for hatchery-origin collections the average percentage of alleles shared is 80% and 75% for collections separated by years divisible and not divisible by four, respectively. Although the percent differences described above are relatively small, they are consistent with the idea that allelic differences between collections are a function of year-to-year variability among different cohorts of four year-old fish.

Summary – The allele frequencies within and between natural- and hatchery-origin collections are significantly different, but there does not appear to be a robust signal indicating that the recent natural-origin collections have diverged greatly from the pre- or early post-supplementation collections. Genetic drift will occur in all populations, but does not appear to be a major factor with the Chiwawa collections. We propose that the differences among collections are a function of differences in allele frequencies among cohorts of the four year-old fish that dominate each collection.

Hatchery Broodstock Versus Natural (In-River) Spawners

We address the following questions with the spawner data set:

1. Are there changes in allele frequencies and allele sharing distances in the natural spawning collections from pre-supplementation to today?
2. Are there changes in allele frequencies and allele sharing distances in the hatchery broodstock collections from early supplementation to today?
3. Are there significant differences in allele frequencies and large allele sharing distances between hatchery and natural spawning adults from a collection year, and has this pattern changed through time?

Genic Differentiation Tests – For the most part there are significant differences in allele frequencies among collections for both the hatchery broodstock and natural spawners (Table 4), and these differences are consistent with the origin data set (Table 3). There are four collection years with paired samples (2001, 2004-2006) where we can compare allele frequency differences between the hatchery broodstock and natural spawners, within the same year. The 2001 hatchery broodstock and natural spawner collections have significantly different allele frequencies, but the level of significance decreased from 2001 to 2004, and become non-significant in 2005 and 2006 (Table 4). This indicates that by 2005, the hatchery broodstock and natural spawners collections were effectively sampling from the same population of fish. Additionally, the percentage of alleles shared between the hatchery broodstock and the natural spawners increased from 76% in 2001 to 86% in 2006 (allele sharing distance matrix, not shown). From this analysis, we conclude that although there are year-to-year differences in allele frequencies within the natural and hatchery spawner collections, *there appears to be a convergence of allele frequencies within collection-year, between the natural and hatchery spawner populations*.

Linkage Disequilibrium – Linkage disequilibrium is the correlation of alleles between two loci, and can occur for several reasons. If two loci are physically linked on the same chromosome, than alleles from each of these loci should be correlated. However, linkage between two loci can occur as a result of population bottlenecks, small population sizes, and natural selection. If any of these conditions had occurred or were occurring within the Chiwawa River system, we would expect to find substantial linkage disequilibrium in many or perhaps all Chiwawa collections. However, many Chiwawa collections, especially the natural-origin collections, do not show linkage disequilibrium (Table 1), and it would appear that the linkage disequilibrium within certain Chiwawa collections is not a function of the processes listed above. Linkage disequilibrium can also result if the collection is composed of an admixture. That is, if two or more reproductively isolated populations are combined into a single collection, the collection will show linkage disequilibrium. Each broodstock and natural spawning collection is composed of natural- and hatchery-origin fish. If these hatchery- and natural-origin fish are drawn from the same population, the spawning collections should not show substantial linkage disequilibrium. However, if the hatchery- and natural-origin fish are from different populations (i.e., full hatchery – natural integration has not been achieved), the spawning collections should show substantial linkage disequilibrium.

There are only three Chiwawa spawning collections that are not composed of both hatchery- and natural-origin samples: 1989 (natural-origin, natural spawner), 1993 (natural-origin, hatchery broodstock), and 2001 (natural-origin, natural spawner). Of the 10 spawning collections with both hatchery- and natural-origin fish, seven show significant linkage disequilibrium. Two of the three collections that did not show linkage disequilibrium are the 1996 and 1998 hatchery broodstock collections, which are composed of only seven natural- and six hatchery-origin fish, and two natural- and 19 hatchery-origin fish, respectively. Within the hatchery broodstock collections with linkage disequilibrium, the percent of loci pairs showing linkage decreased from 32% in 2000 to 13% in 2001 and 2004, to only 1% and 5% in 2005 and 2006, respectively (Table 1). If the homogenization of allele frequencies of natural- and hatchery-origin fish was increasing from 2000 to 2006, we would expect a decrease in linkage disequilibrium among the broodstock collections. This is what occurred within the hatchery broodstock collections, but did not occur within the natural spawner collections, where the percent of loci pairs showing linkage was 18% in 2004, 6% in 2005, and 10% in 2006 (Table 1). Furthermore, the 2001 natural spawner collection, with no hatchery-origin component showed linkage disequilibrium with 9% of loci pairs.

There is no correlation between percent of loci pairs showing linkage disequilibrium and percent of broodstock composed of hatchery-origin fish ($r^2 = 0.0045$). Furthermore, the natural spawner and hatchery broodstock collections were each composed of roughly the same average percentage of hatchery-origin fish (57% and 53%, respectively). If the decrease in linkage disequilibrium among the hatchery broodstock collections from 2000 to 2006 was a result of a homogenization of allele frequencies of natural- and hatchery-origin fish in the broodstock, the same degree of homogenization did not occur within the natural spawner collections. This would occur if natural- and hatchery-origin fish spawning within the river remain segregated, either by habitat or by fish behavior.

Summary – As with the origin data set, there are significant allele frequency differences within and between hatchery broodstock and natural spawner collections. However, in recent years the allele frequency differences between the hatchery broodstock and natural spawner collections has declined. Furthermore, based on linkage disequilibrium, there is a genetic signal that is consistent with increasing homogenization of allele frequencies within hatchery broodstock collections, but a similar homogenization within the natural spawner collection is not apparent. These data suggest that there exists consistent year-to-year variation in allele frequencies among hatchery and natural spawning collections, but there is a trend toward homogenization of the allele frequencies of the natural- and hatchery-origin fish that compose the hatchery broodstock.

Four Treatment Groups

Analyses of genetic differences between hatchery (broodstock) and natural spawner collections is confounded by the fact that each these two groups are composed of fish of natural- and hatchery-origin. To understand the effects of hatchery supplementation on *natural-origin fish that spawn naturally*, we needed to divide the Chiwawa data set into four mutually exclusive groups: (1) hatchery-origin hatchery broodstock, (2) hatchery-origin natural spawner, (3) natural-origin hatchery broodstock, and (4) natural-origin natural spawner, with each group consisting of multiple collection years, for a total of 25 different groups.

Allele-sharing and Nonmetric Multidimensional Scaling –As with previous analyses discussed above, we constructed a pairwise allele-sharing distance matrix for all collections from each of these treatment groups and subjected this matrix to a nonmetric multidimensional scaling analysis, restricting the analysis to two dimensions. Figure 4 shows that five outlier groups dominate the allele-sharing distances within this data set. These outlier groups are also present in Figure 2, as discussed above, and Figure 2 and 4 resemble each other because the same fish are included in each analysis. The difference between Figures 2 and 4 is that in Figure 4 the fish are grouped into collection year and the four treatment groups, rather than collection year and two treatment groups (hatchery- versus natural-origin).

Figure 4 does not provide useful resolution of the groups within the polygon, because the outlier groups dominate the allele sharing distances. We removed the five outlier groups from Figure 4, recalculated the allele sharing distances and subjected this new matrix to a multidimensional scaling analysis (Figure 5). Figure 5 shows separation among the 2001, 2004-2006 collections, but this separation does not necessarily indicate that within-year collections are more similar to each other than any collection is to a collection from another year. For example, the 2006 natural-origin natural spawner and the 2005 natural-origin hatchery broodstock collections share 81% alleles, while the 2006 natural-origin natural spawner and 2006 hatchery-origin hatchery broodstock collections share 75% alleles. There does not appear to be any discernable pattern of change in allele-sharing distance among the collections relevant to pre- or post-supplementation. Although the 1989 pre-supplementation natural-origin collection appears distinct (Figure 5), the 1993 natural-origin hatchery broodstock collection appears quite similar to the 2005 and 2006 natural-origin collections (Figure 5). The 1993 natural-origin hatchery broodstock collection, although not technically pre-supplementation, is composed of fish whose ancestry cannot be traced to any Chiwawa hatchery fish. Therefore, there is no clear pattern of allele sharing change from pre-supplementation to recent collections.

There does appear to be some change in the average percentage of alleles shared within the 2001 to 2006 collections, with an increase from 74% in 2001 and 2004 to 78% and 79% in 2005 and 2006, respectively. The results provided by this analysis are consistent with the results presented in the origin and spawner data sets. That is, there are allele frequency and allele sharing differences among the collections, but analyses do not strongly suggest that these differences are a function of the supplementation program. Furthermore, there is also a weak signal that the hatchery and natural collections within the most recent years are more similar to each other than in the previous years.

Overall Genetic Variance – Although there are signals of allelic differentiation among Chiwawa River collections, there are no robust signs that these collections are substantially different from each other. We used two different analyses to measure the degree of genetic variation that exists among individuals and collections within the Chiwawa River. First, we conducted a principal component analysis using all Chiwawa samples with complete genotypes (i.e., no missing alleles from any locus). Although the first two principal component axes account for only 10.5% of the total molecular variance, a substantially greater portion of that variance is among individual fish, regardless of their identity, rather than among hatchery and natural collections (Figure 6). The variances in principal component scores among individuals are 11 and 13 times greater than the variance in scores among collections, along the first and second axes, respectively.

Second, we conducted a series of analyses of molecular variance (AMOVA) to ascertain the percentage of molecular variance that could be attributed to differences among collections. We organized these analyses to test also for differences in the hierarchical structure of the data. That is, we tested for differences among collections using the following framework:

- No organizational structure – all 25 origin-spawner collections considered separately
- Origin-spawner collections organized into 10 collection year groups
- Origin-spawner collections organized into 2 breeding location groups (hatchery versus natural)
- Origin-spawner collections organized into 2 origin groups (hatchery versus natural)
- Origin-spawner collections organized into the 4 origin-spawner groups

It is clear from this analysis that nearly all molecular variation, no matter how the data are organized, resides within a collection (Table 5). The percentage of total molecular variance occurring within collections ranged from 99.68% to 99.74%. The among group variance component was limited to less than 0.26% and in all organizational structures, except “no structure,” the among group percentage was not significantly greater than zero. Furthermore, none of the organizational structures provided better resolution than “no structure” in terms of accounting for molecular variance within the data set. *These results indicate that if there are significant differences among collections of Chiwawa fish, these differences account for less than one percent of the total molecular variance, and these differences cannot be attributed to fish origin or spawning location.*

Summary and Conclusions

We reject the null hypothesis that the allele frequencies of the hatchery collections equal the allele frequencies of the natural collections, which equals the allele frequency of the donor population. Furthermore, because the allele-sharing distances are not consistent within and among collections years, we also reject the second stated hypothesis discussed above. However, there is an extremely small amount of genetic variance that can be attributed to among collection differences. The allelic differentiation that does exist among collections does not appear to be a function of fish origin, spawning location, genetic drift, or collection year. Figure 5 and related statistics does suggest that hatchery and natural collections in 2005 and 2006 are more similar to each other than previous years’ collections, and this would be expected in a successful integrated hatchery supplementation program.

Since each of these collection years are generally composed of four-year-old fish, the differentiation among these collections for the most part is differentiation among specific cohorts. The slightly greater percentage of alleles shared among collections that are separated in time by multiples of four years, compared with collections that are not separated in time as such, suggests that cohort differences may be the most important factor accounting for differences in allele frequencies among collections.

Task 4: Develop a model of genetic drift.

See Task 3

Task 5: Analyze spring Chinook population samples from the Chiwawa River and Chiwawa Hatchery from multiple generations.

See Task 3

Task 6: Analyze among population differences for upper Wenatchee spring Chinook.

Supplementation of the Chiwawa River spring Chinook population may affect populations within the Wenatchee River watershed other than the Chiwawa River stock. If the stray rate for Chiwawa hatchery-origin fish is greater than that for natural-origin fish, an increase in gene flow from the Chiwawa population into other populations may result. If this gene flow is high enough, Chiwawa River fish may alter the genetic structure of these other populations. Records from field observations indicate that hatchery-origin fish are present in all major spawning aggregates (A.R Murdoch, unpublished data), and these fish are successfully reproducing (Blankenship et al 2006). The intent of this task is to investigate if there have been changes to the genetic structure of the spring Chinook stocks within upper Wenatchee tributaries during the past 15-20 years, and if changes have occurred, are they a function of the Chiwawa River Supplementation Program? Therefore, we ask the following two questions:

1. Are allele frequencies within populations in the upper Wenatchee stable through time? That is, is there significant allelic differentiation among collections within upper Wenatchee populations?
2. Are the recent collections from the upper Wenatchee populations more similar to the Chiwawa population than earlier collections from the same populations?

For this task we analyzed natural spawning collections from the White River (natural-origin), Little Wenatchee River (natural-origin), Nason Creek (natural-origin), and

Wenatchee mainstem (hatchery-origin), and hatchery collections from Leavenworth NFH and Entiat River NFH (Table 1). We also included in the analysis the natural- and hatchery-origin collections from the Chiwawa River. There are no repeated collections from Leavenworth, Entiat, Little Wenatchee, and Wenatchee mainstem (Table 1), so for many of the analyses we have limited our discussion to the Chiwawa River, White River, and Nason Creek collections. Furthermore, genetic structure of the Little Wenatchee collection, which consisted of only 19 samples, was unexpectedly quite different from the other collections. For example, the F_{ST} statistic measures the percent of total molecular variation that can be attributed to differences between populations. The median F_{ST} for all pairwise combinations of collections from all populations, except Little Wenatchee (33 populations, 528 individual F_{ST} statistics) equals 0.010 (1%), with a range of 0.000 to 0.037 (Table 6). The median F_{ST} for the Little Wenatchee paired with all other collections (33 individual F_{ST} statistics) equals 0.106 (10.6%), with a range of 0.074 to 0.121. The ten-fold increase in the F_{ST} statistic indicates that either the Little Wenatchee spring Chinook is unique among the upper Wenatchee River stocks, or this 1993 collection is somehow aberrant. Therefore, we exclude the Little Wenatchee collection from many other analyses.

Population Differentiation – Table 3 provides the levels of significance for all pairwise genic differentiation tests. Most between-collection comparisons are highly significant, with no pattern of increasing or decreasing differentiation with time, and no differences when comparisons are made with Chiwawa hatchery- versus Chiwawa natural-origin fish. For example, excluding the outlier 1996 and 1998 Chiwawa hatchery- and natural-origin collections, Nason Creek showed highly significant allele frequency differences between the Chiwawa hatchery- and natural-origin collections at 100% and 86% of the comparisons, respectively. The same comparisons with the White River produced 100% and 93% highly significant allele frequency comparisons, respectively. Allele frequencies between Nason Creek and White River were likewise differentiated from each other.

The collection allele frequencies within the upper Wenatchee system are significantly different, and these differences do not appear to change as a function of time (Table 3). Nason Creek shows greater within-population year-to-year variation in allele frequencies than does the White River, with 47% of the pairwise comparisons showing highly significant differences, compared with only 13% for the White River. However, the 2005 and 2006 collections from the White River appear to be somewhat more differentiated from not only each other, but from the earlier collections from the White River.

Despite the high degree of temporal and spatial structure suggested by the genic differentiation tests, as described above for within-Chiwawa analysis (Task 3), most of the genetic variation within this data set occurs within populations, rather than between populations (Table 6). The F_{ST} values for most population comparisons are between 0.01 and 0.02, indicating 1% to 2% among-population variance, with the remaining 98% to 99% variance occurring within populations. The White River shows the highest median F_{ST} among the natural-origin collections, equal to 0.014, compared with 0.009 for both the Nason Creek and Chiwawa natural-origin collections. The median F_{ST} for the Chiwawa hatchery-origin collections (0.012) was higher than that for the Chiwawa natural-origin collections.

Table 7 summarizes the information from the F_{ST} analyses, under five different temporal and spatial scenarios. Under all scenarios, over 99% of the molecular variance is within populations. There is significantly greater spatial structure among populations ("Origin") in 2005 and 2006 than from 1989 to 1996. That is, there appears to be more spatial structure among the Chiwawa hatchery-origin, Chiwawa natural-origin, White River, and Nason Creek now, than in 1989 to 1996, despite the potential homogenizing and cumulative effect of hatchery strays. However, we stress that the amount of molecular variance associated with the among population differences, despite being significantly greater than 0.00%, is limited to only 0.43%.

Allele-sharing and Nonmetric Multidimensional Scaling – As in the Chiwawa River data discussed above, we constructed an allele-sharing distance matrix and then subjected that matrix to a multidimensional scaling analysis (Figure 7). Consistent with all previously discussed multidimensional scaling analyses, the 1996 and 1998 adult, and the 1994 smolt collections are outliers. There is clear separation between the White River collections and all other natural-origin and Chiwawa hatchery-origin collections, indicating that there are more alleles shared among the Nason Creek and Chiwawa collections, than with the White River collections. Furthermore, there is a slight separation between the Chiwawa natural-origin natural spawner collections and Nason Creek collections, suggesting different groups of shared alleles between these populations. There is more variation in the allele-sharing distances among collections involved with the Chiwawa hatchery (origin or broodstock) than any of the natural-origin collections, even if we exclude the 1994, 1996, and 1998 collections. This suggests that there is more year-to-year variation in the composition of hatchery-origin and hatchery broodstock than within natural-origin populations throughout the upper Wenatchee. All Wenatchee mainstem fish are hatchery-origin, and if these fish are from the Chiwawa Supplementation Program (rather than from Leavenworth), it is not unexpected that this collection would be plotted within the Chiwawa polygon (Figure 7).

Assignment of Individual to Populations – Finally, we conducted individual assignment tests whereby we assigned each individual fish to a population, based on a procedure developed by Rannala and Mountain (1997) (Table 8 and 9). Individual fish may be correctly assigned to the population from which they were collected, or incorrectly assigned to a different population. Incorrect assignments may occur if the fish is an actual migrant (i.e., source population different from population where collected), or because the genotype for that fish matches more closely with a population different from its source. If there are many individuals from a population incorrectly assigned to populations other than its source population, that original population is either unreal (i.e., an admixture), or there is considerable gene flow between that population and other populations. Furthermore, in assigning individuals to populations, we can either accept the assignment with the highest probability, regardless of how low that probability may be, or we can establish a more stringent criterion, such as to not accept an assignment unless the posterior probability is equal to or greater than 0.90. This value is roughly equal to having the likelihood of the most-likely population equal to 10 times that of the second most-likely population.

We provide a summary of the assignments in Tables 8 and 9. On average, nearly 50% of the fish are assigned incorrectly if we accept all assignments (Table 8), but the incorrect assignment rate drops to roughly 10% when we accept only those assignments with probabilities greater than 0.90. However, with this more stringent criterion, nearly 64% of the fish go unassigned. These results indicate that the allele frequency distributions for these populations are very similar, and it would be very difficult to assign an individual fish of unknown origin to the correct population. If all fish are assigned, there is a 50% chance, overall, of a correct assignment. If you accept only those assignment with the 0.90 criterion, nearly two-thirds of the fish would be unassigned, but there is a 90% chance of correctly assigning those fish that are indeed assigned.

Of all the populations in the data set, there are fewer errors associated with assigning fish to the White River. If all fish are assigned (Table 8), 72% of those fish assigned to the White River, are actually from the White River (115 fish out of a total of 159 fish assigned to the White River). This compares to a rate of only 52% and 53% for Nason Creek and Chiwawa natural-origin, respectively, and 60% for the Chiwawa hatchery-origin collections. With the 0.90 criterion (Table 9), 89% of the fish assigned to the White River, are actually from the White River, compared with 70% and 65% for Nason Creek and Chiwawa natural origin, respectively, and 81% for the Chiwawa hatchery origin.

When all fish are assigned, most of the incorrectly assigned fish from Nason Creek and White River are assigned to Chiwawa River, at roughly equal frequencies to the hatchery- and natural-origin populations. Incorrectly assigned fish to other populations occur at a slightly higher rate in Nason Creek than in the White River. However, when only those fish meeting the 0.90 criterion are assigned (Table 9), incorrectly assigned fish from Nason Creek are distributed among White and Chiwawa Rivers, as well as Leavenworth NFH, and the Entiat NFH. Mis-assignment to the Chiwawa hatchery-origin was the highest among the Nason Creek collections, equal to nearly 14%. This contrasts with the White River where mis-assignments do not exceed 7% anywhere, and there is a roughly even distribution of mis-assignments among Nason Creek and Chiwawa River collections.

Summary and Conclusions – There is little geographic or temporal structure among populations within the upper Wenatchee systems. Among population molecular variance is limited to 1% or less. The little variance that can be attributed to among populations indicates that the White River is more differentiated from the Chiwawa and Nason populations than these populations are from each other. Furthermore, although we cannot rule out a hatchery effect on the Nason Creek and White River populations, there is no indication there has been any temporal changes in allele frequencies within these populations that can be attributed directly to the Chiwawa River Supplementation Program. In fact, Table 7 weakly suggests that there is more differentiation among these populations now, than there was before or at the early stages of Chiwawa supplementation.

Therefore, returning to our two original questions, there are significant differences in allele frequencies among collections within populations, and among populations within the upper Wenatchee spring Chinook stocks. However, these differences account for a very small portion of the overall molecular variance, and these populations overall are very similar to each other. There is no evidence that the Chiwawa River Supplementation Program has changed the allele frequencies in the Nason Creek and White River populations, despite the presence of hatchery-origin fish in both these systems. Finally, of all the populations within the Wenatchee River, the White River appears to be the most distinct. Yet, this distinction is more a matter of detail than of large significance, as the median F_{ST} between White River collections and all other collections (except the Little Wenatchee) is less than 1.5% among population variance.

Task 7: Calculate the inbreeding effective population size using demographic data for each sample year, and document the ratio of census to effective size.

This analysis was completed by Williamson et al. (submitted).

Task 8: Calculate LD N_b using genetic data for each sample year, and document the ratio of census to effective size.

We report N_e estimated for the Chiwawa River collections based on the bias correction method of Waples (2006) implemented in LDNe (Do and Waples unpublished). N_e estimates based on LD are best interpreted as the effective number of breeders (N_b) that produced the sample (Waples 2006).

For collections categorized by spawning location (i.e., hatchery broodstock or natural), estimates of N_b are shown in Table 10. Considering the hatchery broodstock, N_b estimates range from 30.4 (1996) to 274.3 (2005). To obtain N_e /N ratios, the N_b estimate is multiplied by four (i.e., mean generation length) and divided by the total in river (i.e., NOS [natural-origin spawners] plus HOS [hatchery-origin spawners]) census data from four years prior (i.e., major cohort; see Table 2). The observed N_e /N ratios for the broodstock collections range from 11% to 54% of the census estimate, excluding the 2000 collection which is 106%. A ratio greater than one is possible under special circumstances, and certain artificial mating schemes within hatcheries can inflate N_e above N; yet, it is unknown if this is the case for this collection. While no direct comparisons are possible, the N_b estimates reported by Williamson et al. (submitted) for Chiwawa broodstock collections from 2000 – 2003 are similar in magnitude to our estimates. For Chiwawa natural spawner collections, the N_b estimates range from 5.2 (1989) to 231.5 (2005), with observed N_e /N ratios of 22% - 48% of the census estimate.

Task 9: Calculate N_b using the temporal method for multiple samples from the same location.

Estimates of effective number of breeders (N_b) derived from Waples' (1990) temporal method are shown in Tables 11-13. Eight collection years were used for the Chiwawa broodstock collections (Table 11). The harmonic mean of all pairwise estimates of N_b ($\tilde{N}_b$) was 269.4. This estimate is the contemporary N_e for Chiwawa broodstock collections. For the five collection years of Chiwawa in-river spawners (Table 12), the estimated $\tilde{N}_b$ = 224.2. This estimate is the contemporary N_e for Chiwawa River natural spawner collections. Since the Chiwawa Supplementation Program is integrated by design, we also performed another estimation of N_e using composite hatchery and natural samples. There are paired samples from 2004-2006. We combined genetic data for hatchery (HOS) and natural (NOS) origin fish from 2004 – 2006 to create a single Chiwawa River natural spawner sample for each year. The three composite samples from 2004 – 2006 were then analyzed using the temporal method (Table 13), resulting in a $\tilde{N}_b$ = 386.8. This estimate is the contemporary N_e for Chiwawa River.

Williamson et al. (submitted) estimated N_e using Waples' (1990) temporal method for Chinook captured in 2004 and 2005, and used age data to decompose brood years into consecutive cohorts from 2000 – 2003. They report for Chiwawa broodstock a $\tilde{N}_b$ = 50.4. This estimate is not similar to our Chiwawa broodstock estimate. However, if we analyze the hatchery-origin Chinook only, our estimate is $\tilde{N}_b$ = 80.1 for collection years 1989 – 2006 (data not shown). Williamson et al. (submitted) report for Chiwawa naturally spawning Chinook a $\tilde{N}_b$ = 242.7, which is slightly higher than our estimate for in-river spawners from 1989 – 2006, but lower than our estimate from combined NOS and HOS Chinook from 2004 – 2006 collection years.

<u>Task 10:</u> Use available data and the Ryman-Laikre and Wang-Ryman models to determine the expected change of N_e for natural spring Chinook salmon in the Wenatchee River due to hatchery operation.

N_e is generally thought to be between 0.10 and 0.33 of the estimated census size (Bartley et al. 1992; RS Waples pers. comm.). We used this range to generate an estimate of N_e for Chiwawa natural spawners prior to hatchery operation. For brood years 1989 – 1992, the arithmetic mean census size was N=962.7 (Table 2), resulting in an estimated N_e ranging from 96.3 – 317.7. The contemporary estimate of N_e calculated using genetic data for the Chiwawa in-river spawners is N_e=224.2 (Table 12), falling in the middle of the pre-hatchery range. The N_e /N ratio calculated using 224.2 and the arithmetic census of NOS Chinook from 1989 – 2005 is 0.42. A more appropriate contemporary N_e to compare with the pre-hatchery estimate (i.e., 96.3 – 317.7) is the combined NOS and HOS estimate from natural spawners, since the supplementation program is integrated. As discussed above, the contemporary estimate of N_e calculated using genetic data for Chiwawa NOS and HOS Chinook is N_e=386.8 (Table 13), which is slightly larger than the pre-hatchery range, suggesting the N_e has not declined during the period of hatchery operation. The N_e /N ratio calculated using 386.8 and the arithmetic census of NOS and HOS Chinook from 1989 – 2005 is 0.40. These results suggest the Chiwawa Hatchery Supplementation Program has not resulted in a smaller N_e for the natural spawners from the Chiwawa River.

Williamson et al. (submitted) argued that since their combined (i.e., broodstock and natural) N_e estimate was lower than the naturally spawning estimate, the supplementation program likely had a negative impact on the Chiwawa River N_e. We disagree with this interpretation of these data. Since the natural spawning component is mixed hatchery and natural ancestry, the N_e estimates from natural spawning data are the results that bear on possible hatchery impacts. The census data show the population declined in the mid 1990's and rebounded by 2000 (Table 2). This trend is reflected in the N_e results, as shown above, and Williamson et al. (submitted) clearly show in their Table 4 the N_e was lower in 2000 (N_e = 989) than it was in 1992 (N_e = 2683). Yet, the important comparison they make in our view was the natural spawning N_e versus the natural only component N_e (i.e., hypothetically excluding hatchery program). Williamson et al. (submitted) report the 1989 – 1992 N_e estimated from naturally spawning Chinook (i.e., NOS and HOS integrated) was essentially the same as the natural only component estimate, 2683 and 2776, respectively. This result is not surprising since no HOS fish were present between 1989 – 1992. They also report that the 1997 – 2000 N_e estimated from naturally spawning Chinook (i.e., NOS and HOS integrated) was N_e =989, while the natural-origin estimate of N_e in 1997 – 2000 was N_e = 629. Since the natural-origin estimate of 629 is lower than 989, the N_e estimate from all in-river spawners, we argue that their analysis of demographic data show the N_e estimated from naturally spawning Chinook (i.e., NOS and HOS integrated) is larger only if the hatchery Chinook in the river are ignored.

Task 11: Use individual assignment methods to determine the power of self-assignment for upper Wenatchee River tributaries.

See "Assignment of Individual to Populations" in Task 6

Conclusions

Has the Chiwawa Hatchery Supplementation Program succeeded at increasing the census size of the target population while leaving genetic integrity intact? This is an important question, as hatcheries can impact natural populations by reducing overall genetic diversity (Ryman and Laikre 1991), reducing the fitness of the natural populations through relaxation of selection or inadvertent positive selection of traits advantageous in the hatchery (Ford 2002; Lynch and O'Hely 2001), and by reducing the reproductive success of natural populations (McLean et al. 2003). The census data presented here show that the current natural spawning census size is similar to the pre-supplementation census size. Despite large numbers of hatchery-origin fish on the Chiwawa River spawning grounds, the genetic diversity of the natural-origin collections appear unaffected by the supplementation program; heterozygosities are high, and contemporary N_e is similar (perhaps slightly higher) than pre-supplementation N_e. We did find significant year-to-year differences in allele frequencies in both the origin and spawner datasets, but these differences do not appear to be related to fish origin, spawning area, or genetic drift. However, we do suggest that cohort differences may be the most important factor accounting for differences in allele frequencies among collections.

The main objective of this study was to determine the potential impacts of the hatchery program on natural spring Chinook in the upper Wenatchee system. We did this by analyzing temporally replicated collections from the Chiwawa River, and by comparing genetic diversity prior to the presumed effect of the Chiwawa Hatchery Supplementation Program, with contemporary collections. We report that the genetic diversity present in the Chiwawa River is unchanged (allowing for differences among cohorts) from 1989 – 2006, and the contemporary estimate of the effective population size (N_e) using genetic data is approximately the same as the N_e estimate extrapolated from 1989 – 1992 census data (i.e., pre-hatchery collection years). We observed substantial genetic diversity, with heterozygosities ~80% over thirteen microsatellite markers. Yet, temporal variation in allele frequencies was the norm among temporal collections from the same populations (i.e., location). The genetic differentiation of replicated collections from the same population is likely the result of salmon life history in this area, as four-year-old Chinook comprise a majority of returns each year. The genetic tests are detecting the differences of contributing parents for each cohort. An important point related to the temporal variation, is that the hatchery broodstock is composed in part of the natural origin Chinook from the Chiwawa River. When we compared the genetic data (within a collection year) for Chinook brought into the hatchery as broodstock with the Chinook that remained in the river (years 2001, 2004 – 2006), there was a trend of decreasing statistical differences in allele frequencies from 2001 to 2004, and no differences were detected for 2005 and 2006. While the replicated collections may have detectable differences in allele frequencies, those differences reflect actual differences in cohorts, not the result of hatchery operations, and the hatchery broodstock collection method captures the differences in returning Chiwawa River spring adults each year. We conclude from these results that the genetic diversity of natural spring Chiwawa Chinook has been maintained during the Chiwawa Hatchery Supplementation Program.

We observe slight, but statistically significant population differentiation between Chiwawa River, White River, and Nason Creek collections. Murdoch et al (2006) and Williamson et al. (submitted) also observed population differentiation between Chiwawa River, White River, and Nason Creek collections. Yet, 99.3% of the genetic variation observed was within samples, very little variance could be attributed to population differences (i.e., population structure). The AMOVA analysis and poor individual assignment results suggest the occurrence of gene flow among Wenatchee River locations or a very recent divergence of these groups. While Murdoch et al. 2006 did not perform an AMOVA analysis, their F_{ST} results provide comparable data to our among-population results. Murdoch et al. 2006 report F_{ST} ranging from 2%-3% for pairwise comparisons between of Chiwawa, White, and Nason River collections. Since F_{ST} is an estimate of among-sample variance, these results also imply a majority of the genetic variance (i.e., 97%-98%) resides within collections. To provide further context for the magnitude of these variance estimates, we present the among-group data from Murdoch et al. 2006 comparing summer-run and spring-run Chinook from the Wenatchee River. They report that approximately 91% of observed genetic variance is within-collection for comparisons between collections of summer- and spring-run Chinook. Ultimately, the information provided by this and other reports will be incorporated into the management process for Wenatchee River Chinook. However, we would like to emphasize that the application of these genetic data to management is more about the goals related to the distribution of genetic diversity in the future than specific data values reported. If Chinook are collected at Tumwater Dam instead of within the upper Wenatchee River tributaries, a vast majority of the genetic variation present in the basin would be captured, although any differences among tributaries would be mixed. Alternatively, management policies could be crafted to promote and maintain the among-group genetic diversity that genetic studies consistently observe to be non-zero within the Wenatchee River.

We agree with Murdoch et al. (2006) that it appears hatchery Chinook are not contributing to reproduction in proportion to their abundance. Additionally, if the total census size (i.e., NOS and HOS combined) within the Chiwawa River does not continue to increase, genetic diversity may decline within this system, given the smaller N_e within the hatchery-origin collections compared with the natural-origin collections.

Acknowledgements

We would like to thank Denise Hawkins, Craig Busack, and Cheryl Dean for helpful comments regarding this project. This project was funded by Chelan County PUD and the Washington State General Fund.

Literature Cited

Araki H, Waples RS, Ardren WR, Cooper B, Blouin MS (2007) Effective population size of steelhead trout: influence of variance in reproductive success, hatchery programs, and genetic compensation between life-history forms. *Molecular Ecology*, **16**:953-966.

Arden WR and Kapuscinski AR (2003) Demographic and genetic estimates of effective population size (N_e) reveals genetic compensation in steelhead trout. Molecular Ecology 12: 35-49

Banks MA, Blouin MS, Baldwin BA, Rashbrook VK, Fitzgerald HA, Blankenship SM, Hedgecock D (1999) Isolation and inheritance of novel microsatellites in chinook salmon (Oncorhynchus tschawytscha). *Journal of Heredity*, **90**:281-288.

Banks MA, Rashbrook VK, Calavetta MJ et al (2000) Analysis of microsatellite DNA resolves genetic structure and diversity of chinook salmon (*Oncorhynchus tshawytscha*) in California's Central Valley. Canadian Journal of Fisheries and Aquatic Sciences 57:915-927.

Bartley D, Bentley B, Brodziak J, Gomulkiewicz R, Mangel M, and Gall GAE (1992) Geographic variation in population genetic structure of chinook salmon from California and Oregon. Fish. Bull., U.S. 90:77-100.

Blankenship SM, Von Bargen J, and Truscott KD (2006) Genetic analysis of White River juveniles retained for captive brood at AquaSeed to assess the hatchery status of contributing parents. Developed for Grant County PUD.

Blankenship SM and Murdoch AR (2006) Study Plan For Assessing the Genetic Diversity of Natural Chiwawa River Spring Chinook Salmon And Evaluating The Effectiveness Of Its Supportive Hatchery Supplementation Program. Developed for Chelan County PUD and the Habitat Conservation Plan’s Hatchery Committee.

Bugert R (1998) Mechanics of supplementation in the Columbia River. Fisheries 23:11-20.

Cairney M, Taggart JB, Hoyheim B (2000) Characterization of microsatellite and minisatellite loci in Atlantic salmon (*Salmo salar* L.) and cross-species amplification in other salmonids. *Mol Ecol*, **9**:2175-2178.

Campton DE (1987) Natural hybridisation and introgression in fishes: methods of detection and genetic interpretations. In: Population genetics and fisheries management. (Eds. Ryman, N. and Utter, F.), pp. 161-192. Washington Sea Grant Program, University of Washington Press, Seattle, USA.

Chapman D, Giorgi A, Hillman T, Deppert D, Erho M, Hays S, Peven C, Suzumoto B, and Klinge R (1994) Status of summer/fall chinook salmon in the mid-Columbia region. Report for Chelan, Douglas, and Grant County PUDs. 412 p. + app. (Available from Don Chapman Consultants, 3653 Rickenbacker, Ste. 200, Boise, ID 83705.)

Chapman D, Peven C, Giorgi A, Hillman T, and Utter F (1995) Status of spring chinook salmon in the mid-Columbia River. Don Chapman Consultants, Inc., 477 p. (Available from Don Chapman Consultants, 3653 Rickenbacker, Ste. 200, Boise, ID 83705.)

Cockerham CC (1969) Variance of gene frequencies. Evolution 23:72-83.

Craig JA, and Suomela (1941) Time of appearance of the runs of salmon and steelhead trout native to the Wenatchee, Entiat, Methow, and Okanogan rivers. U.S. Fish Wildl. Serv.

Fish FF, and Hanavan MG (1948) A report on the Grand Coulee Fish Maintenance. Project 1939-1947. U.S. Fish Wildl. Serv. Spec. Sci. Rep 55.

Ford MJ (2002) Selection in captivity during supportive breeding may reduce fitness in the wild. Conservation Biology 16(3):815-825

Frankham R, Ballou JD, Briscoe DA (2002). Introduction to Conservation Genetics, Cambridge University Press, Cambridge, UK.

Greig C, Jacobson DP, Banks MA (2003) New tetranucleotide microsatellites for fine-scale discrimination among endangered chinook salmon *(Oncorhynchus tshawytscha*). *Mol Ecol Notes,* **3**:376-379.

Heath DD, Busch C, Kelly J, and Atagi DY (2002) Temporal change in genetic structure and effective population size in steelhead trout (*Oncorhynchus mykiss*). Molecular Ecology 11:197-214

Hedrick P, Hedgecock D (1994) Effective population size in winter-run chinook salmon. *Conservation Biology,* **8**:890-892.

Hill WG (1981) Estimation of effective size from data on linkage disequilibrium. Genetical Research 38: 209-216.

Jensen LF, Hansen MM, Carlsson J et al (2005) Spatial and temporal genetic differentiation and effective population size of brown trout (*Salmo trutta*, *L.*) in small Danish rivers. Conservation Genetics 6:615-621.

Liu, K and Muse SV (2005) PowerMarker: Integrated analysis environment for genetic marker data. Bioinformatics 21:2128-2129.

Lynch M and O'Hely M (2001) Captive breeding and the genetic fitness of natural populations. Conservation Genetics 2:363-378

Manly, BFJ. (1986) Multivariate Statistical Methods. A Primer. Chapman and Hall. London.. 159 + x pp.

McLean JE, Bentzen P, Quinn TP (2003) Differential reproductive success of sympatric, naturally spawning hatchery and wild steelhead trout (*Oncorhynchus mykiss*) through the adult stage. Can. J. Fish. Aquat. Sci., 60:433–440.

Mullan, JW (1987) Status and propagation of chinook salmon in the mid-Columbia River through 1985. U.S. Fish Wildl. Serv. Biol. Rep. 87:111.

Murdoch AR and Peven C (2005) Conceptual Approach to Monitoring and Evaluating the Chelan County Public Utility District Hatchery Programs, Final Report.

Murdoch AR, Pearsons TN, Maitland TW, Ford M, and Williamson K (2006) Monitoring the reproductive success of naturally spawning hatchery and natural spring Chinook salmon in the Wenatchee River. BPA Project No. 2003-039-00, Contract No. 00021391. pp. 96

Nelson WR, and Bodle J (1990) Ninety years of salmon culture at the Little White Salmon National Fish Hatchery. U.S. Fish Wildl. Serv. Biol. Rep. 90:22.

Palm S, Laikre L, Jorde PE, et al (2003) Effective population size and temporal genetic change in stream resident brown trout (*Salmo trutta, L.*). Conservation Genetics 4:249-264.

Olsen JB, Bentzen P, Seeb JS (1998) Characterization of seven microsatellite loci derived from pink salmon. *Molecular Ecology,* **7**:1087-1089

Rannala B, Mountain JL (1997) Detecting immigration by using multilocus genotypes. Proceedings of the National Academy of Sciences 94:9197-9201.

Rexroad CE, Coleman RL, Martin AM, Hershberger WK, Killefer J (2001) Thirty-five polymorphic microsatellite markers for rainbow trout (Oncorhynchus mykiss). *Animal Genetics,* **32**:317-319.

Rohlf, F. J. (2002) NTSYSpc: Numerical Taxonomy System, ver. 2.1. Exeter Publishing, Ltd.

Ryman N, Laikre L (1991) Effects of supportive breeding on the genetically effective population size. Conservation Biology, 5:325-329.

Seeb L, et al. (in review) Development of a Standardized DNA Database for Chinook Salmon. *Fisheries*

Schneider S, Roessli D, Excoffier L (2000) Arlequin ver 2.000: A software for population genetic data analysis. Genetics and Biometry Laboratory. University of Geneva, Switzerland.

The Mathworks (2006) MatLab Release R2006b. Massachusetts.

Utter FM, Chapman DW, and Marshall AR (1995) Genetic population structure and history of chinook salmon of the Upper Columbia River. Am. Fish. Soc. Symp. 17:149-165.

Wang J (2005) Estimation of effective size from data on genetic markers. Trans. Royal. Phil. Soc. B 360: 1395-1409.

Wang J, and Ryman N (2001) Genetic effects of multiple generations of supportive breeding. Conservation Biology 15: 1615-1631.

Wang J, Whitlock MC (2003) Estimating Effective Population Size and Migration Rates From Genetic Samples Over Space and Time. Genetics 163:429-446

Waples RS (1989) A generalized approach for estimating effective population size from temporal changes in allele frequency. Genetics, 121:379-391.

Waples RS (1990) Conservation genetics of Pacific salmon. III. Estimating effective population size. J. Hered. 81: 277-289.

Waples RS (1991) Genetic interactions between hatchery and wild salmonids: Lessons from the Pacific Northwest. Can. J. Fish. Aquat. Sci. 48(Suppl. 1):124-133.

Waples RS (2005) Genetic estimates of contemporary effective population size: to what time periods do the estimates apply? Molecular Ecology, 14:3335-3352

Waples RS (2006) A bias correction for estimates of effective population size based on linkage disequilibrium at unlinked gene loci. Conservation Genetics 7:167-184

Washington Department of Fisheries (WDF). 1934. Forty-second and forty-fifth inclusive annual reports of the State Department of Fisheries for the period from April 1, 1931-March 31, 1935, fiscal years of 1931 to 1934 inclusive. Wash. Dep. Fish., pp. 78

Williamson K, Cordes J, May B (2002) Characterization of microsatellite loci in chinook salmon (*Oncorhynchus tshawytscha*) and cross-species amplification in other salmonids. *Molecular Ecology Notes*, **2**:17-19.

Williamson KS, Murdoch AR, and Ford MJ (submitted) Influence of supportive breeding on genetic diversity of hatchery and natural Wenatchee River spring Chinook salmon.

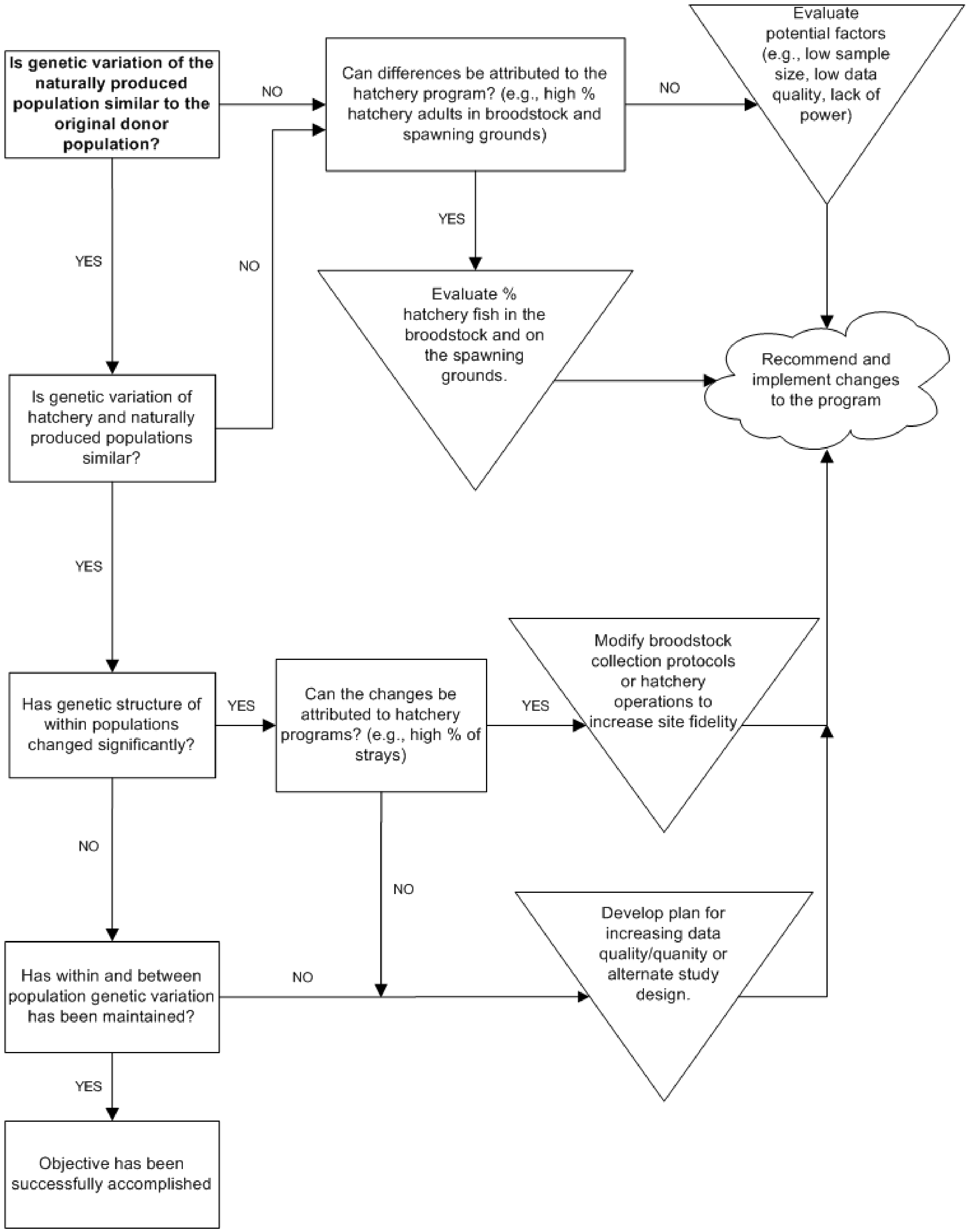


Figure 1. Conceptual process for evaluating potential changes in genetic variation in the Chiwawa naturally produced populations as a result of the supplementation hatchery programs (From Murdoch and Peven 2005).

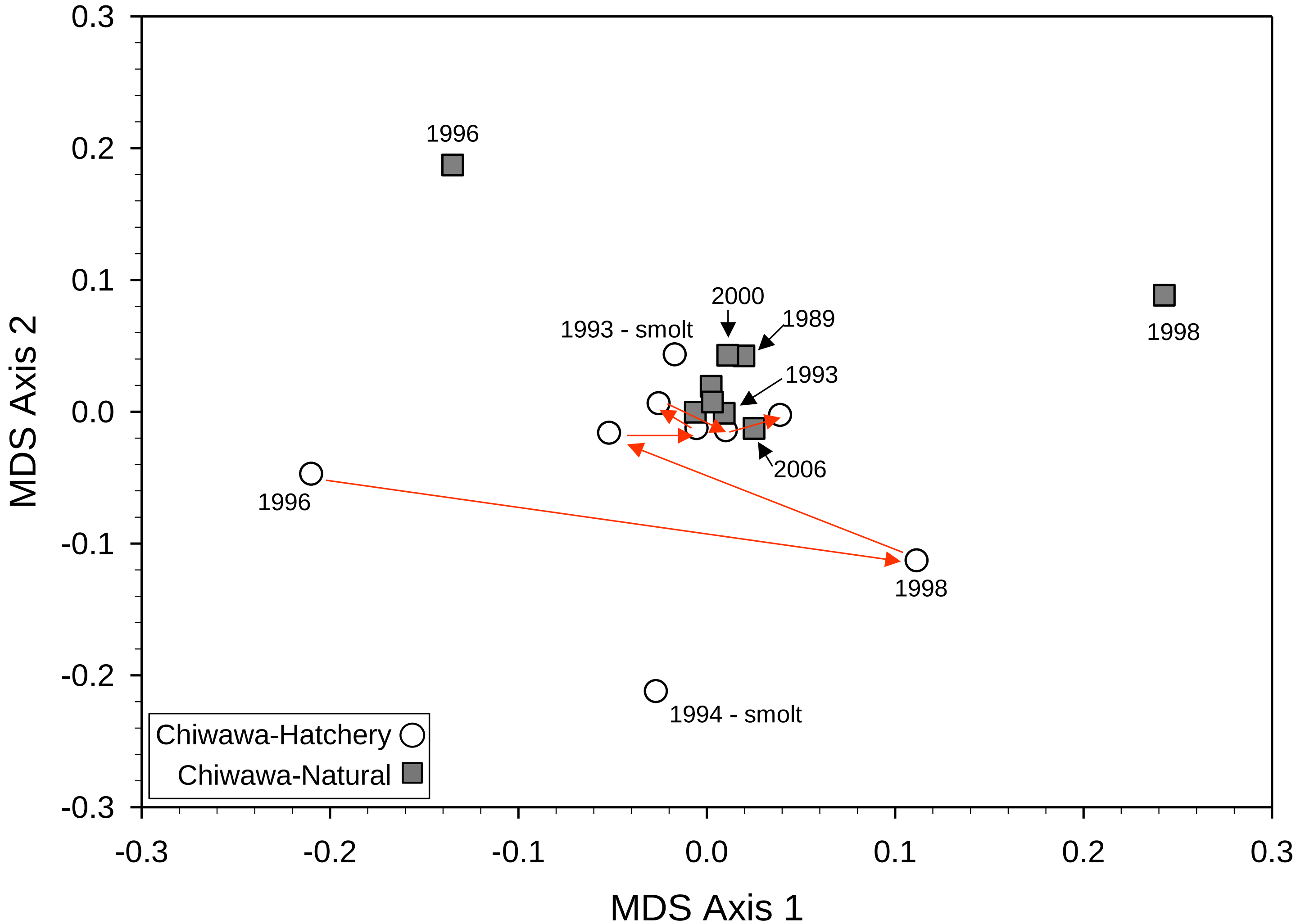


Figure 2. Multidimensional scaling plot from an allele-sharing distance matrix calculated from the Chiwawa data set organized by fish origin (i.e., hatchery versus natural). The red arrows connect consecutive hatchery-origin collections starting with the first adult collection (1996) and ending with the 2006 collection (see Table 1 for collection years).

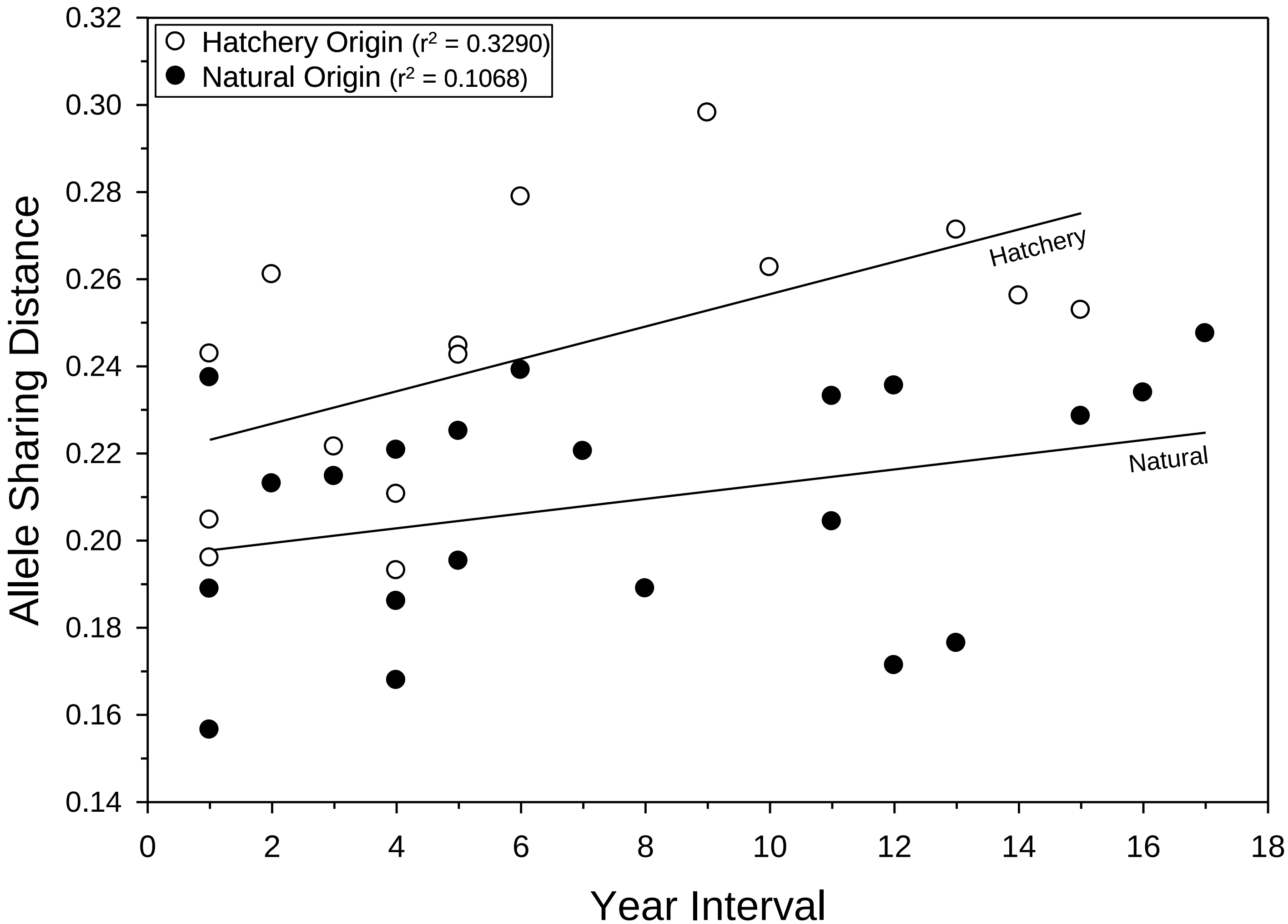


Figure 3. Relationships between the time interval in years and allele sharing distances, with each circle representing the pairwise relationship between two Chiwawa collections. Separate regression lines for the natural- and hatchery-origin collections. The slope for the natural-origin collection is not significantly different from zero (p=0.1483), while the slope for hatchery-origin collection is significantly greater than zero (p=0.0254) indicating a positive relationship between time interval and allele sharing distance.

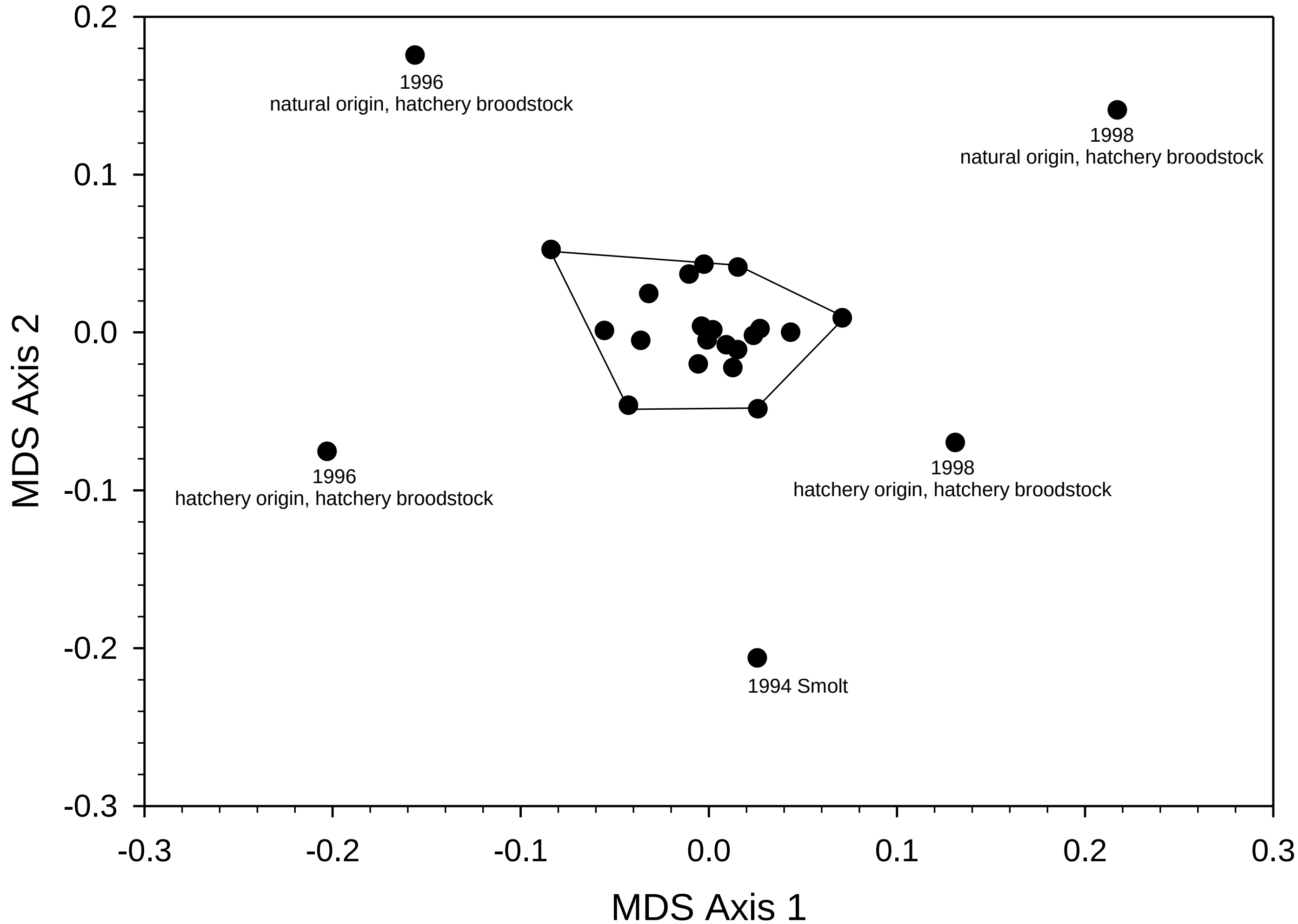


Figure 4. Multidimensional scaling plot from an allele-sharing distance matrix calculated from the Chiwawa data set organized by four treatment groups, as discussed in the text. Each circle represents a single collection within each of the four treatment groups, and the polygon encloses all groups that are not outliers. Each outlier group is specifically labeled.

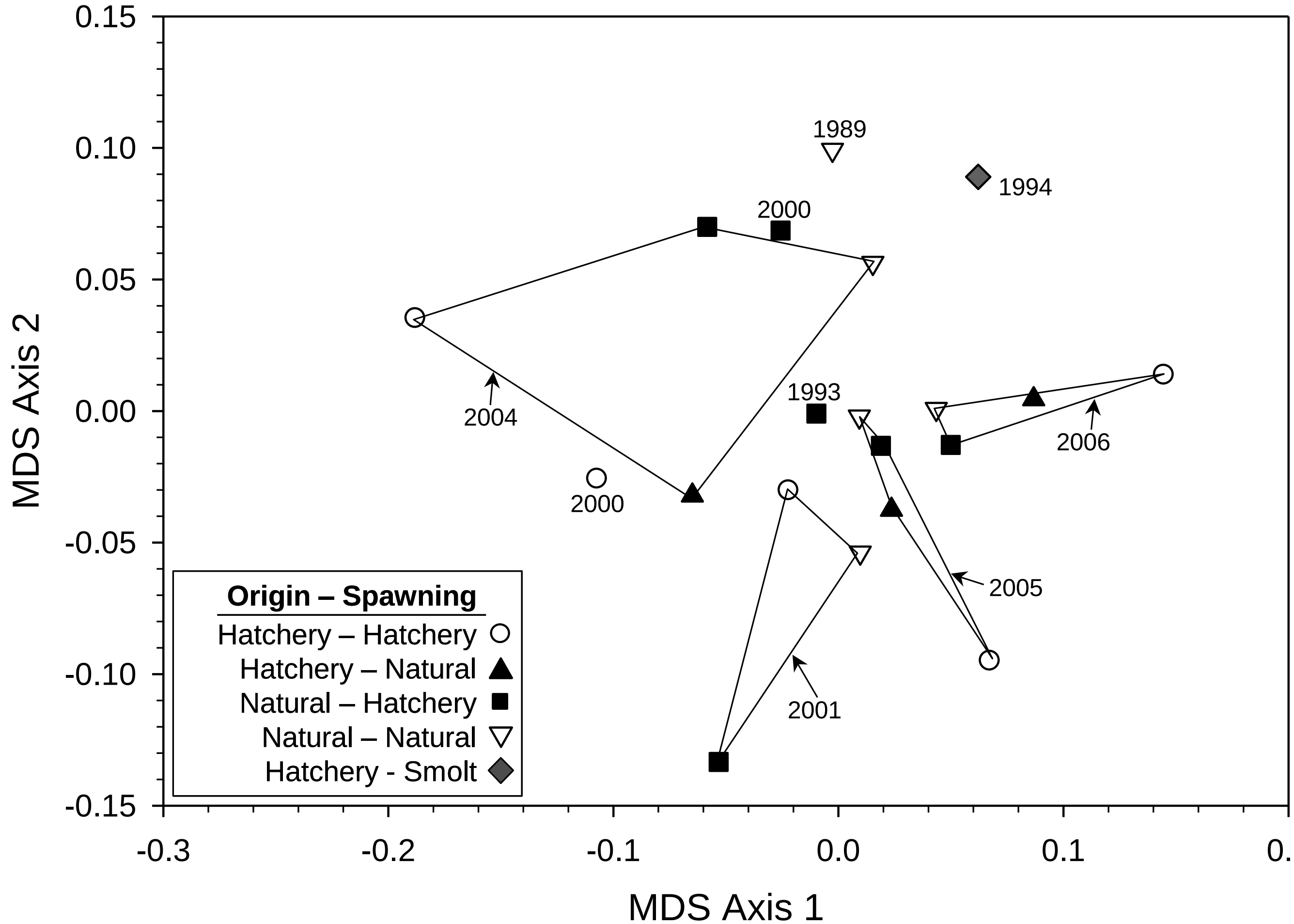


Figure 5. As in Figure 4, but allele-sharing distance matrix recalculated without the five outlier groups shown in Figure 4. Polygons group together treatment groups from the same collection year. Dates associated with symbols also refer to collection year. Collection years 2004-2006 included all four treatment groups, while collection year 2001 did not include a hatchery-origin natural spawner group. Legend is read as follows: Open circles refer to hatchery-origin hatchery spawner group, while filled box refers to natural-origin hatchery spawner group, and so on.

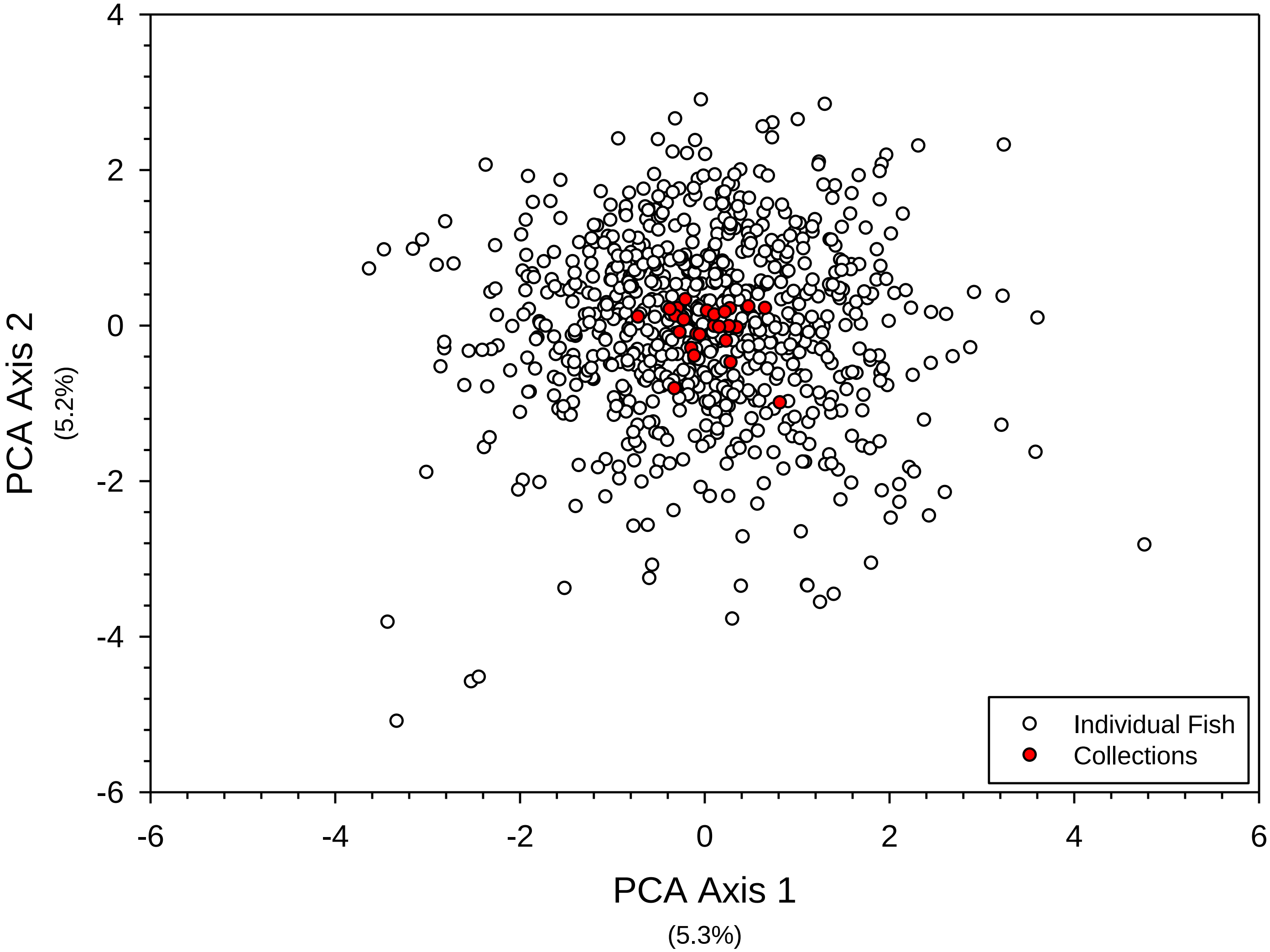


Figure 6. Principal component (PC) analysis of individual fish from the Chiwawa River. Only fish with complete microsatellite genotypes were included in the analysis (n = 757). Open circles are the PC scores for individual fish, and the filled circles are the centroids (bivariate means) for each of the 25 groups discussed in the text. PC axes 1 and 2 account for only 10.5% of the total molecular variance.

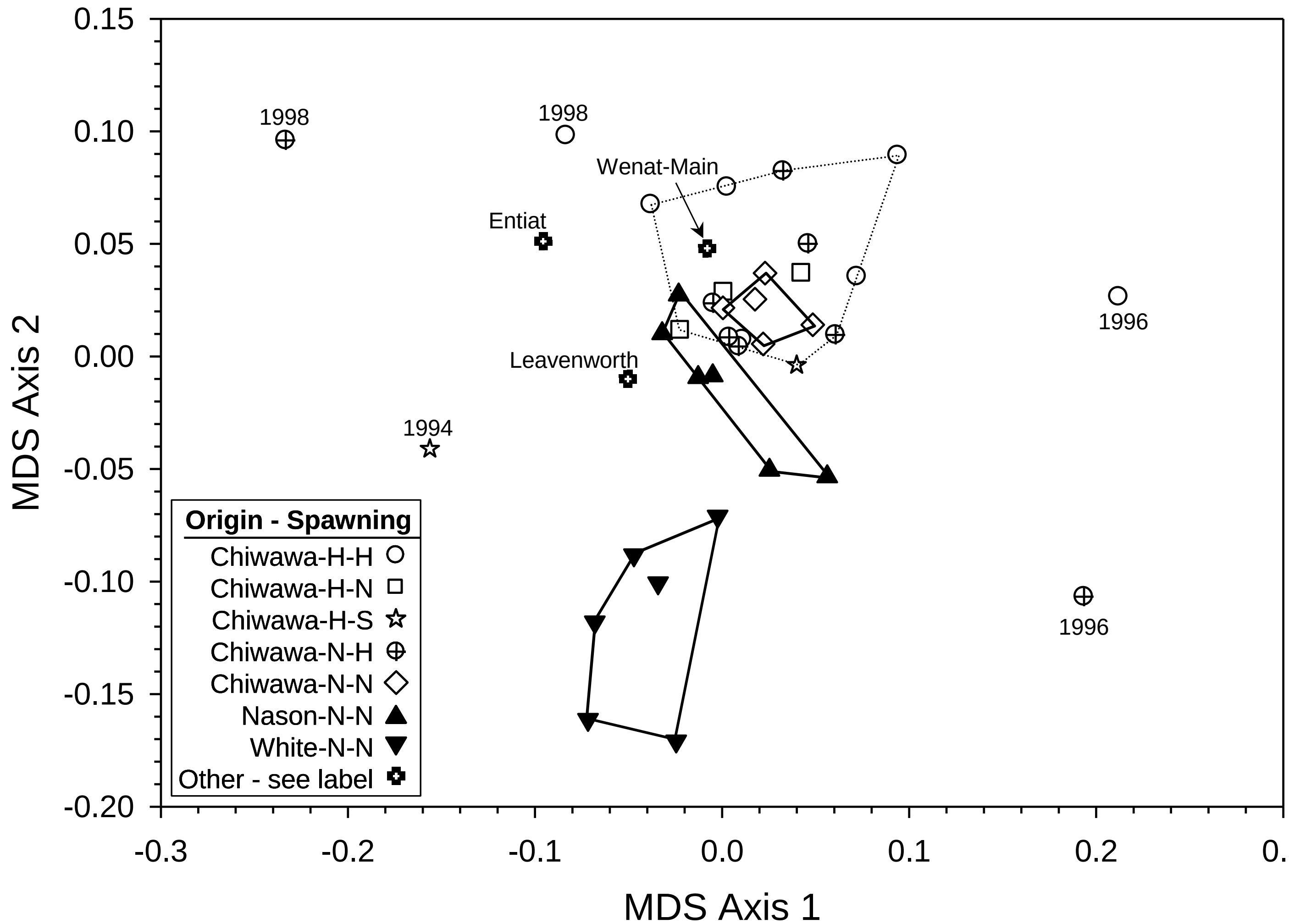


Figure 7. Multidimensional scaling plot from an allele-sharing distance matrix calculated from the Chiwawa origin data set and all other non-Chiwawa collections, except Little Wenatchee River. Legend is read with abbreviations beginning with origin and then spawning location. H=hatchery, N=natural, and S=smolts. Polygons with solid lines enclose the natural-origin natural spawner collections from each population (i.e., river). The polygon with the dotted lines enclose all Chiwawa collections, except for the five outlier collections, as discussed in text.

Table 1 Summary of within population genetic data. Chiwawa collection data are summarized in A) by origin of the sample (i.e., clipped vs. non-clipped). All collection data are summarized in B) by spawning location (i.e., hatchery broodstock or on spawning grounds). Hz is heterozygosity, HWE is the statistical significance of deviations from Hardy-Weinberg expectations (* = 0.05, ** = 0.01, and *** = 0.001), LD is the proportion of pairwise locus tests (across all populations) exhibiting linkage disequilibrium (bolded values are statistically significant), and the last column is mean number of alleles per locus.

Collection	Sample size	Gene Diversity	Observed Hz	HWE	F_{IS}	LD	Mean # Alleles
A) Origin							
1993 Chiwawa Hatchery	95	0.77	0.79	***	-0.02	**0.86**	14.00
1994 Chiwawa Hatchery	95	0.76	0.77	***	-0.01	**0.91**	11.38
1996 Chiwawa Hatchery	8	0.75	0.81	-	-0.01	0.00	8.23
1998 Chiwawa Hatchery	27	0.81	0.82	-	0.00	0.04	12.62
2000 Chiwawa Hatchery	43	0.75	0.78	***	-0.01	**0.19**	12.46
2001 Chiwawa Hatchery	69	0.77	0.80	***	-0.02	**0.14**	15.31
2004 Chiwawa Hatchery	72	0.77	0.77	***	0.01	**0.45**	15.92
2005 Chiwawa Hatchery	91	0.79	0.82	*	-0.03	**0.05**	16.15
2006 Chiwawa Hatchery	95	0.80	0.84	***	-0.05	**0.49**	15.85
1989 Chiwawa Natural	36	0.76	0.78	-	0.01	0.00	12.77
1993 Chiwawa Natural	62	0.78	0.81	-	-0.02	0.04	15.85
1996 Chiwawa Natural	8	0.72	0.78	-	-0.02	0.00	7.54
1998 Chiwawa Natural	10	0.78	0.84	-	0.00	0.00	8.23
2000 Chiwawa Natural	39	0.78	0.79	***	0.00	**0.10**	14.00
2001 Chiwawa Natural	75	0.78	0.80	-	-0.03	0.03	15.31
2004 Chiwawa Natural	85	0.78	0.77	-	0.02	0.01	15.77
2005 Chiwawa Natural	90	0.79	0.79	-	0.01	0.01	16.15
2006 Chiwawa Natural	96	0.80	0.81	-	-0.01	0.01	16.46

Table 1 Within population genetic data analysis summary continued.

Collection	Sample size	Gene Diversity	Observed Hz	HW	F_{IS}	LD	Mean # Alleles
B) Spawning Location							
1993 Chiwawa Broodstock	62	0.78	0.81	-	-0.02	0.00	15.85
1996 Chiwawa Broodstock	16	0.75	0.79	-	-0.02	0.00	10.92
1998 Chiwawa Broodstock	37	0.82	0.83	-	0.00	0.01	14.38
2000 Chiwawa Broodstock	82	0.78	0.78	***	0.00	**0.32**	15.62
2001 Chiwawa Broodstock	89	0.78	0.80	*	-0.02	**0.13**	15.77
2004 Chiwawa Broodstock	61	0.77	0.76	*	0.02	**0.13**	14.92
2005 Chiwawa Broodstock	75	0.79	0.78	*	0.02	0.01	15.85
2006 Chiwawa Broodstock	89	0.80	0.83	-	-0.03	**0.05**	16.46
1989 Chiwawa River	36	0.76	0.78	-	0.01	0.00	12.77
2001 Chiwawa River	55	0.78	0.80	-	-0.02	**0.09**	14.00
2004 Chiwawa River	96	0.78	0.78	*	0.01	**0.18**	17.23
2005 Chiwawa River	106	0.79	0.82	*	-0.02	**0.06**	16.69
2006 Chiwawa River	102	0.80	0.83	***	-0.03	**0.10**	16.77
1989 White River	48	0.75	0.75	-	0.01	0.01	12.85
1991 White River	19	0.76	0.76	-	0.03	0.00	10.92
1992 White River	22	0.75	0.79	-	-0.02	0.01	11.00
1993 White River	21	0.75	0.69	*	0.10	0.00	10.15
2005 White River	29	0.75	0.77	-	-0.01	0.03	12.23
2006 White River	40	0.76	0.76	-	0.01	0.04	13.38

Table 1 Within population genetic data analysis summary continued.

Collection	Sample size	Gene Diversity	Observed Hz	HW	F_{IS}	LD	Mean # Alleles
1993 Little Wenatchee R.	19	0.84	0.85	-	0.02	0.00	11.23
1993 Nason Creek	45	0.78	0.80	-	-0.01	0.01	13.77
2000 Nason Creek	51	0.76	0.78	-	-0.02	**0.13**	13.92
2001 Nason Creek	41	0.79	0.81	-	-0.01	**0.08**	14.23
2004 Nason Creek	38	0.76	0.76	-	0.02	0.03	13.23
2005 Nason Creek	45	0.78	0.82	-	-0.04	0.03	14.92
2006 Nason Creek	48	0.80	0.82	-	-0.01	0.00	15.77
2001 Wenatchee River	32	0.79	0.80	*	0.00	0.04	12.85
2000 Leavenworth NFH	73	0.80	0.82	*	-0.02	**0.15**	16.23
1997 Entiat NFH	37	0.81	0.83	-	-0.01	**0.06**	14.38

Table 2 Demographic data for Chiwawa Hatchery and Chiwawa natural spring Chinook salmon. BS is census size of hatchery broodstock, pNOB is the proportion of hatchery broodstock of natural origin, NOS is the census size of natural-origin spawners present in Chiwawa River, HOS is the census size of hatchery-origin spawners present in Chiwawa River, Total is NOS and HOS combined, and pNOS is the proportion of spawners present in Chiwawa River of natural origin.

	Hatchery		In River			
Brood Year	BS	pNOB	NOS	HOS	Total	pNOS
1989	28	1	1392	0	1392	1.00
1990	18	1	775	0	775	1.00
1991	32	1	585	0	585	1.00
1992	78	1	1099	0	1099	1.00
1993	94	1	677	491	1168	0.58
1994	11	0.64	190	90	280	0.68
1995	0	0	8	50	58	0.14
1996	18	0.44	131	51	182	0.72
1997	111	0.29	210	179	389	0.54
1998	47	0.28	134	45	178	0.75
1999	0	0	119	13	132	0.90
2000	30	0.3	378	310	688	0.55
2001	371	0.3	1280	2850	4130	0.31
2002	71	0.28	694	919	1613	0.43
2003	94	0.44	380	223	603	0.63
2004	215	0.39	820	788	1608	0.51
2005	270	0.33	250	1222	1472	0.17

Table 3 Levels of significance for pairwise tests of genic differentiation among all hatchery- and natural-origin collections used in this analysis. HS = highly significant (P < 0.000095; the Bonferroni corrected p-value for an alpha = 0.05); * = P < 0.05 (nominal critical value for most statistical test); - = P > 0.05 (not significant). A significant result between pairs of populations indicates that the allele frequencies between the pair are significantly different. Results are read by comparing the collections along the rows to collections along columns. The top block for each section is a symmetric matrix, as it compares collections within the same group.

		Chiwawa – Hatchery Origin								
		1993	1994	1996	1998	2000	2001	2004	2005	2006
Chiwawa – Hat. Origin	1993		HS	*	HS	HS	HS	HS	HS	HS
	1994	HS		HS	HS	HS	HS	HS	HS	HS
	1996	*	HS		*	-	*	-	-	*
	1998	HS	HS	*		HS	HS	HS	HS	HS
	2000	HS	HS	-	HS		HS	*	HS	HS
	2001	HS	HS	*	HS	HS		HS	*	HS
	2004	HS	HS	-	HS	*	HS		HS	HS
	2005	HS	HS	-	HS	HS	*	HS		HS
	2006	HS	HS	*	HS	HS	HS	HS	HS	
Chiwawa – Natural Origin	1989	HS	HS	-	HS	HS	*	HS	HS	HS
	1993	HS	HS	-	HS	HS	-	HS	*	HS
	1996	*	HS	-	*	-	-	-	-	-
	1998	HS	HS	-	-	HS	*	*	*	-
	2000	HS	HS	-	HS	HS	HS	*	HS	HS
	2001	HS	HS	-	HS	HS	HS	HS	*	HS
	2004	HS	HS	-	HS	HS	HS	HS	HS	HS
	2005	HS	HS	-	HS	HS	*	HS	*	HS
	2006	HS	HS	-	*	HS	HS	HS	HS	HS
Nason	1996	HS	HS	-	HS	HS	HS	HS	HS	HS
	2000	HS	HS	*	HS	HS	HS	HS	HS	HS
	2001	HS	HS	-	HS	HS	HS	HS	HS	HS
	2004	HS	HS	-	HS	HS	HS	HS	HS	HS
	2005	HS	HS	-	HS	HS	HS	HS	HS	HS
	2006	HS	HS	-	*	HS	HS	HS	HS	HS
White	1989	HS	HS	HS	HS	HS	HS	HS	HS	HS
	1991	HS	HS	-	HS	HS	HS	HS	HS	HS
	1992	HS	HS	*	HS	HS	HS	HS	HS	HS
	1993	HS	HS	*	HS	HS	HS	HS	HS	HS
	2005	HS	HS	-	HS	HS	HS	HS	HS	HS
	2006	HS	HS	HS	HS	HS	HS	HS	HS	HS
Other	Wen-M	HS	HS	*	HS	HS	*	*	-	HS
	Leaven	HS	HS	*	HS	HS	HS	HS	HS	HS
	Entiat	HS	HS	*	HS	HS	HS	HS	HS	HS

Table 3 (con't)

		Chiwawa – Natural Origin								
		1989	**1993**	**1996**	**1998**	**2000**	**2001**	**2004**	**2005**	**2006**
Chiwawa – Natural Origin	**1989**		-	-	-	-	*	*	*	*
	1993	-		-	*	*	*	HS	*	HS
	1996	-	-		-	-	-	-	-	-
	1998	-	*	-		*	*	HS	*	*
	2000	-	*	-	*		HS	-	HS	HS
	2001	*	*	-	*	HS		HS	*	HS
	2004	*	HS	-	HS	-	HS		HS	HS
	2005	*	*	-	*	HS	*	HS		*
	2006	*	HS	-	*	HS	HS	HS	*	
Nason	**1996**	*	*	-	*	*	HS	HS	HS	HS
	2000	HS	HS	HS	HS	HS	HS	HS	HS	HS
	2001	HS	*	-	*	HS	HS	HS	HS	HS
	2004	HS	HS	-	HS	HS	HS	HS	HS	HS
	2005	*	*	-	*	HS	HS	HS	HS	HS
	2006	HS	HS	-	-	HS	HS	HS	HS	HS
White	**1989**	HS	HS	*	HS	HS	HS	HS	HS	HS
	1991	HS	HS	*	-	HS	HS	HS	HS	HS
	1992	HS	HS	-	*	HS	HS	HS	HS	HS
	1993	HS	*	-	*	HS	HS	HS	HS	HS
	2005	HS	*	*	*	HS	HS	HS	*	HS
	2006	HS	HS	*	HS	HS	HS	HS	HS	HS
Other	**Wen-M**	*	-	-	-	*	*	HS	*	*
	Leaven	HS	HS	*	*	HS	HS	HS	HS	HS
	Entiat	HS	HS	*	HS	HS	HS	HS	HS	HS

Table 3 (con't)

		Nason					
		1996	2000	2001	2004	2005	2006
Nason	1996		HS	-	HS	-	*
	2000	HS		HS	HS	HS	HS
	2001	-	HS		*	-	*
	2004	HS	HS	*		*	HS
	2005	-	HS	-	*		-
	2006	*	HS	*	HS	-	
White	1989	HS	HS	HS	HS	HS	HS
	1991	*	HS	HS	HS	*	*
	1992	HS	HS	HS	HS	HS	HS
	1993	*	HS	HS	HS	HS	HS
	2005	*	HS	HS	HS	HS	HS
	2006	HS	HS	HS	HS	HS	HS
Other	Wen-M	HS	HS	HS	HS	*	HS
	Leaven	HS	HS	HS	HS	HS	HS
	Entiat	HS	HS	HS	HS	HS	HS

Table 3 (con't)

		White						Other		
		1989	1991	1992	1993	2005	2006	Wen-M 2001	Leaven 2000	Entiat 1997
White	1989		-	*	-	HS	HS	HS	HS	HS
	1991	-		-	-	*	*	*	HS	HS
	1992	*	-		-	*	*	HS	HS	HS
	1993	-	-	-		*	*	HS	HS	HS
	2005	HS	*	*	*		*	HS	HS	HS
	2006	HS	*	*	*	*		HS	HS	HS
Other	Wen-M	HS	*	HS	HS	HS	HS		HS	HS
	Leaven	HS	HS	HS	HS	HS	HS	HS		HS
	Entiat	HS	HS	HS	HS	HS	HS	HS	HS	

Table 4 Probabilities (above diagonal) and levels of significance (below diagonal) for pairwise tests of genic differentiation among all Chiwawa hatchery broodstock and Chiwawa natural spawner collections used in this analysis. HS = highly significant (P < 0.000476; the Bonferroni corrected p-value for an alpha = 0.05); * = P < 0.05 (nominal critical value for most statistical test); - = P > 0.05 (considered not significant). A significant result between pairs of populations indicates that the allele frequencies between the pair are significantly different. Pairwise comparisons between the hatchery broodstock and natural spawner collections from 2001, 2004, 2005, and 2006, respectively, are highlighted.

		Smolt		**Hatchery Broodstock**								**Natural Spawners**				
		1993	**1994**	**1993**	**1996**	**1998**	**2000**	**2001**	**2004**	**2005**	**2006**	**1989**	**2001**	**2004**	**2005**	**2006**
Smolt	**1993**		0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
	1994	HS		0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
Hatchery Broodstock	**1993**	HS	HS		0.9155	0.0000	0.0073	0.3647	0.0003	0.0694	0.0000	0.2220	0.0039	0.0008	0.0095	0.0000
	1996	HS	HS	-		0.0151	0.8388	0.0452	0.4916	0.3189	0.0716	0.5591	0.0759	0.8101	0.2364	0.0786
	1998	HS	HS	HS	*		0.0000	0.0000	0.0000	0.0000	0.0043	0.0000	0.0000	0.0000	0.0000	0.0005
	2000	HS	HS	*	-	HS		0.0000	0.4720	0.0000	0.0000	0.0036	0.0000	0.0712	0.0000	0.0000
	2001	HS	HS	-	*	HS	HS		0.0000	0.0059	0.0000	0.0003	0.0000	0.0000	0.0126	0.0000
	2004	HS	HS	*	-	HS	-	HS		0.0000	0.0000	0.0001	0.0000	0.0012	0.0000	0.0000
	2005	HS	HS	-	-	HS	HS	*	HS		0.0005	0.0024	0.0137	0.0025	0.7782	0.0018
	2006	HS	HS	HS	-	*	HS	HS	HS	*		0.0000	0.0000	0.0000	0.0000	0.5770
Natural Spawners	**1989**	HS	HS	-	-	HS	*	*	HS	*	HS		0.0023	0.0317	0.0000	0.0003
	2001	HS	HS	*	-	HS	HS	HS	HS	*	HS	*		0.0000	0.2641	0.0000
	2004	HS	HS	*	-	HS	-	HS	*	*	HS	*	HS		0.0000	0.0000
	2005	HS	HS	*	-	HS	HS	*	HS	-	HS	HS	-	HS		0.0000
	2006	HS	HS	HS	-	*	HS	HS	HS	*	-	*	HS	HS	HS	

Table 5 Analysis of molecular variance (AMOVA) for the Chiwawa collections, showing the partition of molecular variance into (1) within collections, (2) among collections but within group, and (3) among group components. Each column in the table represents a separate analysis testing for differences under a different spatial or temporal hypothesis. The different analyses are grouped together in a single table for comparisons. The values within the table are percentages and the parenthetical values are P-values, or probabilities, associated with that percentage. P-values greater than 0.05 indicate that the percentage is not significantly different from zero. For example, when collections are organized by hatchery- versus natural-origin ("Origin" – fourth column), 0.11% of the molecular variance is attributed to among group (i.e., hatchery- versus natural-origin), which is not significantly different from zero. No collections (first column) indicates no organization or grouping among all collections, and the among-group percentage is equal to the F_{ST} for the entire data set.

	No Structure	Collection Year	Spawning Location	Origin	Origin-Spawning Location
Among Groups	0.26 (0.00)	0.20 (0.43)	0.05 (0.48)	0.11 (0.15)	0.11 (0.06)
Among collections - Within groups	-	0.08 (0.003)	0.24 (0.00)	0.21 (0.00)	0.18 (0.06)
Within collections	99.74 (0.00)	99.72 (0.00)	99.71 (0.00)	99.68 (0.00)	99.71 (0.00)

Table 6 F_{ST} values for all pairwise combinations of populations. Each F_{ST} is the median value for all pairwise combinations of collections within each population (the number of collections within each population is shown parenthetically next to each population name on each row). For example, the F_{ST} for the Chiwawa hatchery versus the White River (0.019) is the median value of 54 pairwise comparisons. The bold values along the center diagonal are the median F_{ST} values within each collection. For those populations with only one collection, the diagonal value was set at 0.000.

	Chiwawa-Hatchery	Chiwawa-Natural	Entiat	Leaven-worth	Nason	Wenatchee-main	White	Little Wenatchee
Chiwawa-Hatchery (9)	**0.013**	0.008	0.016	0.012	0.011	0.005	0.019	0.111
Chiwawa-Natural (9)		**0.003**	0.012	0.011	0.007	0.003	0.014	0.105
Entiat (1)			**0.000**	0.005	0.010	0.008	0.019	0.078
Leavenworth (1)				**0.000**	0.007	0.008	0.014	0.092
Nason (6)					**0.006**	0.008	0.015	0.099
Wenatchee-main (1)						**0.000**	0.012	0.098
White (6)							**0.005**	0.113
Little Wenatchee (1)								**0.000**

Table 7 As in Table 5, except data includes Chiwawa hatchery- and natural-origin, Nason Creek, and White River collections

	All Years	All Years	1989-1996	2005-2006	2005-2006
	No Structure	Origin	Origin	Origin	Collection Year
Among Groups	0.28 (0.00)	0.33 (0.00)	-0.07 (0.67)	0.43 (0.01)	-0.06 (0.57)
Among Collections - Within groups	-	0.04 (0.00)	0.22 (0.00)	0.25 (0.00)	0.64 (0.00)
Within Collections	99.72	99.63	99.85	99.32	99.41

Table 8 Individual assignment results reported are the numbers of individuals assigned to each population using the partial Bayesian criteria of Rannala and Mountain (1997) and a "jack-knife" procedure (see Methods). The population with the highest posterior probability is considered the stock of origin (i.e., no unassigned individuals). Individuals from each population are assigned to specific populations (along rows). Bold values indicate correct assignment back to population of origin. Individuals assigned to a population are read down columns. For example, of the 595 individuals from Chiwawa hatchery origin, 134 individuals were assigned to Chiwawa natural origin (reading across). Of the 511 individuals assigned to Chiwawa natural origin (reading down), 60 were from Nason Creek.

Population	Total	Unassigned	1	2	3	4	5	6	7	8
1) Chiwawa Hatchery	595	0	**371**	134	2	16	0	45	15	12
2) Chiwawa Natural	501	0	156	**269**	4	5	0	42	9	16
3) Entiat	37	0	4	5	**13**	8	0	6	1	0
4) Leavenworth	73	0	9	8	3	**33**	0	17	0	3
5) Little Wenatchee	19	0	0	0	0	0	**19**	0	0	0
6) Nason	268	0	49	60	5	11	0	**131**	1	11
7) Wenatchee Mainstem	32	0	12	9	0	1	0	2	**6**	2
8) White	179	0	22	26	0	2	0	13	1	**115**
TOTAL	1704	0	623	511	27	76	19	256	33	159

Table 9 As in Table 8, except the posterior probability from the partial Bayesian criteria of Rannala and Mountain (1997) must be 0.90 or greater, to be assigned to a population. Those individuals with posterior probabilities less than 0.90 are unassigned.

Aggregate	Total	Unassigned	1	2	3	4	5	6	7	8
1) Chiwawa Hatchery	595	332	**214**	31	1	4	0	10	3	0
2) Chiwawa Natural	501	375	30	**82**	0	1	0	5	2	6
3) Entiat	37	24	1	1	**5**	4	0	2	0	0
4) Leavenworth	73	51	0	1	1	**19**	0	1	0	0
5) Little Wenatchee	19	2	0	0	0	0	**17**	0	0	0
6) Nason	268	188	11	6	2	5	0	**53**	0	3
7) Wenatchee Mainstem	32	23	4	3	0	0	0	0	**2**	0
8) White	179	92	4	3	0	1	0	5	1	**73**
TOTAL	1704	1087	264	127	9	34	17	76	8	82

Table 10 Estimates of N_e based on bias correction method of Waples (2006) implemented in LDNe (Do and Waples unpublished). Collections are categorized by spawning location. Sample size is the harmonic mean of the sample size, 95% CI is the confidence interval calculated using Waples' (2006) equation 12, and Major Cohort assumes that each collection is 100% four-year-olds.

	Sample size	Estimated N_b	95% CI	Major Cohort	Census	N_e/N
1993 Chiwawa Broodstock	58.4	103.1	77.0 - 149.7	1989	1392	0.30
1996 Chiwawa Broodstock	15.5	30.4	19.6 - 58.1	1992	1099	0.11
1998 Chiwawa Broodstock	33.4	37.7	29.8 - 49.7	1994	280	0.54
2000 Chiwawa Broodstock	77.8	48.4	41.4 - 57.2	1996	182	1.06
2001 Chiwawa Broodstock	80.4	49.6	42.2 - 59.2	1997	389	0.51
2004 Chiwawa Broodstock	56.6	48.1	39.0 - 60.9	2000	688	0.28
2005 Chiwawa Broodstock	73	274.3	148.9 - 1131.8	2001	4130	0.27
2006 Chiwawa Broodstock	88.4	198.3	136.1 - 340.5	2002	1613	0.49
1989 Chiwawa River	26.6	5.2	3.9 - 6.3	1985		
2001 Chiwawa River	46.7	38.6	31.0 - 49.3	1997	389	0.40
2004 Chiwawa River	88.5	82.6	67.3 - 104.4	2000	688	0.48
2005 Chiwawa River	104.2	231.5	161.8 - 382.7	2001	4130	0.22
2006 Chiwawa River	101.1	107.3	87.2 - 136	2002	1613	0.27

Table 11 Summary of output from program SALMONNb and data for eight Chiwawa broodstock collections from Wenatchee River. For each pairwise comparison of samples *i* and *j*, $\tilde{S}$ is the harmonic mean sample size, *n* is the number of independent alleles used in the comparison, $\hat{N}_{b(i,j)}$ are the pairwise estimates of N_b, and Var [$\hat{N}_{b(i,j)}$] is the variance of $\hat{N}_{b(i,j)}$. $\tilde{N}_b$ is the harmonic mean of the $\hat{N}_{b(i,j)}$. Alleles with a frequency below 0.05 were excluded from the analysis to reduce potential bias.

Year	1993	1996	1998	2000	2001	2004	2005	2006
Pairwise $\tilde{S}$ (above diagonal) and *n* (below diagonal):								
1993	-	24.5	42.5	66.4	67.2	57.2	64.6	70.3
1996	82	-	21.2	25.8	26.0	24.4	25.6	26.4
1998	80	81	-	46.7	47.2	42.0	45.8	48.4
2000	80	82	84	-	78.6	65.2	75.1	82.7
2001	73	77	81	76	-	66.0	76.2	84.2
2004	77	81	75	76	78	-	63.5	69.0
2005	71	75	82	73	73	69	-	80.0
2006	81	80	84	75	74	75	72	-
Pairwise $\hat{N}_{b(i,j)}$ (above diagonal) and Var [$\hat{N}_{b(i,j)}$] (below diagonal):								
1993	-	-742.7	406.9	1240.8	-5432.0	829.8	808.9	729.0
1996	22491.2	-	110.4	-1786.5	765.9	162.8	824.7	382.7
1998	10910.4	67299.1	-	101.8	237.1	69.6	307.0	140.0
2000	6910.0	742895.8	19122.7	-	490.6	1498.2	706.9	201.6
2001	49318.3	21402.8	9754.2	6126.6	-	307.8	82.0	362.5
2004	8338.4	257267.7	24283.0	145043.4	7095.7	-	269.7	140.1
2005	31511.8	22242.5	10015.8	6596.6	114931.1	8240.4	-	599.6
2006	6223.8	43935.2	73518.7	10152.5	5885.3	12827.0	6370.8	-

$\tilde{N}_b = 269.4$

Table 12 Summary of output from program SALMONNb and data for five Chiwawa in-river spawner collections from Wenatchee River. For each pairwise comparison of samples *i* and *j*, $\tilde{S}$ is the harmonic mean sample size, *n* is the number of independent alleles used in the comparison, $\hat{N}_{b(i,j)}$ are the pairwise estimates of N_b, and Var [$\hat{N}_{b(i,j)}$] is the variance of $\hat{N}_{b(i,j)}$. $\tilde{N}_b$ is the harmonic mean of the $\hat{N}_{b(i,j)}$. Alleles with a frequency below 0.05 were excluded from the analysis to reduce potential bias.

Year	1989	2001	2004	2005	2006
Pairwise $\tilde{S}$ (above diagonal) and *n* (below diagonal):					
1989	-	33.3	40.2	41.7	42.2
2001	72	-	60.5	63.9	63.3
2004	72	77	-	95.3	94.0
2005	69	72	75	-	102.5
2006	76	76	77	78	-
Pairwise $\hat{N}_{b(i,j)}$ (above diagonal) and Var [$\hat{N}_{b(i,j)}$] (below diagonal):					
1989	-	118.4	299.0	143.3	165.3
2001	40378.8	-	181.7	-1537.3	153.5
2004	10455.2	7265.5	-	387.1	329.4
2005	20923.6	68660.6	5040.7	-	356.8
2006	16227.2	8886.9	3802.0	4522.8	-

$\tilde{N}_b = 224.2$

Table 13 Summary of output from program SALMONNb and data for three brood years that combined Chiwawa natural- and hatchery-origin samples from Wenatchee River. For each pairwise comparison of samples *i* and *j*, $\tilde{S}$ is the harmonic mean sample size, *n* is the number of independent alleles used in the comparison, $\hat{N}_{b(i,j)}$ are the pairwise estimates of N_b, and Var [$\hat{N}_{b(i,j)}$] is the variance of $\hat{N}_{b(i,j)}$. $\tilde{N}_b$ is the harmonic mean of the $\hat{N}_{b(i,j)}$. Alleles with a frequency below 0.05 were excluded from the analysis to reduce potential bias.

Year	2004	2005	2006
Pairwise $\tilde{S}$ (above diagonal) and *n* (below diagonal):			
2004	-	162	164.3
2005	77	-	188.2
2006	76	75	-
Pairwise $\hat{N}_{b(i,j)}$ (above diagonal) and Var [$\hat{N}_{b(i,j)}$] (below diagonal):			
2004	-	611.3	210.8
2005	9351.5	-	727.5
2006	14965.5	8673.9	-

$\tilde{N}_b$ = 386.8

APPENDIX J

Genetic Diversity of Upper Columbia River Summer Chinook Salmon.

Genetic Structure of upper Columbia River Summer Chinook and Evaluation of the Effects of Supplementation Programs

by

Todd W. Kassler and Scott Blankenship
Washington Department of Fish and Wildlife
Molecular Genetics Laboratory
600 Capitol Way N
Olympia, WA 98501

and

Andrew R. Murdoch
Washington Department of Fish and Wildlife
Hatchery/Wild Interactions
3515 State Highway 97A
Wenatchee, WA 98801

February 2011

Abstract

We investigated genetic relationships among temporally replicated collections of summer Chinook from the Wenatchee River, Methow River, and Okanogan River in the upper Columbia River basin. Samples from the Eastbank Hatchery – Wenatchee stock, Eastbank Hatchery – MEOK stock, and Wells Hatchery were also included in the analysis. Samples of natural- and hatchery-origin summer Chinook were analyzed and compared to determine if the supplementation program has had any impacts to the genetic structure of these populations. We also calculated the effective number of breeders for collection locations of natural- and hatchery-origin summer Chinook from 1993 and 2008. In general, population differentiation was not observed among the temporally replicated collection locations. A single collection from the Okanogan River (1993) was the only collection showing statistically significant differences. The effective number of breeders was not statistically different from the early collection in 1993 in comparison to the late collection in 2008. Overall, these analyses revealed a lack of differentiation among the temporal replicates from the same locations and among the collection from different locations, suggesting the populations have been homogenized or that there has been substantial gene flow among populations. Additional comparisons among summer-run and fall-run Chinook populations in the upper Columbia River were conducted to determine if there was any differentiation between Chinook with different run timing. These analyses revealed pairwise F_{ST} values that were less than 0.01 for the collections of summer Chinook to collections of fall Chinook from Hanford Reach, lower Yakima River, Priest Rapids, and Umatilla. Collections of fall Chinook from Crab Creek, Lyons Ferry Hatchery, Marion Drain, and Snake River had pairwise F_{ST} values that were higher in comparison to the collections of summer Chinook. The consensus clustering analysis did not provide good statistical support to the groupings, but did show relationships among collections based on geographic proximity. Overall the summer and fall run Chinook that have historically been

spawned together were not differentiated while fall Chinook from greater geographic distances were differentiated.

Introduction

The National Marine Fisheries Service (NMFS) recognizes 15 Evolutionary Significant Units (ESU) for Chinook salmon (*Oncorhynchus tshawytscha*) (Myers et al. 1998). The summer Chinook from the upper Columbia River are included in the Upper Columbia River Summer- and Fall-Run ESU, which encompasses all late-run (summer and fall), ocean-type Chinook salmon from the mainstem Columbia River and its tributaries (excluding the Snake River) between Chief Joseph and McNary Dams (Waknitz et al. 1995). Waknitz et al. (1995) concluded that due to high total abundance this ESU was not likely to become at risk from extinction. Yet, a majority of natural spawning activity was in the vicinity of Hanford Reach, and it was unclear whether natural production was self-sustaining given the vast summer Chinook artificial propagation efforts (Waknitz et al. 1995). Additionally, the Biological Review Team expressed concern about potential consequences to genetic and life-history traits from an increasing contribution of hatchery fish to total spawning escapement (Waknitz et al. 1995).

Artificial propagation of ocean-type Chinook from the middle/upper Columbia has been continuous since the implementation of the Grand Coulee Fish Maintenance Project (GCFMP) in 1939 (Myers et al. 1998). The US Fish and Wildlife Service established three hatchery programs for summer/fall Chinook during the GCFMP, Leavenworth NFH, Entiat NFH, and Winthrop NFH. The Washington Department of Fisheries (now Washington Department of Fish and Wildlife) followed with hatchery programs at Rocky Reach (1964), Wells Dam (1967), Priest Rapids (1974), and Eastbank (1990) facilities. Currently, only Leavenworth NFH and Winthrop NFH are not producing summer/fall Chinook. Entiat NFH has resumed production of summer/fall Chinook (Wells FH Stock) in 2009 and released their first yearling summer Chinook smolts in 2010. Since

1941, over 200 million ocean-type Chinook salmon have been released into the middle Columbia River Basin (Myers et al. 1998). Initially, the hatchery programs differentiated between early returning fish (i.e., stream-type) and later returning fish (i.e., ocean-type), but no distinction was made regarding the “summer” and “fall” components of the ocean-type stocks (Waknitz et al. 1995). Therefore, all Chinook salmon now migrating above Rock Island Dam descend from not only a mixture between different stocks from the basin, but also a mixture between the endemic summer and fall life histories. While hatchery protocols have been modified of late to maintain discreet summer and fall Chinook hatchery stocks (Utter et al. 1995; see also HGMP), physical evidence and genetic data suggests that summer and fall Chinook may have become homogenized. During the 1970’s and 80’s, given coded-wire tag recoveries, summer-run Chinook originating from above Rock Island Dam were believed to have spawned extensively with Hanford Reach and Priest Rapids Hatchery fish (Chapman 1994). Stuehrenberg et al. (1995) reported that 10% of their radio tagged summer Chinook were occupying typical fall-run spawning habitat on the mainstem Columbia river, and 25% of fall fish released from Priest Rapids were recovered as summers at (or above) Wells Hatchery. Genetic data reported by Marshall et al. (1995) and Waknitz et al. (1995) corroborate these observations, as genetic distances observed between summer and fall Chinook within the Upper Columbia River Summer- and Fall-Run ESU were essentially zero.

In response to the need for evaluation of the supplementation hatchery programs, both a monitoring and evaluation plan (DCPUD 2005; Murdoch and Peven 2005) and the associated analytical framework (Hays et al. 2006) were developed for the Habitat Conservation Plan’s Hatchery Committee through the joint effort of the fishery co-managers (CCT, NMFS, USFWS, WDFW, and YN) and Chelan County and Douglas County PUDs. These reports outline 10 objectives to be applied to various species assessing the impacts of hatchery operations mitigating the operation of Wells, Rocky Reach, and Rock Island hydroelectric projects. The present monitoring and evaluation study plan differs in scope from previous monitoring and evaluation projects proposed by WDFW Molecular Genetics Lab, in that it does not investigate a single watershed, but instead will encompass all summer Chinook stocks from the upper Columbia River including the three supplementation (Wenatchee, Methow, and Okanogan) and the harvest augmentation program (Wells summer Chinook). The objectives of this study were to determine if genetic diversity, population structure, and effective population size have changed in natural spawning populations as a result of the hatchery programs.

Materials and Methods

Collections

A total of 2,416 summer Chinook were collected from tributaries in the upper Columbia River basin and were analyzed (Table 1). Two collections of natural-origin summer Chinook from 1993 (prior to the supplementation program) were taken from the Wenatchee River Basin and were compared to collections of hatchery and natural-origin from 2006 and 2008 that were post-supplementation. Two pre-supplementation collections from the Methow River (1991 and 1993) were compared to post-supplementation collections from 2006 and 2008. Three pre-supplementation collections from the Okanogan River Basin (1991, 1992, and 1993) were compared with post-supplementation collections from 2006 and 2008. A collection of natural-origin summer Chinook from the Chelan River was also analyzed. Additionally, hatchery collections from Eastbank Hatchery (Wenatchee and MEOK stock) and Wells Hatchery were analyzed and compared to the in-river collections. Summer Chinook data (provided by the USFWS) from the Entiat River was also used for comparison. Lastly, data from eight collections of fall Chinook was compared to the collections of summer Chinook.

Laboratory Analyses

All laboratory analyses were conducted at the WDFW Genetics Laboratory in Olympia, Washington. Genomic DNA was extracted by digesting a small piece of fin tissue using the nucleospin tissue kits obtained from Macherey-Nagel following the recommended conditions in the user manual. Extracted DNA was eluted with a final volume of 100 µL.

Genotype information was generated using thirteen microsatellite markers following standard laboratory protocols and analysis methods. Descriptions of the loci assessed in this study and polymerase chain reaction (PCR) conditions are given in Table 2. PCR reactions were run with a thermal profile consisting of: denaturation at 95^{o}C for 3 min, denaturation at 95^{o}C for 15 sec, anneal for 30 sec at the appropriate temperature for each locus (Table 2), extension at 72^{o}C for 1 min, repeat cycle (steps 2-4), final extension at 72^{o}C for 30 minutes. PCR products were then processed with an ABI-3730 DNA Analyzer. Genotypes were visualized with a known size standard (GS500LIZ 3730) using GENEMAPPER 3.7 software. Alleles were binned in GENEMAPPER using the standardized allele sizes established for the Chinook GAPS dataset (Seeb et al. 2007).

Within-collection Statistical Analyses

Allele frequencies were calculated with CONVERT (version 1.3, Glaubitz 2003). Hardy-Weinberg proportions for all loci within each collection were calculated using GENEPOP (version 3.4, Raymond and Rousset 1995). Heterozygosity (observed and expected) was computed for each collection group using GDA (Lewis and Zaykin 2001).

Allelic richness and F_{IS} (Weir and Cockerham 1984) inbreeding coefficient were calculated using FSTAT (version 2.9.3.2, Goudet 2001). Linkage disequilibrium for each pair of loci in each collection was calculated using GENEPOP v 3.4 (10,000 dememorizations, 100 batches, and 5,000 iterations per batch). Pairwise estimates of genetic differentiation between collection groups were calculated using GENEPOP (version 3.4, Raymond and Rousset 1995). Statistical significance for the tests of Hardy-Weinberg proportions, linkage disequilibrium, and genotypic differentiation was evaluated using a Bonferroni correction of p-values to account for multiple, simultaneous tests (Rice 1989).

Between-collection Statistical Analyses

Pairwise F_{ST} estimates were computed to examine population structure among collections using GENETIX (version 4.03, Belkhir et al. 2001). This estimate uses allelic frequency data and departures from expected heterozygosity to assess differences between pairs of populations.

We used PHYLIP (version 3.5c, Felsenstein 1993) to calculate Cavalli-Sforza and Edwards (1967) pairwise chord distances between collections. Bootstrap calculations were performed using SEQBOOT followed by calculations of genetic distance using GENDIST. The NEIGHBOR-JOINING method of Saitou and Nei (1987) was used to generate the dendrograms and CONSENSE to generate a final consensus tree from the 1,000 replicates. The dendrogram generated in PHYLIP was plotted as an unrooted radial tree using TREEVIEW (version 1.6.6, Page 1996).

Effective Number of Breeders

The effective number of breeders (N_b) was estimated for pre- and post-supplementation program collections (where possible) to investigate whether hatchery programs had affected that genetic metric over the operational period. Wang (2009) derived an equation for effective size (N_e) as a function of the frequency of nested full-sib and half-sib families in a random collection of individuals.

$$\frac{1}{N_e} = \frac{1+3\alpha}{4}\left(Q_1 + Q_2 + 2Q_3\right) - \frac{\alpha}{2}\left(\frac{1}{N_1} + \frac{1}{N_2}\right) \qquad \text{(equation 10)}$$

Where α is a measure of the deviation of genotype frequencies from Hardy-Weinberg expectation (equivalent to Wright's (1969) F_{IS}), Q_i are the probabilities that a pair of offspring are paternal half sibs, maternal half sibs, or full sibs, respectively, and N_1 and N_2 are the number of male and female parents that generation, respectively. Genetic parameters (i.e., sibship distributions) were estimated for summer Chinook collections using algorithms implemented in COLONY (Jones and Wang 2009). To be clear, Wang's (2009) method as implemented here will estimate N_b, given multi-locus genotypes from each collection were partitioned by brood year for this analysis. To obtain an estimate of N_e each N_b value must be multiplied by the mean generation time of that population.

Results

Collections

A total of 2,350 individuals from 32 collections of temporally replicated samples (six locations) were analyzed (Table 1). Temporally replicated collections of hatchery and natural-origin samples were from the Wenatchee, Methow, and Okanogan Rivers. Temporally replicated hatchery-origin summer Chinook were from Wells Hatchery, Eastbank Hatchery - Wenatchee stock, and Eastbank Hatchery - Methow/Okanogan (MEOK) stock. A total of 232 of those individuals were excluded from any analyses because they failed to amplify at nine or more loci. Data for remaining 2,118 individuals were analyzed to assess differences between temporally replicated natural- and hatchery-origin summer Chinook for each location and to compare the differences among the different collection locations. Summer Chinook data from the temporally replicated collection locations were then combined and compared to fall Chinook data from the GAPS v.3.0 dataset.

Statistical Analyses

The population statistics (Hardy-Weinberg equilibrium and F_{IS}) calculated for each of the 32 temporally replicated collection locations were consistent with neutral expectations (i.e., no associations among alleles). Three collections did have a single locus that did not meet expectations (Wenatchee hatchery-origin 2006, Wells hatchery 2006, and Okanogan hatchery-origin 2009). Based on these results we suggest the collections represented randomly breeding groups and were not comprised of mixtures of individuals from different genetic source populations.

Population differentiation was assessed for each of the temporally replicated collections from within each location (Table 3). This analysis revealed the only significant difference observed within a collection location pertained to the collection from 1993 Okanogan River natural-origin samples. Because of the significant difference of this collection to the other temporal replicates it was not included in further analyses.

Given the absence of genetic differentiation observed among the temporally replicated collections, the 32 collections from the Wenatchee, Methow, and Okanogan River were combined to form three location-specific collections for analysis. Population differentiation metrics were compared among the composite Wenatchee, Methow, and Okanogan collections and eight other location-specific collections (11 locations total). Comparing all collections, there were a total of 39 significant genic test comparisons out of a total 496 (Table 4). Thirty-eight of the 39 statistically significant pairwise differences pertained to the Okanogan River and 2006 Wells Hatchery collections (Table 4). F_{ST} results are described further below.

Within-collection genetic metrics were estimated for the 11 location-specific collections of summer Chinook from the upper Columbia River, in addition to eight collections of fall Chinook (Table 1). The population statistics (Hardy-Weinberg equilibrium and F_{IS}) calculated for these collections of summer and fall

Chinook were also consistent with neutral expectations. The collection from Lyons Ferry Hatchery had one locus that did not meet expectations and the collections from Crab Creek and Marion Drain both had three loci that did not meet expectations.

The hatchery collections in general had a higher percentage of significantly linked loci; however the observed genetic diversity were similar for the natural and hatchery-origin collections. Analysis of allelic richness was based on 11 individuals per collection, the minimum number of individuals across all collections with complete multilocus genotypes. The largest number of linked loci occurred in the Crab Creek, Entiat River, and Okanogan natural-origin collections. Allelic richness was on average lower in the collections of summer Chinook (10.7) collections in comparison to the collections of fall Chinook (11.0).

Pairwise F_{ST} (Table 4) estimates revealed low levels of differentiation, where all observed F_{ST} values between the collections of summer Chinook were lower than 0.0096. There were 15 out of 28 comparisons between collections of summer Chinook that were significantly different from zero and occurred primarily from comparisons of the Okanogan River (hatchery and natural-origin) and Wells Hatchery to all other collections. The collection of Eastbank Hatchery – MEOK stock was differentiated from the Wenatchee River natural-origin and Entiat River collections. The collection from the Chelan River had a small sample size of 23 individuals and only differentiated from the Eastbank Hatchery – MEOK stock. F_{ST} estimates regarding pairwise comparisons between each of four fall Chinook collection locations (Crab Creek, Lyons Ferry Hatchery, Marion Drain, and Snake River) to all other collections were significantly different from zero (Table 5). Pairwise comparisons for three other fall Chinook collections (Hanford Reach, lower Yakima River, and Umatilla River) to the collections of summer Chinook were significantly different from zero (Table 6). The only fall Chinook collection that was not significantly differentiated from all of the summer Chinook was Priest Rapids.

The relative genetic relationships among the test groups were assessed using the consensus clustering analysis (Figure 1). Statistical support for the dendrogram topology (i.e., tree shape) was low regarding the branching that separated the collections of summer Chinook from the upper Columbia River. The collections of fall Chinook; however were supported with bootstrap support over 76% with the exception of three collections (lower Yakima River, Crab Creek, and Umatilla River). In other words, 760 of the 1000 bootstrap replicates supported the placement of the node separating summer and fall collections. The collection from the Chelan River had bootstrap support of 68%; however the sample size for that collections was small (N = 23). Even though the bootstrap support was low among the collections of summer Chinook there was concordance between geography and genetic distance.

Where comparisons were possible between pre- and post-supplementation program collections, the effective number of breeders (N_b) estimated to have comprised those collections were slightly lower for contemporary (2008) collections; however in all cases the 95% confidence intervals overlapped between historical and contemporary collections, suggesting statistical equivalency. Regarding Wenatchee River collections, the point estimates of N_b ranged from 134 (08FU) to 190 (93DD), where all collections had overlapping confidence intervals (Table 7). The upper bound of the 1989 brood year for collection 93DD was very large, suggesting the sample size was insufficient for properly inferring the sibship distribution within the collection. Comparing the Okanogan natural collections 93ED and 08GA, the estimated N_b were 142 (CI 102 – 203) and 127 (CI 92 – 180), respectively. For the Eastbank Hatchery MEOK stock comparisons, the N_b estimated for the 93DF collection was 171 (CI 129 – 229), as compared to the 166 (CI 126 – 226) estimated for collection 08MO. In all cases, the estimated N_b can be converted to effective population size (N_e) by multiplying the estimate by the mean generation time.

Discussion

The collections of summer Chinook populations from the upper Columbia River are of interest because census sizes are reduced below historic levels and are the subject of mitigation and supplementation hatchery programs. Concern over the impacts of hatchery supplementation programs on the genetic integrity of natural-origin populations led to our primary objective, which was to evaluate genetic metrics for temporally replicated collections of summer Chinook in the upper Columbia River pre and post hatchery supplementation. A similar analysis by Kassler and Dean (2010) was conducted on spring Chinook in the Tucannon River to evaluate the effects of a supplementation and captive brood program on natural-origin stocks. Additionally, upper Columbia River spring Chinook supplementation programs (Blankenship et al. 2007; Small et al. 2007), spring and fall Chinook populations in the Yakima Basin (Kassler et al. 2008), and a potentially unique population of fall Chinook in Crab Creek (Small et al. 2010) have been evaluated. In the present analysis of summer Chinook populations, collections of pre- and post- supplementation summer Chinook were collected from the Wenatchee River, Methow River, and Okanogan River Basins and analyzed to determine if the genetic profile has changed as a result of the supplementation program. Analysis was then conducted on the collections of summer run to compare the fall run Chinook collections in the upper Columbia River basin.

Allozyme analyses of these three summer run Chinook stocks in the upper Columbia River have identified that each stock was distinct, with a closer relationship detected between the Wenatchee and Methow Rivers (WDF and WDW 1993, Marshall 2002). Wenatchee summer Chinook are thought to be a mixture of native summer Chinook and Chinook from the Grand Coulee Fish Maintenance Project (GCFMP). The goal of the GCFMP project between 1939 and 1943 was to trap migrating Chinook salmon at Rock Island dam (75 miles below Grand Coulee) and homogenize the populations, which reduced the genetic uniqueness of the distinct tributary populations present in the upper Columbia River.

We found allele frequencies for individual temporally replicated hatchery- and natural-origin collection locations of adult summer Chinook were not significantly different from that expected of a single underlying population, except for one collection (1993 Okanogan natural-origin; Table 3). This collection was differentiated to the Okanogan collections in 2006 and 2008; however it was not differentiated from the collection in 1992. The Okanogan collection from 1992 was also not differentiated to any other collection; therefore the difference in the collection from Okanogan 1993 was likely not an indication of genetic change from pre supplementation to post supplementation. The collection was however dropped from further analyses so as to not confuse interpretation of results. The lack of allelic differentiation observed among the temporally replicated collections was interpreted as the genetic metrics from each location in the early 1990's did not differ from the samples collected in 2008. Spanning a few generations, allele frequencies are not expected to change for large populations at genetic equilibrium. In contrast, changes in allele frequencies of small populations may occur due to the stochastic sampling of genes from one generation to the next (i.e., genetic drift).

A second round of analyses was conducted to evaluate the genetic relationships of the summer run collections (temporal collections were combined) with data from the Entiat River, Chelan River, and eight collections of fall Chinook. Assessment of the relationship between the summer run collections in comparison to each other provided very little evidence of genetic differentiation between these collections. While population differentiation did show some significant differences between the Okanogan River and Wells Hatchery collections, all of the pairwise F_{ST} values were below 0.003. Meaning that a very small proportion of the observed genetic variation could be attributed to restrictions in gene flow (i.e., population structure)

The comparison of the hatchery-origin collections revealed a lack of differentiation between the Eastbank Hatchery – Wenatchee stock, Eastbank Hatchery – MEOK stock, and the Wells Hatchery (with exception of the 2006 collection). The genetic similarity or low level of genetic differentiation among these stocks suggests that there has been an integration of natural- and hatchery-origin summer Chinook in the upper Columbia River or a lack of ancestral genetic difference. The difference of the 2006 Wells Hatchery collection to the other collections is most likely a result of sampling effect because of the lack of differentiation among the stocks in the basin. If the 2006 collection had been mixed from different sources of summer Chinook there would not be a detectable level of differentiation as was seen with the 2006 sample.

The analyses to compare summer and fall Chinook collections provided some understanding on the genetic relationships of Chinook with different run timings in the upper Columbia River basin. Historically, the hatchery programs in the upper Columbia River were separated into groups of the early returning fish (i.e., stream-type) and later returning fish (i.e., ocean-type), but the programs did not sort individuals identified as "summer" or "fall" stocks (Waknitz et al. 1995). Now all Chinook salmon that are migrating above Rock Island Dam descend from a mixture of different stocks from the upper Columbia River basin, but also a mixture between the endemic summer and fall life histories.

Small et al. (2010) conducted an analysis on summer run and fall run Chinook in the upper Columbia River and concluded that Crab Creek Chinook in the upper Columbia River were genetically distinct to all other fall and summer run Chinook stocks that were analyzed. They did note a departure from Hardy Weinberg expectation as a result of a null allele at the microsatellite locus *Ogo-4* and a higher linkage disequilibrium value due to the inclusion of family groups in one of their samples. Kassler et al. (2008) found differentiation among spring and fall Chinook populations in the Yakima River.

The tests of pairwise F_{ST} indicated a very low level of genetic differentiation (less than one percent difference) between collections of summer-run Chinook and fall-run Chinook. The range of pairwise F_{ST} values for comparisons between the summer run and fall run collections was 0.0016 – 0.0248. The larger values from the range were associated to the collections from Crab Creek, Lyons Ferry Hatchery, and Marion Drain. Studies by Kassler et al. (2008) and Small et al. (2010) have documented differences among the populations of these collections to others within the upper Columbia River basin. The low pairwise F_{ST} values between Priest Rapids and Hanford Reach collections and the summer run collections were not surprising because summer-run Chinook originating from above Rock Island Dam were believed to have spawned extensively with Hanford Reach and Priest Rapids Hatchery fish during the 1970's and 80's (Chapman 1994). The lack of differentiation among the summer and fall stocks in the Columbia River was also identified by Utter et al. (1995) and the HGMP where they state physical evidence and genetic data suggests that summer and fall Chinook may have become homogenized.

Despite low levels of statistical bootstrap support for dendrogram topology (i.e., tree shape), there was concordance observed between geographic location and the genetic relationships among the summer and fall Chinook populations. The collections from the Okanogan (hatchery and natural-origin) did separate out with collections from Wells Dam Hatchery, Entiat River, and Eastbank Hatchery – MEOK stock, and were next to a group of the Methow and Wenatchee collections. The fall Chinook populations are also separated to the summer collections and the position of all but three of these collections (lower Yakima River, Crab Creek, and Umatilla River) were statistically supported. The geographic proximity of the fall collections seemed to follow the observed pattern in this dendrogram. The relationship of the Snake River and Lyons Ferry Hatchery in proximity to the collection from Marion Drain was not surprising while the relationship between Priest Rapids and Hanford Reach was easily a result of the stocking practices of fall Chinook in the 1970 and 1980's.

A secondary objective of this study was to determine if the effective population size of upper Columbia River summer Chinook populations had changed over time due to supplementation efforts. We observed that the number of effective breeders in the collections from 1993 and 2008 has not changed thus providing reason to believe that the genetic diversity of summer Chinook in the upper Columbia River has not been altered through the supplementation program.

Acknowledgements

Chelan County PUD, Grant County PUD, and Washington State General Funds provided funding for this project. Cherril Bowman (WDFW – Molecular Genetics Laboratory) processed samples in the laboratory. Maureen (Mo) Small provided data for some collections and discussion of the analyses. USFWS provided data from the Entiat River.

References

Banks, M.A., M.S. Blouin, B.A. Baldwin, V.K. Rashbrook, H.A. Fitzgerald, S.M. Blankenship, and D. Hedgecock. 1999. Isolation and inheritance of novel microsatellites in Chinook salmon (*Oncorhynchus tshawytscha*). Journal of Heredity 90:281-288.

Belkhir, K., P. Borsa, L. Chikhi, N. Raufaste, and F. Bonhomme. 2001. *Genetix*, *logiciel sous Windows* TM *pour la genetique des populations*. Laboratoire Genome, Populations, Interactions: CNRS UMR 5000, Universite de Montpellier II, Montpellier, France.

Blankenship, S.M., J.F. VonBargen, K.I. Warheit, and A.R. Murdoch. 2007. Assessing the Genetic Diversity of Natural Chiwawa River Spring Chinook Salmon and Evaluating the Effectiveness of its Supportive Hatchery Supplementation Program. . Final Report. Unpublished Washington Department of Fish and Wildlife Molecular Genetics Laboratory Report submitted to Chelan County PUD.

Cairney, M., J.B. Taggart, and B. Hoyheim. 2000. Characterization of microsatellite and minisatellite loci in Atlantic salmon (*Salmo salar L.)* and cross-species amplification in other salmonids. Molecular Ecology 9:2175–2178.

Cavalli-Sforza, L.L. and A.W.F. Edwards. 1967. Phylogenetic analysis: models and estimation procedures. Evolution 32:550-570.

Chapman, D., A. Giorgi, T. Hillman, D. Deppert, M. Erho, S. Hays, C. Peven, B. Suzumoto, and R. Klinge. 1994. Status of summer/fall chinook salmon in the mid-Columbia region. Report for Chelan, Douglas, and Grant County PUDs. 412 p. + app. (Available from Don Chapman Consultants, 3653 Rickenbacker, Ste. 200, Boise, ID 83705.)

DCPUD. 2005. Conceptual approach for monitoring and evaluating the Douglas County Public Utility District hatchery programs. Douglas County Public Utility District, Wenatchee, Washington. 105 p.

Felsenstein, J. 1993. PHYLIP (Phylogeny Inference Package) version 3.5c. Distributed by the author. Department of Genetics, University of Washington, Seattle, WA.

Glaubitz, J.C. 2003. CONVERT (version 1.2): A user-friendly program to reformat diploid genotypic data for commonly used population genetic software packages. http://www.agriculture.purdue.edu/fnr/html/faculty/Rhodes/Students%20and%20Staff/glaubitz/software.htm.

Goudet, J. 2001. FSTAT, a program to estimate and test gene diversities and fixation indices (version 293). Updated from Goudet (1995). Available from http://www.unilch/izea/softwares/fstat.html.

Greig, C., J.P. Jacobson, and M.A. Banks. 2003. New tetranucleotide microsatellites for fine-scale discrimination among endangered Chinook salmon (Oncorhynchus tshawytscha). Molecular Ecology Notes 3:376-379.

Hays, S., T. Hillman, T. Kahler, R. Klinge, R. Langshaw, B. Lenz, A. Murdoch, K. Murdoch, and C. Peven. 2006. Decision rules for monitoring and evaluating district hatchery programs. Draft study plan. 27 p.

HGMP. Draft Hatchery and Genetic Management Plans (2005) for Wenatchee, Methow, and Okanogan River summer Chinook. Available at Washington Department of Fish and Wildlife, 600 Capitol Way N, Olympia, WA, 98501.

Kassler, T.W., J.F. VonBargen, and D. Hawkins. 2008. DNA-based population of-Origin Assignments of Chinook Salmon Smolts Outmigrating Past Chandler Trap at Prosser Dam (Yakima River) in 2007. Final Report. Unpublished Washington Department of Fish and Wildlife Molecular Genetics Laboratory Report submitted to Bonneville Power Administration (BPA).

Kassler, T.W. and C.A. Dean. 2010. Genetic analysis of natural-origin spring Chinook and comparison to spring Chinook from an integrated supplementation program and captive broodstock program in the Tucannon River. Final Report. Unpublished Washington Department of Fish and Wildlife Molecular Genetics Laboratory Report submitted to Mike Gallinat, WDFW - Snake River Laboratory, Dayton, WA.

Jones, O. and J. Wang. 2009. COLONY: a program for parentage and sibship inference from multilocus genotype data. Molecular Ecology Resources 10: 551–555.

Lewis, P. O. and D. Zaykin. 2001. Genetic Data Analysis: Computer program for the analysis of allelic data. Version 1.0 (d16c). Free program distributed by the authors over the internet from http://lewis.eeb.uconn.edu/lewishome/software.html

Marshall, A.R., C. Smith, R. Brix, W. Dammers, J. Hymer, and L. LaVoy. 1995. Genetic diversity units and major ancestral lineages for chinook salmon in Washington. *In* C. Busack and J. B. Shaklee (eds.), Genetic diversity units and major ancestral lineages of salmonid fishes in Washington, p. 111-173. Wash. Dep. Fish Wildl. Tech. Rep. RAD 95-02. (Available from Washington Department of Fish and Wildlife, 600 Capital Way N., Olympia WA 98501-1091.)

Marshall, A. 2002. 16 August memo to Ann Blakley (WDFW) and Amilee Wilson (WDFW) regarding genetic analyses of selected Washington Chinook stocks. WDFW. Olympia.

Mobrand, L. (chair), J. Barr, L. Blankenship, D. Campton, T. Evelyn, C. Mahnken, P. Seidel, L. Seeb and B. Smoker. 2004. Hatchery Scientific Review Group (HSRG) – March 2004. Hatchery Reform Recommendations for the Puget Sound and Coastal Washington Hatchery Reform Project. Long Live the Kings, 1305 Fourth Avenue, Suite 810, Seattle, WA 98101 (available from www.hatcheryreform.org).

Murdoch, A. and C. Peven. 2005. Conceptual approach for monitoring and evaluating the Chelan County Public Utility District hatchery programs. Chelan County Public Utility District, Wenatchee, Washington. 105 p.

Myers, J.M., R.G. Kope, G.J. Bryant, D. Teel, L.J. Lierheimer, T.C. Wainwright, W.S. Grand, F.W. Waknitz, K. Neely, S.T. Lindley, and R.S. Waples. 1998. Status review of chinook salmon from Washington, Idaho, Oregon, and California. U.S. Dept. Commer., NOAA Tech. Memo. NMFS-NWFSC-35, 443 p.

Olsen, J.B., P. Bentzen, and J.E. Seeb. 1998. Characterization of seven microsatellite loci derived from pink salmon. Molecular Ecology 7(8):1087-1089.

Page, R.D.M. 1996. TREEVIEW: an application to display phylogenetic trees on personal computers. Computer Application Biosciences 12:351-358.

Raymond, M. and F. Rousset. 1995. GENEPOP (Version 3.3): Population genetics software for exact tests and ecumenicism. Journal of Heredity 86:248-249.

Rexroad, C.E., III, R.L. Coleman, A.M. Martin, W.K. Hershberger, and J. Killefer. 2001. Thirty-five polymorphic microsatellite markers for rainbow trout (Oncorhynchus mykiss). Animal Genetics 32:317-319.

Rice, W.R. 1989. Analyzing tables of statistical tests. Evolution 43:223-225.

Saitou, N. and M. Nei. 1987. The neighbor-joining method: A new method for reconstructing phylogenetic trees. Molecular Biology and Evolution 4:406-425.

Seeb, L.W., A. Antonovich, M.A. Banks, *et al*. 2007. Development of a standardized DNA database for Chinook salmon. Fisheries 32:11.

Small, M.P., K.I. Warheit, C.A. Dean, and A.R. Murdoch. 2007. Methow spring Chinook genetic monitoring. Final Report. Unpublished Washington Department of Fish and Wildlife Molecular Genetics Laboratory Report.

Small, M.P., D. Burgess, C. Dean, and K. Warheit. 2010. Does Lower Crab Creek in the Eastern WA desert have a native population of Chinook salmon? Submitted to special edition of American Fisheries Society, Proceedings from the Coastwide Salmonid Genetics Meeting, Boise, ID.

Stuehrenberg, L.C., G.A. Swan, L.K. Timme, P.A. Ocker, M.B. Eppard, R.N. Iwamoto, B.L. Iverson, and B.P. Sanford. 1995. Migrational characteristics of adult spring, summer, and fall chinook salmon passing through reservoirs and dams of the mid-Columbia River. Final report. CZES Division, NWFSC, NMFS, Seattle, WA, 115 p.

Utter, F.M., D.W. Chapman, and A.R. Marshall. 1995. Genetic population structure and history of chinook salmon of the Upper Columbia River. American Fisheries Society Symposium 17:149-165.

Waknitz, F.W., G.M. Matthews, T. Wainwright, and G.A. Winans. 1995. Status review for Mid-Columbia River summer chinook salmon. NOAA Tech. Mem. NMFS-NWFSC-22, 80 p. (Available from Natl. Mar. Fish. Serv., Northwest Fisheries Science Center, Coastal Zone and Estuarine Studies Division, 2725 Montlake Blvd. E., Seattle, WA 98112-2097.)

Wang, J. 2009. A new method for estimating effective population sizes from a single sample of multilocus genotypes. Molecular Ecology 18:2148-2164

Wang, J. and A.W. Santure. 2009. Parentage and sibship inference from multi-locus genotype data under polygamy. Genetics 181: 1579-1594.

Waples R.S. 1990. Conservation genetics of Pacific salmon. III. Estimating effective population size. Journal of Heredity 81:277-289

Waples R.S., M. Masuda, and J. Pella. 2007. SALMONNb: a program for computing cohort-specific effective population sizes (N_b) in Pacific salmon and other semelparous species using the temporal method. Molecular Ecology Notes 7, 21-24

WDF (Washington Department of Fisheries) and WDW (Washington Department of Wildlife). 1993. 1992 Washington state salmon and steelhead stock inventory. Appendix Three. Columbia River stocks. WDF. Olympia, WA.

Weir, B.S. and C.C. Cockerham. 1984. Estimating F-statistics for the analysis of population structure. Evolution 38:1358-1370.

Williamson, K.S., J.F. Cordes, and B.P. May. 2002. Characterization of microsatellite loci in chinook salmon (*Oncorhynchus tshawytscha)* and cross-species amplification in other salmonids. Molecular Ecology Notes 2 (1):17-19.

Wright, S. 1969. Evolution and the Genetics of Populations, Vol. 2, The Theory of Gene Frequencies. The University of Chicago Press, Chicago, Illinois.

Table 1. Samples of adult hatchery- and natural-origin summer and fall Chinook that were analyzed from the upper Columbia River. Total number of individuals that were analyzed / individuals with data for 9 or more loci that were included in the analysis. Collection statistics (allelic richness, linkage disequilibrium (before and after Bonferroni correction), F_{IS}, heterozygosity (H_O and H_E)) and p-values for deviations from Hardy-Weinberg equilibrium (HWE). P-values were defined as significant after implementation of Bonferroni correction for multiple tests (Rice 1989).

WDFW GSI code[a]	Collection location	N =	Allelic Richness[b]	Linkage Disequilibrium[c]	F_{IS} (p-value)[d]	H_O	H_E
93DD	Wenatchee River upstream of Tumwater Dam - natural origin	51 / 45					
93DE	Wenatchee River downstream of Tumwater Dam - natural origin	88 / 88					
06CQ	Wenatchee River upstream of Tumwater Dam - natural origin	95 / 86					
06CR	Wenatchee River downstream of Tumwater Dam - natural origin	95 / 82					
08FV	Wenatchee River upstream of Tumwater Dam - natural origin	95 / 82					
08FW	Wenatchee River downstream of Tumwater Dam - natural origin	95 / 87					
	Wenatchee River - Natural origin combined	**519 / 470**	**10.7**	**17 / 4**	**0.001 (0.403)**	**0.8504**	**0.8513**
06CP	Wenatchee River - hatchery origin	95 / 70					
08FU	Wenatchee River - hatchery origin	95 / 83					
	Wenatchee River - Hatchery origin combined	**190 / 153**	**10.6**	**18 / 6**	**0.018 (0.013)**	**0.8409**	**0.8561**
93EC	Methow River - natural origin	27 / 27					
06CT	Methow River - natural origin	95 / 90					
08FY	Methow River - natural origin	95 / 88					
09CO	Methow River - natural origin	91 / 80					
	Methow River - Natural origin combined	**308 / 285**	**10.7**	**4 / 1**	**0.006 (0.160)**	**0.8506**	**0.8554**
06CS	Methow River - hatchery origin	14 / 8					
08FX	Methow River - hatchery origin	21 / 18					
09CP	Methow River - hatchery origin	19 / 18					
	Methow River - Hatchery origin combined	**54 / 44**	**10.8**	**11 / 2**	**-0.003 (0.593)**	**0.8553**	**0.8523**

Table 1 continued.

92FM	Okanogan River - natural origin	49 / 46					
93ED*	Okanogan River - natural origin	103 / 87					
06CV	Okanogan River - natural origin	95 / 88					
08GA	Okanogan River - natural origin	95 / 92					
09CN	Okanogan River - natural origin	133 / 126					
	Okanogan River - Natural origin combined	**475 / 439**	**10.8**	**9 / 4**	**0.003 (0.304)**	**0.8563**	**0.8596**
* - not included in the combined dataset							
06CU	Okanogan River - hatchery origin	58 / 49					
08FZ	Okanogan River - hatchery origin	19 / 18					
09CM	Okanogan River - hatchery origin	117 / 107					
	Okanogan River - hatchery origin combined	**194 / 174**	**10.8**	**31 / 10**	**-0.011 (0.920)**	**0.8678**	**0.8586**
91FL	Wells Hatchery	68 / 42					
92FK	Wells Hatchery	25 / 23					
93DG	Wells Hatchery	11 / 9					
06DM	Wells Hatchery	95 / 91					
08HY	Wells Hatchery	95 / 91					
	Wells Hatchery combined	**294 / 256**	**10.7**	**8 / 3**	**-0.001 (0.529)**	**0.8670**	**0.8665**
08MN	**Eastbank Hatchery - Wenatchee River stock**	**95 / 90**	**10.7**	**6 / 1**	**0.020 (0.024)**	**0.8326**	**0.8498**
92FO	Eastbank Hatchery - Methow / Okanogan (MEOK) stock	36 / 33					
93DF	Eastbank Hatchery - Methow / Okanogan (MEOK) stock	90 / 86					
08MO	Eastbank Hatchery - Methow / Okanogan (MEOK) stock	95 / 88					
	Eastbank Hatchery - MEOK stock combined	**221 / 207**	**10.7**	**2 / 0**	**-0.005 (0.782)**	**0.8647**	**0.8604**
		2,350 / 2,118					

Table 1 continued.

06KN	**Chelan River**	**70 / 23**	**10.3**	**11 / 0**	**0.027 (0.118)**	**0.8334**	**0.8556**
Data provided by USFWS							
	Entiat River - summer Chinook	**190**	**10.9**	**33 / 10**	**0.008 (0.119)**	**0.8553**	**0.8625**
Data from Small et al. (2010)							
08EH	Crab Creek	108					
09AZ	Crab Creek	291					
	Crab Creek	**399**	**10.5**	**35 / 14**	**0.018 (0.000)**	**0.8519**	**0.8676**
GAPS v.3.0 data							
	Priest Rapids Hatchery - fall Chinook	**81**	**11.1**	**3 / 2**	**0.015 (0.079)**	**0.8591**	**0.8723**
	Hanford Reach - fall Chinook	**220**	**11.3**	**4 / 0**	**0.010 (0.068)**	**0.8661**	**0.8746**
	Umatilla - fall Chinook	**96**	**11.2**	**17 / 6**	**-0.003 (0.623)**	**0.8719**	**0.8693**
	lower Yakima River - fall Chinook	**103**	**11.0**	**3 / 1**	**0.000 (0.511)**	**0.8724**	**0.8721**
	Marion Drain - fall Chinook	**190**	**10.8**	**9 / 4**	**0.022 (0.001)**	**0.8586**	**0.8782**
	Lyons Ferry Hatchery - fall Chinook	**186**	**10.6**	**7 / 4**	**0.013 (0.033)**	**0.8527**	**0.8641**
	Snake River - fall Chinook	**521**	**11.1**	**0 / 0**	**-0.001 (0.634)**	**0.8720**	**0.8708**
		NA / 2,009					

[a] - Year that samples were collected is identifed by the two numbers in the WDFW GSI code

[b] - based on a minimum of 11 diploid individuals

[c] - adjusted alpha p-value = 0.0006

[d] - adjusted alpha p-value = 0.0002

Table 2. PCR conditions and microsatellite locus information (number alleles/locus and allele size range) for multiplexed loci used for the analysis of Chinook. Also included are the observed and expected heterozygosity (H_o and H_e) for each locus.

PCR Conditions			Locus statistics		Heterozygosity		
Poolplex	Locus	Dye Label	# Alleles/ Locus	Allele Size Range (bp)	H_o	H_e	References
Ots-M	*Ots-201b*	blue	49	137 - 334	0.9474	0.9544	Unpublished
	Ots-208b	yellow	56	154 - 378	0.9523	0.9672	Greig et al. 2003
	Ssa-408	red	32	184 - 308	0.9177	0.9214	Cairney et al. 2000
Ots-N	*Ogo-2*	red	22	206 - 260	0.8526	0.8673	Olsen et al. 1998
Ots-O	*Ogo-4*	blue	20	128 - 170	0.6694	0.7028	Olsen et al. 1998
	Ots-213	yellow	45	178 - 370	0.9430	0.9525	Greig et al. 2003
	Ots-G474	red	16	152 - 212	0.6816	0.6838	Williamson et al. 2002
Ots-R	*Ots-3M*	blue	15	128 - 158	0.7854	0.7938	Banks et al. 1999
	Omm-1080	green	54	162 - 374	0.9517	0.9670	Rexroad et al. 2001
Ots-S	*Ots-9*	red	9	99 - 115	0.6531	0.6543	Banks et al. 1999
	Ots-212	blue	33	123 - 251	0.9205	0.9360	Greig et al. 2003
Ots-T	*Oki-100*	blue	50	164 - 361	0.9500	0.9567	Unpublished
	Ots-211	red	34	188 - 327	0.9325	0.9414	Greig et al. 2003

Table 3. Tests of population differentiation for temporal collections of summer Chinook from natural and hatchery-origin populations in the upper Columbia River. P-values that are highlighted grey are significantly different after Bonferroni correction (Rice 1989). Adjusted alpha p-value was 0.0001 . The H and W in the collection identifier is for wild or hatchery-origin and the two digit number identifes the year samples were collected.

Wenatchee River

	WenW93U	WenW93D	WenH06	WenW06U	WenW06D	WenH08	WenW08U	WenW08D
WenW93U	****							
WenW93D	0.0162	****						
WenH06	0.0033	0.0102	****					
WenW06U	0.3039	0.1642	0.4795	****				
WenW06D	0.0261	0.0160	0.0678	0.5300	****			
WenH08	0.1126	0.0708	0.0073	0.4359	0.0893	****		
WenW08U	0.2115	0.1148	0.4191	0.7243	0.3830	0.8856	****	
WenW08D	0.1915	0.0014	0.7047	0.4928	0.1671	0.7755	0.7665	****

D - collection was downstream of Tumwater Dam; U - collection was upstream of Tumwater Dam

Methow River

	MetW93	MetH06	MetW06	MetH08	MetW08	MetW09	MetH09
MetW93	****						
MetH06	0.3962	****					
MetW06	0.5481	0.4688	****				
MetH08	0.1408	0.1192	0.2052	****			
MetW08	0.8219	0.8937	0.6156	0.3779	****		
MetW09	0.2564	0.4282	0.2502	0.0328	0.7309	****	
MetH09	0.1543	0.5678	0.0547	0.0017	0.0098	0.0073	****

Okanogan River

	OkanW92	OkanW93	OkanH06	OkanW06	OkanH08	OkanW08	OkanH09	OkanW09
OkanW92	****							
OkanW93	0.0066	****						
OkanH06	0.0193	0.0000	****					
OkanW06	0.2843	0.0082	0.0031	****				
OkanH08	0.1290	0.1106	0.0652	0.7329	****			
OkanW08	0.0106	0.0029	0.0082	0.4075	0.7396	****		
OkanH09	0.0187	0.0001	0.0094	0.0551	0.2214	0.0281	****	
OkanW09	0.0527	0.0000	0.0024	0.7130	0.0262	0.0065	0.0002	****

Table 3 continued.

Wells Dam Hatchery

	Wells91	Wells92	Wells93	Wells06	Wells08
Wells91	****				
Wells92	0.5863	****			
Wells93	0.0490	0.0784	****		
Wells06	0.0089	0.0100	0.0542	****	
Wells08	0.0819	0.1088	0.2552	0.0256	****

Eastbank Hatchery - Wenatchee and MEOK stocks

	EBHWen08	EBHME92	EBHME93	EBHME08
EBHWen08	****			
EBHME92	0.8681	****		
EBHME93	0.0251	0.8661	****	
EBHME08	0.0086	0.9563	0.1895	****

Table 4. F_{ST} pairwise comparisons and genotypic tests of differentiation for hatchery- and natural-origin summer Chinook from the upper Columbia River. Above the diagonol are the F_{ST} values and below are p-values for the test of genotypic differentiation. Non-significant p-values for the result of the genotypic differentiation test are in bold type and F_{ST} values that are not significantly different from zero are in bold type.

	Wenatchee Hatchery	Wenatchee Natural	Methow Hatchery	Methow Natural	Okanogan Hatchery	Okanogan Natural	Wells Hatchery	Eastbank Wenatchee stock	Eastbank MEOK stock	Entiat River	Chelan River
Wenatchee Hatchery	****	**0.0000**	**0.0011**	**0.0000**	**0.0013**	**0.0010**	0.0015	**0.0004**	**0.0007**	**0.0004**	**0.0072**
Wenatchee Natural	**0.4351**	****	**0.0016**	**0.0000**	0.0014	0.0016	0.0024	**0.0006**	0.0012	0.0009	**0.0068**
Methow Hatchery	**0.3800**	**0.0205**	****	**0.0012**	0.0029	**0.0008**	**0.0027**	**0.0014**	**0.0022**	**0.0019**	**0.0078**
Methow Natural	**0.2237**	**0.6566**	**0.1502**	****	**0.0011**	0.0011	0.0013	**0.0007**	**0.0007**	**0.0008**	**0.0053**
Okanogan Hatchery	0.0001	0.0000	**0.0364**	**0.0008**	****	**0.0010**	**0.0014**	0.0029	**0.0000**	**0.0007**	**0.0055**
Okanogan Natural	0.0000	0.0000	**0.1755**	0.0000	**0.0003**	****	0.0016	0.0023	**0.0005**	**0.0008**	**0.0049**
Wells Hatchery	0.0000	0.0000	**0.0129**	0.0000	0.0000	0.0000	****	0.0036	**0.0006**	**0.0008**	**0.0041**
Eastbank Wenatchee	**0.5261**	**0.4102**	**0.1215**	**0.8404**	**0.0015**	0.0000	0.0000	****	**0.0018**	0.0030	0.0096
Eastbank MEOK stock	**0.0485**	0.0000	**0.4246**	**0.0009**	**0.5786**	**0.0051**	0.0000	**0.0065**	****	**0.0005**	**0.0039**
Entiat River	**0.0565**	0.0000	**0.1795**	**0.0044**	**0.0005**	0.0000	**0.0032**	**0.0039**	**0.0042**	****	**0.0052**
Chelan River	**0.0091**	**0.0026**	**0.0182**	**0.0156**	**0.0048**	**0.0030**	**0.0066**	**0.0059**	**0.0493**	**0.0617**	****

Table 5. F_{ST} pairwise comparisons and genotypic tests of differentiation for fall Chinook. Above the diagonol are the F_{ST} values and below are p-values for the test of genotypic differentiation. Non-significant p-values for the result of the genotypic differentiation test are in bold type and F_{ST} values that are not significantly different from zero are in bold type.

	Crab Creek	Hanford Reach Fall	Lyons Ferry Hatchery Fall	lower Yakima River Fall	Marion Drain Fall	Priest Rapids Fall	Umatilla River Fall	Snake River Fall
Crab Creek	****	0.0087	0.0134	0.0079	0.0143	0.0107	0.0073	0.0097
Hanford Reach Fall	0.0000	****	0.0077	**0.0000**	0.0064	**0.0000**	**0.0000**	0.0022
Lyons Ferry Hatchery Fall	0.0000	0.0000	****	0.0063	0.0074	0.0092	0.0062	0.0029
lower Yakima River Fall	0.0000	**0.4140**	0.0000	****	0.0054	**0.0000**	**0.0000**	0.0018
Marion Drain Fall	0.0000	0.0000	0.0000	0.0000	****	0.0067	0.0061	0.0060
Priest Rapids Fall	0.0000	**0.0695**	0.0000	**0.0083**	0.0000	****	**0.0000**	0.0027
Umatilla River Fall	0.0000	**0.4879**	0.0000	**0.4896**	0.0000	**0.2539**	****	0.0011
Snake River Fall	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	****

Table 6. F_{ST} pairwise comparisons and genotypic tests of differentiation for hatchery- and natural-origin summer Chinook from the upper Columbia River and fall Chinook. Above the diagonol are the F_{ST} values and below are p-values for the test of genotypic differentiation. Non-significant p-values for the result of the genotypic differentiation test are in bold type and F_{ST} values that are not significantly different from zero are in bold type.

Population Differentiation

	Wenatchee Hatchery	Wenatchee Natural	Methow Hatchery	Methow Natural	Okanogan Hatchery	Okanogan Natural	Wells Hatchery	Eastbank Wenatchee stock	Eastbank MEOK stock	Entiat River	Chelan River
Crab Creek	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
Hanford Reach Fall	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	**0.0349**
Lyons Ferry Hatchery Fall	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
lower Yakima River Fall	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	**0.0074**
Marion Drain Fall	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
Priest Rapids Fall	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	**0.0642**
Umatilla River Fall	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	**0.0579**
Snake River Fall	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

Table 6 continued.

Pairwise F_{ST}

	Crab Creek	Hanford Reach Fall	Ferry Hatchery	Yakima River	Marion Drain Fall	Priest Rapids Fall	Umatilla River Fall	Snake River Fall
Wenatchee Hatchery	0.0158	0.0054	0.0180	0.0056	0.0153	**0.0025**	0.0053	0.0103
Wenatchee Natural	0.0162	0.0059	0.0185	0.0063	0.0157	0.0030	0.0059	0.0102
Methow Hatchery	0.0191	0.0104	0.0248	0.0095	0.0220	0.0069	0.0107	0.0165
Methow Natural	0.0148	0.0057	0.0182	0.0051	0.0148	0.0033	0.0055	0.0101
Okanogan Hatchery	0.0146	0.0041	0.0166	0.0042	0.0151	**0.0016**	0.0041	0.0082
Okanogan Natural	0.0163	0.0064	0.0187	0.0062	0.0170	0.0035	0.0068	0.0113
Wells Hatchery	0.0120	0.0051	0.0135	0.0044	0.0120	0.0028	0.0046	0.0077
Wenatchee stock	0.0184	0.0073	0.0203	0.0074	0.0167	0.0047	0.0084	0.0128
Eastbank MEOK stock	0.0128	0.0036	0.0143	0.0038	0.0135	**0.0019**	0.0038	0.0079
Entiat River	0.0147	0.0059	0.0176	0.0057	0.0156	0.0028	0.0056	0.0100
Chelan River	0.0074	**0.0046**	0.0110	**0.0040**	0.0160	**0.0047**	**0.0035**	0.0072

Table 7. Effective number of breeders per brood year with the largest number of samples of summer Chinook in the upper Columbia River. Brood years with sample size less than 19 individuals (shown in bold type) were not analyzed with exception of the 2008 Wells Hatchery collection. A comparison could not be made between an early and late collection from Wells Hatchery.

WDFW Code	Collection Location	Sample Size	Nb =	CI95(L) =	CI95(U) =
93DD[A]	Wenatchee Natural - upstream	23 / 19	152 / 190	77 / 87	616 / 2,147,483,647
08FV	Wenatchee Natural - upstream	56	162	112	249
93DE[A]	Wenatchee Natural - downstream	39 / 34	145 / 152	94 / 95	256 / 302
08FW	Wenatchee Natural - downstream	67	140	105	199
08FU	Wenatchee Hatchery	60	134	90	213
93EC[A]	Methow Natural	**10 / 15**	---	---	---
08FY	Methow Natural	62	150	106	218
08FX	Methow Hatchery	**9**	---	---	---
93ED	Okanogan Natural	69	142	102	203
08GA	Okanogan Natural	59	127	92	180
08FZ	Okanogan Hatchery	**16**	---	---	---
93DG	Wells Hatchery	**6**	---	---	---
08HY[B]	Wells Hatchery	24 / 39	---	---	---
08MN	Eastbank Hatchery - Wenatchee	88	190	144	263
93DF	Eastbank Hatchery - MEOK	84	171	129	229
08MO	Eastbank Hatchery - MEOK	88	166	126	226

[A] - calculations were made for samples from brood year 1988 / brood year 1989

[B] - samples were collected from brood year 2003 / brood year 2004

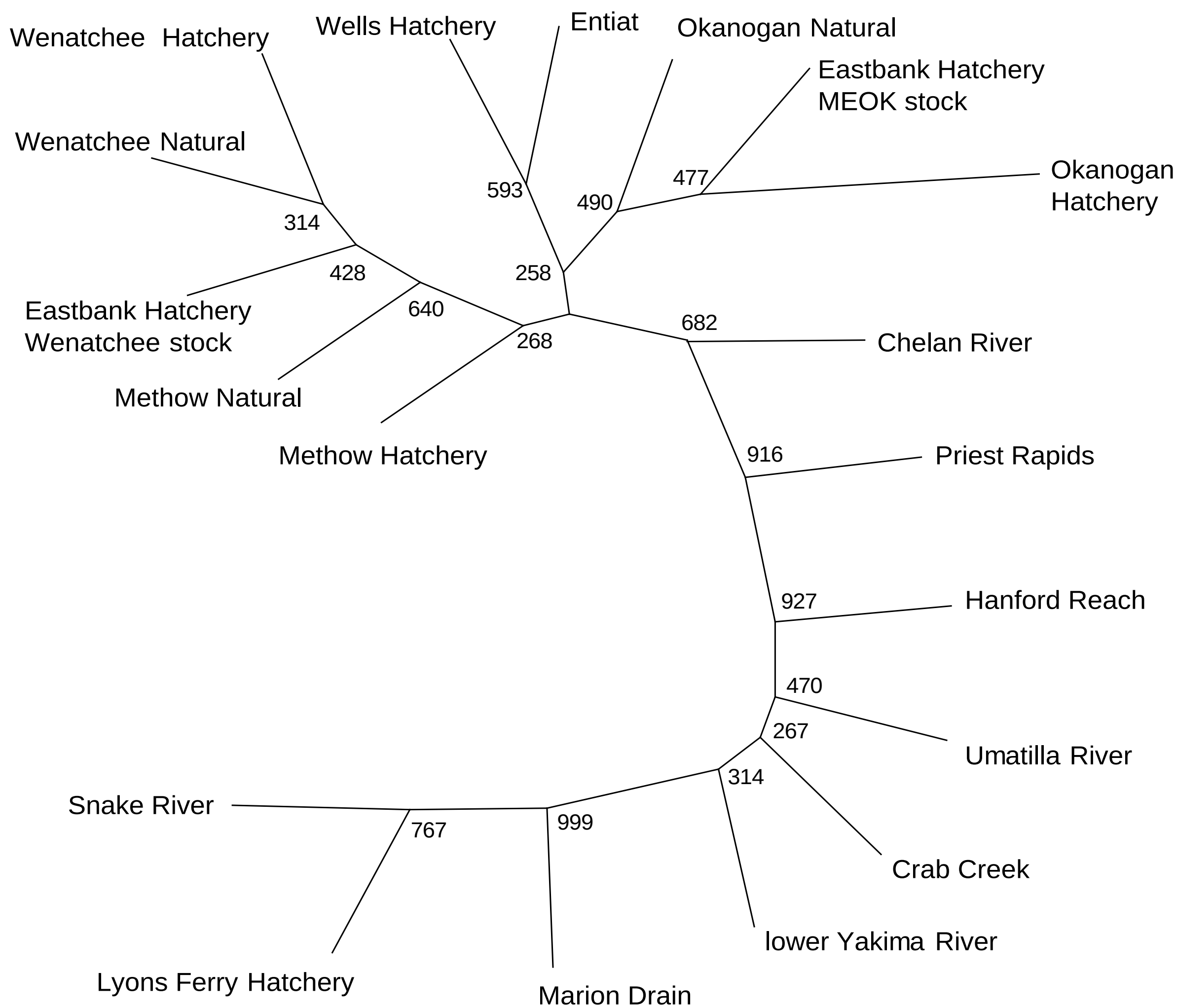


Figure 1. Relationship of natural- and hatchery-origin Chinook collections from the upper Columbia River basin using Cavalli-Sforza and Edwards (1967) chord distance. Bootstrap values are shown at each node.

APPENDIX K

Summer Chinook Spawning Ground Surveys in the Methow and Okanogan Basins, 2010.

BioAnalysts, Inc.℠
4725 North Cloverdale Road, Ste 102
Boise Idaho 83713

January 11, 2011

To: HCP Hatchery Committee

From: Denny Snyder and Mark Miller

Re: 2010 Spawning Ground Surveys in the Okanogan and Methow Basins

The purpose of this memo is to provide information on the hatchery-supplemented natural spawning population of summer Chinook in the Methow and Okanogan basins. This work is part of a larger effort focused on monitoring and evaluating Chelan PUD's hatchery supplementation program. The tasks and objectives associated with implementing Chelan PUD's hatchery M&E plan for 2010 are outlined in several documents (Murdoch and Peven 2005; Peven 2006; Hays et al. 2006). Figures and tables are presented at the end of this memo.

METHODS

Spawning ground surveys were conducted by foot, raft, and aircraft beginning the last week of September and ending mid-November. During aerial surveys an observer recorded the location and number of redds on topographic maps. We did not use aerial surveys on the Methow River because past work has demonstrated that ground counts were more accurate than aerial surveys (Miller and Hillman 1997). Because of the depth of redds, aerial surveys were the only census method used for the Columbia River downstream from Wells (tailrace area only) and Chief Joseph dams. Ground surveys were used to provide more accurate counts and a complete census of Chinook redds within their spawning distribution. Observers floated through sampling reaches and recorded the location and numbers of redds each week. Observers recorded the date, water temperature, river mile, and constructed a drawing of the area where redds were located. A different symbol was used each week to record the number of new and incomplete redds.

To maintain consistency, at least one observer surveyed the same stream reach on successive dates. In areas where numerous summer Chinook spawn, we constructed detailed maps of the river and used the cell-area method (Hamilton and Bergersen 1984) to identify the number of redds within each cell. Cells were bound by noticeable landmarks along the banks (e.g., bridges or trees) or at stream habitat boundaries (e.g., transitions between pools and riffles). The number of redds were then recorded in the corresponding grid on the map. When possible, observers estimated the number of redds in a large disturbed area by counting females that defended their redds. We assumed that the area or territory defended by a female was one redd.

During redd surveys, we sampled carcasses of summer Chinook to describe the spawning population. Biological data included collection of scale samples for age analysis, length measurements (POH and FKL), gender, egg voidance, and a check for tags or marks. These data will be used to assess length-at-age, size-at-age, egg voidance, origin (hatchery or naturally produced), and stray rates. No DNA samples were collected on summer Chinook this year. Information on summer Chinook spawning in the Chelan River was collected by Chelan PUD and is presented in the results.

RESULTS

Methow

There were 887 summer Chinook redds counted within seven reaches of the Methow River (Table 1). This was the fifth highest redd count observed in the last 19 years for the Methow River (Table 3). Spawning began the last week of September and peaked the second week of October and continued into the second week of November (Table 1; Figure 1). Stream temperatures in the Methow River, when spawning began, varied from 6.5-12.0 °C. Peak spawning occurred in reaches (M2-M6) of the Methow River during the second week of October. The lowest reach (M1) had spawning throughout October with a slight peak the second week. Most redds (87%) were located in reaches (M1-M3) downstream from the town of Twisp and in reach (M5) between Methow Valley Irrigation Diversion (MVID) and Winthrop Bridge (Table 1). Few summer Chinook spawned (1%) upstream from the Winthrop Bridge in reaches M6 and M7. Estimated escapement based on redd counts and the sex-ratio observed at Wells Dam during broodstock collection suggests that 2,492 summer Chinook (887 redds x 2.81 fish/redd) escaped to the Methow River.

There were 577 summer Chinook salmon carcasses sampled within the different reaches of the Methow River (Table 2). Twenty-three percent of the fish returning to the Methow River were sampled based on the estimated escapement of 2,492 summer Chinook. Females made up 46% and males 54% of the carcasses examined. Mean percent egg voidance assessed from 266 female carcasses was 98%. Two females (1%) died before spawning (i.e., they retained all their eggs). Ad-clipped hatchery fish made up 46% and naturally produced fish were 54% of the sample collected (Table 2). The distribution of ad-clipped hatchery and naturally produced fish showed that more than half (92%) of the ad-clipped hatchery fish were located in the lower three reaches while naturally produced fish were more evenly distributed (Figure 2).

Okanogan

There were 1,011 summer Chinook redds counted within six reaches of the Okanogan River (Table 1). This was the tenth highest redd count observed in the last 21 years for the Okanogan River (Table 3). Peak aerial redd counts (688 redds) were about 68 percent of redds counted from the ground. Spawning began the last week of September and peaked two weeks later in mid-October (Figure 1). Spawning was initiated in the Okanogan River when the stream temperature varied from 8.5-16°C. Spawning activity ended after the first week of November (Table 1; Figure 1). Peak spawning in the Okanogan River occurred during the second week of October for reaches O4 through O6 with the lower reaches peaking the following two week. Most redds (78%) were located in the upper reaches (O5 and O6) between Zosel Dam and the town of Riverside (Table 1). Estimated escapement (1,011 redds x 2.81 fish/redd) to the Okanogan River was 2,841 summer Chinook.

There were 678 summer Chinook salmon carcasses sampled within 6 reaches of the Okanogan River (Table 2). Twenty-four percent of the fish returning to the Okanogan River were sampled based on the estimated escapement of 2,841 summer Chinook. Females made up 44% and males 56% of the carcasses examined. Mean percent egg voidance from 297 female carcasses was 99%. No females died before they spawned. Ad-clipped hatchery fish made up 41% and naturally produced fish 59% of the sample collected (Table 2). Most naturally produced (52%) and ad-clipped hatchery fish (35%) were collected in the upper reaches (O5 and O6) of the Okanogan River closely following the distribution of redds (Figure 2).

Similkameen

There were 1,107 summer Chinook redds counted within the two reaches of the Similkameen River (Table 1). This was the eight highest redd count recorded in the Similkameen River in the last 22 years (Table 3). The peak aerial count (642 redds) was about 58% of redds counted on the ground. Spawning began the last week of September and peaked the second week in October (Figure 5). Spawning was initiated in the Similkameen River when the temperature varied from 13.5-15°C. Spawning activity ended by the first week of November (Table 1). Most (81%) spawning occurred in the lower reach from the Oroville Bridge, downstream to the Driscoll channel on the Similkameen River. Estimated escapement (1,107 redds x 2.81 fish/redd) to the Similkameen River was 3,111 summer Chinook.

There were 775 summer Chinook salmon carcasses sampled within the two reaches of the Similkameen River (Table 2). Twenty-five percent of the fish returning to the Similkameen River were sampled based on the estimated escapement of 3,111 summer Chinook. Females made up 65% and males 35% of the carcasses examined. Mean percent egg voidance from 505 female carcasses was 99%. One female (1%) died before it spawned. Ad-clipped hatchery fish made up 47% and naturally produced fish 53% of the sample collected (Table 2).

Chelan River

Chelan County PUD biologists counted 398 redds in the Chelan River area. Spawning activity in the Chelan River began mid-October and peaked two weeks later (Table 1).

Spawning ended the third week of November. The majority (86%) of spawning occurred in the Chelan tailrace and in the habitat channel (Table 1). Estimated escapement (398 redds x 2.81 fish/redd) to the Chelan River was 1,118 summer Chinook.

There were 106 summer Chinook carcasses sampled in the Chelan River area (Table 2). Nine percent of the summer Chinook returning to the Chelan River were sampled based on the estimated escapement of 1,118 fish. Sampling focused on collection of CWT snouts, especially during the earlier surveys, thus the proportion of unmarked (ad present) fish in the data set is biased low. Females made up 85% and males 15% of the carcasses examined. The sample rate was likely higher for females and low for the males. Mean percent egg voidance from 76 female carcasses was 93%. Five females (7%) died before spawning. Ad-clipped hatchery fish made up 56.6% and naturally produced fish 43.4% of the sample collected.

Columbia River

Aerial surveys were used to count the number of redds in the Columbia River. The surveys were conducted downstream from Wells Dam and in Wells pool. The redd counts likely underestimate the true number of redds because aerial surveys only count visible redds and it is likely that spawning may occur in deep water. Aerial surveys in 2010 were also hampered by poor visibility or weather conditions. There were 48 Chinook redds counted in the Columbia River (Table 1). Twenty two redds were located downstream from Wells Dam in an area that has been documented before (Giorgi 1992). An aerial survey in Wells pool located an estimated 26 redds downstream from Chief Joseph Dam between the bridge and Foster Creek near the left bank. Observations in this area were difficult because distinct outlines of some redds were not readily apparent and most of the spawning occurred in a large single cluster. During the aerial survey, we observed at least five carcasses downstream from Chief Joseph dam.

A radiotelemetry study on movement and migration patterns of summer Chinook in the Wells Pool suggests that spawning occurs in the Columbia River (Ashbrook et al. 2008). Many of the radio-tagged Chinook resided near the tailrace of Chief Joseph Dam along the right and left banks near the location where the redds were observed. Next year we plan to investigate this area to confirm these observations by retrieving carcasses and to see if snorkeling is a viable method for observing redds at this locations. Estimated escapement (48 redds x 2.81 fish/redd=135 fish) based on aerial surveys suggests that at least 135 Chinook spawned in the Columbia River. No carcasses were examined for these two spawning areas.

REFERENCES

Ashbrook, C. E., E.A. Schwartz, C. M. Wallibillig, and K. W. Hassel. 2008. Migration and movement patterns of adult Chinook salmon above Wells Dam. Washington Department of Fish and Wildlife, Fish Program Science Division, Olympia, WA.

Hays, S., T. Hillman, T. Kahler, R. Klinge, R. Langshaw, B. Lenz, A. Murdoch, K. Murdoch, C. Peven. 2006. Analytical Framework for Monitoring and Evaluating PUD Hatchery Programs. Prepared for Habitat Conservation Plans Hatchery Committee.

Giorgi, A. E. 1992. Fall Chinook spawning in the Rocky Reach Pool: Effects of a three foot increase in pool elevation. Report to Chelan County PUD. Don Chapman Consultants, Redmond, WA.

Hamilton, K. and E. P. Bergersen. 1984. Methods to estimate aquatic habitat variables. Report for Bureau of Reclamation, Division of Planning and Technical Services, Denver, Colorado. Colorado Cooperative Fishery Research Unit, Colorado State University, Fort Collins, Colorado.

Miller, M. D. and T. W. Hillman. 1997. Summer/fall Chinook salmon spawning ground surveys in the Methow and Okanogan river basins, 1997. Report to Chelan County PUD. Don Chapman Consultants, Inc. Boise, ID.

Murdoch, A. and C. Peven. 2005. Conceptual Approach to Monitoring and Evaluating the Chelan County Public Utility District Hatchery Programs. Prepared for Chelan PUD Habitat Conservation Plan’s Hatchery Committee. Chelan PUD, Wenatchee, WA.

Peven, Chuck. 2005. Chelan County PUD Hatchery Implementation Plan 2006. Prepared for Chelan PUD Habitat Conservation Plan’s Hatchery Committee, Chelan PUD, Wenatchee, WA.

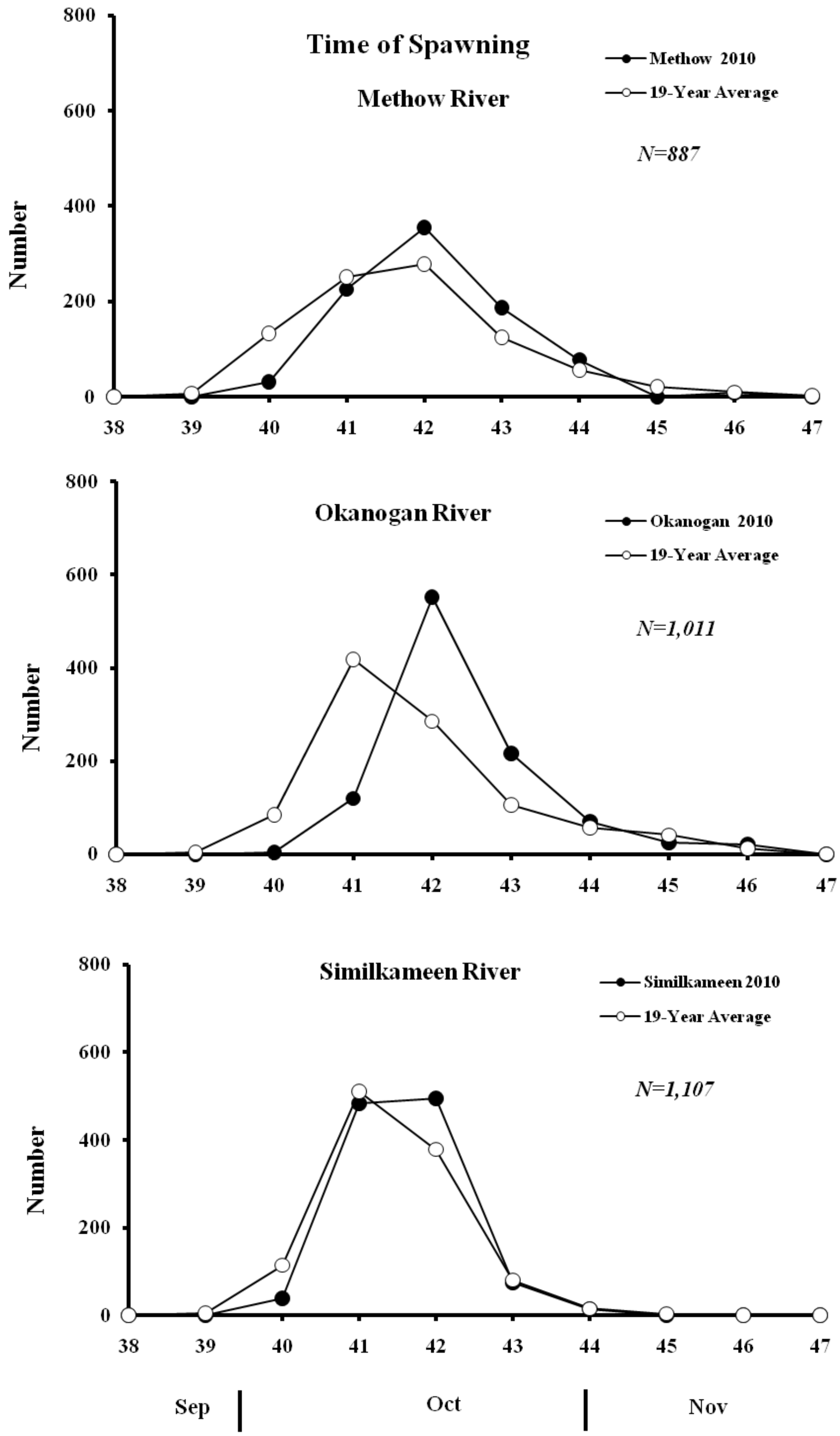


Figure 1. Number of new redds counted each week from mid-September to mid-November. The figure displays the beginning, peak, and end of spawning for summer Chinook in the Methow, Okanogan, and Similkameen rivers in 2010 compared to a 19-year average (1991-2009).

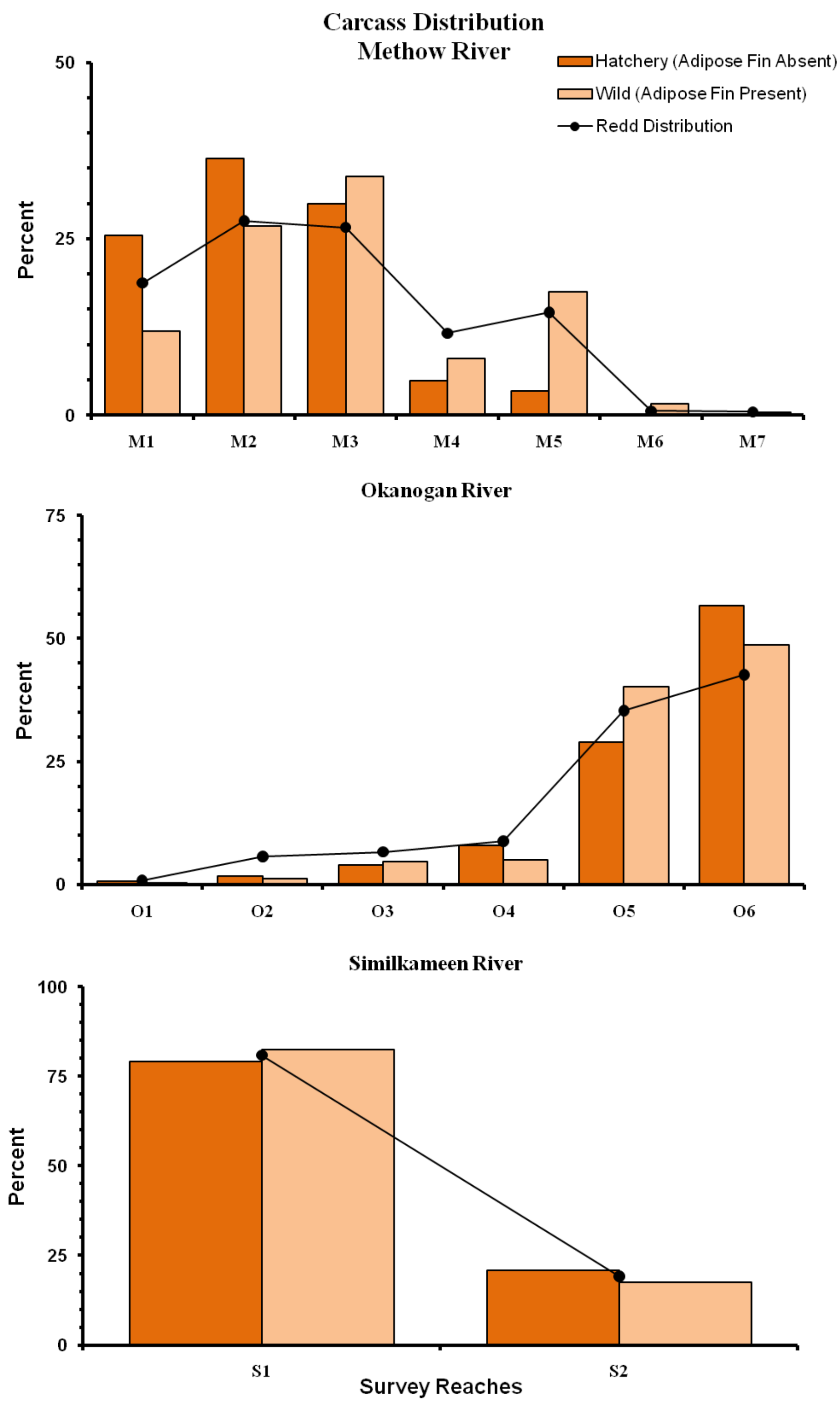


Figure 2. Percent distribution of ad-clipped hatchery and naturally produced fish plotted against the percent distribution of redds observed in reaches of the Methow, Okanogan, and Similkameen rivers, 2010.

Table 1. Number of summer Chinook redds observed each week within the Methow, Okanogan, Similkameen, Chelan, and Columbia rivers, 2010. Dashes indicate no survey occurred and poor visibility is indicated as PV during aerial surveys on the Columbia River.

Reach	Location (Rkm)	Sep		Oct					Nov		Total	Percent
		19-25	26-2	3-9	10-16	17-23	24-30	31-6	7-13	14-20		
		39	40	41	42	43	44	45	46	47		
Methow River												
M1	0.0-25.0	0	0	8	59	57	34	0	8	---	**166**	**18.7**
M2	25.0-45.9	0	28	81	81	43	11	0	0	---	**244**	**27.5**
M3	45.9-63.6	0	4	65	97	41	28	1	0	---	**236**	**26.6**
M4	63.6-75.8	0	0	36	43	20	4	0	0	---	**103**	**11.6**
M5	75.8-84.2	0	0	34	71	23	1	0	0	---	**129**	**14.5**
M6	84.2-87.2	0	0	2	2	1	0	0	0	---	**5**	**0.6**
M7	87.2-90.2	0	0	0	2	2	0	0	0	---	**4**	**0.5**
	Total:	**0**	**32**	**226**	**355**	**187**	**78**	**1**	**8**		**887**	**100.0**
Okanogan River												
O1	0.0-27.2	0	0	0	0	2	3	2	2	---	**9**	**0.9**
O2	27.2-41.9	0	0	0	4	19	22	7	6	---	**58**	**5.7**
O3	41.9-49.4	0	0	0	15	17	15	10	10	---	**67**	**6.6**
O4	49.4-65.4	0	0	0	32	20	27	7	3	---	**89**	**8.8**
O5	65.4-91.4	0	3	51	214	87	2	0	0	---	**357**	**35.3**
O6	91.4-129.6	0	1	69	287	72	2	0	0	---	**431**	**42.6**
	Total:	**0**	**4**	**120**	**552**	**217**	**71**	**26**	**21**	---	**1,011**	**100.0**
Similkameen River												
S1	0.0-2.9	0	39	387	402	54	13	0	0	---	**895**	**80.8**
S2	2.9-9.1	0	0	97	93	20	2	0	0	---	**212**	**19.2**
	Total:	**0**	**39**	**484**	**495**	**74**	**15**	**0**	**0**	---	**1,107**	**100.0**
Chelan River												
Chelan PH. T.R.		---	---	---	3	36	111	46	27	11	**234**	**58.8**
Pool		---	---	---	1	1	4	1	0	0	**7**	**1.8**
Habitat Channel		---	---	---	6	32	19	38	11	1	**108**	**27.1**
Col. River T.R.		---	---	---	0	13	11	17	7	1	**49**	**12.3**
	Total:	---	---	---	**10**	**82**	**145**	**102**	**45**	**14**	**398**	**100.0**
Columbia River												
Wells	827.2-828.8	---	---	---	3	8	22	---	PV	---	**22**	**45.8**
Chief Joseph	876.3-876.9	---	---	---	---	0	---	---	---	26	**26**	**54.2**

Table 2. Number and percent of hatchery (ad-clipped) and naturally produced (not ad-clipped) summer Chinook collected in the Methow, Okanogan, and Chelan river basins, 2010.

Reach	Location (Rkm)	Ad-Clipped Hatchery				Naturally Produced				Reach Total
		Male	Female	Total	Percent	Male	Female	Total	Percent	
Methow River										
M1	0.0-23.8	43	25	68	64.8	22	15	37	35.2	**105**
M2	23.8-43.8	60	37	97	53.9	37	46	83	46.1	**180**
M3	43.8-63.7	43	37	80	43.2	50	55	105	56.8	**185**
M4	63.7-72.3	8	5	13	34.2	14	11	25	65.8	**38**
M5	72.3-80.1	5	4	9	14.3	26	28	54	85.7	**63**
M6	80.1-83.0	0	0	0	0.0	3	2	5	100.0	**5**
M7	83.0-96.1	0	0	0	0.0	0	1	1	100.0	**1**
	Total:	**159**	**108**	**267**	**46.3**	**152**	**158**	**310**	**53.7**	**577**
Okanogan River										
O1	0.0-27.2	2	0	2	66.7	1	0	1	33.3	**3**
O2	27.2-42.0	2	3	5	50.0	2	3	5	50.0	**10**
O3	42.0-49.4	5	6	11	36.7	10	9	19	63.3	**30**
O4	49.4-65.5	7	15	22	52.4	4	16	20	47.6	**42**
O5	65.5-91.4	42	38	80	33.2	66	95	161	66.8	**241**
O6	91.4-124.6	125	32	157	44.6	115	80	195	55.4	**352**
	Total:	**183**	**94**	**277**	**40.9**	**198**	**203**	**401**	**59.1**	**678**
Similkameen River										
S1	0.0-2.9	133	155	288	45.9	109	230	339	54.1	**627**
S2	2.9-9.2	18	58	76	51.4	10	62	72	48.6	**148**
	Total:	**151**	**213**	**364**	**47.0**	**119**	**292**	**411**	**53.0**	**775**
Chelan River[1]										
Chelan PH. T.R.		1	7	8	100.0%	0	0	0	0.0%	8
Pool		1	0	1	100.0%	0	0	0	0.0%	1
Habitat Channel		9	30	39	51.3%	2	29	37[2]	34.9%	76
Col. River T.R.		1	11	12	57.1%	1	8	9	8.5%	21
	Total:	**12**	**48**	**60**	**56.6%**	**3**	**37**	**46**	**43.4%**	**106**

[1] Chelan PUD examined 106 carcasses. Sampling was focused on collection of CWT snouts, especially during the earlier surveys, thus the proportion of naturally produced Chinook (ad present) in the data set is biased low.

[2] Six fish of the 37 naturally produced Chinook examined in the habitat channel were not assigned a gender.

Table 3. Historical aerial and ground redd counts of summer Chinook in the Methow, Okanogan, and Similkameen rivers, 1957-2010.

Year	Methow		Okanogan		Similkameen	
	Aerial	Ground	Aerial	Ground	Aerial	Ground
1956	109	--	37	--	30	--
1957	451	--	53	--	30	--
1958	335	--	94	--	31	--
1959	130	--	50	--	23	--
1960	194	--	29	--	--	--
1961	120	--	--	--	--	--
1962	678	--	--	--	17	--
1963	298	--	9	--	51	--
1964	795	--	112	--	67	--
1965	562	--	109	--	154	--
1966	1,275	--	389	--	77	--
1967	733	--	149	--	107	--
1968	659	--	232	--	83	--
1969	329	--	103	--	357	--
1970	705	--	656	--	210	--
1971	562	--	310	--	55	--
1972	325	--	182	--	64	--
1973	366	--	138	--	130	--
1974	223	--	112	--	201	--
1975	432	--	273	--	184	--
1976	191	--	107	--	139	--
1977	365	--	276	--	268	--
1978	507	--	195	--	268	--
1979	622	--	173	--	138	--
1980	345	--	118	--	172	--
1981	195	--	55	--	121	--
1982	142	--	23	--	56	--
1983	65	--	36	--	57	--
1984	162	--	235	--	301	--
1985	164	--	138	--	309	--
1986	169	--	197	--	300	--
1987	211	--	201	--	164	--
1988	123	--	113	--	191	--
1989	126	--	134	--	221	370
1990	229	--	88	47	94	147
1991	--	153	55	64	68	91
1992	--	107	35	53	48	57
1993	--	154	144	162	152	288
1994	--	310	372	375	463	777
1995	--	357	260	267	337	616
1996	--	181	100	116	252	419
1997	--	205	149	158	297	486
1998	--	225	75	88	238	276
1999	--	448	222	369	903	1,275
2000	--	500	384	549	549	993
2001	--	675	883	1,108	865	1,540
2002	--	2,013	1,958	2,667	2,000[a]	3,358
2003	--	1,624	1,099	1,035	103	378

Year	Methow		Okanogan		Similkameen	
	Aerial	Ground	Aerial	Ground	Aerial	Ground
2004	--	973	1,310	1,327	2,127	1,660
2005	--	874	1,084	1,611	1,111	1,423
2006	--	1,353	1,857	2,592	1,337	1,666
2007	--	620	1,265	1,301	523	707
2008	--	599	1,019	1,146	673	1,000
2009	--	692	1,109	1,672	907	1,298
2010	--	887	688	1,011	642	1,107