

Tucannon River Spring Chinook Salmon Hatchery Evaluation Program

2004 Annual Report

by

Michael P. Gallinat
Lance A. Ross

Washington Department of Fish and Wildlife
Fish Program/Science Division
600 Capitol Way North
Olympia, Washington 98501-1091

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U.S. Fish and Wildlife Service
Lower Snake River Compensation Plan Office
1387 S. Vinnell Way, Suite 343
Boise, Idaho 83709
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Abstract

Lyons Ferry Hatchery (LFH) and Tucannon Fish Hatchery (TFH) were built/modified under the Lower Snake River Fish and Wildlife Compensation Plan. One objective was to compensate for the estimated annual loss of 1,152-spring chinook (Tucannon River stock) caused by hydroelectric projects on the Snake River. The standard supplementation production goal is 132,000 fish for release as yearlings at 30 g/fish (15 fish per pound). The captive brood production goal is 150,000 yearlings at 30 g/fish. This report summarizes activities of the Washington Department of Fish and Wildlife Lower Snake River Hatchery Evaluation Program for Tucannon River spring chinook for the period April 2004 to April 2005.

Four hundred sixty-six fish were captured in the TFH trap in 2004 (309 natural adults, 2 natural jacks, 102 hatchery adults, and 53 hatchery jacks); 92 were collected and hauled to LFH for broodstock and the remaining fish were passed upstream.

During 2004, four salmon that were collected for broodstock died. Prespawning mortality has been low since broodstock began being held at LFH in 1992, and is generally less than 10% each year.

Spawning of supplementation fish in 2004 at LFH occurred between August 24 and September 21, with peak eggtake on September 14. A total of 140,459 eggs were collected from 28 wild and 18 hatchery-origin fish. Egg mortality to eye-up was 4.5% (6,383 eggs), with an additional loss of 5,199 (3.9%) sac-fry. Total fry ponded for production in the rearing ponds was 128,877.

A total of 205 captive brood females were spawned from August 31 to October 5, 2004 producing 310,819 eggs. Egg mortality to eye-up was 49% leaving 158,902 live eggs. An additional 18,028 dead eggs/fry (11.3%) were picked at ponding leaving 140,874 fish for rearing.

WDFW staff conducted spawning ground surveys in the Tucannon River between September 1 and September 30, 2004. One hundred-sixteen redds and 78 carcasses were found above the adult trap and 44 redds and 43 carcasses were found below the trap. Based on redd counts, broodstock collection, and in-river pre-spawning mortalities, the estimated escapement for 2004 was 573 fish (400 wild adults, 0 wild jacks and 151 hatchery-origin adults, 22 hatchery jacks).

Length and weight samples were collected twice during the rearing cycle for 2003 brood year (BY) juveniles at TFH and Curl Lake Acclimation Pond. All 2003 BY juveniles were marked in October at LFH, transported to TFH, and transported again in February to Curl Lake for acclimation and volitional release during April.

Snorkel surveys were conducted during the summer of 2004 to determine the population of subyearling and yearling spring chinook in the Tucannon River. We estimated 40,900 subyearlings (BY 2003) and 1,205 yearlings (BY 2002) were present in the river. Evaluation staff also operated a downstream migrant trap. During the 2003/2004 emigration, we estimated that 60,530 (BY 2002) wild spring chinook smolts emigrated from the Tucannon River.

Monitoring survival rate differences between natural and hatchery-reared salmon continues. Smolt-to-adult return rates (SAR) for natural salmon consistently average about four times higher than for hatchery salmon. However, hatchery salmon survive about three times greater than natural salmon from parent to adult progeny. Due to the low SAR for hatchery fish, the mitigation goal of 1,152 salmon of Tucannon River stock was not achieved as only 173 hatchery-origin fish returned in 2004.

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Introduction

Program Objectives

Congress authorized implementation of the Lower Snake River Fish and Wildlife Compensation Plan (USACE 1975). As a result, Lyons Ferry Hatchery (LFH) was constructed and Tucannon Fish Hatchery (TFH) was modified. One objective of these hatcheries is to compensate for the estimated annual loss of 1,152 Tucannon River spring chinook salmon adults caused by hydroelectric projects on the Snake River. In 1984, Washington Department of Fish and Wildlife (WDFW) began to evaluate the success of these two hatcheries in meeting the mitigation goal, and identifying factors that would improve performance of the hatchery fish. The WDFW also initiated the Tucannon River Spring Chinook Captive Broodstock Program in 1997 which is funded by the Bonneville Power Administration (BPA) through its Fish and Wildlife Program. The project goal is to rear captive salmon selected from the supplementation program (1997-2001 brood years) to adults, rear their progeny, and release approximately 150,000 smolts (30 g/fish) annually into the Tucannon River between 2003-2007. These smolt releases, in combination with the current hatchery supplementation program (goal = 132,000 smolts; 30 g/fish) and wild production, are expected to produce 600-700 returning adult spring chinook to the Tucannon River each year from 2005-2010. This report summarizes work performed by the WDFW Spring Chinook Evaluation Program from April 2004 through April 2005.

Facility Descriptions

Lyons Ferry Hatchery is located on the Snake River (rkm 90) at its confluence with the Palouse River (Figure 1). It is used for adult broodstock holding and spawning, and early life incubation and rearing. All juvenile fish are marked and returned to TFH for final rearing and acclimation. Tucannon Fish Hatchery, located at rkm 59 on the Tucannon River, has an adult collection trap on site (Figure 1). Juveniles rear at TFH through winter. In February, the fish are transported to Curl Lake Acclimation Pond (AP) and volitionally released.

Tucannon River Watershed Characteristics

The Tucannon River empties into the Snake River between Little Goose and Lower Monumental Dams approximately 622 rkm from the mouth of the Columbia River (Figure 1). Stream elevation rises from 150 m at the mouth to 1,640 m at the headwaters (Bugert et al. 1990). Total watershed area is approximately 1,295 km². Local habitat problems related to logging, road

building, recreation, and agriculture/livestock grazing have limited the production potential of spring chinook in the Tucannon River. Land use in the Tucannon watershed is approximately 36% grazed rangeland, 33% dry cropland, 23% forest, 6% WDFW, and 2% other use (Tucannon Subbasin Summary 2001). Five unique strata have been distinguished by predominant land use, habitat, and landmarks (Table 1).

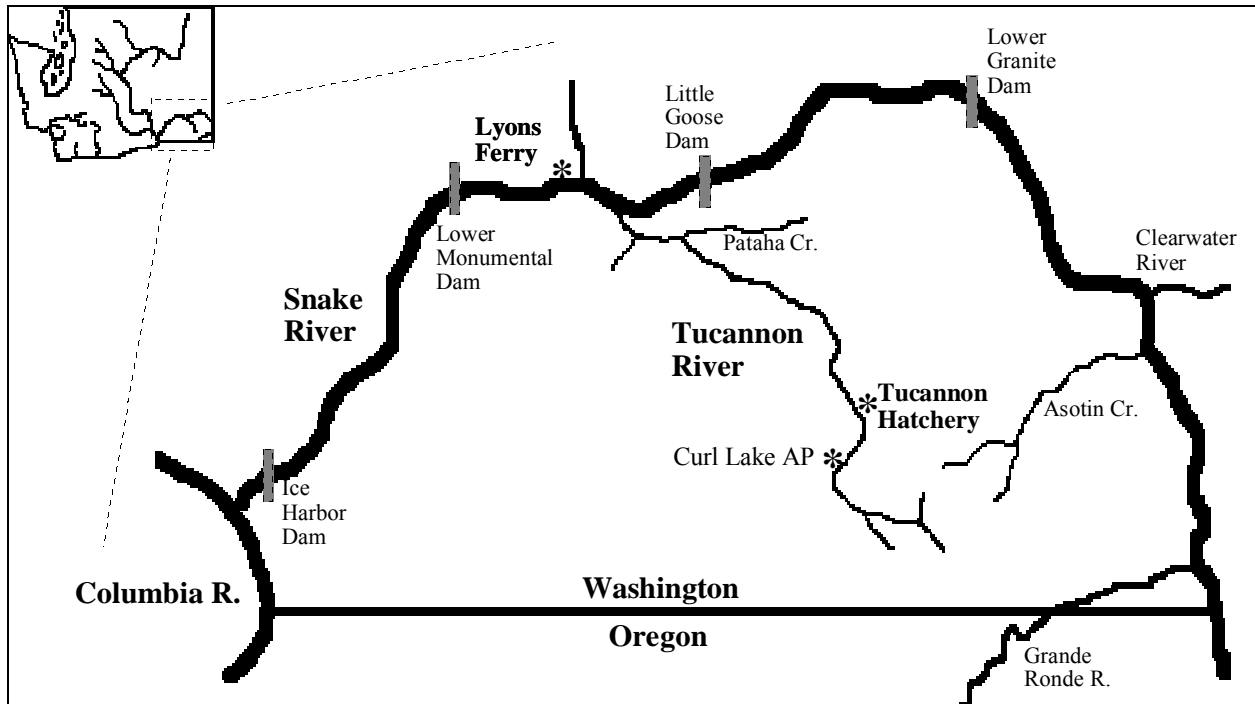


Figure 1. Location of the Tucannon River, and Lyons Ferry and Tucannon Hatcheries within the Snake River Basin.

Table 1. Description of five strata within the Tucannon River.

Strata	Land Ownership/Usage	Spring Chinook Habitat	River Kilometer^a
Lower	Private/Agriculture & Ranching	Not-Usable (temperature limited)	0.0-20.1
Marengo	Private/Agriculture & Ranching	Marginal (temperature limited)	20.1-39.9
Hartsock	Private/Agriculture & Ranching	Fair to Good	39.9-55.5
HMA	State & Forest Service/Recreational	Good/Excellent	55.5-74.5
Wilderness	Forest Service/Recreational	Excellent	74.5-86.3

^a Rkm descriptions: 0.0–mouth at the Snake River; 20.1-Territorial Rd.; 39.9–Marengo Br.; 55.5-HMA Boundary Fence; 74.5-Panjab Br.; 86.3-Rucherts Camp.

Evaluation program staff deployed 17 continuous recording thermographs throughout the Tucannon River to monitor daily minimum and maximum water temperatures (temperatures are recorded every 1-1.2 hours) from May through October. Data from each of these water temperature recorders are kept on an electronic file in our Dayton office. During 2004, maximum temperatures near the mouth (rkm 3) of the Tucannon River reached 26.7° C (80° F) on three different days. Maximum temperatures where spring chinook juveniles were rearing during the hottest part of the summer ranged from 15.5° C (59.9° F) in the upper HMA stratum (rkm 74.5) to 23.3° C (73.9° F) in the lower Hartsock stratum (rkm 43.3)(Figure 2).

The upper lethal temperature for chinook fry is 25.1° C (77.2° F) while the preferred temperature range is 12-14° C (53.6-57.2° F) (Scott and Crossman 1973, McCullough 1999). The optimum range of temperature in freshwater, which controls the rate of growth and survival of young, is 13-17° C (55.4-62.6° F) (Becker 1983). Theurer et al. (1985) estimated that spring chinook production in the Tucannon River would be zero for all stream reaches having maximum daily July water temperatures greater than 23.9° C (75° F) (or average mean temperature of 20° C (68.0° F)). Based on the preferred and optimum temperature limits, fish returning to the upper watershed have the best chance for survival (Figure 2).

It is hoped that recent initiatives to improve habitat within the Tucannon Basin, such as the Tucannon River Model Watershed Program, will: 1) restore and maintain natural stream stability; 2) reduce water temperatures; 3) reduce upland erosion and sediment delivery rates; and 4) improve and re-establish riparian vegetation. Theurer et al. (1985) estimated that improving riparian cover and channel morphology in the Tucannon River mainstem would increase chinook-rearing capacity present in the early 1980s by a factor of 2.5. Habitat

restoration efforts should permit increased utilization of habitat by spring chinook salmon in the marginal sections of the middle reaches of the Tucannon River and increase fish survival.

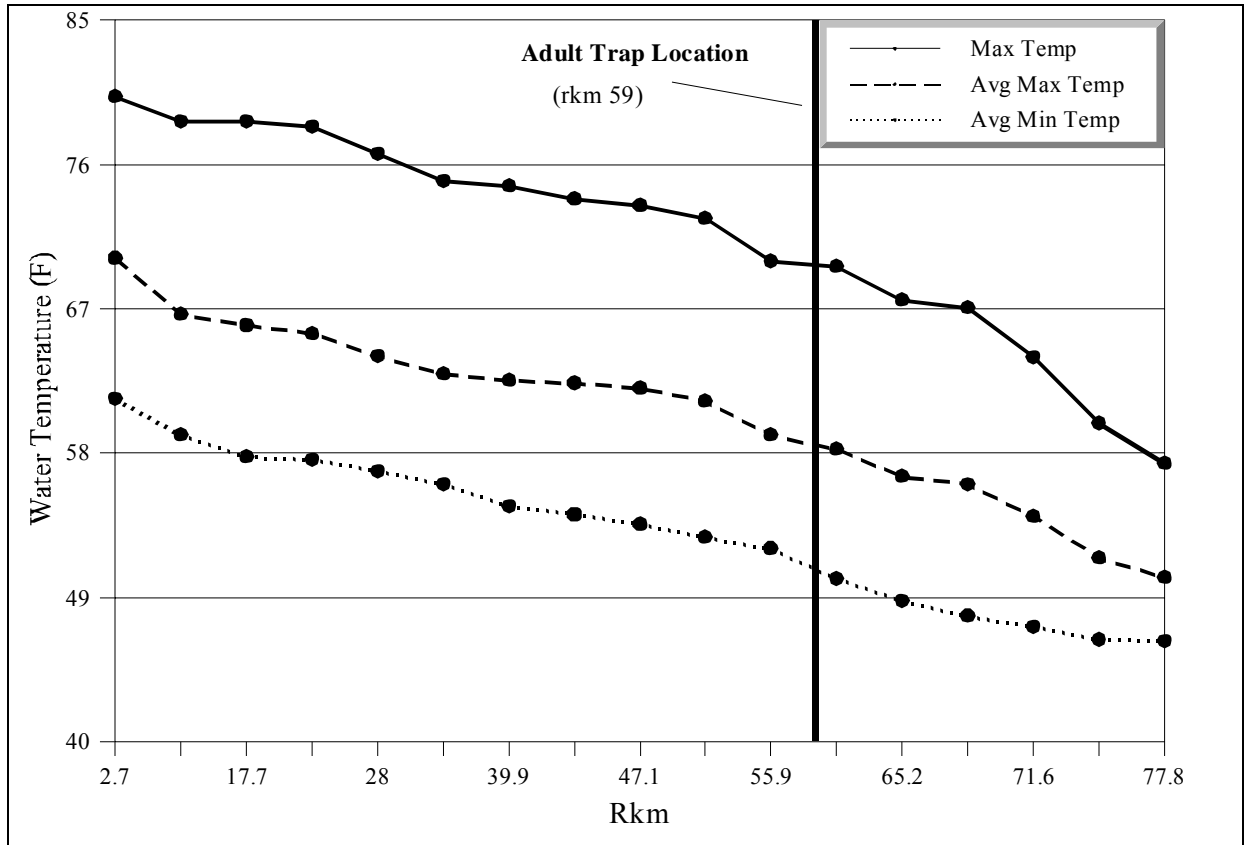


Figure 2. Maximum temperature, average maximum temperature, and average minimum temperature recorded by thermographs at 17 selected sites along the Tucannon River, May-October, 2004.

Adult Salmon Evaluation

Broodstock Trapping

The annual collection goal for broodstock is 50 natural and 50 hatchery adults collected throughout the duration of the run. Additional jack salmon may be collected to contribute to the broodstock if necessary. Jack contribution to the broodstock can be no more than their percentage in the overall run. Returning hatchery salmon were identified by coded-wire tag (CWT) in the snout or presence of a visible implant elastomer tag.

The TFH adult trap began operation in February (for steelhead) with the first spring chinook captured April 28. The trap was operated through September. A total of 466 fish entered the trap (309 natural adults, 2 natural jacks, 102 hatchery adults, and 53 hatchery jacks), and 51 wild (51 adults, 0 jacks) and 41 hatchery (37 adults, 4 jacks) spring chinook were collected and hauled to LFH for broodstock (Table 2, Appendix A). Fish not collected for broodstock were passed upstream. Adults collected for broodstock were injected with erythromycin and oxytetracycline (0.5 cc/4.5 kg); jacks were given half dosages. Fish received formalin drip treatments during holding at 167 ppm every other day at LFH to control fungus.

Based on previous years' returns, we anticipated catching unmarked Umatilla River origin hatchery fish. We decided prior to broodstock trapping that scale samples would be collected from all unmarked fish for scale pattern analysis in the hope of identifying hatchery origin fish. Unmarked fish collected for broodstock were injected with a Passive Integrated Transponder (PIT) tag for individual identification. If scale analysis determined that a "wild" fish collected for broodstock was actually of hatchery origin, that fish would be identified by its PIT tag number and killed. However, none of the wild fish kept for broodstock in 2004 had hatchery origin scale patterns.

Table 2. Numbers of spring chinook salmon captured, trap mortalities, fish collected for broodstock, or passed upstream to spawn naturally at the TFH trap from 1986-2004.

Year	Captured at Trap		Trap Mortality		Broodstock Collected		Passed Upstream	
	Natural	Hatchery	Natural	Hatchery	Natural	Hatchery	Natural	Hatchery
1986	247	0	0	0	116	0	131	0
1987	209	0	0	0	101	0	108	0
1988	267	9	0	0	116	9	151	0
1989	156	102	0	0	67	102	89	0
1990	252	216	0	1	60	75	191	134
1991	109	202	0	0	41	89	68	105
1992	242	305	8	3	47	50	165	202
1993	191	257	0	0	50	47	130	167
1994	36	34	0	0	36	34	0	0
1995	10	33	0	0	10	33	0	0
1996	76	59	1	4	35	45	33	7
1997	99	160	0	0	43	54	47	76
1998 ^a	50	43	0	0	48	41	1	1
1999 ^b	1	139	0	1	1	135	0	0
2000 ^c	28	177	0	17	12	69	13	94
2001	405	276	0	0	52	54	353	222
2002	168	610	0	0	42	65	126	545
2003	84	151	0	0	42	35	42	116
2004	311	155	0	0	51	41	260	114

^a Two males (one natural, one hatchery) captured were transported back downstream to spawn in the river.

^b Three hatchery males that were captured were transported back downstream to spawn in the river.

^c Seventeen stray LV and ADLV fish were killed at the trap.

Broodstock Mortality

Four of the 92 salmon collected for broodstock died prior to spawning in 2004 (Table 3). Table 3 shows that prespawning mortality in 2004 was comparable to the mortality documented since broodstock holding at LFH began in 1992. Higher mortality was experienced when fish were held at TFH (1986-1991).

Table 3. Numbers of pre-spawning mortalities and percent of fish collected for broodstock at TFH and held at TFH (1985-1991) or LFH (1992-2004).

Year	Natural			% of collected	Hatchery			% of collected
	Male	Female	Jack		Male	Female	Jack	
1985	3	10	0	59.1	—	—	—	—
1986	15	10	0	21.6	—	—	—	—
1987	10	8	0	17.8	—	—	—	—
1988	7	22	0	25.0	—	—	9	100.0
1989	8	3	1	17.9	5	8	22	34.3
1990	12	6	0	30.0	14	22	3	52.0
1991	0	0	1	2.4	8	17	32	64.0
1992	0	4	0	8.2	2	0	0	4.0
1993	1	2	0	6.0	2	1	0	6.4
1994	1	0	0	2.8	0	0	0	0.0
1995	1	0	0	10.0	0	0	3	9.1
1996	0	2	0	5.7	2	1	0	6.7
1997	0	4	0	9.3	2	2	0	7.4
1998	1	2	0	6.3	0	0	0	0.0
1999	0	0	0	0.0	3	1	1	3.8
2000	0	0	0	0.0	1	2	0	3.7
2001	0	0	0	0.0	0	0	0	0.0
2002	0	0	0	0.0	1	1	0	3.1
2003	0	1	0	2.4	0	0	1	2.9
2004	0	3	0	5.9	0	0	1	2.4

Broodstock Spawning

Spawning at LFH occurred once a week from August 24 to September 21, with peak eggtake occurring on September 14. A total of 140,459 eggs were collected (Table 4). Eggs were initially disinfected and water hardened for one hour in iodophor (100 ppm). Fungus on the incubating eggs was controlled with formalin applied every-other day at 1,667 ppm for 15 minutes. Mortality to eye-up was 4.5% with an additional 3.9% (5,199) loss of sac-fry, which left 128,877 fish for production.

To prevent any stray fish from contributing to the population, all CWT were read prior to spawning. No hatchery strays were found in the broodstock in 2004. Scales from unmarked fish were read prior to spawning to check for hatchery growth patterns. Carcasses were returned to the upper Tucannon River (above rkm 59) for stream nutrient enrichment.

Table 4. Number of fish spawned and killed, estimated egg collection, and egg mortality of Tucannon River spring chinook salmon at LFH in 2004.

Spawn Date	Natural			Hatchery		
	Male ^a	Female	Eggs Taken	Male ^a	Female	Eggs Taken
8/24		1	5,062			
8/31		3	11,778	1	3	7,990
9/07	2	5	19,394	3	7	18,548
9/14	5	15	45,947	18	5	12,176
9/21	13	4	11,454		3	8,110
Totals	20	28	93,635	22	18	46,824
Egg Mortality			5,401			982

^a Does not include live spawned fish.

Eggs were also collected as part of the Tucannon River Captive Broodstock Program. A total of 205 captive brood females were spawned from August 31 to October 5, 2004. From the total 310,819 captive brood eggs collected, mortality to eye-up was 48.9%, leaving 158,902 live eggs in the incubators. An additional 18,028 dead eggs/fry (11.3%) were picked at ponding leaving 140,874 live fish for rearing. The Tucannon River Captive Broodstock Program results achieved to date are more thoroughly described in the annual Tucannon River Spring Chinook Captive Broodstock Report (Gallinat 2005).

Natural Spawning

Spawning ground surveys were conducted on the Tucannon River weekly from September 1 to September 30, 2004, to count redds and determine the temporal and spatial distribution of spawners. One hundred sixty redds were counted and 100 natural and 21 hatchery origin carcasses were recovered (Table 5). One hundred sixteen redds (73% of total) and 78 carcasses (64% of total) were found above the adult trap.

While conducting redd surveys in 2004 we also snorkeled 15 redds to observe adult hatchery/wild interactions and look for possible precocious male spawning. We observed 24 adults (11 males and 13 females) and 2 jacks on the redds. We also observed juvenile (33 yearling and 52 subyearling) spring chinook salmon in and near the redds. With the exception of one yearling, these juvenile fish had the coloration of parr and were determined not to be precocious males. Efforts will be made in 2005 to capture and physically examine the juvenile chinook. In addition to the spring chinook, 6 bull trout, 43 wild juvenile steelhead and 1 hatchery endemic juvenile steelhead were observed in or near the redds.

Table 5. Numbers and general locations of salmon redds and carcasses recovered on the Tucannon River spawning grounds, 2004 (the Tucannon Hatchery adult trap is located at rkm 59).

Stratum	Rkm ^a	Number of redds	Carcasses Recovered	
			Natural	Hatchery
Wilderness	78-84	8	1	0
	75-78	9	1	0
HMA	73-75	20	3	0
	68-73	27	14	1
	66-68	7	9	2
	62-66	21	9	5
	59-62	24	28	5
		Tucannon Fish Hatchery Trap		
Hartsock	56-59	25	26	6
	52-56	9	8	1
	47-52	4	0	0
	43-47	0	0	0
	40-43	6	0	1
Marengo	34-40	0	1	0
	28-34	0	0	0
Totals	28-84	160	100	21

^a Rkm descriptions: 84-Sheep Cr.; 78-Lady Bug Flat CG; 75-Panjab Br.; 73-Cow Camp Bridge; 68-Tucannon CG; 66-Curl Lake; 62-Beaver/Watson Lakes Br.; 59-Tucannon Hatchery Intake/Adult Trap; 56-HMA Boundary Fence; 52-Br. 14; 47-Br. 12; 43-Br. 10; 40-Marengo Br.; 34-King Grade Br.; 28-Enrich Br.

Historical Trends

Two general trends were evident from the program's inception in 1985 through 1999:

- 1) The proportion of the total number of redds occurring below the trap increased; and
- 2) The density of redds (redds/km) decreased in the Tucannon River.

In part, this resulted from a greater emphasis on broodstock collection to keep the spring chinook population from extinction. However, increases in the SAR rates beginning with the 1995 brood have subsequently resulted in increased spawning above the trap and higher redd densities (Table 6). Also, moving the release location from TFH upstream to Curl Lake AP has affected the spawning distribution, with higher numbers of fish and redds in the Wilderness and HMA strata compared to previous years.

Table 6. Number of spring chinook salmon redds and redds/km (in parenthesis) by stratum and year, and the number and percent of redds above and below the TFH adult trap in the Tucannon River, 1985-2004.

Year	Strata				Total Redds	TFH Adult Trap			
	Wilderness	HMA	Hartsock	Marengo		Above	%	Below	%
1985	97 (8.2)	122 (6.2)	–	–	219	–	–	–	–
1986	53 (4.5)	117 (6.2)	29 (1.9)	0 (0.0)	200	163	81.5	37	18.5
1987	15 (1.3)	140 (7.4)	30 (1.9)	–	185	149	80.5	36	19.5
1988	18 (1.5)	79 (4.2)	20 (1.3)	–	117	90	76.9	27	23.1
1989	29 (2.5)	54 (2.8)	23 (1.5)	–	106	74	69.8	32	30.2
1990	20 (1.7)	94 (4.9)	64 (4.1)	2 (0.3)	180	96	53.3	84	46.7
1991	3 (0.3)	67 (2.9)	18 (1.1)	2 (0.3)	90	40	44.4	50	55.6
1992	17 (1.4)	151 (7.9)	31 (2.0)	1 (0.2)	200	130	65.0	70	35.0
1993	34 (3.4)	123 (6.5)	34 (2.2)	1 (0.2)	192	131	68.2	61	31.8
1994	1 (0.1)	10 (0.5)	28 (1.8)	5 (0.9)	44	2	4.5	42	95.5
1995	0 (0.0)	2 (0.1)	3 (0.2)	0 (0.0)	5	0	0.0	5	100.0
1996	1 (0.1)	33 (1.7)	34 (2.2)	0 (0.0)	68	11	16.2	58	83.8
1997	2 (0.2)	43 (2.3)	27 (1.7)	1 (0.2)	73	30	41.1	43	58.9
1998	0 (0.0)	3 (0.2)	20 (1.3)	3 (0.5)	26	3	11.5	23	88.5
1999	1 (0.1)	34 (1.8)	6 (0.4)	0 (0.0)	41	3	7.3	38	92.7
2000	4 (0.4)	68 (3.6)	20 (1.3)	0 (0.0)	92	45	48.9	47	51.1
2001	24 (2.7)	189 (9.9)	84 (5.3)	1 (0.2)	298	168	56.4	130	43.6
2002	13 (1.4)	227 (11.9)	46 (2.9)	13 (1.1)	299	197	65.9	102	34.1
2003	0 (0.0)	(11.9)	28 (1.8)	0 (0.0)	118	62	52.5	56	47.5
2004	17 (1.9)	90 (4.7)	19 (1.2)	0 (0.0)	160	116	72.5	44	27.5
		124 (6.5)							

Note: – indicates the river was not surveyed in that section during that year.

Genetic Sampling

During 2004 we collected 157 DNA samples (opercle punches) from adult salmon (98 natural origin and 59 hatchery origin) and 300 samples from captive broodstock spawners. These samples were sent to the WDFW genetics lab in Olympia, Washington for analysis.

A total of 480 spring chinook samples from the 2003 collections of Tucannon River spring chinook salmon (75 supplementation spawners, 59 in-river spawners, and 346 captive brood spawners) were genotyped at 14 microsatellite loci (Ogo-2, Ogo-4, Ots-3M, Ssa-197, Oki-100, Ots-201b, Ots-208b, Ssa-408, Omm-1080, Ots-213, Ots-G474, Ots-9, Ots-211, and Ots-212)

using an Applied Biosystems 3730 DNA analyzer. Hawkins and Frye (2005) found evidence that the captive broodstock program has been an effective method of preserving genetic variation, and that the supplementation hatchery practices have been effective in minimizing differences between the hatchery and natural origin fish (Appendix B). Genotypes, allele frequencies, and tissue samples are stored at WDFW’s Genetics Laboratory in Olympia.

Age Composition, Length Comparisons, and Fecundity

One objective of the monitoring program is to track the age composition of each years’ returning adults. This allows us to annually compare ages of natural and hatchery-reared fish, and to examine long-term trends and variability in age structure. Overall, hatchery origin fish return at a younger age than natural origin fish (Figure 3). This difference is likely due to smolt size-at-release (hatchery origin smolts are generally 25-30 mm greater in length than natural smolts).

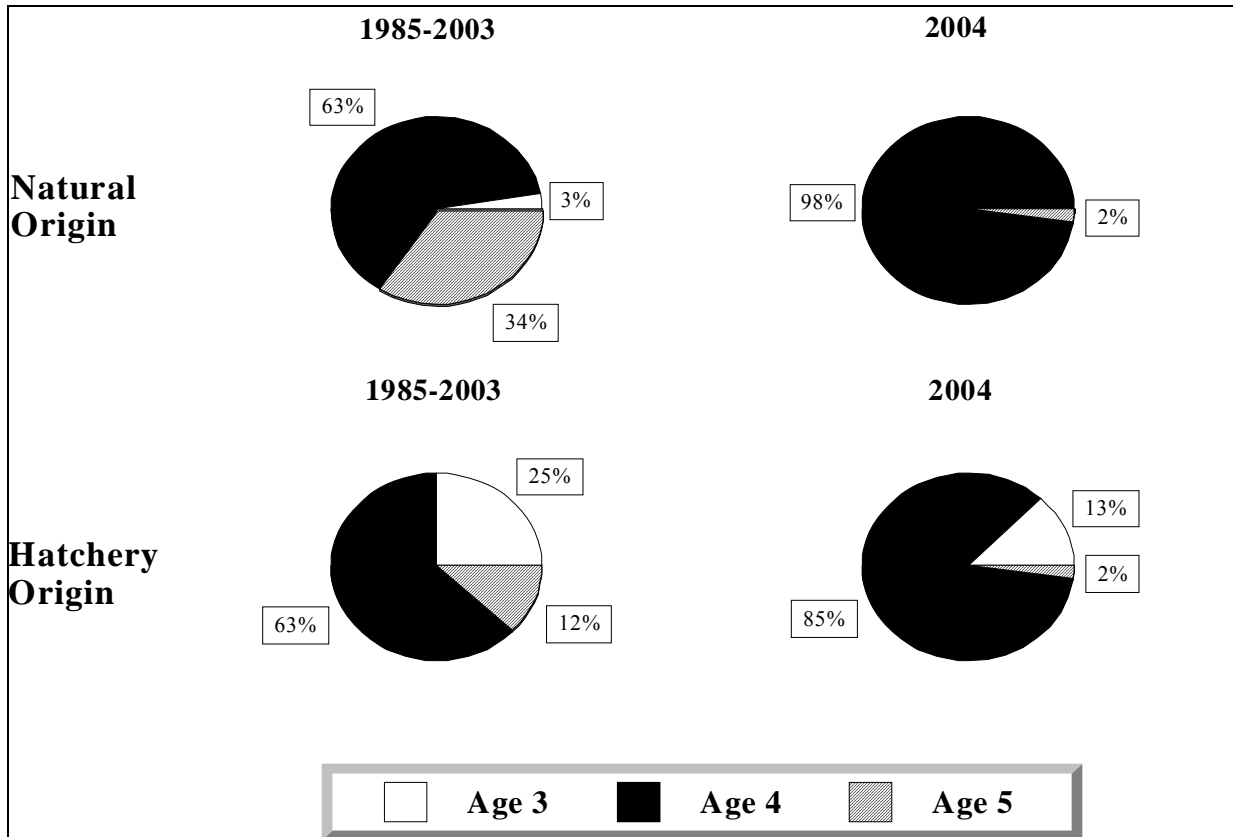


Figure 3. Historical (1985-2003), and 2004 age composition for spring chinook in the Tucannon River.

An unusually large proportion of Age 4 fish were observed during the 2004 run for both the hatchery and wild components of the population (Figure 3). This was likely due to higher survival rates associated with recent desirable ocean conditions.

Another comparison we conduct on returning adult natural and hatchery origin fish is the difference between mean post-eye to hypural-plate lengths. It was reported in the past (Bumgarner et al. 1994) that hatchery fish were generally shorter than natural origin fish of the same age. For many of the early return years this appeared to be true (Figures 4, 5, 6, and 7). However, overall for all return years, there is no difference in mean length between natural and hatchery origin fish, even though they migrate as smolts at significantly different sizes (Bugert et al. 1990; Bugert et al. 1991).

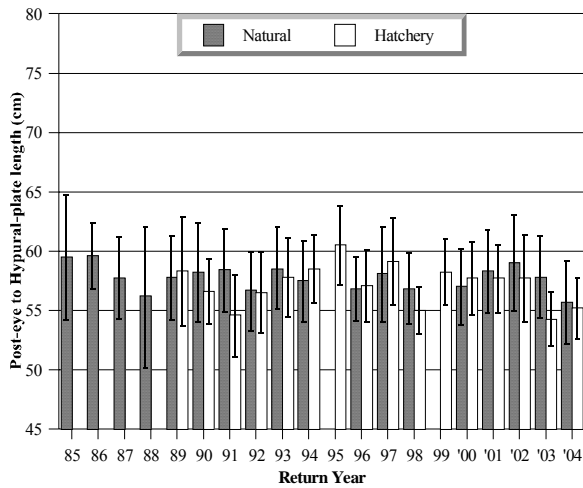


Figure 4. Mean length and SD of Age 4 females.

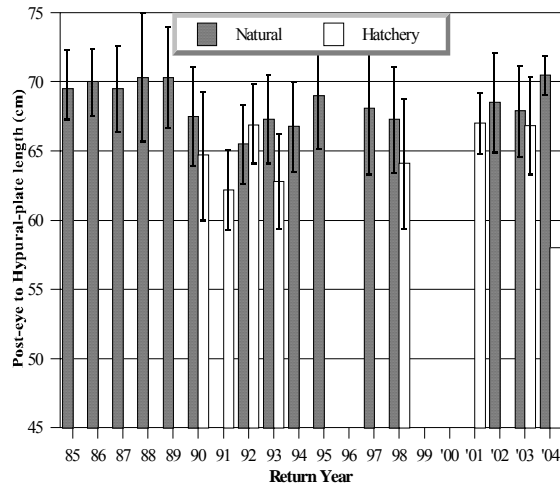


Figure 5. Mean length and SD of Age 5 females.

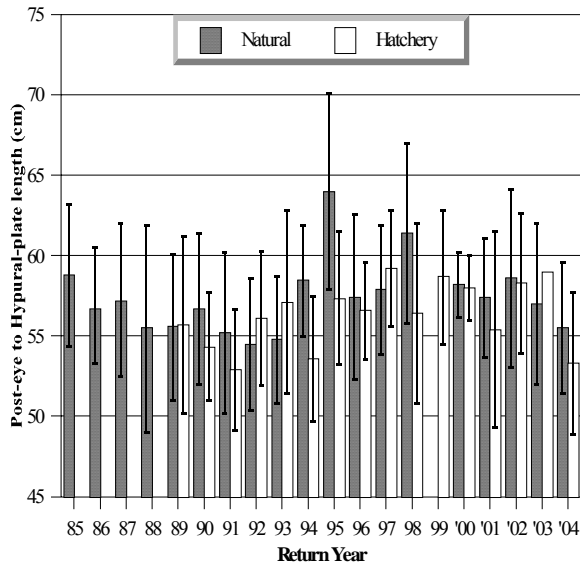


Figure 6. Mean length and SD of Age 4 males.

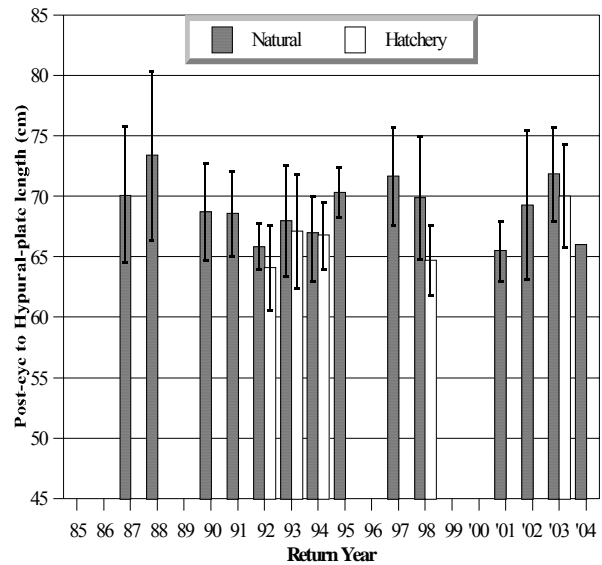


Figure 7. Mean length and SD of Age 5 males.

Fecundities (number of eggs/female) of natural and hatchery origin fish from the Tucannon River program have been documented since 1990 (Table 7). Analysis of variance was performed to determine if there were significant differences in mean fecundities at the 95% confidence level. Natural origin females were significantly more fecund than hatchery origin fish for both Age 4 ($P < 0.001$) and 5-year-old fish ($P < 0.001$).

Mean egg size of natural origin Age 4 spring chinook from the Tucannon River averaged 0.224 g/egg and hatchery origin eggs averaged 0.238 g/egg. This difference was statistically significant at the 95% confidence level ($P < 0.05$). This may explain why Age 4 hatchery origin females are less fecund. Mean egg size in Age 5 salmon was 0.270 g/egg for natural origin and 0.284 g/egg for hatchery origin females. Although the difference was not significant ($P = 0.09$), we suspect that egg size is a factor affecting the fecundity difference.

Table 7. Average number of eggs/female (n, SD) by age group of Tucannon River natural and hatchery origin broodstock, 1990-2004.

Year	Age 4				Age 5			
	Natural		Hatchery		Natural		Hatchery	
1990	3,691	(13, 577.3)	2,794	(18, 708.0)	4,383	(8, 772.4)	No	Fish
1991	2,803	(5, 363.3)	2,463	(9, 600.8)	4,252	(11, 776.0)	3,052	(1, 000.0)
1992	3,691	(16, 588.3)	3,126	(25, 645.1)	4,734	(2, 992.8)	3,456	(1, 000.0)
1993	3,180	(4, 457.9)	3,456	(5, 615.4)	4,470	(1, 000.0)	4,129	(1, 000.0)
1994	3,688	(13, 733.9)	3,280	(11, 630.3)	4,906	(9, 902.0)	3,352	(10, 705.9)
1995	No	Fish	3,584	(14, 766.4)	5,284	(6, 136.1)	3,889	(1, 000.0)
1996	3,509	(17, 534.3)	2,833	(18, 502.3)	3,617	(1, 000.0)	No	Fish
1997	3,487	(15, 443.1)	3,290	(24, 923.3)	4,326	(3, 290.9)	No	Fish
1998	4,204	(1, 000.0)	2,779	(7, 375.4)	4,017	(28, 680.5)	3,333	(6, 585.2)
1999	No	Fish	3,121	(34, 445.4)	No	Fish	3,850	(1, 000.0)
2000	4,144	(2, 1,111.0)	3,320	(34, 545.4)	3,618	(1, 000.0)	4,208	(1, 000.0)
2001	3,612	(27, 508.4)	3,225	(24, 690.6)	No	Fish	3,585	(2, 842.5)
2002	3,584	(14, 740.7)	3,368	(24, 563.7)	4,774	(7, 429.1)	No	Fish
2003	3,342	(10, 738.1)	2,723	(2, 107.0)	4,428	(7, 894.7)	3,984	(17, 772.1)
2004	3,376	(26, 686.9)	2,628	(17, 385.9)	5,191	(1, 000.0)	2,151	(1, 000.0)
Mean	3,545		3,146		4,390		3,649	
SD	624.6		661.5		849.3		771.4	

Coded-Wire Tag Sampling

Broodstock collection, pre-spawn mortalities, and carcasses recovered from spawning ground surveys provide representatives of the annual run that can be sampled for CWT study groups (Table 8). In 2004, based on the estimated escapement of fish to the river, we sampled approximately 37% of the run (Table 9).

Table 8. Coded-wire tag codes of hatchery salmon sampled at LFH and the Tucannon River, 2004.

CWT Code	Broodstock Collected			Recovered in Tucannon River			Totals
	Died in Pond	Killed Outright	Spawned	Dead in Trap	Pre-spawn Mortality	Spawned	
63 (Age 3)						1	1
63-06-81	1		3			3	7
63-02-75			1				1
63-08-87			35			11	46
No tags			1 ^a				1
Total	1	0	40	0	0	15	56

^a This fish did not have CWT but it did have a right red VIE and was Age 4 which would make it 63-08-87.

Table 9. Spring chinook salmon (natural and hatchery) sampled from the Tucannon River, 2004.

	2004		
	Natural	Hatchery	Total
Total escapement to river	400	173	573
Broodstock collected	51	41	92
Fish dead in adult trap	0	0	0
Total hatchery sample	51	41	92
Total fish left in river	349	132	481
In-river pre-spawn mortality	0	1	1
Spawned carcasses recovered	100	20	120
Total river sample	100	21	121
Carcasses sampled	151	62	213

Arrival and Spawn Timing Trends

Peak arrival and spawn timing have always been monitored to determine whether the hatchery program has caused a shift (Table 10). Peak arrival dates were based on greatest number of fish trapped on a single day. Peak spawn in the hatchery was determined by the day when the most females were spawned. Peak spawning in the river was determined by the highest weekly redd count.

Peak arrival to the trap during 2004 was within the expected historical range (Table 10). Peak spawning date of hatchery fish was also within the range found from previous years. The peak of active spawning in the Tucannon River was a week earlier than the historical mean, but within the historical range.

Table 10. Peak dates of arrival of natural and hatchery salmon to the TFH adult trap and peak (date) and duration (number of days) for spawning in the hatchery and river, 1986-2004.

Year	Peak Arrival at Trap		Spawning in Hatchery			Spawning in River	
	Natural	Hatchery	Natural	Hatchery	Duration	Combined	Duration
1986	5/27	–	9/17	–	31	9/16	36
1987	5/15	–	9/15	–	29	9/23	35
1988	5/24	–	9/07	–	22	9/17	35
1989	6/06	6/12	9/15	9/12	29	9/13	36
1990	5/22	5/23	9/04	9/11	36	9/12	42
1991	6/11	6/04	9/10	9/10	29	9/18	35
1992	5/18	5/21	9/15	9/08	28	9/09	44
1993	5/31	5/27	9/13	9/07	30	9/08	52
1994	5/25	5/27	9/13	9/13	22	9/15	29
1995 ^a	–	6/08	9/13	9/13	30	9/12	21
1996	6/06	6/20	9/17	9/10	21	9/18	35
1997	6/15	6/17	9/09	9/16	30	9/17	50
1998	6/03	6/16	9/08	9/16	36	9/17	16
1999 ^a	–	6/16	9/07	9/14	22	9/16	23
2000	6/06	5/22	–	9/05	22	9/13	30
2001	5/23	5/23	9/11	9/04	20	9/12	35
2002	5/29	5/29	9/10	9/03	22	9/11	42
2003	5/25	5/25	9/09	9/02	36	9/12	37
Mean	5/30	6/03	9/12	9/10	28	9/15	35
2004	6/04	6/02	9/14	9/07	29	9/08	30

^a Too few natural salmon were trapped in 1995 and 1999 to determine peak arrival.

Total Run-Size

In general, redd counts have been directly related to total run-size entering the Tucannon River and passage of adult salmon at the TFH adult trap (Bugert et al. 1991). For 2004, we used sex ratios from collected broodstock and sex ratio observations on the spawning grounds to estimate the number of fish/redd. The run-size estimate for 2004 was calculated by adding the estimated number of fish upstream of the TFH adult trap, the estimated fish below the weir based on the

fish/redd ratio, the number of pre-spawn mortalities below the weir, and the number of broodstock collected (Table 11). Total run-size for 2004 was estimated at 573 fish (400 wild adults, 0 wild jacks and 151 hatchery-origin adults, 22 hatchery jacks). The total run for jacks and adults by origin has been estimated since 1985 (Appendix C).

Table 11. Estimated spring chinook salmon run to the Tucannon River, 1985-2004.

Year^a	Total Redds	Fish/Redd Ratio^b	Spawning fish In the river	Broodstock Collected	Pre-spawning Mortalities^c	Total Run-Size	Percent Natural
1985	219	2.60	569	22	0	591	100
1986	200	2.60	520	116	0	636	100
1987	185	2.60	481	101	0	582	100
1988	117	2.60	304	125	0	429	96
1989	106	2.60	276	169	0	445	76
1990	180	3.39	611	135	8	754	66
1991	90	4.33	390	130	8	528	49
1992	200	2.82	564	97	92	753	56
1993	192	2.27	436	97	56	589	54
1994	44	1.59	70	70	0	140	70
1995	5	2.20	11	43	0	54	39
1996	68	2.00	136	80	16	232	63
1997	73	2.00	146	97	45	288	47
1998	26	1.94	51	89	4	144	59
1999	41	2.60	107	136	2	245	1
2000	92	2.60	239	81	19	339	24
2001	298	3.00	894	106	12	1,012	71
2002	299	3.00	897	107	1	1,005	35
2003	118	3.10	366	77	1	444	56
2004	160	3.00	480	92	1	573	70

^a In 1994, 1995, 1998 and 1999, fish were not passed upstream, and in 1996 and 1997, high pre-spawning mortality occurred in fish passed above the trap, therefore; fish/redd ratio was based on the sex ratio of broodstock collected.

^b From 1985-1989 the TFH trap was temporary, thereby underestimating total fish passed upstream of the trap. The 1985-1989 fish/redd ratios were calculated from the 1990-1993 average, excluding 1991 because of a large jack run.

^c Effort in looking for pre-spawn mortalities has varied from year to year with more effort expended during years with poor conditions.

Stray Salmon into the Tucannon River

Spring chinook from other river systems (strays) have periodically been recovered in the Tucannon River, though generally at a low proportion of the total run (Bumgarner et al. 2000). Through 1998 the incidence of stray spring chinook salmon was negligible (Appendix D). However, in 1999, Umatilla River strays accounted for 8% of the total Tucannon River run, and that rate increased to 12% in 2000 (Gallinat et al. 2001). The increase in the number of strays, particularly from the Umatilla River, is of concern since it exceeds the allowable 5% stray rate of hatchery fish deemed acceptable by NOAA Fisheries (formerly NMFS) and is contrary to WDFW management intent for the Tucannon River. Beginning with the 1997 brood year releases, the Oregon Department of Fish and Wildlife (ODFW) and Confederated Tribes of the Umatilla Indian Reservation (CTUIR) ceased marking a portion of Umatilla River origin spring chinook with an RV or LV fin clip (65-70% of releases). Because of this action, some fish that returned in 2004 were physically indistinguishable from wild origin Tucannon River spring chinook. For 2004, scale samples were collected from all wild fish collected for broodstock and passed upstream at the adult trap. None of these fish were determined to be of hatchery origin based on scale pattern analysis. However, scale analysis is not as accurate as genetic analysis and in future years we hope to identify a genetic marker that will allow us to separate unmarked Umatilla origin fish (1997-1999 BYs) from wild Tucannon origin fish. The proportion of hatchery and wild fish (Table 11) may change for the affected years after this analysis is completed. Beginning with the 2000 BY, Umatilla River hatchery-origin spring chinook will be 100% marked. This will help ensure that Tucannon River spring chinook genetic integrity is maintained by allowing selective removal of strays from the hatchery broodstock.

No known (CWT) hatchery strays were recovered during 2004. However, we did recover six 4-year-old AD only clipped fish on the spawning grounds. Based on our marks for that age class (VIE/CWT), and past straying events, we believe those fish were likely Umatilla River origin strays. After expansions, those strays accounted for an estimated 3.0% of the total run (Appendix D).

Juvenile Salmon Evaluation

Hatchery Rearing, Marking, and Release

Hatchery Rearing and Marking

Supplementation juveniles (2003 BY) were marked with a red elastomer tag (VIE) behind the right eye and tagged with CWTs on October 5-14, 2004 (73,369 fish). Supplementation fish were transported to TFH during October. The 2003 BY captive brood juveniles (130,596 fish) were marked on October 19-21 with a CWT in the snout and transported to TFH during October.

Length and weight samples were collected twice on the 2003 BY fish during the rearing cycle (Table 12). During February, fish were sampled for length, weight and mark quality, and were PIT tagged for outmigration comparisons (1,000 supplementation fish and 1,000 captive brood progeny) before transfer to Curl Lake AP.

Table 12. Sample sizes (N), mean lengths (mm), coefficients of variation (CV), condition factors (K), and fish/lb (fpp) of 2003 BY juveniles sampled at TFH and Curl Lake.

Brood/ Date	Progeny Type	Sample Location	N	Mean Length	CV	K	FPP
2003							
2/03/05	Supplementation	TFH	300	120.7	11.1	1.30	19.4
3/31/05	Supplementation	Curl Lake	250	138.8	16.2	1.26	12.7
2/02/05	Captive Brood	TFH	250	124.5	13.5	1.28	17.7
3/31/05	Captive Brood	Curl Lake	250	135.0	17.3	1.29	13.4

2003 Brood Release

The 2003 BY pre-smolts were transported to Curl Lake in February 2005 for acclimation and volitional release. Volitional release began March 28 and continued until April 15 when the remaining fish were forced out. Mortalities were low in Curl Lake and WDFW released an estimated 71,154 supplementation fish (12.7 fish/lb) and 130,064 captive broodstock progeny (13.4 fish/lb) (Table 13). Historical hatchery releases are summarized in Appendix E.

Table 13. Yearling spring chinook releases in the Tucannon River, 2003 brood year.

Release Year	(BY)	Release		CWT Code	Total Released	Number CWT	Additional mark/cross	lbs	Fish lb
		Location	Date						
2005	(03)	Curl Lake	3/28-4/15	63/24/82	71,154	69,831	Rt. Red VI, Mixed	5,603	12.7
2005	(03CB)	Curl Lake	3/28-4/15	63/27/78	130,064	125,304	No VI, Mixed	9,706	13.4

N/A = Not applicable.

Natural Parr Production

Program evaluation staff surveyed the Tucannon River at index sites in 2004 to estimate the density and population of subyearling (Table 14, Appendix F) and yearling spring chinook salmon. Snorkel surveys were conducted using a total count method (Griffith 1981, Schill and Griffith 1984). Population size was determined by multiplying the mean fish density (fish/100 m²) for a stratum by the estimated total area within each stratum. Fifty 50 m sites were snorkeled in 2004 (July 26–August 11), representing approximately 5.0% of the suitable rearing habitat in the Tucannon River. A total of 1,999 subyearling and 63 yearling spring chinook were counted during the surveys. We estimated that 40,900 (± 10,581) subyearling and 1,205 (± 538) yearling chinook were present in the river (Table 14).

Table 14. Number of sites, area snorkeled, mean density (fish/100 m²), population estimates, and 95% confidence intervals for subyearling and yearling spring chinook within the Tucannon River, 2004.

Stratum	Number of sites	Area (m ²) Snorkeled	Subyearling			Yearling		
			Mean Density	Pop. Estimate	C.I.	Mean Density	Pop. Estimate	C.I.
Marengo	6	3,438	2.92	1,942	2,146	0.00	0	0
Hartsock	14	7,830	6.17	10,768	6,042	0.07	122	163
HMA	20	11,977	11.79	26,836	9,125	0.33	757	369
Wilderness	10	3,665	1.90	1,354	1,779	0.46	325	268
Total	50	26,910	7.18	40,900	10,581	0.24	1,205	538

Natural Smolt Production

Program staff operated a 1.5 m rotary screw trap at rkm 3 on the Tucannon River from October 13, 2003 to June 21, 2004 to estimate numbers of migrating natural and hatchery spring chinook. Numbers of selected species captured during the 2004 outmigration can be found in Appendix G. Other data such as peak outmigration, other species captured, etc., have not been reported here for simplicity. Those data are available upon request.

Natural spring chinook emigrating from the Tucannon River (BY 2002) averaged 107 mm (Figure 8). This is in comparison to an average length of 142 mm for hatchery-origin fish (BY 2002) released from Curl Lake Acclimation Pond (Gallinat 2004).

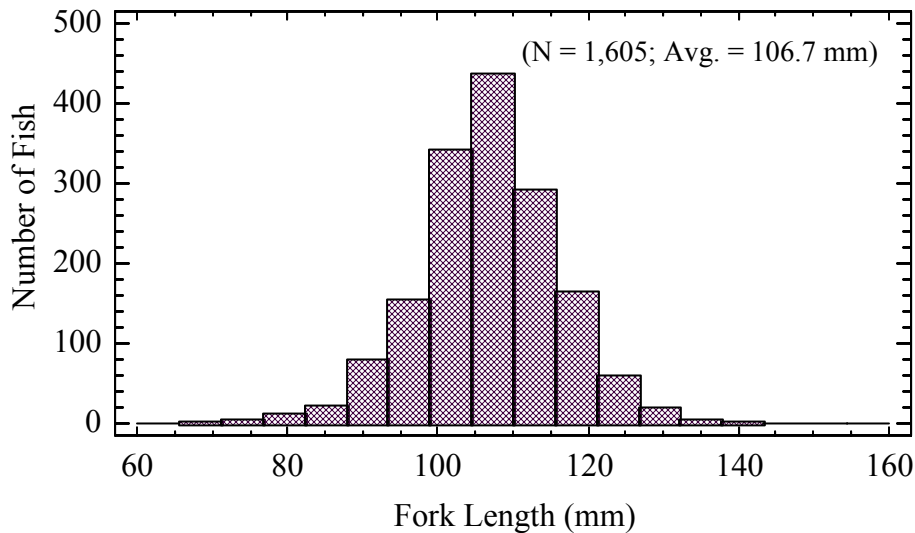


Figure 8. Length frequency distribution of sampled wild spring chinook salmon captured in the Tucannon River smolt trap, 2003/2004 season.

Regression analysis was used to examine the influence of specific abiotic variables on spring chinook emigration during the last seven trapping seasons (1997/1998 to 2003/2004). Significant relationships were found between the total number of wild spring chinook smolts captured (\log_{10} transformed for normality) emigrating from the Tucannon River and flow

(ft³/sec) ($r^2 = 0.20$, $P < 0.01$), staff gauge level ($r^2 = 0.29$, $P < 0.01$), time of year ($r^2 = 0.14$, $P < 0.01$), and water temperature ($r^2 = 0.05$, $P < 0.01$). Although these variables are statistically significant, they account for only a small amount of the variability in the number of emigrating fish. This is understandable as smoltification is a physiological process and the resulting outmigration may only be slightly influenced by abiotic factors. No significant relationship was found between number of wild spring chinook smolts emigrating and secchi disk reading (indicator of turbidity). Also, no significant relationships were found between the number of hatchery spring chinook smolts captured (\log_{10} transformed) and flow, staff gauge level, time of year, water temperature, or, secchi disk reading.

Each week we attempted to determine trap efficiency by clipping a portion of the caudal fin on a representative subsample of captured migrants and releasing them one kilometer upstream. The percent of marked fish recaptured was used as an estimate of weekly trapping efficiency. To calculate trapping efficiency during weeks when low numbers of fish were caught we examined the relationship between trap efficiency and the variables flow, staff gauge, number of fish captured, water temperature, and time of year (week). There were no statistically significant relationships between trap efficiency for wild and hatchery spring chinook and any of the variables examined using regression analysis. Cheng and Gallinat (2004) used a generalized linear model with a binomial response (link function – logit) for Tucannon River smolt trap data and found that staff gauge level and flow were the most important factors affecting trap efficiency.

Flow is the dominant factor affecting downstream migrant trapping operations in any system according to Seiler et al. (1999). Groot and Margolis (1991) state that the rate of downstream migration of chinook fingerlings appears to be both time and size dependent and may also be related to river discharge and the location of fish in the river. They state that during years of low and stable river flow; the rate of downstream migration was negatively correlated with discharge, whereas, when flows were higher and more variable, the rate of migration was positively correlated with discharge. Despite our finding of low statistical power, we believe that trap efficiency decreases on the Tucannon as flow increases.

Mean daily flow data was from by the U.S. Geological Survey gauge station at Starbuck, WA (rkm 12.7). Correlation analysis indicated a statistically significant relationship between flow and the staff gauge level at the smolt trap at the 99% confidence level ($r^2 = 0.97$). As the U.S.G.S. flow data is computer monitored on a continuous basis, is in relatively close proximity to the smolt trap, and there was a strong statistically significant relationship between our staff

gauge and the flow data, trap efficiencies were estimated with the following equations:

$$\text{Trap Efficiency} = 18.72 + 0.01 (\text{Flow}) \quad (P=0.77)$$

$$\text{Trap Efficiency} = 29.52 - 0.06 (\text{Flow}) \quad (P=0.09)$$

To estimate potential juvenile migrants passing when the trap was not operated for short intervals, such as periods when freshets washed out large amounts of debris from the river, we calculated the average number of fish trapped for three days before and three days after non-trapping periods. The mean number of fish trapped daily was then divided by the estimated trap efficiency to calculate fish passage. The estimated number of fish passing each day was then applied to each day the trap was not operated.

We estimated that 60,530, or 84% of the 2002 BY parr estimates, passed the smolt trap during 2003-2004 (Table 15). We also estimated that 46% of the hatchery supplementation fish and 64% of the captive brood progeny released from Curl Lake AP (2002 BY) passed the smolt trap.

Table 15. Monthly and total population estimates for natural and hatchery origin (supplementation and captive brood) emigrants from the Tucannon River, 2004.

Month	Natural	Hatchery	Captive Brood
Sept.-Feb.	1,398	0	0
March	4,451	0	0
April	42,681	31,571	14,256
May	11,837	24,681	14,288
June	163	34	37
Total	60,530	56,286	28,581
% Survival^a	83.8	45.5	63.8

^a Percent survival to smolt based on estimated number of parr from summer snorkel surveys (natural origin) or from TFH release numbers (hatchery origin).

Juvenile Migration Studies

In 2004, WDFW used Passive Integrated Transponder (PIT) tags to study the emigration timing and relative success of our supplementation hatchery fish with our captive brood progeny. We tagged 1,012 supplementation and 1,029 captive brood progeny hatchery-origin fish during early February before transferring them to Curl Lake AP for acclimation and volitional release (Table 16). No fish were killed during PIT tagging, though it is likely that some delayed mortality occurred after release. Detection rates were low, but similar to rates from previous releases at Curl Lake AP (Bumgarner et al. 1998).

Table 16. Cumulative detection (one unique detection per tag code) and travel time in days (TD) of PIT tagged hatchery spring chinook salmon released from Curl Lake Acclimation Pond (rkm 65.6) on the Tucannon River at downstream Snake and Columbia River Dams during 2004 (Fish were volitionally released from 4/01/04-4/20/04).

Hatchery Origin	Release Data			Recapture Data										
	N	Mean Length	SD	Mean Length	LMJ		MCJ		JDJ		BONN		Total N	%
Supplementation	1,012	136.8	16.9	139.0	44	9.6	108	12.1	34	18.3	7	16.1	193	(19.1)
Captive Brood	1,029	125.5	16.6	128.9	41	10.4	106	12.4	41	17.6	6	17.1	194	(18.9)

Note: Mean travel times listed are from the total number of fish detected at each dam, not just unique recoveries for a tag code. Abbreviations are as follows: LMJ-Lower Monumental Dam, MCJ- McNary Dam, JDJ-John Day Dam, BONN-Bonneville Dam, TD- Mean Travel Days.

Survival probabilities were estimated by the Cormack Jolly-Seber methodology using the Survival Under Proportional Hazards (SURPH2) computer model. The data files were created using the CAPHIST program. Data for input into CAPHIST was obtained directly from PTAGIS. Survival estimates from Curl Lake to Lower Monumental Dam were 0.53 (\pm 0.12) and 0.50 (\pm 0.11) for supplementation and captive brood progeny, respectively. While survival estimates were slightly lower for captive brood progeny fish the differences were not significant.

Survival Rates

Point estimates of population sizes have been calculated for various life stages (Tables 17 and 18) of natural origin fish from spawning ground and juvenile mid-summer population surveys, smolt trapping, and fecundity estimates. From these two tables, survivals between life stages have been calculated for both natural and hatchery salmon to assist in the evaluation of the hatchery program. These survival estimates provide insight as to where efforts should be directed to improve not only the survival of fish produced within the hatchery, but fish in the river as well.

As expected, juvenile (egg-parr-smolt) survival rates for hatchery fish are considerably higher than for naturally reared salmon (Table 19) because they have been protected in the hatchery. However, smolt-to-adult return rates (SAR) of natural salmon were about four times higher than for hatchery-reared salmon (Tables 20 and 21). The mean hatchery SARs (0.15%) documented from the 1985-1999 broods were below the LSRCP survival goal of 0.87%. Hatchery SARs for Tucannon River salmon need to substantially improve to meet the mitigation goal of 1,152 hatchery adult salmon.

Table 17. Estimates of natural Tucannon spring chinook salmon abundance by life stage for 1985-2004 broods.

Brood Year	Females in River		Mean ^a Fecundity		Number of eggs	Number ^b of parr	Number of Smolts	Progeny ^c (returning adults)
	Natural	Hatchery	Natural	Hatchery				
1985	219	-	3,883	-	850,377	90,200	42,000	392
1986	200	-	3,916	-	783,200	102,600	58,200	468
1987	185	-	4,096	-	757,760	79,100	44,000	238
1988	117	-	3,882	-	454,194	69,100	37,500	527
1989	103	3	3,883	2,606	407,767	58,600	30,000	158
1990	128	52	3,993	2,697	651,348	86,259	49,500	94
1991	51	39	3,741	2,517	288,954	54,800	30,000	7
1992	119	81	3,854	3,295	725,521	103,292	50,800	194
1993	112	80	3,701	3,237	673,472	86,755	49,560	204
1994	39	5	4,187	3,314	179,863	12,720	7,000	12
1995	5	0	5,224	0	26,120	0	75	6
1996	53	16	3,516	2,843	231,836	2,845	1,612	69
1997	39	33	3,609	3,315	250,146	32,913	21,057	799
1998	19	7	4,023	3,035	97,682	8,453	5,508	375
1999	1	40	3,965	3,142	129,645	15,944	8,157	141
2000	26	66	3,969	3,345	323,964	44,618	20,045	395
2001	219	79	3,612	3,252	1,047,936	63,412	38,079	0
2002	104	195	3,981	3,368	1,070,784	72,197	60,530	
2003	67	51	3,789	3,812	448,275	40,900		
2004	117	43	3,444	2,601	514,791			

^a 1985 and 1989 mean fecundity of natural females is the average of 1986-88 and 1990-93 brood years.

^b Number of parr estimated from electrofishing (1985-1989), Line transect snorkel surveys (1990-1992), and Total Count snorkel surveys (1993-1999).

^c Numbers do not include down river harvest or other out-of-basin recoveries.

Table 18. Estimates of Tucannon spring chinook salmon abundance (spawned and reared in the hatchery) by life stage for 1985-2004 broods.

Brood Year	Females Spawned		Mean ^a Fecundity		Number of Eggs	Number of parr	Number of smolts	Progeny ^b (returning adults)
	Natural	Hatchery	Natural	Hatchery				
1985	4	-	3,883	-	14,843	13,401	12,922	45
1986	57	-	3,916	-	187,958	177,277	153,725	339
1987	48	-	4,096	-	196,573	164,630	152,165	190
1988	49	-	3,882	-	182,438	150,677	146,200	447
1989	28	9	3,883	2,606	133,521	103,420	99,060	243
1990	21	23	3,993	2,697	126,334	89,519	85,800	28
1991	17	11	3,741	2,517	91,275	77,232	74,060	25
1992	28	18	3,854	3,295	156,359	151,727	87,752 ^c	81
1993	21	28	3,701	3,237	168,366	145,303	138,848	207
1994	22	21	4,187	3,314	161,707	132,870	130,069	34
1995	6	15	5,224	0	85,772	63,935	62,272	180
1996	18	19	3,516	2,843	117,287	80,325	76,219	260
1997	17	25	3,609	3,315	144,237	29,650	24,184	181
1998	30	14	4,023	3,035	161,019	136,027	127,939	830
1999	1	36	3,965	3,142	113,544	106,880	97,600	29
2000	3	35	3,969	3,345	128,980	123,313	102,099	175
2001	29	27	3,612	3,252	184,127	174,934	146,922	19
2002	22	25	3,981	3,368	169,364	151,531	123,586	
2003	17	20	3,789	3,812	140,658	126,400	71,154	
2004	28	18	3,444	2,601	140,459	128,877		

^a 1985 and 1989 mean fecundity of natural females is the average of 1986-88 and 1990-93 brood years; 1999 mean fecundity of natural fish is based on the mean of 1986-1998 brood years.

^b Numbers do not include down river harvest or other out-of-basin recoveries.

^c Number of smolts is less than actual release number. 57,316 parr were released in October 1993, with an estimated 7% survival. Total number of hatchery fish released from the 1992 brood year was 140,725. We therefore use the listed number of 87,752 as the number of smolts released.

Table 19. Percent survival by brood year for juvenile salmon and the multiplicative advantage of hatchery-reared salmon over naturally-reared salmon in the Tucannon River.

Brood Year	Natural			Hatchery			Hatchery Advantage		
	Egg to Parr	Parr to Smolt	Egg to Smolt	Egg to Parr	Parr to Smolt	Egg to Smolt	Egg to Parr	Parr to Smolt	Egg to Smolt
1985	10.6	46.6	4.9	90.3	96.4	87.1	8.5	2.1	17.6
1986	13.1	56.7	7.4	94.3	86.7	81.8	7.2	1.5	11.0
1987	10.4	55.6	5.8	83.8	92.4	77.4	8.0	1.7	13.3
1988	15.2	54.3	8.3	82.6	97.0	80.1	5.4	1.8	9.7
1989	14.4	51.2	7.4	77.5	95.8	74.2	5.4	1.9	10.1
1990	13.2	57.4	7.6	70.9	95.8	67.9	5.4	1.7	8.9
1991	19.0	54.7	10.4	84.6	95.9	81.1	4.5	1.8	7.8
1992	14.2	49.2	7.0	97.0	57.8	56.1	6.8	1.2	8.0
1993	12.9	57.1	7.4	86.3	95.6	82.5	6.7	1.7	11.2
1994	7.1	55.0	3.9	82.2	97.9	80.4	11.6	1.8	20.7
1995	0.0	0.0	0.3	74.5	97.4	72.6	--	--	--
1996	1.2	56.7	0.7	68.5	94.9	65.0	55.8	1.7	--
1997	13.2	64.0	8.4	20.6	81.6	16.8	1.6	1.3	2.0
1998	8.7	65.2	5.6	84.5	94.1	79.5	9.8	1.4	14.1
1999	12.3	51.2	6.3	94.1	91.3	86.0	7.7	1.8	13.7
2000	13.8	44.9	6.2	95.6	82.8	79.2	6.9	1.8	12.8
2001	6.1	60.1	3.6	95.0	84.0	79.8	15.7	1.4	22.0
2002	6.7	83.8	5.7	89.5	81.6	73.0	13.3	0.9	11.8
2003	9.1			89.9	56.3	50.6	9.8		
2004				91.8					
Mean	10.6	53.5	5.9	82.7	88.2	72.2	10.6	1.6	12.2
SD	4.8	15.9	2.6	16.8	12.3	16.5	11.8	0.3	5.0

Table 20. Adult returns and SARs of natural salmon to the Tucannon River for brood years 1985-1999.

Brood Year	Estimated Number of Smolts	Number of Adult Returns, observed (obs) and expanded (exp) ^a						SAR (%)	
		Age 3		Age 4		Age 5		w/ Jacks	No Jacks
		Obs	Exp	Obs	Exp	Obs	Exp		
1985	42,000	8	19	110	255	36	118	0.93	0.89
1986 ^b	58,200	1	2	115	376	28	90	0.80	0.80
1987	44,000	0	0	52	167	29	71	0.54	0.54
1988	37,500	1	3	136	335	74	189	1.41	1.40
1989	30,000	5	12	47	120	23	26	0.53	0.49
1990	49,500	3	8	63	72	12	14	0.19	0.17
1991	30,000	0	0	4	5	1	2	0.02	0.02
1992	50,800	2	2	84	159	16	33	0.38	0.38
1993	49,560	1	2	62	127	58	75	0.41	0.41
1994	6,000	0	0	8	10	1	2	0.20	0.20
1995	75	0	0	1	1	2	5	8.00 ^c	8.00 ^c
1996	1,612	0	0	27	63	2	6	4.28	4.28
1997	21,057	6	14	234	703	29	82	3.79	3.73
1998	5,508	3	9	86	245	43	121	6.81	6.64
1999	8,157	3	9	44	124	3	8	1.73	1.62
Geometric Mean of 1985-1999 broods								0.70	0.68

^a Expanded numbers are calculated from the proportion of each known age salmon recovered in the river and from broodstock collections in relation to the total estimated return to the Tucannon River. Expansions do not include down river harvest or Tucannon River fish straying to other systems.

^b One known (expanded to two) Age 6 salmon was recovered.

^c 1995 SAR not included in mean.

Table 21. Adult returns and SARs of hatchery salmon to the Tucannon River for brood years 1985-1999.

Brood Year	Estimated Number of Smolts	Number of Adult Returns, known and expanded (exp.)						SAR (%)	
		Age 3		Age 4		Age 5		w/ Jacks	No Jacks
		Known	Exp.	Known	Exp.	Known	Exp.		
1985	12,922	9	19	25	26	0	0	0.35	0.20
1986	153,725	79	83	99	238	8	18	0.22	0.17
1987	152,165	9	22	70	151	8	17	0.12	0.11
1988	146,200	46	99	140	295	26	53	0.31	0.24
1989	99,057	7	15	100	211	14	17	0.25	0.23
1990	85,500	3	6	16	20	2	2	0.03	0.03
1991	74,058	4	5	20	20	0	0	0.03	0.03
1992	87,752	11	11	50	66	2	4	0.09	0.08
1993	138,848	11	15	93	174	15	18	0.15	0.14
1994	130,069	2	4	21	25	4	5	0.03	0.02
1995	62,272	13	16	117	160	2	4	0.29	0.26
1996	76,219	44	60	100	186	5	14	0.34	0.26
1997	24,186	7	13	59	168	0	0	0.75	0.69
1998	127,939	36	103	164	577	39	150	0.65	0.57
1999	97,600	2	7	5	19	1	3	0.03	0.02
Geometric Mean of 1985-1999 broods								0.15	0.12

As previously stated, overall survival of hatchery salmon to return as adults was higher than for naturally reared fish because of the early-life survival advantage (Table 19). With the exception of the 1988 and 1997-2000 brood years, naturally produced fish have been below the replacement level (Figure 9; Table 22). Based on adult returns from the 1985-1999 broods, naturally reared salmon produced only 0.6 adults for every spawner, while hatchery reared fish produced 1.8 adults.

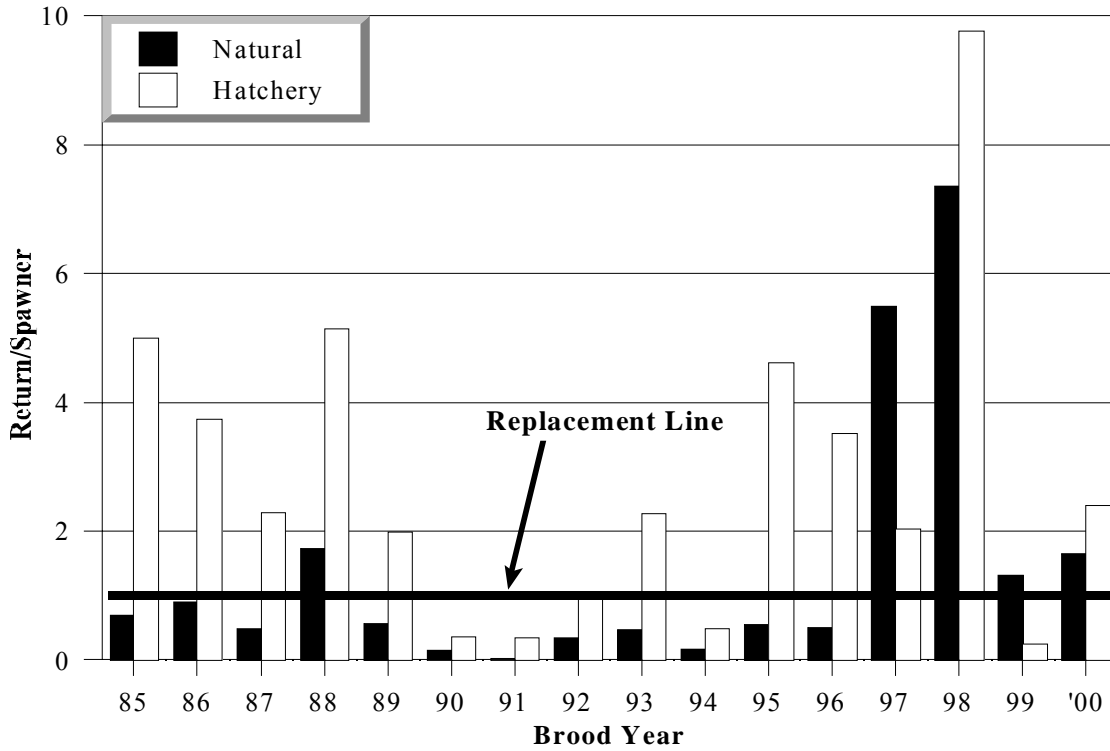


Figure 9. Return per spawner ratio (with replacement line) for the 1985-2000 brood years (2000 incomplete brood year).

Table 22. Parent-to-progeny survival estimates of Tucannon River spring chinook salmon from 1985 through 2000 brood years (2000 incomplete).

Brood Year	Natural Salmon			Hatchery Salmon			Hatchery to Natural Advantage
	Number of Spawners	Number of Returns	Return/ Spawner	Number of Spawners	Number of Returns	Return/ Spawner	
1985	569	392	0.69	9	45	5.00	7.2
1986	520	468	0.90	91	339	3.73	4.1
1987	481	238	0.49	83	190	2.29	4.7
1988	304	527	1.73	87	447	5.14	3.0
1989	276	158	0.57	122	243	1.99	3.5
1990	611	94	0.15	78	28	0.36	2.4
1991	390	7	0.02	72	25	0.35	17.5
1992	564	194	0.34	83	81	0.98	2.9
1993	436	204	0.47	91	207	2.27	4.8
1994	70	12	0.17	69	34	0.49	2.9
1995	11	6	0.55	39	180	4.62	8.4
1996	136	69	0.51	74	260	3.51	6.9
1997	146	799	5.47	89	181	2.03	0.4
1998	51	375	7.35	85	830	9.76	1.3
1999	107	141	1.32	122	29	0.24	0.2
2000	239	395	1.65	73	175	2.40	1.5
Geometric Mean			0.63			1.79	2.9

Fishery Contribution

An original goal of the LSRCP supplementation program was to enhance wild (natural) returns of salmon to the Tucannon River by providing 1,152 hatchery-reared fish (the number estimated to have been lost due to the construction of the Lower Snake River hydropower system) to the river. Such an increase would allow for limited harvest and increased spawning. However, hatchery adult returns have always been below the program goal. Moreover, natural escapement, with the exception of the 2001 run, has been low (Figure 10). Based on 1985-1999 brood year CWT recoveries from the RMIS database (Appendix H), sport and commercial harvest combined has only accounted for 7.9% of the adult hatchery fish recovered annually. However, fishing mortality (both sport and commercial) has increased in recent years to 22% and 20% for the 1997 and 1998 brood years, respectively (Appendix H). Fishing mortality is one form of mortality managers can control. Adipose clipped hatchery fish have traditionally been targeted in the sport fishery. This hatchery fin clip was abandoned for Tucannon River spring chinook

smolts starting with the 2000 BY to mitigate fishing mortality on this ESA listed population (Gallinat et al. 2001). Supplementation fish are now marked with a CWT and a red VIE tag behind the right eye. Captive brood progeny are marked only with agency-only wire tags or CWT to distinguish them from supplementation origin fish. Out-of-basin stray rates of Tucannon River spring chinook have been low (Appendix H), with an average of 3.1% of the adult hatchery fish straying to other river systems/hatcheries for brood years 1985-2000 (range 0-20%).

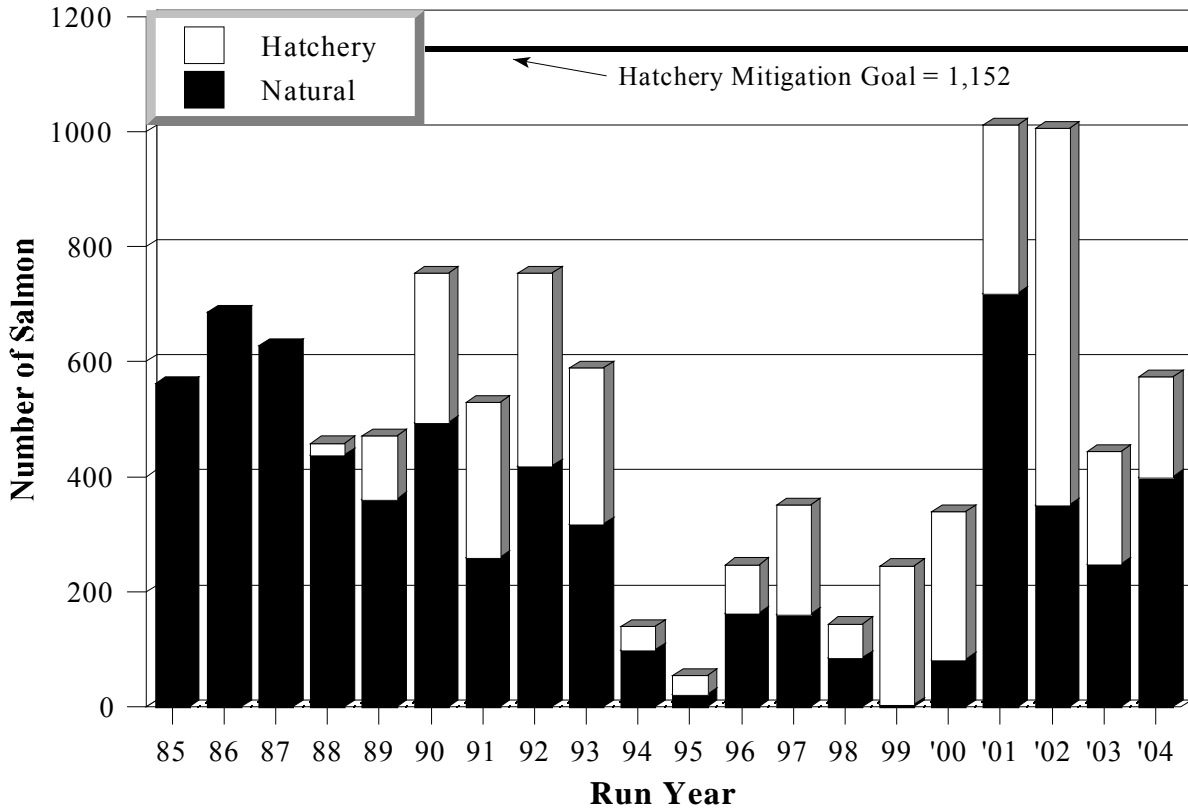


Figure 10. Total escapement for Tucannon River spring chinook salmon for the 1985-2004 run years.

Conclusions and Recommendations

Washington's LSRCP hatchery spring chinook salmon program has failed to return adequate numbers of adults to meet the mitigation goal. This occurred because SARs of hatchery origin fish have consistently been below the predicted SAR, even though hatchery returns have generally been at 2-3 times the replacement level. Further, the natural spring chinook population in the river has declined and remained below the replacement level for most years, with the majority (95%) of the mortality occurring between the green egg and smolt stages. Ocean conditions and mortality within the mainstem migration corridor have also contributed to poor survival. The result has been a slow but steady replacement of the natural population with the hatchery population. While this neither was, nor is the desired result of the program, in many ways the hatchery program has helped conserve the natural population by returning adults to spawn in the river. System survivals (in-river, migration corridor, ocean) must increase in the future for the hatchery program and the natural run to reach their full potential, and the spring chinook run returned to its historic level.

Until that time, the evaluation program will continue to document and study life history survivals, genotypic and phenotypic traits, and examine procedures within the hatchery that can be improved to benefit the program and the natural population. Based on our previous studies and current data involving survival and physical characteristics we recommend the following:

1. We continue to see annual differences in phenotypic characteristics of returning salmon (i.e., hatchery fish are generally younger in age and less fecund than natural origin fish), yet other traits such as run and spawn time are little changed over the program's history. Further, genetic analysis to date indicates little change in the natural population as a result of hatchery actions.

Recommendation: Continue to collect as many carcasses as possible for the most accurate age composition data. Continue to assist hatchery staff with picking eyed eggs to obtain fecundity estimates for each spawned female. Collect other biological data (length, run timing, spawn timing, DNA samples, juvenile parr production, smolt trapping, and life stage survival) to continue the documentation of the effects (positive or negative) that the hatchery program may have on the natural population.

2. Documenting the success of hatchery origin fish spawning in the river has become an important topic among managers within the Snake River Basin and with NOAA Fisheries. Little data exists on this subject. With the hatchery population in the Tucannon River slowly replacing the natural population, we have an opportunity to study the effects of the hatchery spawners in the natural environment.

Recommendation: Continue to seek funding for a DNA based pedigree analysis study to examine the reproductive success of hatchery fish in the natural environment. Continue to use snorkel surveys during the summer months to estimate spring chinook parr production in the river. Examine the relationship between redd counts and the following-year's parr production, smolt numbers and returning adults in context of the proportion of hatchery spawners in the river. Publish the results.

3. Subbasin and recovery planning for ESA listed species in the Tucannon River will identify factors limiting the spring chinook population and strategies to recover the population. Development of a recovery goal for the population that is consistent with NOAA's VSP criteria would be helpful in developing and evaluating recovery strategies for habitat, hydropower, harvest, and hatcheries.

Recommendation: Assist subbasin planning in the development of a recovery goal for spring chinook in the Tucannon River. Determine carrying capacity of the Tucannon River so that stocking is appropriate. Determine impacts to other species (e.g., steelhead).

4. Smolt and adult detection capabilities for PIT tagged salmon within the Columbia and Snake River basins are becoming more widespread. These capabilities can help estimate survival rates for release groups to aid in evaluation of program success.

Recommendation: Continue to utilize the SURPH2 PIT tag model software and present summaries of juvenile rates in future reports. Increase sample size of PIT tags if necessary, and document stray Tucannon fish above lower Granite Dam.

5. We have documented that hatchery juvenile (egg-parr-smolt) survival rates are considerably higher than naturally reared salmon, and hatchery smolt-to-adult return rates are much lower. We need to identify and address the factors that limit hatchery SAR's in order to meet mitigation goals.

Recommendation: Compare survival rates from different watersheds under different rearing

and release strategies. Provide recommendations to improve SAR, or a list of recommended research topics for managers to consider that would provide answers to improve hatchery survival. Monitor smolts per redd to evaluate effects of habitat improvement over time.

Literature Cited

- Becker, G. C. 1983. *Fishes of Wisconsin*. University of Wisconsin Press.
- Bugert, R., P. LaRiviere, D. Marbach, S. Martin, L. Ross, and D. Geist. 1990. Lower Snake River Compensation Plan Salmon Hatchery Evaluation Program 1989 Annual Report to U.S. Fish and Wildlife Service, AFF 1/LSR-90-08, Cooperative Agreement 14-16-0001-89525. Washington Department of Fisheries, Olympia, Washington.
- Bugert, R., C. Busack, G. Mendel, L. Ross, K. Petersen, D. Marbach, and J. Dedloff. 1991. Lower Snake River Compensation Plan Tucannon River Spring Chinook Salmon Hatchery Evaluation Program 1990 Annual Report to U.S. Fish and Wildlife Service, AFF 1/LSR-91-14, Cooperative Agreement 14-16-0001-90524. Washington Department of Fisheries, Olympia, Washington.
- Bumgarner, J. D., G. Mendel, L. Ross, D. Milks, and J. Dedloff. 1994. Lower Snake River Compensation Plan Tucannon River Spring Chinook Salmon Hatchery Evaluation Program 1993 Annual Report to U.S. Fish and Wildlife Service, Aff1/LSR-94-09, Cooperative Agreement 14-16-0001-93539. Washington Department of Fish and Wildlife, Olympia, Washington.
- Bumgarner, J., D. Milks, L. Ross, and M. Varney. 1998. Tucannon River Spring Chinook Salmon Hatchery Evaluation Program. 1997 Annual Report to U.S. Fish and Wildlife Service, Boise, ID. Washington Department of Fish and Wildlife, Fish Program/Hatcheries Division, Olympia, WA 98501-1091. Report # H98-06. 43 p.
- Bumgarner, J., L. Ross, and M. Varney. 2000. Lower Snake River Compensation Plan Tucannon River Spring Chinook Salmon Hatchery Evaluation Program 1998 and 1999 Annual Reports to U.S. Fish and Wildlife Service, Cooperative Agreements 1448-14110-98-J057 and CA-14110-9-J070. Washington Department of Fish and Wildlife, Olympia, Washington. Report # FPA00-17.
- Cheng, Y. W., and M. P. Gallinat. 2004. Statistical analysis of the relationship among environmental variables, inter-annual variability and smolt trap efficiency of salmonids in the Tucannon River. *Fisheries Research* 70: 229-238.
- Gallinat, M. P., J. D. Bumgarner, L. Ross, and M. Varney. 2001. Tucannon River Spring Chinook Salmon Hatchery Evaluation Program 2000 Annual Report to U.S. Fish and Wildlife Service, Cooperative Agreement 1411-09-J070. Washington Department of Fish and Wildlife, Olympia, Washington. Report # FPA01-05.
- Gallinat, M. P. 2004. Tucannon River Spring Chinook Salmon Hatchery Evaluation Program

- 2003 Annual Report to U.S. Fish and Wildlife Service, Cooperative Agreement 1411-03-J051. Washington Department of Fish and Wildlife, Olympia, Washington. Report # FPA 04-12.
- Gallinat, M. P. 2005. Tucannon River Spring Chinook Salmon Captive Broodstock Program-FY2004 Annual Report. Washington Department of Fish and Wildlife, Olympia, Washington. Report to BPA. Project #2000-019-00.
- Griffith, J. S. 1981. Estimation of the age-frequency distribution of stream-dwelling trout by underwater observation. *Progressive Fish-Culturist* 43: 51-53.
- Groot, C., and L. Margolis. 1991. Pacific salmon life histories. UBC Press. Vancouver, B.C. 564 p.
- Hawkins, D., and A. Frye. 2005. Microsatellite DNA analysis of Tucannon River spring chinook: 2003 collections of supplementation hatchery spawners, redd survey carcasses from the river, and captive brood spawners. Washington Dept. of Fish and Wildlife. Olympia, Washington. 24 p.
- McCullough, D. A. 1999. A review and synthesis of effects of alterations to the water temperature regime on freshwater life stages of salmonids, with special reference to chinook salmon. Prepared by Columbia River Inter-Tribal Fish Commission for U.S. EPA. Report #EPA 910-R-99-010. 279 pp.
- Scott, W. B., and E. J. Crossman. 1973. Freshwater fishes of Canada. Fisheries Research Board of Canada Bulletin 184.
- Schill, D. J., and J. S. Griffith. 1984. Use of underwater observations to estimate cutthroat trout abundance in the Yellowstone River. *North American Journal of Fisheries Management* 4: 479-487.
- Seiler, D., L. Kishimoto, and S. Neuhauser. 1999. 1998 Skagit River wild 0+ chinook production evaluation. Washington Department of Fish and Wildlife. Rept. 98504-1091. Olympia, Washington. 73 pp.
- Theurer, F. D., I. Lines, and T. Nelson. 1985. Interaction between riparian vegetation, water temperature, and salmonid habitat in the Tucannon River. *Water Resources Bull.* 21(1): 53-64.
- Tucannon Subbasin Summary. 2001. L. Gephart and D. Nordheim, editors. Prepared for the Northwest Power Planning Council. Dayton, Washington.
- USACE (U.S. Army Corps of Engineers), 1975. Special Reports: Lower Snake River Fish and

Wildlife Compensation Plan. Walla Walla, Washington.

**Appendix A: Spring Chinook Captured, Collected,
or Passed Upstream at the Tucannon Hatchery
Trap in 2004**

Appendix A. Spring chinook salmon captured, collected, or passed upstream at the Tucannon Hatchery trap in 2004.

(Trapping began in February; last day of trapping was September 30).

Date	Captured in Trap		Collected for Broodstock		Passed Upstream	
	Natural	Hatchery	Natural	Hatchery	Natural	Hatchery
4/28	1				1	
5/4	1				1	
5/5	2				2	
5/8	11	1			11	1
5/10	3		3			
5/12	3		3			
5/14	5	1	5	1		
5/15	3	1			3	1
5/16	4				4	
5/17	3				3	
5/18	9	1	3		6	1
5/19	5	2	3		2	2
5/20	20	3			20	3
5/21	6	2	3	1	3	1
5/22	3				3	
5/24	1				1	
5/25	2	1			2	1
5/26	8	1			8	1
5/27	9	3	4	2	5	1
5/28	7	8	4	2	3	6
5/29	8	4			8	4
5/31	4	5			4	5
6/1	6	6			6	6
6/2	11	11	5	5	6	6
6/3	12	9			12	9
6/4	25	10	3	3	22	7
6/5	5	6			5	6
6/6	5	3			5	3
6/7	3	1	2	1	1	
6/8	3	3	1	1	2	2
6/9	1	1	1	1		
6/10	5	3			5	3
6/11	1	4	1	2		2
6/13	3	6			3	6
6/14	2	8	1	4	1	4
6/15	4	2	2	1	2	1
6/16	5	4	2	2	3	2
6/17	4	1		1	4	
6/18	3	5		3	3	2
6/19	5				5	
6/20	4	1			4	1
6/21	6	1			6	1
6/22	5				5	
6/23	4	3		1	4	2
6/24		1				1
6/25	1	2			1	2
6/26	8	1			8	1
6/27	3	4			3	4
6/28		3		1		2
6/30	4	2			4	2

Appendix A (continued). Spring chinook salmon captured, collected, or passed upstream at the Tucannon Hatchery trap in

2004.						
Date	Captured in trap		Collected for broodstock		Passed upstream	
	Natural	Hatchery	Natural	Hatchery	Natural	Hatchery
7/1		1				1
7/2	2				2	
7/3	1				1	
7/4	3				3	
7/5	2				2	
7/6		1				1
7/8		1		1		
7/9	1	1			1	1
7/13	1				1	
7/14		1		1		
7/16	1				1	
7/20	1	1			1	1
7/27	1	1			1	1
7/28	1	1			1	1
8/23	1		1			
8/27	1	1	1	1		
8/29	3		2		1	
8/31	5				5	
9/1	2	3		3	2	
9/2	1	1			1	1
9/3	7				7	
9/4	2	3			2	3
9/5	2				2	
9/7	3	2		1	3	1
9/8	4				4	
9/9	7	3		3	7	
9/13	1				1	
9/14		1				1
9/19	1				1	
Totals	310	156	50	42	260	114
Corrected #'s after spawning^a	311	155	51	41	260	114

^a One wild fish collected for broodstock was inadvertently identified as a hatchery fish due to a fish hook in its gullet.

Appendix B: 2003 Microsatellite DNA Analysis

Appendix B. Microsatellite DNA Analysis of Tucannon River Spring Chinook: 2003 collections of supplementation hatchery spawners, redd survey carcasses from the river, and captive brood spawners

Microsatellite DNA Analysis of Tucannon River Spring Chinook: 2003 collections of supplementation hatchery spawners, redd survey carcasses from the river, and captive brood spawners

Denise Hawkins, Alice Frye
Genetics Laboratory
Conservation Biology Unit
Science Division
Fish Program
Washington Department of Fish and Wildlife
(WDFW)

Final Report

Abstract

A total of 480 spring Chinook samples from 2003 collections of Tucannon River spring Chinook (75 supplementation spawners, 59 in-river spawners, and 346 captive brood spawners) were analyzed at 14 microsatellite loci (*Oki-100*, *Ots-201b*, *Ots-208b*, *Ssa-408*, *Ogo-2*, *Ssa-197*, *Omm-1080*, *Ogo-4*, *Ots-213*, *Ots-G474*, *Ots-3M*, *Ots-9*, *Ots-211*, and *Ots-212*). All three collections were found to exhibit relatively high and similar levels of genetic diversity. Genotypic tests of differentiation indicated highly significant differences between the captive brood spawners and either of the other two spawner groups, but that the supplementation spawners were not different from the in-river spawners. Further analysis of the collections regrouped by genetic origin (based on coded-wire tags) indicated highly significant differences among hatchery origin, natural origin and captive brood.

Introduction

Prior to 1985, artificial production of spring Chinook in the Tucannon River was nearly nonexistent, with only two fry releases in the 1960s. In August 1962 and June 1964 16,000 Klickitat (2.3 g fish) and 10,500 Willamette, Oregon (2.6 g fish) spring Chinook stock, respectively, were released by WDFW into the Tucannon River. Neither of these releases is believed to have returned any significant number of adults (Gallinat 2004). In 1985, WDFW began the hatchery spring Chinook production program by trapping wild (unmarked) adults for the hatchery broodstock. Hatchery-origin fish have been returning to the Tucannon since 1988. The hatchery broodstock since 1989 has consisted of both natural and hatchery-origin fish. The Tucannon River spring Chinook were listed as threatened in 1995 under the ESA. The supplementation program is part of the Lower Snake River Compensation Plan (LSRCP) mitigation program, and will continue as long as mitigation is required under the LSRCP. In 1994, the adult escapement declined severely to less than 150 fish, and the run in 1995 was estimated at 54 fish. WDFW and the co-managers believed the risk of extinction was high enough that aggressive intervention beyond the supplementation program, in the form of a captive broodstock program, was warranted. The captive broodstock program collected fish from the 1997-2001 supplementation program brood years (BY) to be raised to adults and spawned. Males were also collected from the 2002 BY in order to have enough to spawn with the captive brood females towards the end of the program. Each year, fish that mature from the initial group of captive broodstock are spawned. The captive brood program is scheduled to terminate with the final release of smolts in 2008. Both of the hatchery programs (supplementation and captive brood) are being conducted with the recognition that artificial propagation may have potentially deleterious direct and indirect effects on the listed fish. These effects may include genetic and ecological hazards that cause maladaptive genetic, physiological, or behavioral changes in the donor or target populations, with attendant losses in natural productivity. See Gallinat 2004 for a complete description of the Tucannon River spring Chinook program.

The current report addresses the genetic analysis and comparison of the 2003 collections of Tucannon River spring Chinook.

Materials and Methods

A total of 480 spring Chinook samples from the 2003 collections of Tucannon River spring Chinook (supplementation spawners, in-river spawners, and captive brood spawners) were analyzed at 14 microsatellite loci for this study. Collections were grouped in two ways for analysis. The first comparisons (spawner) involved groups comprised of fish that actually spawned during the 2003 spawning season in the various environments (i.e., supplementation hatchery, in-river, or part of the captive brood program), and therefore, represent the parents of the 2003 broodyear (BY) Tucannon River spring Chinook. Both the supplementation spawner and in-river spawner groups are comprised of fish of natural and hatchery origin (to minimize differences between the two spawner groups). Marking and tagging operations in the hatchery make it possible to identify where each of the fish spawned in 2003 was hatched (i.e., hatchery or natural) and then to re-shuffle these spawner groups based on their genetic origin. The second comparisons (genetic origin) involved these re-shuffled groups and allow comparisons among hatchery, natural and captive brood origin fish. The captive brood group is the same in both sets of comparisons. Tissue samples were collected for all fish spawned in both the supplementation and captive broodstock programs in 2003. Therefore, these samples represent complete genetic collections for spawner group comparisons. However, not all of the fish that spawned in-river were genetically sampled, thus, the entire Tucannon River spring Chinook escapement was not represented. Overall, the total escapement to the river was comprised of 248 natural origin fish and 196 hatchery origin fish in 2003 (Gallinat pers. comm.). Of these fish, 35% of the natural origin fish and 27% of the hatchery origin fish were genetically sampled. Collection codes, number of samples analyzed per collection, sample types and collection sources are given in Table 1.

DNA was extracted using silica membrane based kits obtained from Machery-Nagel. The protocol was: incubate tissue fragments 6 hours to overnight at 56° C in 200 µl proteinase K solution, add 200 µl Buffer B3 and 200 µl 100% ethanol, mix and transfer the supernatant into a Tissue Binding Plate containing the silica binding membranes, centrifuge 10 min, add 500 µl Buffer BW, centrifuge 2 min, add 700 µl Buffer B5, centrifuge 4 min, place Tissue Binding Plate on a collection rack, incubate 10 min at 70° C to remove residual ethanol, add 100 µl Buffer BE (elution buffer) at 70° C, incubate 1 min, centrifuge 2 min, dispose of Tissue Binding Plate, refrigerate eluted DNA or store at -20° C.

Table 1. Collection information and microsatellite scoring success rates. N indicates the total number of samples analyzed per collection. The first three collections are comprised of fish that actually spawned in 2003 in the various environments (i.e., supplementation hatchery, in-river, or part of the captive brood), and therefore represent the parents of the 2003 broodyear Tucannon spring chinook. The last two collections are based on the genetic origin of the same fish based on tagging information. All hatchery origin fish originated in the hatchery in their respective brood year and all natural origin fish were spawned naturally and originated in the river in their respective broodyear.

Collection Description	Collection		Sample Type														
	Code	N	0 loci	1 loci	2 loci	3 loci	4 loci	5 loci	6 loci	7 loci	8 loci	9 loci	10 loci	11 loci	12 loci	13 loci	14 loci
Captive brood spawners	03EM	346	opercle punches														
Number of loci scored			0 loci	1 loci	2 loci	3 loci	4 loci	5 loci	6 loci	7 loci	8 loci	9 loci	10 loci	11 loci	12 loci	13 loci	14 loci
Number of fish scored per collection			3	0	1	0	0	0	1	0	4	5	7	12	35	88	190
Percent of collection			0.87	0.00	0.29	0.00	0.00	0.00	0.29	0.00	1.16	1.45	2.02	3.47	10.12	25.43	54.9
Supplementation spawners	03EK and 03EL	75	opercle punches														
Number of loci scored			0 loci	1 loci	2 loci	3 loci	4 loci	5 loci	6 loci	7 loci	8 loci	9 loci	10 loci	11 loci	12 loci	13 loci	14 loci
Number of fish scored per collection			0	0	0	0	0	0	0	0	0	0	0	3	13	20	39
Percent of collection			0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.00	17.33	26.67	52.0
In-river spawners	03EK and 03EL	59	opercle punches														
Number of loci scored			0 loci	1 loci	2 loci	3 loci	4 loci	5 loci	6 loci	7 loci	8 loci	9 loci	10 loci	11 loci	12 loci	13 loci	14 loci
Number of fish scored per collection			4	2	2	1	5	1	1	0	2	3	0	4	3	11	20
Percent of collection			6.78	3.39	3.39	1.69	8.47	1.69	1.69	0.00	3.39	5.08	0.00	6.78	5.08	18.64	33.9
Hatchery origin	03EK	50	opercle punches														
Number of loci scored			0 loci	1 loci	2 loci	3 loci	4 loci	5 loci	6 loci	7 loci	8 loci	9 loci	10 loci	11 loci	12 loci	13 loci	14 loci
Number of fish scored per collection			4	0	0	0	3	0	0	0	2	1	0	2	6	12	20
Percent of collection			8.00	0.00	0.00	0.00	6.00	0.00	0.00	0.00	4.00	2.00	0.00	4.00	12.00	24.00	40.0
Natural origin	03EL	84	opercle punches														
Number of loci scored			0 loci	1 loci	2 loci	3 loci	4 loci	5 loci	6 loci	7 loci	8 loci	9 loci	10 loci	11 loci	12 loci	13 loci	14 loci
Number of fish scored per collection			0	2	2	1	2	1	1	0	0	2	0	5	10	19	39
Percent of collection			0.00	2.38	2.38	1.19	2.38	1.19	1.19	0.00	0.00	2.38	0.00	5.95	11.90	22.62	46.4

Descriptions of the loci assessed in this study and PCR conditions are given in Table 2. PCR reactions were run separately for each microsatellite locus using an M-J Research PTC-200 thermal cycler, with a simple thermal profile consisting of: denature at 95° C for 3 min., denature at 95° C for 15 sec., anneal for 30 sec. at the appropriate temperature (see Table 2), extend at 72° C for 1 min., repeat cycle (steps 2-4) as given in Table 2, final extension at 72° C for 30 min. PCR products were subsequently pooled and genotypes were visualized using an ABI-3730 DNA Analyzer with internal size standards (GS500LIZ 3730) and GeneMapper 3.0 software. Allele binning and naming were accomplished using MicrosatelliteBinner-v1h (Young, WDFW available from the author). MicrosatelliteBinner creates groups (bins) of alleles with similar mobilities (alleles with the same number of repeat units). The upper and lower bounds of the bins are determined by identifying clusters of alleles separated by gaps (nominally 0.4 base pairs in size) in the distribution of allele sizes. The bins are then named as the mean allele size for the cluster rounded to an integer.

The 2003 collections (grouped for both the spawner comparisons and the genetic origin comparisons) were genetically characterized and compared. Each locus was tested for deviations from Hardy-Weinberg equilibrium (HWE) over all groups, and pairwise linkage disequilibrium with all other loci using Genepop 3.4 (Raymond and Rousset 1995) with 100 batches and 1000 iterations; all groups were also tested for deviations from HWE at each locus and over all loci, and linkage disequilibrium using Genepop 3.4 with 100 batches and 1000 iterations to determine loci and/or collections that violate the assumptions of the statistical analyses. Measures of within-population genetic diversity were calculated for each group (gene diversity, number of alleles per locus, and allelic richness – the number of alleles corrected for sample size, FSTAT 2.9.3 Goudet 2001; observed and expected heterozygosity, GDA 1.1 Lewis and Zaykin 2001; and the number of unique alleles found in each group Convert 1.3 Glaubitz 2003). Weir and Cockerham's (1984) inbreeding coefficient (F_{IS}) was also calculated using GDA for each group across all loci to look for genetic effects of small population size. To explore population structure among the groups, pairwise F_{ST} values and pairwise genotypic population differentiation tests were calculated using Genepop 3.4. Within a group, the coefficient of identity (I Identix 1.1 Belkhir et. al. 2002) was calculated between each pair of samples to explore the overall relatedness of the fish in the groups. Using this measure of relatedness, a value of 0.5 is expected for a full-sib relationship (individuals sharing the same mother and father) between two individuals. Statistical significance of all tests was determined using a Bonferroni corrected P-value to account for multiple, simultaneous tests (Rice 1989). An allele frequency table (Convert 1.3) has also been included.

Table 2. PCR conditions and microsatellite locus information (including designated repeat unit length, and observed allele size range) for poolplexed loci. Also included are the observed and expected heterozygosity (He and Ho) for each locus, P-values for deviations from Hardy-Weinberg equilibrium (HWE, values significant after Bonferroni correction for multiple, simultaneous tests are in bold), and the number of significant linkage disequilibrium tests after Bonferroni correction (Link). Because HWE and linkage disequilibrium are dependent on the fish combined in a group, values are given for both the spawner group collections and the genetic origin collections (see text for detailed description of these groups).

Poolplex x	Locus	Annealing Primer			Cycles	Designated Repeat Unit	Observed Allele Size Range (bp)	Ho ^c	He ^c	Spawner Genetic		Spawner Group Link ^b	Genetic Origin Link ^b
		Dye Label	temp (°C)	conc. (mM)						HWE P-value ^a	HWE P-value ^a		
Ots-M	<i>Oki-100*</i>	vic	50	0.36	40	4	248-327	0.9009	0.9044	0.8533	0.8453	8	7
	<i>Ots-201b*</i>	6fam	50	0.32	40	4	184-330	0.9324	0.9167	0.9042	0.9551	10	7
	<i>Ots-208b*</i>	ned	50	0.18	40	4	188-287	0.9215	0.9193	0.3157	0.7844	5	6
	<i>Ssa-408*</i>	pet	50	0.20	40	4	211-324	0.8764	0.8935	0.0594	0.0715	5	7
Ots-N	<i>Ogo-2*</i>	pet	63	0.07	40	2	231-260	0.6400	0.6260	0.7384	0.9325	12	8
	<i>Ssa-197*</i>	ned	63	0.25	40	4	189-301	0.8698	0.8803	0.1595	0.1970	8	7
Ots-O	<i>Ogo-4*</i>	6fam	56	0.18	40	2	165-198	0.7895	0.7823	0.7502	0.7905	7	9
	<i>Omm-1080*</i>	vic	56	0.22	40	4	218-377	0.8966	0.9145	0.0091	0	6	1
	<i>Ots-213*</i>	ned	56	0.18	40	4	252-359	0.8722	0.8972	0.0257	0.0190	8	5
	<i>Ots-G474*</i>	pet	56	0.14	40	4	188-231	0.5480	0.5255	0.9101	0.9107	8	11
Ots-P	<i>Ots-3M*</i>	6fam	63	0.12	40	2	146-183	0.5123	0.5012	0.8225	0.8421	9	8
	<i>Ots-9*</i>	ned	63	0.04	40	2	132-138	0.6304	0.6030	0.9267	0.9223	7	7
Ots-Q	<i>Ots-211*</i>	ned	63	0.07	40	4	237-340	0.8422	0.8759	0.1800	0.1914	5	9
	<i>Ots-212*</i>	6fam	63	0.30	40	4	161-258	0.8550	0.8735	0.2695	0.3400	8	8

a: Bonferroni corrected P-value = 0.0036 (0.05/14)

b: Bonferroni corrected P-value = 0.0006 (0.05/91)

c: value calculated using GDA 1.1

Results and Discussion

Good quality DNA was obtained and analyzed for all three collections. Nearly complete genotypes were collected for most samples. All samples with genotypes for seven or more loci were included in the analysis, and over all three collections only 21 samples were excluded. Table 1 contains a summary of the scoring success rate for each group. The in-river spawner group suffered the greatest loss with just over 27% of the group excluded due to missing data. This is likely due to the inferior quality of samples taken from dead, decaying fish and the subsequent increased difficulty in obtaining high quality DNA. Based on the results of the Hardy-Weinberg Equilibrium (HWE) and linkage disequilibrium tests (Table 2), none of the loci were excluded from analysis. Although the locus *Omm-1080* was out of HWE over all genetic origin groups combined, it was not consistently out in all groups individually and was therefore included in the analysis. All 14 loci exhibited some linkage disequilibrium, but no pair of loci was consistently linked in all groups. Thus, there was not an indication of physical linkage of two loci, which would yield non-independent data, and therefore all loci were retained.

Large positive values of the inbreeding coefficient (F_{IS}) are an indication of an excess of homozygotes in a collection and can result from small population size and inbreeding. Allelic richness and gene diversity are two additional measures of population diversity and therefore indications of the health and stability of the population; high values indicate increased genetic diversity. In general, all groups exhibited relatively high and similar levels of gene diversity and allelic richness, and neither the F_{IS} values nor the observed heterozygosities indicated an excess of homozygotes (which would be an indication of inbreeding) (Table 3). However, there were many significant linkage disequilibria detected in the captive brood group (Table 3). Linkage disequilibrium can be caused by genetic drift, inclusion of family groups within collections, assortative mating and/or analysis of an admixed collection. The linkage disequilibria detected in the captive brood collection is likely the result of sampling a relatively small number of families of related individuals, effectively creating an admixed collection. Table 4 gives the average and modal coefficient of identity for each collection. The captive brood, in-river spawners, and the hatchery origin groups have an average value greater than the modal value, which indicates that some of the identity coefficients are larger than the average value. Thus, these groups contain individuals that are more related than would be expected in a model of random mating and unbiased sampling (family groups have been sampled). The coefficient of identity for the natural origin group indicates that these fish are as related as expected under the null hypothesis of

Table 3. Descriptive statistics of the collections analyzed, including the number of significant pairwise linkage disequilibria detected (Link, calculated with Genepop 3.4), observed and expected heterozygosities (H_o , H_e , calculated with GDA 1.1), P-values for deviations from Hardy Weinberg Equilibrium (HWE, values significant after Bonferroni correction for multiple, simultaneous tests are in bold, calculated with Genepop 3.4), allelic richness (number of alleles corrected for sample size, averaged over all loci, calculated with Fstat 2.9.3), gene diversity (a measure of expected heterozygosity corrected for sample size, averaged over all loci, calculated with Fstat 2.9.3), inbreeding coefficient (F_{IS} GDA 1.1), and the number of unique alleles found each collection (Convert 1.3).

Collection	Collection Code	Number of Fish Included in Analysis (scored at 7 or more loci)	Link ^a		H_o	H_e	HWE P-value ^b	Allelic Richness ^c	Gene Diversity	F_{IS}	Number of Unique Alleles
			Number of (significant before/ significant after Bonferroni correction)								
Captive brood spawners	03EM	341	79 / 44		0.7865	0.7910	0.0320	11.60	0.787	0.006	36
Supplementation spawners	03EK and 03EL	75	11 / 3		0.7956	0.7981	0.2765	12.53	0.798	0.003	13
In-river spawners	03EK and 03EL	43	13 / 3		0.8271	0.7892	1.0000	11.96	0.789	0.049	8
Hatchery origin	03EK	43	16 / 3		0.7961	0.7872	0.6431	10.97	0.787	0.012	4
Natural origin	03EL	75	20 / 2		0.8127	0.7952	0.9937	12.03	0.795	0.022	23

a: Bonferroni corrected P-value = 0.0006 (0.05/91)

b: Bonferroni corrected P-value = 0.0167 (0.05/3)

c: Allelic richness based on 14 loci, and 33 individuals (spawner groups) or 30 individuals (genetic origin).

Table 4. Coefficient of identity (I) for each collection (calculated with Identix 1.1); a value of 0.5 indicates full-sib offspring. The most common value of I for each collection is also shown (Modal I), as well as the total number of pairwise comparisons calculated for each collection, and the percent of the total comparisons with I values greater than 0.5.

Collection	Collection Code	Number of Fish Included in		Average I	Modal I	Number of total comparisons	Percent of comparisons > 0.5
		Analysis (scored at 7 or more loci)					
Captive brood spawners	03EM	341		0.25	0.22	62,970	2.2
Supplementation spawners	03EK and 03EL	75		0.22	0.23	2,775	0.6
	03EK and 03EL	43		0.26	0.19	903	3.4
In-river spawners	03EL	43		0.26	0.22	903	3.2
Hatchery origin	03EK	43		0.26	0.22	903	3.2
Natural origin	03EL	75		0.23	0.23	2,775	1.6

random mating (average coefficient of identity equal to the modal value). As would be expected, when natural origin and hatchery origin fish are combined in the supplementation hatchery, the average coefficient of identity is lower than the most common value.

The results of the pairwise comparisons of F_{ST} and genotypic differentiation (Table 5A and 5B) appear to be somewhat contradictory. The pairwise F_{ST} values are all quite small (yet still significantly different from zero) indicating little genetic difference among the collections, grouped either by spawner location or genetic origin. F_{ST} values are highly affected by the level of heterozygosity of the populations compared; the observed heterozygosities in this study were quite high (Table 2) which results in smaller F_{ST} values. However, based on the genotypic tests a different picture emerges. In the genetic origin comparison, all three groups are highly significantly different from each other in tests over all loci, and these differences are retained for many of the loci when tested individually (Table 5A, right side). Yet, when the hatchery origin and natural origin fish (significantly different from each other) are re-grouped as either supplementation spawners or in-river spawners, they are not significantly different from each other (Table 5A). A look at the number and distribution of the alleles observed in each group can give insights into the pairwise genotypic differentiation test results. A side-by-side comparison of the unique alleles (Table 7) facilitates an understanding of why the genotypic differentiation results differ depending on how the fish are grouped. In many cases, alleles that are unique to the natural origin fish have been split between the supplementation and in-river spawners. This effectively homogenizes the two groups and spreads the genetic diversity found in the natural population between the two spawner groups. Because this hatchery program is a supplementation hatchery designed to augment the natural production, this homogenization and spreading of the natural genetic diversity is a desired result. The alleles of *Oki-100* are a good example of this effect. Both allele number 18 and 20 are observed only in the natural group. However, allele 18 is distributed between the supplementation spawners and the in-river spawners, while allele 20 is only present in the supplementation spawners. In this case, allele 18 is represented by 3 copies in the natural group; these copies of allele 18 are distributed as 2 copies in the supplementation spawners and 1 copy in-river. There are many other examples of this homogenization of genetic diversity throughout the loci. Additionally, there is one example of an allele unique to the hatchery origin fish moving into the in-river spawners, and thus becoming part of the 2003 BY natural origin fish (*Ots-3M* allele number 6). Therefore, it is probable that these distribution differences of particular alleles are driving the genotypic differences observed among the groups even though all of these groups were recently derived from the same population.

Table 5A. P-values for pairwise tests of genotypic differentiation across all loci (Fisher's method, Genepop 3.4). Values significant before Bonferroni correction for multiple tests are underlined; values still significant after correction are underlined and bold. H.S. indicates highly significant results with a chi-squared value of infinity. Number of statistically significant individual loci tests before and after Bonferroni correction (before/after) shown in parentheses.

Table 5B. Table of pairwise F_{ST} values (Genepop 3.4). Bold values are significantly different from zero.

A. Pairwise genotypic tests

Spawner comparison

	<u>in-river</u>	<u>captive brood</u>
supplementation	0.0925 (1/0)	<u>H.S.</u> (10/9)
in-river		<u>H.S.</u> (11/10)

Genetic origin comparison

	<u>natural origin</u>	<u>captive brood</u>
hatchery origin	<u>H.S.</u> (7/6)	<u>H.S.</u> (11/8)
natural origin		<u>H.S.</u> (11/11)

Bonferroni corrected P-value = 0.0167 (0.05/3)

B. Pairwise F_{ST}

Spawner comparison

	<u>in-river</u>	<u>captive brood</u>
supplementation	0.001	0.006
in-river		0.007

Genetic origin comparison

	<u>natural origin</u>	<u>captive brood</u>
hatchery origin	0.008	0.010
natural origin		0.007

Although the overall number of alleles observed is relatively similar in all groups (Table 6), the captive brood spawners have more unique alleles than any of the other groups (Table 3), and these unique alleles are spread throughout all of the loci except *Ots-9*, which is not surprising because *Ots-9* is the least polymorphic of the loci analyzed (Table 7). In theory, it would be expected that a natural population would exhibit higher genetic diversity and thus contain more unique alleles than a captive broodstock. Here, the captive brood group has more alleles observed than the natural origin group for 11 of the 14 loci examined (Table 6) and many of these alleles are unique to the captive brood (Table 7). One hypothesis for the observed results is that the natural and supplementation hatchery populations of Tucannon River spring Chinook have undergone severe bottleneck events and have lost many of the alleles observed uniquely in the captive broodstock. Many of the unique alleles are observed at low frequencies and would thus be easily lost. If this is the case, this analysis has demonstrated that the captive brood program has effectively preserved the genetic diversity of the Tucannon River spring Chinook. However, it is also possible that once collections of fish from other broodyears are examined, these unique alleles will be observed in other groups, and will no longer be unique. Due to the small population sizes of each of the three types of Tucannon River spring Chinook, shifts in the frequencies of various alleles would be expected from broodyear to broodyear. Furthermore, even though 100% of the supplementation hatchery spawners and captive broodstock were sampled, we were unable to get complete genetic data for 21 fish (see Table 1 for distribution of these lost fish). Therefore, the genotypes of these 21 fish are unknown and could possibly contain some of the alleles currently observed only in the captive broodstock collection. Finally, due to the difficulties of obtaining samples from fish spawning in-river, we do not have complete knowledge of all of the alleles present in the entire Tucannon River spring Chinook population outside of the captive broodstock, and therefore, some of the currently defined unique alleles are likely a result of incomplete genetic information. Yet, the evidence still suggests that the 2003 captive broodstock possess many alleles not represented in the other 2003 spawning groups.

Table 6. Number of alleles observed per locus for each collection. See text for detailed description of the collections.

Collection	Collection Code	Average number of samples per locus included in analysis	Oki-	Ots-	Ots-	Ssa-	Ogo-	Ssa-	Ogo-	Omm-	Ots-	Ots-	Ots-	Ots-	Ots-	Ots-
			100	201b	208b	408	2	197	4	1080	213	G474	3M	9	211	212
Captive brood spawners	03EM	322	18	24	23	19	9	18	12	30	19	7	7	4	19	15
Supplementation spawners	03EK and 03EL	71	17	22	24	19	7	15	11	26	19	5	6	4	17	12
In-river spawners	03EK and 03EL	39	16	16	15	19	7	13	10	23	17	4	7	4	12	11
Hatchery origin	03EK	40	15	16	19	14	5	12	10	22	16	4	4	4	13	9
Natural origin	03EL	70	18	23	21	21	7	17	10	25	18	5	6	4	18	14
Number of alleles in all collections		432	20	26	29	24	9	21	12	34	22	8	11	4	20	17

Table 7. Table of allele frequencies for each locus. Private allele column identifies alleles observed in only one collection and indicates in which collection that allele is uniquely found. The groups in comparison **A** are comprised of the fish that actually spawned in 2003 in the various environments (i.e., supplementation hatchery, in the river, or part of the captive brood), and therefore represent the parents of the 2003 broodyear Tucannon spring chinook. The captive brood group is the same in both comparisons and represents all of the fish spawned in 2003. The groups in comparison **B** were based on the genetic origin of the fish based on tagging information. All hatchery origin fish originated in the hatchery in their respective brood year, all natural origin fish were spawned naturally and originated in the river in their respective broodyear, and all captive brood were progeny of the captive brood program.

A. 2003 Spawner Comparison						B. Genetic origin comparison			
Oki-100						Hatchery	Natural	Captive	Private
Allele#	Size (bp)	Supple- mentation	In-River	Captive Brood	Private Allele	Origin	Origin	Brood	Allele
1	248	0.0135	0.0256	0.0393		0.0256	0.0135	0.0393	
2	256	0	0	0.003	Captive brood spawners	0	0	0.003	Captive brood
3	260	0.0135	0	0.0166		0.0128	0.0068	0.0166	
4	264	0.0338	0.0256	0.0393		0.0256	0.0338	0.0393	
5	268	0.1081	0.0897	0.1254		0.1282	0.0878	0.1254	
6	272	0.0473	0.0385	0.0408		0.0769	0.027	0.0408	
7	276	0.0473	0.0513	0.1012		0.0385	0.0541	0.1012	
8	280	0.027	0.0128	0.0196		0.0256	0.0203	0.0196	
9	284	0.0541	0.0128	0.0363		0.0513	0.0338	0.0363	
10	288	0.1419	0.1795	0.0937		0.1026	0.1824	0.0937	
11	292	0	0	0.003	Captive brood spawners	0	0	0.003	Captive brood
12	295	0.0743	0.1026	0.0861		0.0897	0.0811	0.0861	
13	297	0.0541	0.0256	0.0438		0.0769	0.027	0.0438	
14	299	0.1959	0.1923	0.1782		0.1923	0.1959	0.1782	
15	303	0.0946	0.1154	0.0166		0.0769	0.1149	0.0166	
16	307	0.0203	0.0128	0.0196		0.0256	0.0135	0.0196	
17	311	0.0541	0.0897	0.1239		0.0513	0.0743	0.1239	
18	315	0.0135	0.0128	0		0	0.0203	0	Natural origin
19	323	0	0.0128	0.0136		0	0.0068	0.0136	
20	327	0.0068	0	0	Supplementation spawners	0	0.0068	0	Natural origin
number of samples		74	39	331		39	74	331	

Table 7 (continued). Table of allele frequencies for each locus. Private allele column identifies alleles observed in only one collection and indicates in which collection that allele is uniquely found. The groups in comparison **A** are comprised of the fish that actually spawned in 2003 in the various environments (i.e., supplementation hatchery, in the river, or part of the captive brood), and therefore represent the parents of the 2003 broodyear Tucannon spring chinook. The captive brood group is the same in both comparisons and represents all of the fish spawned in 2003. The groups in comparison **B** were based on the genetic origin of the fish based on tagging information. All hatchery origin fish originated in the hatchery in their respective brood year, all natural origin fish were spawned naturally and originated in the river in their respective broodyear, and all captive brood were progeny of the captive brood program.

Ots-201b

Allele#	Size (bp)	Supplemen tation	In-river	Captive brood	Private Allele	Hatchery origin	Natural origin	Captive brood	Private Allele
1	184	0.0903	0.0303	0.054		0.05	0.0846	0.054	
2	196	0.0139	0	0.017		0	0.0154	0.017	
3	200	0	0	0.0015	Captive brood spawners	0	0	0.0015	Captive brood
4	204	0	0	0.0031	Captive brood spawners	0	0	0.0031	Captive brood
5	208	0.1042	0.0303	0.0586		0.1125	0.0615	0.0586	
6	212	0.0486	0.0455	0.0756		0.05	0.0462	0.0756	
7	215	0.1181	0.1818	0.1466		0.1875	0.1077	0.1466	
8	219	0.0972	0.1212	0.1728		0.1	0.1077	0.1728	
9	223	0.0625	0.1212	0.0478		0.0625	0.0923	0.0478	
10	227	0.0417	0	0.037		0.0125	0.0385	0.037	
11	231	0.0208	0	0.0262		0	0.0231	0.0262	
12	235	0.0139	0.0303	0.0093		0.0125	0.0231	0.0093	
13	239	0.0486	0.0152	0.0139		0.0375	0.0385	0.0139	
14	243	0.0208	0	0.0324		0	0.0231	0.0324	
15	247	0.0764	0.0152	0.0633		0.0625	0.0538	0.0633	
16	251	0.0625	0.1515	0.1204		0.075	0.1	0.1204	
17	255	0.0417	0.0303	0.0309		0.0625	0.0231	0.0309	
18	258	0.0069	0	0.0062		0	0.0077	0.0062	
19	262	0.0208	0.0455	0.0093		0.0625	0.0077	0.0093	
20	266	0.0417	0.0758	0.0247		0.05	0.0538	0.0247	
21	275	0	0	0.0015	Captive brood spawners	0	0	0.0015	Captive brood
22	278	0.0069	0	0.0015		0	0.0077	0.0015	
23	282	0.0139	0	0.0123		0	0.0154	0.0123	
24	306	0.0417	0.0606	0.034		0.05	0.0462	0.034	
25	314	0.0069	0.0152	0		0.0125	0.0077	0	
26	330	0	0.0303	0	In-river spawners	0	0.0154	0	Natural origin
number of samples		72	33	324		40	65	324	

Table 7 (continued). Table of allele frequencies for each locus. Private allele column identifies alleles observed in only one collection and indicates in which collection that allele is uniquely found. The groups in comparison **A** are comprised of the fish that actually spawned in 2003 in the various environments (i.e., supplementation hatchery, in the river, or part of the captive brood), and therefore represent the parents of the 2003 broodyear Tucannon spring chinook. The captive brood group is the same in both comparisons and represents all of the fish spawned in 2003. The groups in comparison **B** were based on the genetic origin of the fish based on tagging information. All hatchery origin fish originated in the hatchery in their respective brood year, all natural origin fish were spawned naturally and originated in the river in their respective broodyear, and all captive brood were progeny of the captive brood program.

Ots-208b		Supple-	Captive		Hatchery	Natural	Captive	Private	
Allele#	Size (bp)	mentation	In-river	brood	Private Allele	origin	origin	brood	Allele
1	188	0.0533	0.093	0.0564		0.0698	0.0667	0.0564	
2	193	0	0	0.003	Captive brood spawners	0	0	0.003	Captive brood
3	200	0.0067	0	0	Supplementation spawners	0.0116	0	0	Hatchery origin
4	201	0.0067	0	0	Supplementation spawners	0.0116	0	0	Hatchery origin
5	204	0.0067	0	0.0198		0.0116	0	0.0198	
6	208	0	0.0233	0.0488		0	0.0133	0.0488	
7	212	0.0133	0.0581	0.0091		0	0.0467	0.0091	
8	216	0	0	0.0168	Captive brood spawners	0	0	0.0168	Captive brood
9	219	0.02	0	0.0381		0.0233	0.0067	0.0381	
10	223	0	0	0.0046	Captive brood spawners	0	0	0.0046	Captive brood
11	224	0.16	0.1163	0.1296		0.1744	0.1267	0.1296	
12	228	0.08	0.0698	0.0168		0.0814	0.0733	0.0168	
13	232	0.04	0.0349	0.003		0.0465	0.0333	0.003	
14	235	0.0067	0	0	Supplementation spawners	0	0.0067	0	Natural origin
15	236	0.0533	0.0233	0.0259		0.0233	0.0533	0.0259	
16	240	0.0333	0	0.061		0.0465	0.0067	0.061	
17	244	0.0333	0.0465	0		0	0.06	0	Natural origin
18	248	0.0267	0	0.0534		0.0349	0.0067	0.0534	
19	251	0.0133	0	0.0061		0.0116	0.0067	0.0061	
20	252	0.0067	0.0116	0.003		0.0116	0.0067	0.003	
21	255	0.0467	0.0581	0.0381		0.0581	0.0467	0.0381	
22	259	0.1333	0.1279	0.1448		0.1395	0.1267	0.1448	
23	263	0.08	0.093	0.0991		0.1744	0.0333	0.0991	
24	267	0.1	0.093	0.1372		0.0349	0.1333	0.1372	
25	270	0.0133	0	0	Supplementation spawners	0.0233	0	0	Hatchery origin
26	271	0.04	0.0465	0.0198		0	0.0667	0.0198	
27	275	0.02	0.1047	0.0564		0.0116	0.0733	0.0564	
28	279	0	0	0.0091	Captive brood spawners	0	0	0.0091	Captive brood
29	287	0.0067	0	0	Supplementation spawners	0	0.0067	0	Natural origin
number of samples		75	43	328		43	75	328	

Table 7 (continued). Table of allele frequencies for each locus. Private allele column identifies alleles observed in only one collection and indicates in which collection that allele is uniquely found. The groups in comparison **A** are comprised of the fish that actually spawned in 2003 in the various environments (i.e., supplementation hatchery, in the river, or part of the captive brood), and therefore represent the parents of the 2003 broodyear Tucannon spring chinook. The captive brood group is the same in both comparisons and represents all of the fish spawned in 2003. The groups in comparison **B** were based on the genetic origin of the fish based on tagging information. All hatchery origin fish originated in the hatchery in their respective brood year, all natural origin fish were spawned naturally and originated in the river in their respective broodyear, and all captive brood were progeny of the captive brood program.

Ssa-408

Allele#	Size (bp)	Supple- mentation	In-river	Captive brood	Private Allele	Hatchery origin	Natural origin	Captive brood	Private Allele
1	211	0.0652	0.0641	0.0579		0.0571	0.0685	0.0579	
2	215	0.1594	0.2051	0.1409		0.1714	0.1781	0.1409	
3	219	0.0362	0.0641	0.0401		0.0429	0.0479	0.0401	
4	222	0.1377	0.1923	0.2255		0.1429	0.1644	0.2255	
5	226	0.0435	0.0256	0.0208		0.0857	0.0137	0.0208	
6	230	0.0725	0.0897	0.0519		0.0286	0.1027	0.0519	
7	234	0.1594	0.1026	0.1261		0.2	0.1096	0.1261	
8	238	0.0652	0.0128	0.0401		0.0857	0.0274	0.0401	
9	242	0.0145	0	0.0134		0	0.0137	0.0134	
10	250	0.0652	0.0256	0.0593		0.0429	0.0548	0.0593	
11	253	0.0145	0.0128	0.0163		0.0143	0.0137	0.0163	
12	257	0.0145	0.0128	0.0178		0	0.0205	0.0178	
13	261	0.0072	0	0	Supplementation spawners	0	0.0068	0	Natural origin
14	265	0.0145	0.0256	0		0.0429	0.0068	0	
15	269	0.0145	0	0.0163		0.0286	0	0.0163	
16	273	0	0.0128	0.0104		0	0.0068	0.0104	
17	277	0	0.0128	0	In-river spawners	0	0.0068	0	Natural origin
18	296	0.0072	0.0128	0		0	0.0137	0	Natural origin
19	300	0	0	0.0119	Captive brood spawners	0	0	0.0119	Captive brood
20	306	0	0.0128	0	In-river spawners	0	0.0068	0	Natural origin
21	308	0.0072	0.0128	0.0015		0	0.0137	0.0015	
22	312	0.0362	0.0385	0.0608		0.0143	0.0479	0.0608	
23	320	0.0652	0.0641	0.0846		0.0429	0.0753	0.0846	
24	324	0	0	0.0045	Captive brood spawners	0	0	0.0045	Captive brood
number of samples		69	39	337		35	73	337	

Table 7 (continued). Table of allele frequencies for each locus. Private allele column identifies alleles observed in only one collection and indicates in which collection that allele is uniquely found. The groups in comparison **A** are comprised of the fish that actually spawned in 2003 in the various environments (i.e., supplementation hatchery, in the river, or part of the captive brood), and therefore represent the parents of the 2003 broodyear Tucannon spring chinook. The captive brood group is the same in both comparisons and represents all of the fish spawned in 2003. The groups in comparison **B** were based on the genetic origin of the fish based on tagging information. All hatchery origin fish originated in the hatchery in their respective brood year, all natural origin fish were spawned naturally and originated in the river in their respective broodyear, and all captive brood were progeny of the captive brood program.

Ogo-2

Allele#	Size (bp)	Supple- mentation	In-river	Captive brood	Private Allele	Hatchery origin	Natural origin	Captive brood	Private Allele
1	231	0	0	0.0015	Captive brood spawners	0	0	0.0015	Captive brood
2	242	0.1818	0.1176	0.1369		0.2333	0.1186	0.1369	
3	244	0.5364	0.5	0.5893		0.5667	0.5	0.5893	
4	246	0.0182	0.0147	0.0164		0	0.0254	0.0164	
5	248	0.1818	0.2059	0.1205		0.1333	0.2203	0.1205	
6	250	0.0364	0.1176	0.0536		0.0167	0.0932	0.0536	
7	254	0.0182	0.0147	0.0134		0	0.0254	0.0134	
8	256	0.0273	0	0.0283		0.05	0	0.0283	
9	260	0	0.0294	0.0402		0	0.0169	0.0402	
number of samples		55	34	336		30	59	336	

Table 7 (continued). Table of allele frequencies for each locus. Private allele column identifies alleles observed in only one collection and indicates in which collection that allele is uniquely found. The groups in comparison **A** are comprised of the fish that actually spawned in 2003 in the various environments (i.e., supplementation hatchery, in the river, or part of the captive brood), and therefore represent the parents of the 2003 broodyear Tucannon spring chinook. The captive brood group is the same in both comparisons and represents all of the fish spawned in 2003. The groups in comparison **B** were based on the genetic origin of the fish based on tagging information. All hatchery origin fish originated in the hatchery in their respective brood year, all natural origin fish were spawned naturally and originated in the river in their respective broodyear, and all captive brood were progeny of the captive brood program.

Ssa-197

Allele#	Size (bp)	Supple- mentation	In-river	Captive brood	Private Allele	Hatchery origin	Natural origin	Captive brood	Private Allele
					Supplementation				
1	189	0.0133	0	0	0 spawners	0	0.0133	0	Natural origin
2	201	0.06	0.0814	0.0791		0.1163	0.04	0.0791	
3	209	0.0133	0	0.0657		0	0.0133	0.0657	
4	217	0	0	0.003	Captive brood spawners	0	0	0.003	Captive brood
					Supplementation				
5	221	0.02	0	0	0 spawners	0.0116	0.0133	0	
					Supplementation				
6	233	0.0067	0	0	0 spawners	0	0.0067	0	Natural origin
7	242	0	0	0.0015	Captive brood spawners	0	0	0.0015	Captive brood
8	249	0	0.0116	0.0149		0	0.0067	0.0149	
9	253	0.0467	0.0116	0.0179		0.0233	0.04	0.0179	
10	257	0.02	0.0465	0.1149		0.0116	0.04	0.1149	
11	261	0.0533	0.093	0.0299		0.0581	0.0733	0.0299	
12	265	0.1867	0.186	0.2179		0.1744	0.1933	0.2179	
13	269	0.0667	0.1395	0.0448		0.0465	0.12	0.0448	
14	273	0.2467	0.2093	0.197		0.2674	0.2133	0.197	
15	277	0.08	0.0349	0.0433		0.0581	0.0667	0.0433	
16	281	0	0.0233	0.0299		0	0.0133	0.0299	
17	285	0.0733	0.0233	0.0567		0.0698	0.0467	0.0567	
18	289	0.02	0.0116	0.0104		0.0233	0.0133	0.0104	
19	293	0.0933	0.1279	0.0612		0.1395	0.0867	0.0612	
20	297	0	0	0.006	Captive brood spawners	0	0	0.006	Captive brood
21	301	0	0	0.006	Captive brood spawners	0	0	0.006	Captive brood
number of samples		75	43	335		43	75	335	

Table 7 (continued). Table of allele frequencies for each locus. Private allele column identifies alleles observed in only one collection and indicates in which collection that allele is uniquely found. The groups in comparison **A** are comprised of the fish that actually spawned in 2003 in the various environments (i.e., supplementation hatchery, in the river, or part of the captive brood), and therefore represent the parents of the 2003 broodyear Tucannon spring chinook. The captive brood group is the same in both comparisons and represents all of the fish spawned in 2003. The groups in comparison **B** were based on the genetic origin of the fish based on tagging information. All hatchery origin fish originated in the hatchery in their respective brood year, all natural origin fish were spawned naturally and originated in the river in their respective broodyear, and all captive brood were progeny of the captive brood program.

Ogo-4

Allele#	Size (bp)	Supple- mentation	In-river	Captive brood	Private Allele	Hatchery origin	Natural origin	Captive brood	Private Allele
1	165	0.0405	0.0116	0.0177		0.0119	0.04	0.0177	
2	169	0.0541	0.1047	0.0236		0.0476	0.0867	0.0236	
3	171	0.0068	0	0.0074		0.0119	0	0.0074	
4	182	0.1892	0.2791	0.3274		0.2143	0.2267	0.3274	
5	184	0	0	0.0103	Captive brood spawners	0	0	0.0103	Captive brood
6	186	0.0068	0.0116	0.0059		0	0.0133	0.0059	
7	188	0.0676	0.0465	0.0265		0.0357	0.0733	0.0265	
8	190	0.3108	0.2791	0.3097		0.2857	0.3067	0.3097	
9	192	0.2432	0.1628	0.1445		0.3214	0.1533	0.1445	
10	194	0.0473	0.0116	0.0369		0.0476	0.0267	0.0369	
11	196	0.0203	0.0698	0.0398		0.0119	0.0533	0.0398	
12	198	0.0135	0.0233	0.0501		0.0119	0.02	0.0501	
number of samples		74	43	339		42	75	339	

Table 7 (continued). Table of allele frequencies for each locus. Private allele column identifies alleles observed in only one collection and indicates in which collection that allele is uniquely found. The groups in comparison **A** are comprised of the fish that actually spawned in 2003 in the various environments (i.e., supplementation hatchery, in the river, or part of the captive brood), and therefore represent the parents of the 2003 broodyear Tucannon spring chinook. The captive brood group is the same in both comparisons and represents all of the fish spawned in 2003. The groups in comparison **B** were based on the genetic origin of the fish based on tagging information. All hatchery origin fish originated in the hatchery in their respective brood year, all natural origin fish were spawned naturally and originated in the river in their respective broodyear, and all captive brood were progeny of the captive brood program.

Omm-1080									
Allele#	Size (bp)	Supple- mentation	In-river	Captive brood	Private Allele	Hatchery origin	Natural origin	Captive brood	Private Allele
1	218	0.0068	0	0.0341		0.0125	0	0.0341	
2	221	0.0135	0.0441	0		0.0125	0.0294	0	
3	233	0.0405	0.1029	0.0735		0	0.0956	0.0735	
4	241	0	0.0147	0.0072		0	0.0074	0.0072	
5	245	0.0068	0	0.0305		0	0.0074	0.0305	
6	249	0	0	0.0072	Captive brood spawners	0	0	0.0072	Captive brood
7	257	0.2027	0.1176	0.2437		0.175	0.1765	0.2437	
8	261	0.0338	0.0294	0.0161		0.025	0.0368	0.0161	
9	269	0.0203	0.0147	0.0036		0.025	0.0147	0.0036	
10	273	0	0.0147	0	In-river spawners	0	0.0074	0	Natural origin
11	277	0.0068	0	0	Supplementation spawners	0	0.0074	0	Natural origin
12	281	0	0.0147	0	In-river spawners	0	0.0074	0	Natural origin
13	285	0.0338	0.0147	0.0645		0.0125	0.0368	0.0645	
14	289	0.0405	0.0147	0.0627		0.075	0.0074	0.0627	
15	293	0	0	0.0054	Captive brood spawners	0	0	0.0054	Captive brood
16	297	0.0338	0.0441	0.0125		0.0125	0.0515	0.0125	
17	301	0.0135	0	0.0018		0	0.0147	0.0018	
18	309	0.0203	0.0147	0.0305		0.025	0.0147	0.0305	
19	313	0.0338	0.0588	0.0018		0.0125	0.0588	0.0018	
20	318	0.0135	0.0147	0.0108		0.025	0.0074	0.0108	
21	322	0.027	0.0147	0.009		0.025	0.0221	0.009	
22	326	0.0473	0.1029	0.0699		0.0875	0.0515	0.0699	
23	330	0.1014	0.0735	0.0538		0.125	0.0735	0.0538	
24	334	0.0338	0	0.009		0.025	0.0221	0.009	
25	338	0.0135	0.0147	0.0018		0.0375	0	0.0018	
26	342	0.0405	0.0588	0.0143		0.025	0.0588	0.0143	
27	346	0.0608	0.0441	0.0412		0.0625	0.0515	0.0412	
28	350	0.0135	0	0.0197		0.025	0	0.0197	
29	354	0.0473	0.0882	0.086		0.0375	0.0735	0.086	
30	358	0	0	0.009	Captive brood spawners	0	0	0.009	Captive brood
31	365	0.0878	0.0588	0.052		0.1	0.0662	0.052	
32	369	0	0	0.0161	Captive brood spawners	0	0	0.0161	Captive brood
33	373	0.0068	0.0294	0.0018		0.0375	0	0.0018	
34	377	0	0	0.0108	Captive brood spawners	0	0	0.0108	Captive brood
number of samples		74	34	279		40	68	279	

Table 7 (continued). Table of allele frequencies for each locus. Private allele column identifies alleles observed in only one collection and indicates in which collection that allele is uniquely found. The groups in comparison **A** are comprised of the fish that actually spawned in 2003 in the various environments (i.e., supplementation hatchery, in the river, or part of the captive brood), and therefore represent the parents of the 2003 broodyear Tucannon spring chinook. The captive brood group is the same in both comparisons and represents all of the fish spawned in 2003. The groups in comparison **B** were based on the genetic origin of the fish based on tagging information. All hatchery origin fish originated in the hatchery in their respective brood year, all natural origin fish were spawned naturally and originated in the river in their respective broodyear, and all captive brood were progeny of the captive brood program.

Ots-213

Allele#	Size (bp)	Supple- mentation	In-river	Captive brood	Private Allele	Hatchery origin	Natural origin	Captive brood	Private Allele
1	252	0.0333	0	0.0442		0.0233	0.02	0.0442	
2	256	0	0	0.003	Captive brood spawners	0	0	0.003	Captive brood
3	260	0.0467	0.0233	0		0.0698	0.02	0	
4	263	0.04	0.0233	0.0244		0.0465	0.0267	0.0244	
5	267	0.0133	0	0.0076		0	0.0133	0.0076	
6	275	0.02	0.0116	0		0.0233	0.0133	0	
7	279	0	0	0.003	Captive brood spawners	0	0	0.003	Captive brood
8	283	0.02	0.0233	0		0	0.0333	0	Natural origin
9	287	0.1333	0.093	0.157		0.1047	0.1267	0.157	
10	291	0.0067	0.0698	0.0229		0.0233	0.0333	0.0229	
11	295	0.2067	0.2558	0.2043		0.2442	0.2133	0.2043	
12	299	0.04	0.093	0.0107		0	0.0933	0.0107	
13	303	0.0467	0.0349	0.0701		0.0349	0.0467	0.0701	
14	307	0.0267	0.0233	0.0137		0.0581	0.0067	0.0137	
15	315	0.0333	0.0581	0.0366		0.0349	0.0467	0.0366	
16	319	0.0467	0.0814	0.1082		0.0349	0.0733	0.1082	
17	323	0.0533	0.0814	0.0366		0.0349	0.08	0.0366	
18	327	0.1067	0.0814	0.1037		0.1047	0.0933	0.1037	
19	331	0.04	0.0233	0.0732		0.0116	0.0467	0.0732	
20	335	0.0133	0.0116	0.0137		0.0116	0.0133	0.0137	
21	339	0.0733	0.0116	0.0625		0.1395	0	0.0625	
22	359	0	0	0.0046	Captive brood spawners	0	0	0.0046	Captive brood
number of samples		75	43	328		43	75	328	

Table 7 (continued). Table of allele frequencies for each locus. Private allele column identifies alleles observed in only one collection and indicates in which collection that allele is uniquely found. The groups in comparison **A** are comprised of the fish that actually spawned in 2003 in the various environments (i.e., supplementation hatchery, in the river, or part of the captive brood), and therefore represent the parents of the 2003 broodyear Tucannon spring chinook. The captive brood group is the same in both comparisons and represents all of the fish spawned in 2003. The groups in comparison **B** were based on the genetic origin of the fish based on tagging information. All hatchery origin fish originated in the hatchery in their respective brood year, all natural origin fish were spawned naturally and originated in the river in their respective broodyear, and all captive brood were progeny of the captive brood program.

Ots-G474

Allele#	Size (bp)	Supple- mentation	In-river	Captive brood	Private Allele	Hatchery origin	Natural origin	Captive brood	Private Allele
1	188	0.62	0.6744	0.6441		0.6163	0.6533	0.6441	
2	196	0	0	0.0074	Captive brood spawners	0	0	0.0074	Captive brood
3	200	0.2733	0.2209	0.2294		0.3488	0.2	0.2294	
4	211	0	0	0.0044	Captive brood spawners Supplementation	0	0	0.0044	Captive brood
5	215	0.0133	0	0	spawners	0	0.0133	0	Natural origin
6	219	0	0	0.0015	Captive brood spawners	0	0	0.0015	Captive brood
7	223	0.0533	0.0465	0.0588		0.0116	0.0733	0.0588	
8	231	0.04	0.0581	0.0544		0.0233	0.06	0.0544	
number of samples		75	43	340		43	75	340	

Ots-3M

Allele#	Size (bp)	Supple- mentation	In-river	Captive brood	Private Allele	Hatchery origin	Natural origin	Captive brood	Private Allele
1	146	0	0.0116	0	In-river spawners	0	0.0067	0	Natural origin
2	159	0	0.0116	0	In-river spawners	0	0.0067	0	Natural origin
3	163	0	0	0.0015	Captive brood spawners	0	0	0.0015	Captive brood
4	169	0.0133	0	0.041		0.0233	0	0.041	
5	171	0	0	0.0046	Captive brood spawners	0	0	0.0046	Captive brood Hatchery
6	173	0.0133	0.0349	0		0.0581	0	0	origin
7	175	0	0	0.0198	Captive brood spawners	0	0	0.0198	Captive brood
8	177	0.3133	0.3023	0.2432		0.3488	0.2867	0.2432	
9	179	0.6333	0.6163	0.6657		0.5698	0.66	0.6657	
10	181	0.02	0.0116	0.0243		0	0.0267	0.0243	
11	183	0.0067	0.0116	0		0	0.0133	0	Natural origin
number of samples		75	43	329		43	75	329	

Table 7 (continued). Table of allele frequencies for each locus. Private allele column identifies alleles observed in only one collection and indicates in which collection that allele is uniquely found. The groups in comparison **A** are comprised of the fish that actually spawned in 2003 in the various environments (i.e., supplementation hatchery, in the river, or part of the captive brood), and therefore represent the parents of the 2003 broodyear Tucannon spring chinook. The captive brood group is the same in both comparisons and represents all of the fish spawned in 2003. The groups in comparison **B** were based on the genetic origin of the fish based on tagging information. All hatchery origin fish originated in the hatchery in their respective brood year, all natural origin fish were spawned naturally and originated in the river in their respective broodyear, and all captive brood were progeny of the captive brood program.

Ots-9

Allele#	Size (bp)	Supple- mentation	In-river	Captive brood	Private Allele	Hatchery origin	Natural origin	Captive brood	Private Allele
1	132	0.02	0.0119	0.0185		0.0349	0.0068	0.0185	
2	134	0.4467	0.4167	0.3611		0.4884	0.4054	0.3611	
3	136	0.46	0.5119	0.4938		0.3953	0.527	0.4938	
4	138	0.0733	0.0595	0.1265		0.0814	0.0608	0.1265	
number of samples		75	42	324		43	74	324	

Ots-211

Allele#	Size (bp)	Supple- mentation	In-river	Captive brood	Private Allele	Hatchery origin	Natural origin	Captive brood	Private Allele
1	237	0.0246	0.0303	0.0196		0	0.0424	0.0196	
2	253	0.0082	0.0152	0		0	0.0169	0	Natural origin
3	264	0	0	0.0375	Captive brood spawners	0	0	0.0375	Captive brood
4	268	0.0902	0.0152	0.0857		0.0429	0.0763	0.0857	
5	272	0.0164	0.0455	0.0607		0.0286	0.0254	0.0607	
6	280	0.0164	0	0.0054		0	0.0169	0.0054	
7	284	0.0164	0	0.0143		0.0143	0.0085	0.0143	
8	288	0.0246	0	0.0125		0.0286	0.0085	0.0125	
9	292	0.0082	0	0.0071		0	0.0085	0.0071	
10	296	0.041	0.0909	0.0732		0.0714	0.0508	0.0732	
11	300	0.0902	0.0455	0.0625		0.0571	0.0847	0.0625	
12	304	0.3361	0.4697	0.2482		0.3714	0.3898	0.2482	
13	308	0.0656	0.0303	0.0321		0.0714	0.0424	0.0321	
14	312	0.1475	0.197	0.0911		0.1714	0.161	0.0911	
15	316	0.0246	0.0152	0.0839		0.0286	0.0169	0.0839	
16	320	0	0.0152	0.0411		0	0.0085	0.0411	
17	324	0	0	0.0125	Captive brood spawners	0	0	0.0125	Captive brood
18	332	0.0574	0.0303	0.0893		0.0857	0.0254	0.0893	
19	336	0.0164	0	0.0089		0.0143	0.0085	0.0089	
20	340	0.0164	0	0.0143		0.0143	0.0085	0.0143	
number of samples		61	33	280		35	59	280	

Table 7 (continued). Table of allele frequencies for each locus. Private allele column identifies alleles observed in only one collection and indicates in which collection that allele is uniquely found. The groups in comparison **A** are comprised of the fish that actually spawned in 2003 in the various environments (i.e., supplementation hatchery, in the river, or part of the captive brood), and therefore represent the parents of the 2003 broodyear Tucannon spring chinook. The captive brood group is the same in both comparisons and represents all of the fish spawned in 2003. The groups in comparison **B** were based on the genetic origin of the fish based on tagging information. All hatchery origin fish originated in the hatchery in their respective brood year, all natural origin fish were spawned naturally and originated in the river in their respective broodyear, and all captive brood were progeny of the captive brood program.

Ots-212

Allele#	Size (bp)	Supple- mentation	In-river	Captive brood	Private Allele	Hatchery origin	Natural origin	Captive brood	Private Allele
1	161	0.0076	0	0.0222		0	0.0078	0.0222	
2	165	0.0909	0.0882	0.0819		0.0417	0.1172	0.0819	
3	169	0.0606	0.0735	0.0751		0.0833	0.0547	0.0751	
4	173	0.1136	0.1912	0.1877		0.125	0.1484	0.1877	
5	177	0.0909	0.0882	0.0188		0.0833	0.0938	0.0188	
6	181	0.1894	0.1471	0.1604		0.2361	0.1406	0.1604	
7	185	0.2348	0.1765	0.1792		0.2778	0.1797	0.1792	
8	189	0.1364	0.1618	0.116		0.0972	0.1719	0.116	
9	193	0.0227	0	0.0666		0.0278	0.0078	0.0666	
10	198	0	0.0294	0.0137		0	0.0156	0.0137	
11	202	0.0303	0.0147	0.0512		0.0278	0.0234	0.0512	
12	210	0.0152	0.0147	0.0085		0	0.0234	0.0085	
13	214	0	0.0147	0	In-river spawners	0	0.0078	0	Natural origin
14	234	0	0	0.0068	Captive brood spawners	0	0	0.0068	Captive brood
15	238	0	0	0.0102	Captive brood spawners	0	0	0.0102	Captive brood
					Supplementation				
16	254	0.0076	0	0	spawners	0	0.0078	0	Natural origin
17	258	0	0	0.0017	Captive brood spawners	0	0	0.0017	Captive brood
number of samples		66	34	293		36	64	293	

Conclusions

In summary, based on the measures of genetic diversity reported here, none of the analyzed groups exhibited a severe loss of diversity. Yet, despite the fact that these groups were recently derived from the same population, there were significant genetic differences observed among the groups (with the exception of the supplementation and in-river spawners). This result is most likely due to the high numbers and distribution of unique alleles and is not surprising given the overall small population size (causing genetic drift to have a strong affect), and the relatively small number of families (varying in the number of individuals per family) of both the supplementation spawners and the captive brood spawners. This study provides evidence both that the captive broodstock program has been an effective method of preserving genetic variation, and that the supplementation hatchery practices (despite using only a small percentage of the entire escapement each year) have been effective in minimizing differences between the hatchery and natural origin fish.

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Literature Cited

- Belkhir, K., Castric, V., and Bonhomme, F. 2002. Identix, a software to test for relatedness in a population using permutation methods. *Mole. Ecol. Notes.* 2:611-614.
- Gallinat, M. P. 2004. Tucannon River Spring Chinook Captive Broodstock Program. BPA 2003 annual report. 39 pages.
- 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/software/fstat.html>.
- Lewis, P. O., and Zaykin, D. 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>
- Raymond, M. and F. Rousset. 1995. GENEPOP (Version 3.3): Population genetics software for exact tests and ecumenicism. *Journal of Heredity.* 86:248-249.
- Rice, W.R. 1989. Analyzing tables of statistical tests. *Evolution* 43:223-225.
- Weir, B.S. and C.C. Cockerham. 1984. Estimating F-statistics for the analysis of population structure. *Evolution* 38:1358-1370.

**Appendix C: Estimated Total Run-Size of
Tucannon River Spring Chinook Salmon (1985-
2004)**

Appendix C. Total estimated run-size of spring chinook salmon to the Tucannon River, 1985-2004.

Run Year	Wild Jacks	Wild Adults	Total Wild	Hatchery Jacks	Hatchery Adults	Total Hatchery	Total Run-Size
1985	0	591	591	0	0	0	591
1986	6	630	636	0	0	0	636
1987	6	576	582	0	0	0	582
1988	19	391	410	19	0	19	429
1989	2	334	336	83	26	109	445
1990	0	494	494	22	238	260	754
1991	3	257	260	99	169	268	528
1992	12	406	418	15	320	335	753
1993	8	309	317	6	266	272	589
1994	0	98	98	5	37	42	140
1995	2	19	21	11	22	33	54
1996	2	145	147	15	70	85	232
1997	0	134	134	3	151	154	288
1998	0	85	85	16	43	59	144
1999	0	3	3	60	182	242	245
2000	14	68	82	16	241	257	339
2001	9	709	718	111	183	294	1,012
2002	9	341	350	11	644	655	1,005
2003	3	245	248	27	169	196	444
2004	0	400	400	22 ^a	151	173	573

^a Three of which are captive brood progeny.

**Appendix D: Stray Hatchery-Origin Spring
Chinook Salmon in the Tucannon River (1990-
2004)**

Appendix D. Summary of identified stray hatchery origin spring chinook salmon that escaped into the Tucannon River (1990-2004).

Year	CWT Code or Fin clip	Agency	Origin (stock)	Release Location / Release River	Number Observed/ Expanded ^a	% of Tuc. Run	
1990	074327	ODFW	Carson (Wash.)	Meacham Cr. / Umatilla River	2 / 5		
	074020	ODFW	Rapid River	Lookingglass Cr. / Grande Ronde	1 / 2		
	232227	NMFS	Mixed Col.	Columbia River / McNary Dam	2 / 5		
	232228	NMFS	Mixed Col.	Columbia River / McNary Dam	1 / 2		
Total Strays					14	1.9	
Total Umatilla River					5	0.7	
1992	075107	ODFW	Lookingglass Cr.	Bonifer Pond / Columbia River	2 / 6		
	075111	ODFW	Lookingglass Cr.	Meacham Cr. / Umatilla River	1 / 2		
	075063	ODFW	Lookingglass Cr.	Meacham Cr. / Umatilla River	1 / 2		
	Total Strays					10	1.3
Total Umatilla River					4	0.5	
1993	075110	ODFW	Lookingglass Cr.	Meacham Cr. / Umatilla River	1 / 2		
	Total Strays					2	0.3
	Total Umatilla River					2	0.3
1996	070251	ODFW	Carson (Wash.)	Imeqes AP / Umatilla River	1 / 1		
	LV clip	ODFW	Carson (Wash.)	Imeqes AP / Umatilla River	1 / 2		
	Total Strays					3	1.3
Total Umatilla River					3	1.3	
1997	103042	IDFG	South Fork Salmon	Knox Bridge / South Fork Salmon	1 / 2		
	103518	IDFG	Powell	Powell Rearing Ponds / Lochsa R.	1 / 2		
	RV clip	ODFW	Carson (Wash.)	Imeqes AP / Umatilla River	3 / 5		
	Total Strays					9	2.6
Total Umatilla River					5	1.4	
1999	091751	ODFW	Carson (Wash.)	Imeqes AP / Umatilla River	2 / 3		
	092258	ODFW	Carson (Wash.)	Imeqes AP / Umatilla River	1 / 1		
	104626	UI	Eagle Creek NFH	Eagle Creek NFH / Clackamas R.	1 / 1		
	LV clip	ODFW	Carson (Wash.)	Imeqes AP / Umatilla River	2 / 2		
	RV clip	ODFW	Carson (Wash.)	Imeqes AP / Umatilla River	8 / 13		
Total Strays					20	8.2	
Total Umatilla River					19	7.8	

^a All CWT codes recovered from groups that were 100% marked were given a 1:1 expansion rate. Groups that were not 100% marked were expanded based on the percentage of unmarked fish. The expansion is based on the percent of stray carcasses to Tucannon River origin carcasses and the estimated total run in the river.

Appendix D (continued). Summary of identified stray hatchery origin spring chinook salmon that escaped into the Tucannon River (1990-2004).

Year	CWT Code or Fin clip	Agency	Origin (stock)	Release Location/Release River	Number Observed/Expanded ^a	% of Tuc. Run
2000	092259	ODFW	Carson (Wash.)	Imeques AP / Umatilla River	4 / 4	
	092260	ODFW	Carson (Wash.)	Imeques AP / Umatilla River	1 / 1	
	092262	ODFW	Carson (Wash.)	Imeques AP / Umatilla River	1 / 3	
	105137	IDFG	Powell	Walton Creek/ Lochsa R.	1 / 3	
	636330	WDFW	Klickitat (Wash.)	Klickitat Hatchery	1 / 1	
	636321	WDFW	Lyons Ferry (Wash.)	Lyons Ferry / Snake River	1 / 1	
	LV clip	ODFW	Carson (Wash.)	Imeques AP / Umatilla River	18 / 31	
	Ad clip	ODFW	Carson (Wash.)	Imeques AP / Umatilla River	2 / 2	
			Total Strays	46	13.6	
			Total Umatilla River	41	12.1	
2001	076040	ODFW	Umatilla R.	Umatilla Hatch. /Umatilla River	1/7	
	092828	ODFW	Imnaha R. & Tribs.	Lookingglass/Imnaha River	1/3	
	092829	ODFW	Imnaha R. & Tribs.	Lookingglass/Imnaha River	1/3	
				Total Strays	13	1.3
			Total Umatilla River	7	0.7	
2002	054208	USFWS	Dworshak	Dworshak NFH/Clearwater	1/29	
	076039	ODFW	Umatilla R.	River	1/8	
	076040	ODFW	Umatilla R.	Umatilla Hatch./Umatilla River	2/16	
	076041	ODFW	Umatilla R.	Umatilla Hatch./Umatilla River	2/16	
	076049	ODFW	Umatilla R.	Umatilla Hatch./Umatilla River	1/8	
	076051	ODFW	Umatilla R.	Umatilla Hatch./Umatilla River	1/8	
	076138	ODFW	Umatilla R.	Umatilla Hatch./Umatilla River	1/8	
	105412	IDFG	Powell	Umatilla Hatch./Umatilla River	1/4	
				Clearwater Hatch./Powell	97	9.7
				Ponds	64	6.4
			Total Strays			
			Total Umatilla River			
2003	100472	IDFG	Salmon R.	Sawtooth Hatch./Nature's Rear.	1/1	
				Total Strays	1	0.2
				Total Umatilla River	0	0.0
2004	Ad clip	Unknown	Unknown ^b	Unknown	6/17	
				Total Strays	17	3.0
				Total Umatilla River^b	17	3.0^b

^a All CWT codes recovered from groups that were 100% marked were given a 1:1 expansion rate. Groups that were not 100% marked were expanded based on the percentage of unmarked fish. The expansion is based on the percent of stray carcasses to Tucannon River origin carcasses and the estimated total run in the river.

^b Based on the mark (Ad clip, no wire), brood year (2000), historical stray rates, and large number of releases (670,570) we believe these fish are probable Umatilla River origin strays.

Appendix E: Historical Hatchery Releases (1985- 2002 Brood Years)

Appendix E. Historical hatchery spring chinook releases from the Tucannon River, 1985-2002 brood years. (Totals are summation by brood year, not by release year.)

Release Year	Brood	Release		CWT Code ^b	Number CWT	Ad-only marked	Additional Tag/location/cross ^c	Lbs	Fish/lb
		Type ^a	Date						
1987	1985	H-Acc	4/6-10	34/42	12,922			2,172	6
Total					12,922				
1988	1986	H-Acc	3/7	33/25	12,328	512		1,384	10
		"	"	41/46	12,095	465		1,256	10
		"	"	41/48	13,097	503		1,360	10
		"	4/13	33/25	37,893	1,456		3,735	10
		"	"	41/46	34,389	1,321		3,571	10
		"	"	41/48	37,235	1,431		3,867	10
Total					147,037	5,688			
1989	1987	H-Acc	4/11-13	49/50	151,100	1,065		16,907	9
Total					151,100	1,065			
1990	1988	H-Acc	3/30-4/10	55/01	68,591	3,007		6,509	11
Total					139,050	6,096			
1991	1989	H-Acc	4/1-12	14/61	75,661	989		8,517	9
Total					97,779	1,278			
1992	1990	H-Acc	3/30-4/10	40/21	51,149		BWT, RC, WxW	4,649	11
		"	"	43/11	21,108		BWT, LC, HxH	1,924	11
		"	"	37/25	13,480		Mixed	1,225	11
Total					85,737				
1993	1991	H-Acc	4/6-12	46/25	55,716	796	VI, LR, WxW	3,714	15
		"	"	46/47	16,745	807	VI, RR, HxH	1,116	15
Total					72,461	1,603			
1993	1992	Direct	10/22-25	48/23	24,883	251	VI, LR, WxW	698	36
		"	"	48/24	24,685	300	VI, RR, HxH	694	36
		"	"	48/56	7,111	86	Mixed	200	36
1994	1992	H-Acc	4/11-18	48/10	35,405	871	VI, LY, WxW	2,591	14
		"	"	49/05	35,469	2,588	VI, RY, HxH	2,718	14
		"	"	48/55	8,277	799	Mixed	648	14
Total					135,830	4,895			
1995	1993	H-Acc	3/15-4/15	53/43	45,007	140	VI, RG, HxH	3,166	14
		"	"	53/44	42,936	2,212	VI, LG, WxW	3,166	14
		P-Acc	3/20-4/3	56/15	11,661	72	VI, RR, HxH	782	15
		"	"	56/17	10,704	290	VI, LR, WxW	733	15
		"	"	56/18	13,705	47	Mixed	917	15
		Direct	3/20-4/3	56/15	3,860	24	VI, RR, HxH	259	15
		"	"	56/17	3,542	96	VI, LR, WxW	243	15
		"	"	56/18	4,537	15	Mixed	303	15
Total					135,952	2,896			
1996	1994	H-Acc	3/16-4/22	56/29	89,437		VI, RR, Mixed	5,123	17.7
		P-Acc	3/27-4/19	57/29	35,334	35	VI, RG, Mixed	2,628	15.2
		Direct	3/27	43/23	5,263		VI, LG, Mixed	369	13.3
Total					130,034	35			

Appendix E (continued). Historical hatchery spring chinook releases from the Tucannon River, 1985-2002 brood years. (Totals are summation by brood year, not by release year.)									
Release Year	Brood	Release		CWT Code ^b	Number CWT	Ad-only marked	Additional Tag/location/cross ^c	Lbs	Fish/lb
		Type ^a	Date						
1997	1995	H-Acc	3/07-4/18	59/36	42,160	40	VI, RR, Mixed	2,411	17.5
		P-Acc	3/24-3/25	61/41	10,045	50	VI, RB, Mixed	537	18.8
		Direct	3/24	61/40	9,811	38	VI, LB, Mixed	593	16.6
Total					62,144	128			
1998	1996	H-Acc	3/11-4/17	03/60	14,308	27	Mixed	902	15.9
		C-Acc	3/11-4/18	61/25	23,065	62	“	1,498	15.8
		“	“	61/24	24,554	50	“	1,557	15.8
		Direct	4/03	03/59	14,101	52	“	863	16.4
Total					76,028	191			
1999	1997	C-Acc	3/11-4/20	61/32	23,664	522	Mixed	1,550	15.6
Total					23,664	522			
2000	1998	C-Acc	3/20-4/26	12/11	125,192	2,747	Mixed	10,235	12.5
Total					125,192	2,747			
2001	1999	C-Acc	3/19-4/25	02/75	96,736	864	Mixed	9,207	10.6
Total					96,736	864			
2002	2000	C-Acc	3/15-4/23	08/87	99,566	2,533 ^e	VI, RR, Mixed	6,587	15.5
Total					99,566	2,533^e			
2002	2000CB	C-Acc	3/15/4/23	63	3,031	24 ^f	CB, Mixed	343	8.9
Total					3,031	24^f			
2002	2001	Direct	5/06	14/29	19,948	1,095	Mixed	170.5	123.4
Total					19,948	1,095			
2002	2001CB	Direct	5/06	14/30	20,435	157	CB, Mixed	124.8	165
Total					20,435	157			
2003	2001	C-Acc	4/01-4/21	06/81	144,013	2,909 ^e	Mixed	11,389	12.9
Total					144,013	2,909^e			
2003	2001CB	C-Acc	4/01-4/21	63	134,401	5,995 ^f	CB, Mixed	10,100	13.9
Total					134,401	5,995^f			
2004	2002	C-Acc	4/01-4/20	17/91	121,774	1,812 ^e	Mixed	10,563	11.7
Total					121,774	1,812^e			
2004	2002CB	C-Acc	4/01-4/20	63	42,875	1,909 ^f	CB, Mixed	3,393	13.2
Total					42,875	1,909^f			

^a Release types are: Tucannon Hatchery Acclimation Pond (H-Acc); Portable Acclimation Pond (P-Acc); Curl Lake Acclimation Pond (C-Acc); and Direct Stream Release (Direct).

^b All tag codes start with agency code 63.

^c Codes listed in column are as follows: BWT - Blank Wire Tag; CB - Captive Brood; VI-Visual Implant (elastomer); LR - Left Red, RR - Right Red, LG-Left Green, RG - Right Green, LY - Left Yellow, RY - Right Yellow, LB - Left Blue, RB - Right Blue; Crosses: WxW - wild x wild progeny, HxH - hatchery x hatchery progeny, Mixed - wild x hatchery progeny.

^d No tag loss data due to presence of both CWT and BWT in fish.

^e VI tag only.

^f No wire.

**Appendix F: Numbers and Density Estimates
(Fish/100 m²) of Juvenile Salmon Counted by
Snorkel Surveys in the Tucannon River in 2004**

Appendix F. Numbers and density estimates of subyearling and yearling natural salmon, and yearling hatchery chinook counted by snorkel surveys in the Tucannon River, 2004.

Stratum	Site ^a	Date	Number of Salmon			Snorkeled Area (m ²)	Density (fish/100m ²)			
			Natural		Hatchery		Natural		Hatchery	
			0+	> 1+	> 1+		0+	> 1+	> 1+	
Marengo	TUC01	7/26	6	0	0	568	1.06	0.00	0.00	
	↓	01A	7/26	13	0	0	632	2.06	0.00	0.00
		TUC02	7/26	6	0	0	518	1.16	0.00	0.00
		02A	7/26	6	0	0	615	0.98	0.00	0.00
		TUC03	7/26	8	0	0	720	1.11	0.00	0.00
Hartsock		03A	7/26	43	0	0	385	11.17	0.00	0.00
	↓	TUC04	7/26	6	0	0	472	1.27	0.00	0.00
		04A	7/26	22	0	0	457	4.81	0.00	0.00
		TUC05	7/26	12	0	0	782	1.53	0.00	0.00
		05A	7/26	38	0	0	520	7.31	0.00	0.00
		TUC06	7/26	29	0	0	560	5.18	0.00	0.00
		06A	7/26	5	0	0	589	0.85	0.00	0.00
		TUC07	7/26	37	0	0	849	4.36	0.00	0.00
		07A	7/26	56	0	0	422	13.27	0.00	0.00
		TUC08	7/26	50	0	0	421	11.88	0.00	0.00
		08A	7/26	1	0	0	516	0.19	0.00	0.00
		TUC09	7/27	0	0	0	630	0.00	0.00	0.00
		09A	7/27	0	0	0	593	0.00	0.00	0.00
		TUC10	8/11	130	3	0	615	21.14	0.49	0.00
	HMA		010A	8/11	59	2	0	404	14.60	0.50
↓		TUC11	8/11	145	3	0	608	23.85	0.49	0.00
		011A	8/11	129	4	0	709	18.19	0.56	0.00
		TUC13	7/27	148	2	0	549	26.96	0.36	0.00
		13A	7/27	61	0	0	663	9.20	0.00	0.00
		TUC14	7/27	102	0	0	528	19.32	0.00	0.00
		14A	7/27	202	4	0	625	32.32	0.64	0.00
		TUC16	7/27	83	2	0	517	16.05	0.39	0.00
		16A	7/27	24	0	0	618	3.88	0.00	0.00
		TUC17	8/10	18	1	0	518	3.47	0.19	0.00
	17A	8/10	99	3	0	665	14.89	0.45	0.00	
	TUC19	8/10	99	2	0	456	21.71	0.44	0.00	
	19A	8/10	45	0	0	771	5.84	0.00	0.00	
	TUC20	8/10	16	0	0	710	2.25	0.00	0.00	
	20A	8/10	38	0	0	566	6.71	0.00	0.00	

Appendix F (continued). Numbers and density estimates of subyearling and yearling natural salmon, and yearling hatchery chinook counted by snorkel surveys in the Tucannon River, 2004

Stratum	Site ^a	Date	Number of Salmon			Snorkeled Area (m ²)	Density (fish/100m ²)		
			Natural		Hatchery		Natural		Hatchery
			0+	> 1+	> 1+		0+	> 1+	> 1+
HMA	TUC21	8/10	61	9	0	671	9.09	1.34	0.00
(cont.)	21A	8/10	21	0	0	625	3.36	0.00	0.00
↓	TUC22	8/11	38	4	0	553	6.87	0.72	0.00
	22A	8/11	13	0	0	442	2.94	0.00	0.00
	TUC23	8/11	39	5	0	555	7.03	0.90	0.00
	23A	8/11	12	1	0	628	1.91	0.16	0.00
Wilderness	TUC24	8/10	33	8	0	403	8.19	1.99	0.00
↓	24A	8/10	46	3	0	424	10.85	0.71	0.00
	TUC25	8/10	0	0	0	325	0.00	0.00	0.00
	25A	8/10	0	1	0	303	0.00	0.33	0.00
	TUC26	8/10	0	1	0	413	0.00	0.24	0.00
	26A	8/10	0	0	0	388	0.00	0.00	0.00
	TUC27	8/10	0	3	0	418	0.00	0.72	0.00
	27A	8/10	0	2	0	340	0.00	0.59	0.00
	TUC28	8/10	0	0	0	274	0.00	0.00	0.00
	28A	8/10	0	0	0	377	0.00	0.00	0.00
Totals			1,999	63	0	26,910			

^a Specific site locations are available by request from the Snake River Lab.

Appendix G: Numbers of Selected Species Captured in the Tucannon River Smolt Trap During the 2004 Outmigration

Appendix G. Numbers of selected species captured in the Tucannon River smolt trap during the 2004 outmigration.

Coho Salmon	Fall Chinook	Bull Trout	Grass Pickerel	Sand Roller	Pink Salmon	Steelhead Smolts	Steelhead Parr	Pacific Lamprey		
								Ammo- coetes	Macrophthal- mia	Adults
224	19,365	18	3	4	1	2,770	1,493	483	258	14

**Appendix H: Recoveries of Coded-Wire Tagged
Salmon Released Into the Tucannon River for the
1985-2000 Brood Years**

Appendix H. Observed and estimated recoveries of coded-wire tagged salmon released into the Tucannon River with percent return to the Tucannon Basin, out-of-basin returns, and estimated survival and exploitation rates for the 1985-2000 brood years. (Data from RMIS database.)

Brood Year	1985		1986		1987	
Smolts Released	12,922		147,037		151,100	
Fish/Lb	6.0		10.0		9.0	
CWT Codes^a	34/42		33/25, 41/46, 41/48		49/50	
Release Year	1987		1988		1989	
Agency (fishery/location)	Observed Number	Estimated Number	Observed Number	Estimated Number	Observed Number	Estimated Number
WDFW						
Tucannon River			30	84	28	130
Kalama R., Wind R.						
Fish Trap - F.W.						
Treaty Troll			1	2		
Lyons Ferry Hatch. ^b	32	38	136	280	53	71
F.W. Sport			1	4		
ODFW						
Test Net, Zone 4	1	1	1	1		
Treaty Ceremonial			2	4	1	2
Three Mile, Umatilla R.						
Spawning Ground						
Fish Trap - F.W.						
F.W. Sport						
Hatchery						
CDFO						
Non-treaty Ocean Troll			1	4		
Mixed Net & Seine						
Ocean Sport						
USFWS						
Warm Springs Hatchery						
Dworshak NFH						
IDFG						
Hatchery						
Total Returns	33	39	172	379	82	203
Tucannon (%)	97.4		96.0		99.0	
Out-of-Basin (%)	0.0		0.0		0.0	
Commercial Harvest (%)	2.6		1.3		1.0	
Sport Harvest (%)	0.0		2.6		0.0	
Survival	0.30		0.26		0.13	

^a WDFW agency code prefix is 63. ^b Fish trapped at TFH and held at LFH for spawning.

Appendix H (continued). Observed and estimated recoveries of coded-wire tagged salmon released into the Tucannon River with percent return to the Tucannon Basin, out-of-basin returns, and estimated survival and exploitation rates for the 1985-2000 brood years. (Data from RMIS database.)						
Brood Year	1988		1989		1990	
Smolts Released	139,050		97,779		85,737	
Fish/Lb	11.0		9.0		11.0	
CWT Codes^a	01/42, 55/01		01/31, 14/61		37/25, 40/21, 43/11	
Release Year	1990		1991		1992	
Agency (fishery/location)	Observed Number	Estimated Number	Observed Number	Estimated Number	Observed Number	Estimated Number
WDFW						
Tucannon River	107	370	61	191	2	6
Kalama R., Wind R.						
Fish Trap - F.W.	1	1				
Treaty Troll			2	2		
Lyons Ferry Hatch. ^b	83	86	55	55	19	19
F.W. Sport	1	4				
ODFW						
Test Net, Zone 4	3	3	2	2		
Treaty Ceremonial	8	17	4	8		
Three Mile, Umatilla R.						
Spawning Ground						
Fish Trap - F.W.						
F.W. Sport						
Hatchery						
CDFO						
Non-treaty Ocean Troll						
Mixed Net & Seine						
Ocean Sport						
USFWS						
Warm Springs Hatchery						
Dworshak NFH	1	1				
IDFG						
Hatchery						
Total Returns	204	482	124	258	21	25
Tucannon (%)	94.6		95.3		100.0	
Out-of-Basin (%)	0.4		0.0		0.0	
Commercial Harvest (%)	4.1		3.9		0.0	
Sport Harvest (%)	0.8		0.8		0.0	
Survival	0.35		0.26		0.03	

^aWDFW agency code prefix is 63. ^b Fish trapped at TFH and held at LFH for spawning.

Appendix H (continued). Observed and estimated recoveries of coded-wire tagged salmon released into the Tucannon River

with percent return to the Tucannon Basin, out-of-basin returns, and estimated survival and exploitation rates for the 1985-2000 brood years. (Data from RMIS database.)						
Brood Year	1991		1992		1992	
Smolts Released	72,461		56,679		79,151	
Fish/Lb	15.0		36.0		14.0	
CWT Codes^a	46/25, 46/47		48/23, 48/24, 48/56		48/10, 48/55, 49/05	
Release Year	1993		1993		1994	
Agency (fishery/location)	Observed Number	Estimated Number	Observed Number	Estimated Number	Observed Number	Estimated Number
WDFW						
Tucannon River					11	34
Kalama R., Wind R.						
Fish Trap - F.W.						
Treaty Troll						
Lyons Ferry Hatch. ^b	24	24	2	2	45	49
F.W. Sport						
ODFW						
Test Net, Zone 4						
Treaty Ceremonial	1	3			1	1
Three Mile, Umatilla R.						
Spawning Ground	1	3			2	4
Fish Trap - F.W.			1	1	5	9
F.W. Sport					2	2
Hatchery						
CDFO						
Non-treaty Ocean Troll						
Mixed Net & Seine			1	2		
Ocean Sport						
USFWS						
Warm Springs Hatchery					3	3
Dworshak NFH						
IDFG						
Hatchery						
Total Returns	26	30	4	5	69	102
Tucannon (%)	80.0		40.0		81.4	
Out-of-Basin (%)	10.0		20.0		15.7	
Commercial Harvest (%)	10.0		40.0		0.9	
Sport Harvest (%)	0.0		0.0		2.0	
Survival	0.04		0.01		0.13	

^a WDFW agency code prefix is 63.

^b Fish trapped at TFH and held at LFH for spawning.

Appendix H (continued). Observed and estimated recoveries of coded-wire tagged salmon released into the Tucannon River with percent return to the Tucannon Basin, out-of-basin returns, and estimated survival and exploitation rates for the 1985-2000 brood years. (Data from RMIS database.)						
Brood Year	1993		1994		1995	
Smolts Released	135,952		130,034		62,016	
Fish/Lb	14.0-15.0		13.0-18.0		17.0-19.0	
CWT Codes^a	56/15, 56/17-18, 53/43-44		43/23, 56/29, 57/29		59/36, 61/40, 61/41	
Release Year	1995		1996		1997	
Agency (fishery/location)	Observed Number	Estimated Number	Observed Number	Estimated Number	Observed Number	Estimated Number
WDFW						
Tucannon River Kalama R., Wind R. Fish Trap - F.W. Treaty Troll	42	138	3	8	36	92
Lyons Ferry Hatch. ^b F.W. Sport	66	138	21	24	94	93
ODFW						
Test Net, Zone 4 Treaty Ceremonial Three Mile, Umatilla R. Spawning Ground	3	3			1	1
Fish Trap - F.W. F.W. Sport Hatchery	1	1			1	1
CDFO						
Non-treaty Ocean Troll Mixed Net & Seine Ocean Sport	1	3				
USFWS						
Warm Springs Hatchery Dworshak NFH						
IDFG						
Hatchery						
Total Returns	117	287	24	32	132	187
Tucannon (%)	96.2		100.0		98.9	
Out-of-Basin (%)	1.7		0.0		1.1	
Commercial Harvest (%)	1.0		0.0		0.0	
Sport Harvest (%)	1.0		0.0		0.0	
Survival	0.21		0.02		0.30	

^a WDFW agency code prefix is 63.

^b Fish trapped at TFH and held at LFH for spawning.

Appendix H (continued). Observed and estimated recoveries of coded-wire tagged salmon released into the Tucannon River with percent return to the Tucannon Basin, out-of-basin returns, and estimated survival and exploitation rates for the 1985-2000 brood years. (Data from RMIS database.)						
Brood Year	1996		1997		1998	
Smolts Released	76,028		23,509		124,093	
Fish/Lb	16.0		16.0		13.0	
CWT Codes^a	03/59-60, 61/24-25		61/32		12/11	
Release Year	1998		1999		2000	
Agency (fishery/location)	Observed Number	Estimated Number	Observed Number	Estimated Number	Observed Number	Estimated Number
WDFW						
Tucannon River	43	139	17	85	147	680
Kalama R., Wind R.						
Fish Trap - F.W.						
Treaty Troll						
Lyons Ferry Hatch. ^b	96	99	44	46	83	121
F.W. Sport					3	13
Non-treaty Ocean Troll					1	2
ODFW						
Test Net, Zone 4					1	1
Treaty Ceremonial						
Three Mile, Umatilla R.						
Spawning Ground					1	1
Fish Trap - F.W.	1	1	2	2	7	9
F.W. Sport					2	4
Hatchery	2	2	1	1		
Columbia R. Gillnet			7	22	32	87
Columbia R. Sport			2	15	17	94
CDFO						
Non-treaty Ocean Troll						
Mixed Net & Seine						
Ocean Sport						
USFWS						
Warm Springs Hatchery						
Dworshak NFH						
IDFG						
Hatchery	1	1	1	--		
Total Returns	143	242	74	171	294	1,012
Tucannon (%)	98.3		76.6		79.2	
Out-of-Basin (%)	1.7		1.8		1.0	
Commercial Harvest (%)	0.0		12.9		8.9	
Sport Harvest (%)	0.0		8.8		11.0	
Survival	0.32		0.73		0.82	

^a WDFW agency code prefix is 63.

^b Fish trapped at TFH and held at LFH for spawning.

Appendix H (continued). Observed and estimated recoveries of coded-wire tagged salmon released into the Tucannon River with percent return to the Tucannon Basin, out-of-basin returns, and estimated survival and exploitation rates for the 1985-2000 brood years. (Data from RMIS database.)						
Brood Year	1999		2000 ^c			
Smolts Released	97,600		102,099			
Fish/Lb	10.6		15.5			
CWT Codes^a	02/75		08/87			
Release Year	2001		2002			
Agency (fishery/location)	Observed Number	Estimated Number	Observed Number	Estimated Number	Observed Number	Estimated Number
WDFW						
Tucannon River	2	12	2	12		
Kalama R., Wind R.						
Fish Trap - F.W.						
Treaty Troll						
Lyons Ferry Hatch. ^b	5	9	4	4		
F.W. Sport						
Non-treaty Ocean Troll						
ODFW						
Test Net, Zone 4						
Treaty Ceremonial						
Three Mile, Umatilla R.						
Spawning Ground						
Fish Trap - F.W.						
F.W. Sport						
Hatchery						
Columbia R. Gillnet	1	3				
Columbia R. Sport						
CDFO						
Non-treaty Ocean Troll						
Mixed Net & Seine						
Ocean Sport						
USFWS						
Warm Springs Hatchery						
Dworshak NFH						
IDFG						
Hatchery						
Total Returns	8	24	6	16		
Tucannon (%)	87.5		100.0			
Out-of-Basin (%)	0.0		0.0			
Commercial Harvest (%)	12.5		0.0			
Sport Harvest (%)	0.0		0.0			
Survival	0.02		0.02			

^a WDFW agency code prefix is 63.

^b Fish trapped at TFH and held at LFH for spawning.

^c Data for the 2000 brood year is incomplete.

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Office of External Programs
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Arlington, VA 22203