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IDAHO SUPPLEMENTATION STUDIES

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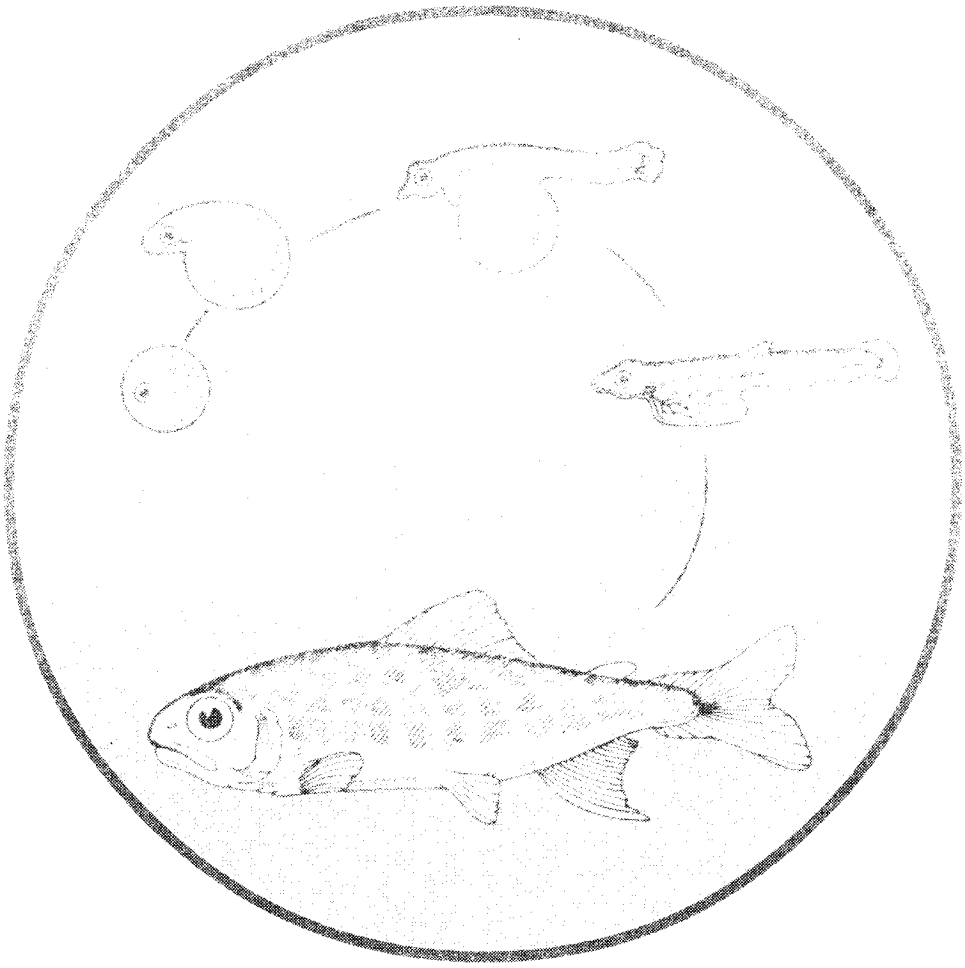

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IDAHO SUPPLEMENTATION STUDIES

ANNUAL REPORT 1994

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ABSTRACT

Adult and jack chinook salmon escapement were indexed by redd counts and weir returns. Escapement in 1994 was low and in some cases approached the lowest on record.

Although stream flow conditions and parr abundance were conducive to precise parr population estimates, some streams continued to exhibit wide confidence intervals. Different methods used to calculate the estimates yielded inconsistent results with regard to increasing or decreasing the population estimate and improving the precision of the estimates. No single method appeared definitively better for all streams.

Emigrant traps captured 78,138 chinook salmon fry, parr, and smolts in 1994. Application of a weekly trap efficiency adjusted for stream flow produced emigration estimates that were up to 30% larger than when a seasonal trap efficiency was used.

Detection rates for smolts tagged in some streams were similar to detection rates for parr tagged during the fall of the previous year. This was unexpected because overwinter mortality usually results in a lower detection rate for fall-tagged fish.

Low escapement in 1994 severely hampered Idaho Supplementation Studies (ISS) broodstock development. The inability to develop local broodstocks for supplementation is the most important factor threatening the implementation of the ISS.

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INTRODUCTION

The Idaho Supplementation Studies (ISS) was developed to help define the potential role of supplementation in managing Idaho's anadromous fisheries (IDFG 1991) and as a recovery tool for Snake River basin chinook salmon (Northwest Power Planning Council 1987; Supplementation Technical Workgroup 1988). Supplementation was defined by the Regional Assessment of Supplementation Project (RASP) group as the use of artificial propagation in the attempt to maintain or increase natural production while maintaining the long term fitness of the target population, and keeping the ecological and genetic impacts on non-target populations within specified biological limits (RASP 1992).

The experimental design for the ISS was published in 1991 (Bowles and Leitzinger 1991). By 1992, data was being collected on most ISS study streams (Leitzinger et al. 1993). Research associated with this study will help determine the best hatchery practices (e.g., broodstock, rearing and release strategies, etc.) for rebuilding natural populations of chinook salmon in various streams, and the effects of these hatchery activities on target and non-target natural anadromous and resident populations. Ultimately, the goal of the ISS is to determine if hatchery supplementation is a viable means of rebuilding natural populations of Idaho's chinook salmon to fishable levels (Idaho Department of Fish and Game 1991). The ISS is designed to extend at least to the year 2007.

OBJECTIVES

1. Monitor and evaluate the effects of supplementation with hatchery-reared smolts and presmolts on naturally-produced presmolt and smolt numbers and resulting spawning escapement of naturally-produced chinook salmon.

2. Monitor and evaluate changes in natural productivity and genetic composition of target and adjacent populations following supplementation.

3. Determine which supplementation strategies (broodstock and release stage) provide the quickest and highest response in natural production without adverse effects on productivity.

4. Develop supplementation recommendations.

The ISS is broad in scope, including streams throughout the Salmon River and Clearwater River drainages. As a result, data collection responsibilities have been assigned to a number of different agencies and tribes. This report deals primarily with data and activities collected and performed by Idaho Department of Fish and Game (IDFG) personnel.

This document reports adult and jack escapement, natural production of juvenile chinook, PIT tag detections of migrating juveniles at Lower Snake River dams, and ISS related hatchery chinook releases for the period January 1, 1994 through December 31, 1994. Baseline genetic information from chinook salmon collected in 1993 and 1994 is presented under a separate cover by the Genetics Unit of the Washington Department of Fish and Wildlife and is attached as Appendix A. The ISS experimental design provides a more detailed discussion of these evaluation points (Bowles and Leitzinger 1991). To provide a more

comprehensive presentation and analysis of the data collected by the ISS, a report will be produced in 1997 assimilating all data collected by the ISS cooperators through 1996. The exceptions are the genetic and behavioral aspects of the ISS objectives which will be addressed under separate contracts conducted by other entities.

Study Area

The ISS research effort incorporates treatment and control streams throughout the Salmon River drainage (Figure 1, Table 1) and Clearwater River drainage (Figure 2, Table 1).

Most study streams are relatively sterile, draining granitic parent material associated with the Idaho batholith (IDFG et al. 1990; Nez Perce Tribe (NPT) and IDFG 1990). Exceptions are the relatively fertile Lemhi River and Pahsimeroi River basins in the eastern Salmon River drainage. These streams originate in basaltic parent material and are spring fed.

Study streams are predominantly low to moderate gradient "headwater" streams with B- and C-channel characteristics (Rosgen 1985). Water quality is generally high with minimal contaminants and acceptable water temperatures. Habitat quality is adequate to support chinook salmon, although sedimentation, channelization, irrigation withdrawal, and riparian degradation affects many streams (IDFG et al. 1990; NPT and IDFG 1990).

Fish communities are similar throughout the study streams. Anadromous fish include wild, natural, and hatchery-produced spring or summer chinook salmon *Oncorhynchus tshawystscha* and summer steelhead *O. mykiss*. Resident fish include bull trout *Salvelinus confluentus*, cutthroat trout *O. clarki*, rainbow trout *O. mykiss*, brook trout *S. fontinalis*, mountain whitefish *Prosopium williamsoni*, northern squawfish *Ptychocheilus oregonensis*, redside shiner *Richardsonius balteatus*, sculpin *Cottus spp.*, dace *Rhinichthys spp.*, and suckers *Catostomus spp.* Pacific lamprey *Lampetra tridentata* occur in disjunct areas of the Salmon River and Clearwater River drainages.

MATERIALS AND METHODS

Weir Returns

Weirs designed to capture adult and jack chinook salmon, were operated in South Fork Salmon River, Marsh Creek, Pahsimeroi River, upper Salmon River, Crooked River, Red River, and Crooked Fork Creek to capture adult chinook salmon. All fish captured at Marsh Creek, Pahsimeroi River, and Crooked Fork Creek were passed above the weir to spawn naturally. Varying proportions of the fish returning to the other weirs were kept for broodstock or passed above the weir to spawn naturally.

Redd Surveys

Redd surveys (Hassemer 1991) were conducted in all study streams from mid-August through mid-October. Most streams were surveyed in ISS index areas two or three times using

ground counts. One-time aerial surveys were conducted on other streams. Redds observed during ground surveys were flagged to avoid duplicate counts. All carcasses encountered were measured (fork length) and sexed. Where possible, unspent eggs were counted to determine the degree of egg retention. After data were collected, the tail was cut off at the caudal peduncle to prevent counting the carcass twice.

Spring and Summer/Fall Emigrants

Juvenile traps were operated in South Fork Salmon River, Marsh Creek, Lemhi River, Pahsimeroi River, upper Salmon River, Crooked River, Red River, and Crooked Fork Creek. Traps were typically located below the primary chinook spawning grounds.

In most streams, emigrating juvenile chinook were trapped during the spring (about mid-March through mid-June) and summer/fall (about mid-August through mid-November) using either rotary screw traps (EG Solutions, Corvallis, Oregon) or inclined plane (humphries) traps. Exceptions were the Lemhi River, trap which was operated continuously from mid-March through mid- November, and the Pahsimeroi River trap, which in addition to spring trapping was operated from mid-September through late-December due to later migration timing (personal communication, Kurtis Plaster, IDFG, Nampa Fisheries Research).

Chinook salmon were removed from the trap daily and anesthetized with MS-222. Length and weight were recorded and chinook salmon down to 52 mm fork length (FL) were tagged with a PIT tag. PIT tagging procedures were defined by Kiefer and Forster (1991) and the PIT Tag Steering Committee (1992). PIT tagging data was recorded following methods outlined in Prentice et al. 1990. PIT-tagged chinook salmon were placed in flow-through containers located in the stream and released at dusk. Newly tagged fish were released upstream of the trap at least above the next riffle to determine trap efficiency. Previously tagged (recaptured) fish were released downstream of the trap.

The emigrant estimate was arrived at by dividing fish trapped (excluding recaptured fish) during the entire trapping period (spring or summer/fall) by the trap efficiency for the entire trapping period. Trap efficiency was calculated by dividing the number of recaptured fish over the entire trapping period by the number of marked fish released above the trap over the entire trapping period. Fall emigrants in the Pahsimeroi River, Red River, and Crooked Fork Creek were also estimated by using a weekly efficiency. This method was identical to the one used above with the exception that trap efficiency and the number of emigrants past the trap were estimated for shorter periods of time. Generally, the data was divided into seven-day periods which were then adjusted for conditions which could change the efficiency of the trap such as stream flow. Trap efficiency and emigrants past the trap were estimated for these shorter periods of time. The smaller estimates were summed to estimate the total number of emigrants past the trap.

A PIT tagging goal of at least 500 spring migrants and 700 fall migrants per study stream was set (Bowles and Leitzinger 1991) to ensure at least 60 detections at the lower Snake River dams for statistical analysis (Kiefer and Forster 1990; Buettner and Nelson 1990).

All other captured salmonids were identified, measured, and released below the trap. Non-salmonid fish were identified, counted, and released below the trap. Data on non-target species are stored at the IDFG Nampa Research office.

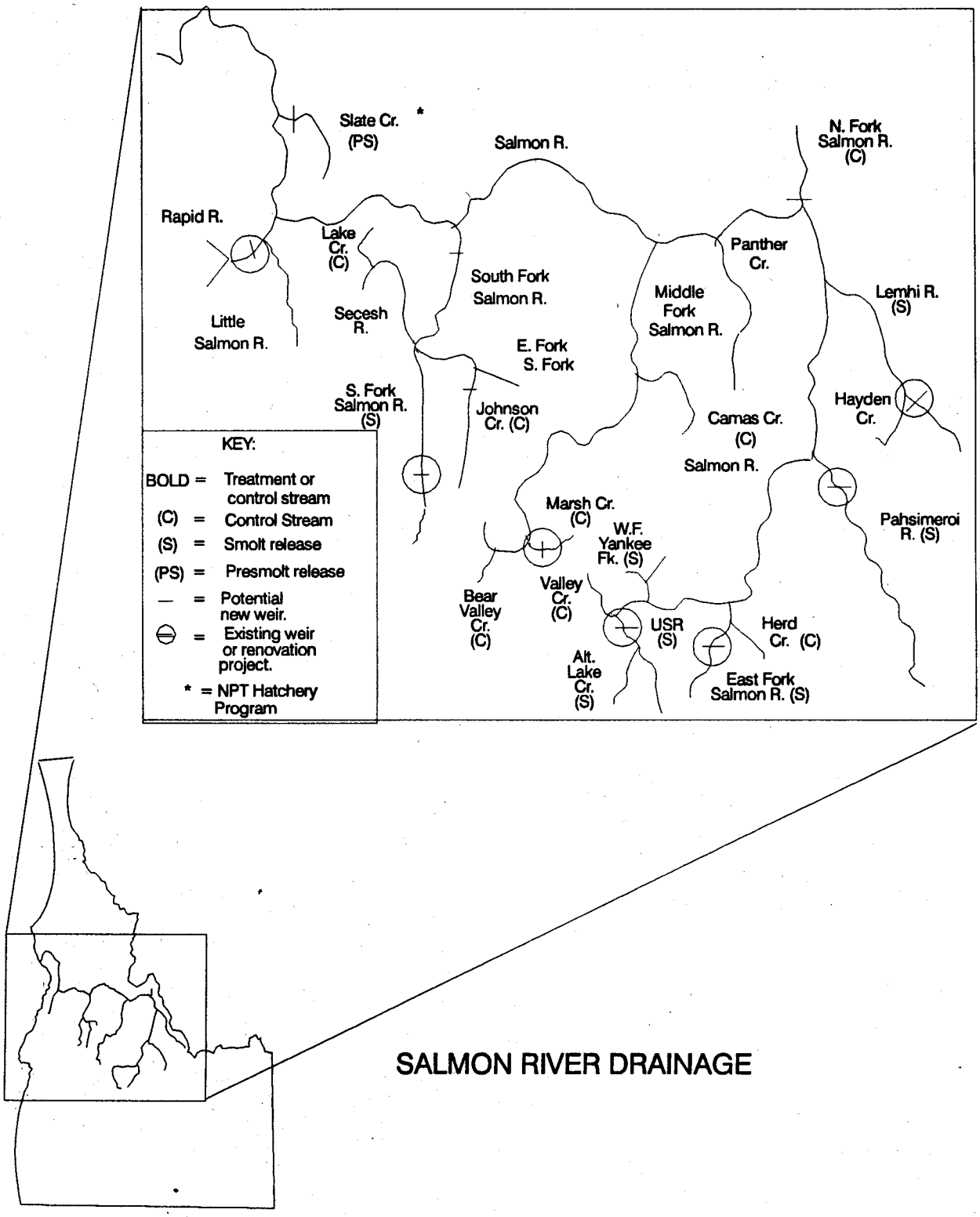
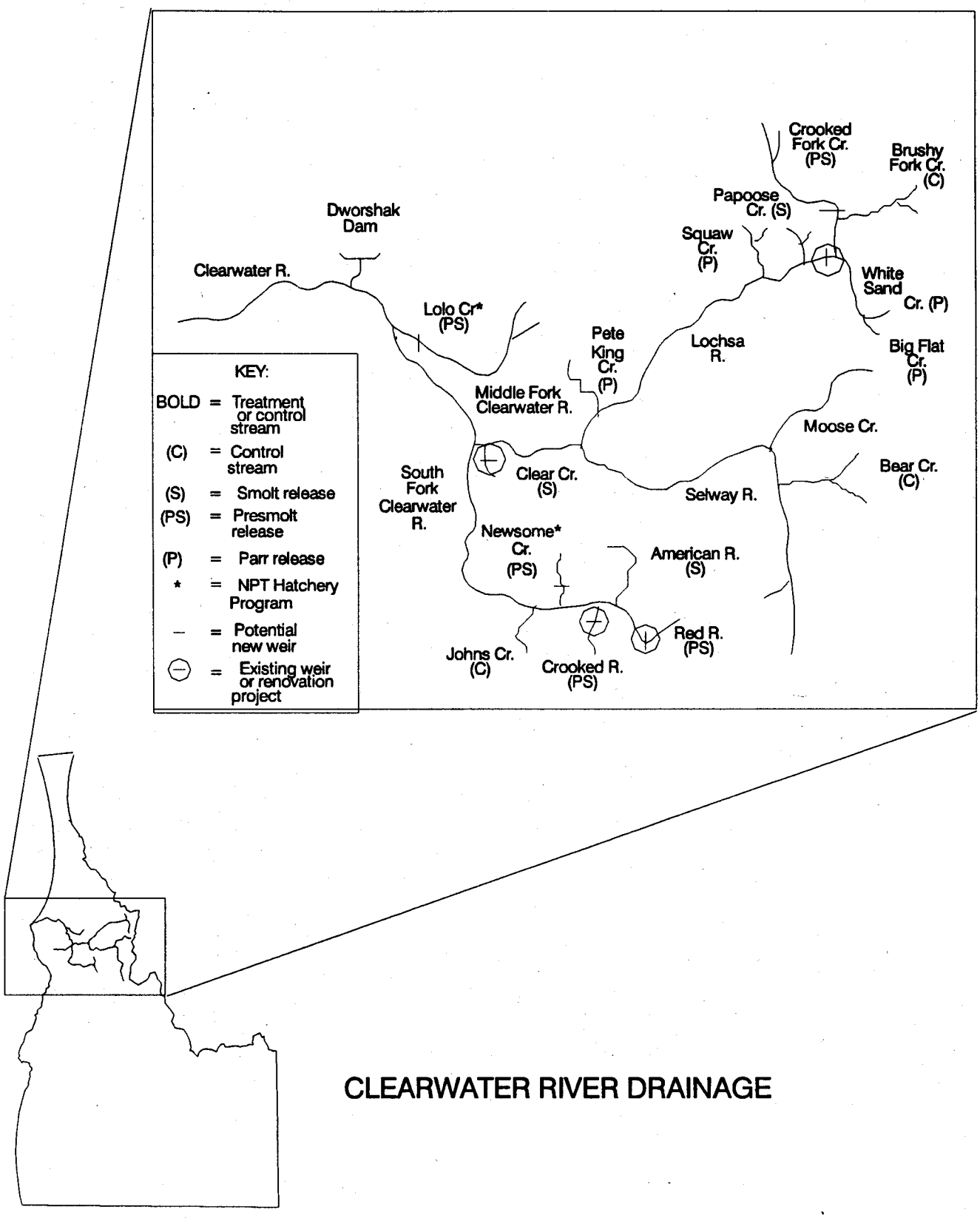


Figure 1. Treatment and control streams in the Salmon River drainage associated with Idaho Supplementation Studies.

Table 1. ISS study streams and responsible agencies, 1994.

Agency	Stream	Treatment/ control (T/C)
IDFG Idaho supplementation studies research crew	Marsh Creek	C
	Pahsimeroi River	T
	Crooked Fork Creek	T
	Brushy Fork Creek	C
	White Sand Creek	T
	Big Flat Creek	T
IDFG Southwest Region	Sulphur Creek	C
IDFG Salmon Region	North Fork Salmon River	C
	Lemhi River	T
IDFG McCall Region	Johnson Creek	C
IDFG Clearwater Region	American River	T
	Red River	T
	Johns Creek	C
	White Cap Creek	C
IDFG Intensive smolt monitoring project	Crooked River	T
	Alturas Lake Creek	T
	Upper Salmon River	T
United States Fish and Wildlife Service	Pete King Creek	T
	Clear Creek	T
Nez Perce Tribe	Lolo Creek	T
	Squaw Creek	T
	Papoose Creek	T
	Newsome Creek	T
	Slate Creek	T
	Secesh River/Lake Creek	C
Shoshone-Bannock Tribes	Valley Creek	C
	West Fork Yankee Fork River	T
	East Fork Salmon River	T
	Herd Creek	C
	South Fork Salmon River	T
	Bear Valley Creek	C



CLEARWATER RIVER DRAINAGE

Figure 2. Treatment and control streams in the Clearwater River drainage associated with Idaho Supplementation Studies.

Summer Parr Abundance

Chinook salmon parr abundance was estimated during July and August through mask and snorkel counts in seven streams in the Salmon River drainage and seven streams in the Clearwater River drainage.

Date, time, water temperature, and visibility were recorded. Global positioning site coordinates of reach boundaries were recorded where possible. Heavy streamside canopy and steep canyon walls prevented coordinates from being established for some reaches. Juvenile chinook were counted and identified as age 0 or 1. Salmonids other than chinook were identified and recorded by species and inch class. The presence of non-game fish was also recorded.

Streams were divided into strata based on stream morphology. Confined, steep gradient reaches were considered Type B strata and meandering, flatter gradient reaches were considered Type C strata (Rosgen 1985). Stratum length was determined by using Environmental Protection Agency (EPA) reach information or IDFG data. Representative stream reaches were snorkeled throughout the stratum. Reach length was measured and an average width was calculated based on at least three width measurements.

The chinook parr population was calculated for each stratum by the following method:

Total Area of Stratum = (Total length of stratum)(Mean width of reaches snorkeled)

Number of Possible Reaches Within the Stratum = $\frac{\text{(Total length of stratum)}}{\text{(Mean length of reaches snorkeled)}}$

Average Area of all Possible Reaches = $\frac{\text{(Total Area)}}{\text{(Number of possible reaches within stratum)}}$

Adjusted Number of Parr for Individual Reaches Snorkeled = $\frac{\text{(Number of parr observed)(Average area of possible reaches)}}{\text{(Area of actual reaches snorkeled)}}$

Population Estimate for Stratum = (Mean number of adjusted parr for stratum sampled)(Number of possible reaches within the stratum)

Confidence Interval for Stratum = $\frac{\text{Pop est} \pm (\text{t value}_{(n-1df)})(\text{Std dev of chin. between reaches})}{\text{Square root of the number of reaches}}$

The chinook parr population of the stream was calculated by adding the population estimates for all strata within the stream (strata method).

In an effort to narrow the confidence intervals around the population estimates arrived at by the strata method, another method was applied to most streams beginning in 1993. This method entailed recording fish counts by habitat type (pool, run, riffle, or pocket water) in each stratum (habitat by stratum method). The proportion of each habitat type in each stratum was estimated by categorizing the habitat throughout the stratum every standard unit of length (e.g., every 40 paces) and extrapolating the resulting frequencies over the entire stratum. A population estimate for each habitat type within each stratum was calculated. These population estimates by habitat type were then summed across all habitat types and strata to produce the population estimate.

In Johnson Creek, American River, Red River, and White Cap Creek an additional population estimate was derived as described above except population estimates for each habitat type were calculated independent of strata (habitat method).

A fourth method was used in Johnson Creek in 1994. Rather than partitioning the stream based on stream channel characteristics, Type B or Type C strata (Rosgen 1985), Johnson Creek was divided into six strata based on the presence or absence of spawning adult chinook salmon in 1993. Population estimates of chinook salmon parr in 1994 were then calculated for these six strata as described above.

PIT Tagging Rearing Parr

Chinook salmon parr were collected with a beach seine in eight streams in the Salmon River drainage and six streams in the Clearwater River drainage during July and August. Collection and PIT tagging occurred only when water temperatures were less than 20°C. Following tagging, parr were dispersed throughout the area from which they were captured.

Detections

A portion of the chinook salmon smolts traveling to the ocean pass through PIT tag detection facilities (interrogation sites) located in Snake River and Columbia River dams. These facilities differ in design and function, and operate at different efficiencies. Detection efficiency varies from year-to-year for any given detection facility depending upon the use and timing of spill.

PIT tag detections at Snake River and Columbia River dams for migratory year 1994 were obtained from the PIT tag information system. Interrogation sites were Lower Granite Dam, Little Goose Dam, Lower Monumental Dam, and McNary Dam.

Hatchery Releases

Supplementation fish were reared in existing hatcheries and satellite facilities. Hatchery personnel incorporated adult allocation and spawning protocols identified in the ISS experimental design (Bowles and Leitzinger 1991). A minimum of 500 smolts and 1,000 parr were PIT-tagged for each stream release. All chinook salmon were marked with a right or left pelvic fin clip to ensure differentiation from naturally-produced adults during broodstock collection in future years. Supplementation fish were released on-station from the Pahsimeroi River Hatchery and Sawtooth Hatchery (upper Salmon River). Off-station releases occurred in South Fork Salmon River, upper Salmon River, Crooked River, Red River (acclimation ponds used), Crooked Fork Creek, White Sand Creek, and Big Flat Creek. Releases into White Sand Creek and Big Flat Creek were from a helicopter; all other releases were trucked.

RESULTS

Adult and Jack Escapement

During return year 1994, the greatest number of chinook salmon returned to the South Fork Salmon River weir and upper Salmon River weir with 455 and 90 adults captured respectively (Table 2). Marsh Creek and Crooked Fork Creek had the fewest returning chinook salmon with 16 and 0 fish captured, respectively (Table 2).

Redd counts in 1994 were lower than in 1993 (Table 3). The South Fork Salmon River had the most redds with 76 (Table 3). Johnson Creek had the next highest redd count with 26 followed by Red River and upper Salmon River with 23 and 22 redds, respectively.

Chinook Salmon Spring Emigrants

Crooked Fork Creek had the greatest estimated number of smolts migrating past the trap (9,371), followed by South Fork Salmon River (7,617) (Table 4). An estimated 5,430 chinook salmon fry migrated past the Pahsimeroi trap. Chinook salmon fry in the other study streams were not large enough to tag during most of their migration, consequently, an emigrant estimate for the other streams was not possible. A total of 3,455 chinook salmon smolts and fry were PIT-tagged during the spring (Table 5). Fifty-six percent (1,935) of these fish were tagged in the South Fork Salmon River.

During the spring trapping season for all streams sampled, 5,649 smolts were trapped and from these 80 died for a mortality rate of 1.4% (Table 4). During the same period, 19,481 fry were trapped and 225 died for a mortality rate of 1.1%.

Table 2. Adult chinook salmon weir returns in 1994.

Weir location	Weir operational	Males		Females	
		Jacks	Adults	Jills	Adults
South Fork Salmon River	6/7-9/16	72	178	0	277
Marsh Creek	6/9-8/24	0	9	0	7
Pahsimeroi River	6/9-8/24	9	11	0	16
Upper Salmon River	5/31-10/26	6	50	0	40
Crooked River	6/2-9/5	0	8	1	18
Red River	6/1-9/11	0	18	0	13
Crooked Fork Creek	6/9-10/1	0	0 [a]	0	0 [a]

[a] Two adult chinook salmon were observed about 400 m below the weir.

Table 3. Number of chinook salmon redds observed in ISS index areas, 1992-1994.

Stream	1994	1993	1992
South Fork Salmon River[a]	76	694 [b]	454 [b]
Johnson Creek	26 [c]	170 [d]	87 [e]
Sulphur Creek	0	84	1
Marsh Creek	9	47	66
North Fork Salmon River	3	17	12
Lemhi River	20	37	15 [f]
Pahsimeroi River	19 [g]	63	32
Upper Salmon River	22 [f]	ND	ND
South Fork Clearwater River	8 [f]	ND	ND
Ten Mile Creek	0 [f]	ND	ND
Johns Creek	0 [f]	ND	ND
Newsome Creek	0 [f]	ND	ND
Crooked River	4	ND	ND
American River	9	209 [h]	5
Red River	23	69	44
South Fork Red River	2	ND	ND
White Cap Creek	2 [f]	6	2
Crooked Fork Creek	0	13	13
Brushy Fork Creek and Spruce Creek	0 [f,i]	25	7

[a] The reach surveyed was from the adult weir to upper Stolle Meadows, about 1,000 m above the mouth of Rice Creek.
[b] One hundred pairs of adult chinook salmon were outplanted in Stolle Meadows.
[c] Includes 23 redds between Deadhorse Rapids and Moose Creek, surveyed by the Nez Perce tribe.
[d] Lower Johnson Creek had 126 redds, upper Johnson Creek had 44 redds.
[e] Lower Johnson Creek had 76 redds, upper Johnson Creek had 11 redds.
[f] Aerial survey.
[g] Includes 16 redds counted in an aerial survey, 2.4 km upstream of the hatchery to the town of May.
[h] One hundred and sixty -five pairs of adult chinook salmon were outplanted from Rapid River hatchery.
[i] A single adult chinook salmon was observed in Brushy Fork Creek during snorkeling activities prior to the beginning of redd counts.

Table 4. Wild and natural chinook salmon trapped by lifestage, number of mortalities, and spring emigrant estimates from data collected with emigrant traps, 1994.

Stream	Lifestage Smolt/Fry	Number Trapped	Number Mortalities	Emigrant Estimate
South Fork Salmon River	Smolt	2,276	69	7,617
	Fry	15,559	173	NE
Marsh Creek	Smolt	165	0	1,680
	Fry	1,165	12	NE
Lemhi River	Smolt	72	0	NE
	Fry	725	0	NE
Pahsimeroi River	Smolt	262	7	3,507
	Fry	669	14	5,430
Upper Salmon River	Smolt	239	1	4,345
	Fry	570	4	NE
Crooked River	Smolt	1,729	0	4,223
	Fry	231	0	NE
Red River	Smolt	385	0	2,567
	Fry	22	0	NE
Crooked Fork Creek	Smolt	521	3	9,371
	Fry	540	22	NE

Table 5. Summary of chinook salmon PIT-tagged in streams studied by the Idaho Fish and Game for the Idaho Supplementation Studies in the spring[a], summer[b], and summer/fall[a] of 1994.

	Spring	Summer	Summer/Fall
South Fork Salmon River	1,931	1,570	2,427
Johnson Creek	0	193	0
Sulphur Creek	0	729	0
Marsh Creek	163	1,575	3,598
Capehorn Creek	0	1,444	0
North Fork Salmon River	0	520	0
Lemhi River	122	0	1,730 [c]
Pahsimeroi River	509	999	1,847
Upper Salmon River	239	3,584	1,141
Crooked River	436	2,242	1,165
American River	0	696	0
Red River	385	650	1,543
White Cap Creek	0	85	0
Crooked Fork Creek	345	193	2,709
Brushy Fork Creek	0	127	0

[a] Chinook salmon during these periods were captured with an emigrant trap. Chinook salmon captured during the spring are primarily chinook salmon smolts but may also include fry.
[b] Chinook salmon were captured with a beach seine or electrofisher. Fish were tagged by Idaho Department of Fish and Game personnel or National Marine Fisheries Service personnel.
[c] These fish were captured during June 1- November 30.

Chinook Salmon Summer Parr

Four of the 12 streams for which alternative methods of calculating rearing parr populations were used resulted in a significantly different population estimate (nonoverlapping confidence intervals) (Table 6). There was nearly a five-fold difference in the point estimate for Sulphur Creek with the habitat by strata method resulting in the higher estimate. Conversely, the strata method resulted in a point estimate that was almost twice as high as the habitat by strata method in Crooked Fork Creek. No one method resulted in consistently narrower confidence intervals than another.

Idaho Department of Fish and Game and National Marine Fisheries Service personnel captured and PIT tagged 14,607 chinook salmon parr in IDFG ISS study streams during the summer of 1994 (Table 5).

Chinook Salmon Summer/Fall Emigrants

Crooked Fork Creek had the largest estimated number of emigrating parr past the trap (84,454), followed by Crooked River (17,547), and Pahsimeroi River (17,287) (Table 7). A total of 16,160 emigrating chinook salmon juveniles were PIT-tagged (Table 5). When weekly trap efficiencies were applied to emigrating chinook parr in Pahsimeroi River, Red River, and Crooked Fork Creek, the respective emigrant estimates increased by 16%, 28%, and 30%. During the fall trapping season for all streams sampled, approximately 53,030 chinook parr were trapped. The mortality rate for summer/fall trapping was 0.2%.

While collecting data for summer parr population estimates, and prior to screw trap installation, snorkelers observed large numbers of chinook salmon parr moving downstream. Consequently, the actual number of summer/fall emigrants was probably higher than estimated for some streams.

Releases of Hatchery Chinook

The following release numbers reflect hatchery chinook salmon released in 1994 for the purpose of the ISS. Additional hatchery chinook may have been released in some of these streams for general hatchery production purposes. Hatchery-reared chinook salmon smolts were released into the Pahsimeroi River and South Fork Salmon River (Table 8). Chinook salmon parr were released into upper Salmon River, Crooked River, Red River, White Sand Creek and Big Flat Creek. Chinook salmon parr were also released into Pete King Creek and Squaw Creek as a component of the ISS being conducted by the Idaho Cooperative Fish and Wildlife Research Unit (Table 8). All hatchery-produced ISS chinook salmon were fin-clipped (Table 8).

Table 6. Chinook salmon parr population estimates (90% confidence interval expressed as percent of population estimate) as determined by mask and snorkel counts and by method of calculation, 1994.

	Population estimate (PE) by method							
Stream	Strata method	90% CI as % of PE	Habitat by strata method	90% CI as % of PE	Habitat method	90% CI as % of PE	Proximity to redd	90% CI as % of PE
Johnson Creek	123,794 ± 45,804	37	158,820 ± 39,705	25	135,843 ± 44,828	33	111,944 ± 24,628	22
Sulphur Creek	9,266 ± 2,687	29	45,976 ± 12,414	27	NE	NE	NE	NE
Marsh Creek	15,607 ± 3,277	21	31,587 ± 13,267	42	NE	NE	NE	NE
North Fork Salmon River	23,639 ± 8,893	38	29,388 ± 13,225	45	NE	NE	NE	NE
Lemhi River	10,793 ± 6,692	62	7,117 ± 4,413	62	NE	NE	NE	NE
Upper Salmon River	152,172 ± 54,782	36	NE	NE	NE	NE	NE	NE
Crooked River	45,567 ± 12,303	27	NE	NE	NE	NE	NE	NE
American River	206,470 ± 24,776	12	156,996 ± 15,700	10	203,490 ± 24,419	12	NE	NE
Red River	101,742 ± 15,261	15	111,870 ± 27,968	25	132,250 ± 38,353	29	NE	NE
White Cap Creek	12,357 ± 7,291	59	11,681 ± 7,009	60	12,035 ± 5,536	46	NE	NE
Crooked Fork Creek	18,315 ± 5,678	31	9,712 ± 2,719	28	NE	NE	NE	NE
Brushy Fork Creek	41,170 ± 14,821	36	18,062 ± 5,238	29	NE	NE	NE	NE
White Sand Creek	175 ± 189	106	147 ± 131	89	NE	NE	NE	NE
Big Flat Creek	4,270 ± 6,277	147	3,138 ± 5,429	173	NE	NE	NE	NE

Broodstock Collection

No chinook salmon broodstock were collected at the Pahsimeroi River weir or Crooked Fork Creek weir in 1994. Seven chinook were collected from the upper Salmon River, ten from Crooked River, and seven from Red River. A total of 527 chinook salmon adults and jacks were collected from the South Fork Salmon River weir. One hundred and one males and 104 females were released above the weir with the remainder retained for broodstock.

Detections

Chinook salmon parr were PIT-tagged in the fall of 1993 (brood year 1992), smolted, and were detected in the spring of 1994. Chinook smolts (brood year 1992) were PIT-tagged in the spring of 1994 and detected in the spring of 1994.

Chinook salmon smolts tagged in the Pahsimeroi River during the spring of 1994 had the highest detection rate (65%) and Marsh Creek the lowest (14%) (Table 9). Detection rates for parr tagged in the fall of 1993 (spring 1994 smolts) ranged from 12% for chinook parr in upper Salmon River to 28% for chinook parr in Crooked Fork Creek. Detection rates for parr tagged in the summer of 1993 ranged from 0% to 18%.

Detection rates of chinook salmon parr PIT-tagged in the fall of 1993 and chinook salmon smolts PIT-tagged in the spring of 1994 were very similar for chinook salmon from the South Fork Salmon River, Crooked River, and Crooked Fork Creek. Chinook salmon parr PIT-tagged in Marsh Creek during the fall of 1993 were detected at a rate which was roughly twice as high as the smolts PIT-tagged in the spring of 1994. For Pahsimeroi River migrants, chinook salmon smolts were detected at a rate which was almost five times higher than chinook salmon parr PIT-tagged during the fall emigration.

Detection rates for hatchery-reared smolts tagged and released into the South Fork Salmon River and Pahsimeroi River were 36% and 22%, respectively (Table 9). The detection rate for hatchery-reared smolts released into the South Fork Salmon River was about twice that for wild smolts. Hatchery parr detection rate was highest for Red River (7%).

DISCUSSION

Adult and jack chinook escapement in most streams in 1994 were orders of magnitude lower than in 1993 and approached the lowest on record for many streams (Riley and Elms-Cockrum 1995). As a result, smolt abundance should be low in 1996 and low escapement of 2-ocean and 3-ocean adult chinook salmon is expected in 1998 and 1999, respectively.

Table 7. Wild and natural chinook salmon trapped, number of mortalities, and summer/fall emigrant estimates from data collected with emigrant traps, 1994.

Stream	Number Trapped	Number of Mortalities	Emigrant Estimate
South Fork Salmon River	13,839	43	NE
Marsh Creek	11,243 [a]	20	14,420
Lemhi River	2,166	12	8,664
Pahsimeroi River	1,856	0	17,287
Upper Salmon River	1,144	2	10,895
Crooked River	6,703	0	17,547
Red River	3,285	13	14,738
Crooked Fork Creek	12,794	19	84,454

[a] Estimated.

Table 8. Releases of hatchery chinook salmon reared for the ISS[a] into treatment streams, 1994.

Stream	Release date	Number released		Fin clip	Number PIT-tagged	Adult collection site	Rearing facility
		Smolt	Parr				
South Fork Salmon River	04/04	235,439	0	LV	498	SF Salmon[b]	McCall Hatchery
Pahsimeroi River	04/12	46,342	0	RV	998	Pahsimeroi	Pahsimeroi Hatchery
Upper Salmon River	10/24	0	161,905	RV	1,200	Sawtooth	Sawtooth Hatchery
Crooked River	9/19	0	199,255	RV	1,000	Crooked River	Clearwater Hatchery
Red River	9/25	0	80,047	LV	1,000	Red River	Clearwater Hatchery
Pete King Creek[c]	07/05	0	15,080	RV	1,000	Powell[d]	Clearwater Hatchery
Squaw Creek[c]	07/05	0	14,977	RV	1,000	Powell	Clearwater Hatchery
White Sand Creek	07/08	0	99,808	RV	1,000	Powell	Clearwater Hatchery
Big Flat Creek	07/08	0	49,954	RV	1,000	Powell	Clearwater Hatchery

[a] Other differentially marked hatchery-reared chinook may have been released into these streams for general production purposes.
[b] The adult collection site for the South Fork Salmon River is located about a mile below Knox Bridge on Warm Lake Road.
[c] These fish are part of an ISS behavioral study conducted by the Idaho Cooperative Fish and Wildlife Research Unit.
[d] The Powell adult collection site is located on Walton Creek, immediately downstream of the confluence of White Sand and Crooked Fork creeks.

Table 9. Number of unique detections from Lower Snake River dams for chinook salmon tagged in Idaho Department of Fish and Game study streams in the summer of 1993, fall of 1993, and spring of 1994.

Stream	Migrant type [a]	Total detected	Fish tagged	Detection rate (%)
South Fork Salmon River	Summer	79	805	10
	Fall	757	4,677	16
	Spring	356	1,931	18
	Hatchery smolt	178	498	36
Johnson Creek	Summer	0	43	0
Marsh Creek	Summer	135	960	14
	Fall	1,603	6,625	24
	Spring	22	161	14
Beaver Creek	Summer	151	856	18
North Fork Salmon River	Fall	41	318	13
Lemhi River	Fall	161	813	20
	Spring	30	63	48
Pahsimeroi River	Summer	15	130	12
	Fall	116	844	14
	Spring	174	267	65
	Hatchery smolt	224	998	22
Upper Salmon River	Spring	62	239	26
	Fall	12	100	12
Crooked River	Spring	436	1,726	25
	Fall	81	368	22
Red River	Fall	224	1,005	22
	Spring	110	386	29
	Hatchery parr	68	1,000	7
Crooked Fork Creek	Summer	18	223	8
	Fall	522	1,868	28
	Spring	83	328	25
Brushy Fork Creek	Summer	0	162	0
White Sand Creek	Hatchery parr	55	1,002	6
Big Flat Creek	Hatchery parr	56	1,000	6

[a] Fall migrants and hatchery parr are chinook that were PIT-tagged in the fall of 1993 (brood year 1992) but smolted and were detected in the spring of 1994. Spring migrants and hatchery smolts are chinook that were PIT-tagged in the spring on 1994 as smolts (brood year 1992) and were detected in the spring of 1994.

The high abundance of rearing parr observed during snorkeling and the large number of emigrating parr trapped, indicates that the smolt migration in the spring of 1995 should be quite large. If smolt to adult survival rates are comparable to the past three years, jack returns in 1996, returns of 2-ocean adults in 1997, and 3-ocean adults in 1998 should be markedly improved relative to 1994 and 1995.

Estimates of juvenile chinook salmon emigration in the past have been determined by applying a single trap efficiency calculated over the entire trapping season. Generally, the bulk of emigrating chinook salmon in any given year migrate over a relatively short period of time under very dynamic conditions. These conditions are not represented when a seasonal efficiency is used and as a result estimates based on a seasonal efficiency probably underestimate actual emigration. Use of a weekly efficiency, that is adjusted for stream flow, however, does reflect changing conditions over the trapping season. Calculation of a weekly estimate that is adjusted for stream flow, however, requires that enough fish are trapped and tagged during most weeks to provide reliable estimates of trap efficiency. In years of low smolt and parr abundance, this may not be possible. As a result, in addition to reporting emigration based on weekly efficiencies in the future, continued reporting of emigration based on a seasonal trap efficiency may still be useful for comparisons between years for any given stream.

With the exception of the Pahsimeroi River, a production estimate of emigrating fry was not possible. (Pahsimeroi River chinook salmon fry attain a taggable size earlier than fry in other streams, presumably due to the high productivity of the Pahsimeroi River.) Emigrating fry are too small to mark to determine trap efficiency, and in many streams, still have a yolk-sac when captured. Button-up fry could be marked by removing the tip of one of the lobes of the caudal fin if permitted by NMFS.

Population estimates of rearing parr were calculated by a number of different methods in 1994 with the objective of finding a method that would improve the precision of the estimates. Although low water and relatively high chinook parr abundance provided favorable conditions no single method resulted in consistently narrower confidence intervals. Population estimates were not significantly different under the different methods of calculation in most streams.

Generally, detection rates for chinook salmon PIT tagged as smolts are expected to be substantially higher than for chinook salmon tagged during the fall due to overwinter mortality and this was the case in 1993 (Leitzinger et al. 1994). In 1994, however, detection rates for parr tagged in the fall and smolts tagged in the spring were fairly similar for chinook salmon from the South Fork Salmon River, Crooked River, and Crooked Fork Creek. In Marsh Creek, approximately twice as many chinook salmon tagged in the fall were detected as those tagged in the spring; however, in the case of Marsh Creek this may have been due to the small sample size. Crooked River also had a small sample size tagged during the fall of 1993. Arrival time of these chinook salmon at the various interrogation sites relative to when spill began (detection rate decreases when spill begins) did not explain these data. Other possible explanations include: some other aspect of dam operations changed, survival of fall-tagged chinook salmon improved, or survival of spring tagged chinook salmon decreased. Detection rates for smolts tagged in the spring of 1994 were much lower than detection rates for smolts tagged and migrating in the spring of 1993 (Leitzinger et al. 1994). Detection rates for chinook salmon parr tagged in the fall of 1992 (1993 smolt migrants) and 1993 (1994 smolt migrants) were similar (Leitzinger et al. 1994). This suggests that survival of smolts tagged in 1994 in at least South Fork Salmon River and Crooked Fork Creek may have been poor.

In response to low parr abundance in 1995, forecasted low adult and jack returns in 1995, and the tenuous status of the species in Idaho, a number of changes to the ISS will be implemented in 1995. To eliminate mortality associated with collecting and PIT tagging, chinook salmon parr will not be collected and PIT-tagged in the summer of 1995 by IDFG personnel. In addition, to minimize harassment of returning jack and adult chinook salmon, the weir in Marsh Creek and Crooked Fork Creek will not be installed.

The ISS experimental design is a very ambitious and comprehensive examination of the effectiveness of hatchery supplementation at rehabilitating chinook salmon populations. Efforts through 1994 have been successful at quantifying a number of production variables and have demonstrated deficiencies in quantifying others. Precariously low returns of adult and jack chinook salmon to Idaho have hampered a number of experimental design elements. Probably the most important element to the experimental design is development of locally-adapted hatchery broodstocks, and rearing of sufficient quantities of juvenile hatchery chinook salmon for release into treatment streams. Unfortunately, due to low adult returns this element is not being adequately met.

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LITERATURE CITED

Bowles, E.C., and E.J. Leitzinger. 1991. Salmon supplementation studies in Idaho rivers. U. S. Department of Energy, Bonneville Power Administration Contract No. DE-B179-89BPO1466. Portland, Oregon.

Buettner, E., and L. Nelson. 1990. Smolt condition and timing of arrival at Lower Granite Reservoir. Idaho Department of Fish and Game, Annual Report to Bonneville Power Administration, Contract DE-AI79-83BP11631, Project 83-323B.

Hassemer, P.F. 1991. Draft redd count manual. Idaho Department of Fish and Game, Boise, Idaho. 19 p.

Idaho Department of Fish and Game. 1991. Anadromous fisheries management plan, 1991-1995. Boise, Idaho.

Idaho Department of Fish and Game, Nez Perce Tribe of Idaho, and Shoshone-Bannock Tribes of Fort Hall. 1990. Salmon River sub-basin salmon and steelhead production plan. Northwest Power Planning Council, Portland, Oregon.

Kiefer, R., and K. Forster. 1990. Intensive evaluation and monitoring of chinook salmon and steelhead trout production, Crooked River and upper Salmon River sites, Idaho. Idaho Department of Fish and Game, Annual Report to Bonneville Power Administration, Contract DE-AI79-84BP13381, Project 83-7, Boise.

Kiefer, R., and K. Forster. 1991. Intensive evaluation and monitoring of chinook salmon and steelhead trout production, Crooked River and upper Salmon River sites, Idaho. Idaho Department of Fish and Game, Annual Report to Bonneville Power Administration, Contract DE-AI79-84BP13381, Project 83-7, Boise.

Leitzinger, E., K. Plaster, P. Hassemer, and P. Sankovich. 1994. Idaho Supplementation Studies. Idaho Department of Fish and Game, Annual Report to Bonneville Power Administration, Project 89-098

Nez Perce Tribe of Idaho and Idaho Department of Fish and Game. 1990. Clearwater River sub-basin salmon and steelhead production plan. Prepared for Northwest Power Planning Council, Portland, Oregon.

Northwest Power Planning Council. 1987. Columbia River Basin Fish and Wildlife Program. Portland, Oregon.

PIT Tagging Steering Committee. 1992. PIT tag specification document, Columbia River Basin PIT tag information system, data source input specifications. 33 p.

Prentice, E.F., T.A. Flagg, C.S. McCutcheon, D.F. Brastow, and D.C. Cross. 1990. Equipment, methods, and an automated data-entry station for PIT tagging. American Fisheries Society Symposium 7:335-340, 1990.

Regional Assessment of Supplementation Project. 1992. Supplementation in the Columbia Basin. Part I: RASP Summary Report Series. Background, Description, Performance Measures, Uncertainty, and Theory. Prepared for the Bonneville Power Administration. Project Number 85-62.

Riley, S., and T.E. Cockrum. 1995. Salmon Spawning Ground Surveys, 1993. Idaho Department of Fish and Game, Annual Report 95-6.

Rosgen, D.L. 1985. A stream classification system. Pages 91-95 *in* Riparian ecosystems and their management: reconciling conflicting uses. First North American Riparian Conference, Arizona.

Supplementation Technical Work Group. 1988. Supplementation research - proposed five-year work plan. Northwest Power Planning Council, Portland, Oregon.

APPENDICES

Appendix A.

GENETIC ANALYSIS OF 1993-94 IDAHO CHINOOK SALMON BASELINE COLLECTIONS, AND A MULTI-YEAR COMPARATIVE ANALYSIS

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INTRODUCTION

The work described in this report is a component of a project being carried out by Idaho Fish and Game (IDFG) entitled "Salmon supplementation studies in Idaho rivers". This report presents results of the genetic analysis of chinook baseline samples collected in July, August, and October 1993 from seven rivers, and in January 1994 from two hatcheries in Idaho. It also includes a comparative analysis among all the Idaho chinook baseline collections made for this project since 1991 (see Marshall 1993 and 1992), where sample sizes permitted. A broader comparative analysis was also carried out using genetic data for other Snake River basin spring and summer chinook populations that were available in Waples et al. (1993).

Chinook juveniles were sampled by personnel from University of Idaho (UI) and IDFG and sent to the Washington Department of Fish and Wildlife (WDFW) Genetics Lab for the analysis. WDFW staff responsible for various laboratory tasks of this project were: Bruce Baker, Susan Cierebiej, Bill Ingram, Norm Switzler, and Beth Vorderstrasse. Craig Busack provided assistance with computer programs for data analysis, and he and Stevan Phelps assisted with data interpretation.

METHODS

Laboratory

Four tissues, muscle, eye, heart, and liver, were dissected from the whole chinook juveniles sent to our lab. The tissue samples were placed in labeled test tubes and stored at -80°C prior to electrophoresis. Horizontal starch-gel electrophoresis was carried out using the electrophoretic protocol provided in Appendix I. The 26 enzymes screened provided data for 57 presumptive gene loci. Three enzymes added to this year's screening were ADH, ALAT, and βGLUA to test for variability of these systems in the 1993-94 samples. The ADH locus had been found monomorphic in the 1991 Idaho samples, but was reported as variable in other Snake River chinook by Waples et al. (1993). Chinook variable loci and their alleles, with relative mobilities and data codes, are listed in Appendix II.

Phenotype data from the gels were entered directly into computer files as presumed genotypes via WDFW's interactive scoring program. All gels were independently double-

scored at all loci. Many loci were screened in two or more tissues and on two different buffers in order to ensure accuracy of the data, as well as resolve all known alleles. Samples were rerun to resolve any scoring discrepancies or uncertainties found in the initial analysis.

The nine 1993/94 baseline collections were given unique codes in our lab. These codes are on the test tube labels as well as in the computer data files for each collection. The names of the collections, their codes, and sample sizes are listed in Table 1.

Table 1. Chinook salmon juvenile collections made in 1993-94 by UI and IDFG, with WDFW collection codes and sample sizes.

Collection Code	Location sampled	Sample Size
93EX	Pahsimeroi R.	29
93FJ	Lemhi R.	54*
93FT	Red R.	50
93FU	North Fork Salmon R.	50
93FV	Bear Valley Creek	50
93FW	Brushy Fork Creek	13
93FX	Lolo Creek	40
94DG	Dworshak Hatchery	100
94DH	East Fork Salmon at Sawtooth Hatchery	100

*Although 60 fish were collected from Lemhi R., electrophoretic analysis showed that 6 of them were not chinook; they were most likely Oncorhynchus mykiss.

Data Analysis

The genotype data gathered by electrophoresis was analyzed using the BIOSYS-1 program (Swofford and Selander 1981) to compute allele frequencies, chi-square tests for conformance to Hardy-Weinberg genotypic proportions, and several variability measures, including average heterozygosities. The BIOSYS-1 program was also used to calculate genetic distance statistics using 29 variable loci, and to perform cluster analyses based on the genetic distance values. The unweighted pair-group method (Sneath and Sokal 1973) was used in the cluster analyses to produce the dendrograms illustrating relationships among samples. G-tests (log-likelihood ratio tests) of the heterogeneity of allele frequencies were performed using 29 variable loci for various pair-wise comparisons of samples as described further in the Results section. For comparisons among populations (locations), I combined the genetic data from all years for each population sampled in more than one year.

The 29 loci used for genetic distance and G-test calculations are the same set of variable loci used in previous analyses in this study, and have been variable at the .99 level in one or

more collections (see Appendix IV for this group of loci). Two variable isoloci (sAAT-1,2, sMDH-B1,2), and two loci in which only homozygotes can be reliably scored (GPIr, sMEP-2) had to be excluded from some of the above calculations, and these cases are described in the Results section.

An electronic file of allele frequency data for twelve Snake River basin spring and summer chinook populations was provided for comparative purposes by Robin Waples and David Teel, National Marine Fisheries Service (NMFS-Seattle). These are the same data that are presented in Appendix Table 3 of Waples et al. 1993, and include samples from 1989 and 1990. Data standardization that had to be done between the two data sets is described in the Results section. Cluster analyses were performed with these twelve populations and the fifteen available from this study to gain a view of relationships among chinook populations throughout the Snake basin.

RESULTS

1993-94 COLLECTIONS

Samples

The amount of heart tissue available from many of the wild juveniles sampled in 1993 was often inadequate for the resolution of some enzymes. This was especially the case for the loci mAH-1, mAH-2, and sSOD-2, which we screen in heart tissue only. The hatchery juveniles, sampled in January 1994, were large enough to allow good resolution for most loci in heart tissue. The Lemhi collection had six fish that were not chinook, and enzyme patterns for these suggested they were *Oncorhynchus mykiss*. Otherwise, sample quality, in terms of enzyme activity and resolution, was generally quite good.

The sample sizes of three 1993 collections, Brushy Fork Creek (N=13), Pahsimeroi River (N=29), and Lolo Creek (N=40), were below our preferred minimum sample size (N=50) for genetic characterization. The Brushy Fork Creek and Pahsimeroi collections were not used for genetic variability analysis or in measuring genetic relationships among the 1993-94 collections. However, data for these two were used subsequently in combination with data from previous years from the same locations for population characterization and comparison. I did use the Lolo Creek collection in the analyses described above, but the smaller sample size should be kept in mind when reviewing results.

Genetic Variation

Allele frequencies for all nine 1993-94 collections at 51 loci are presented in Appendix III. Data for four isolocus pairs (sAAT-1,2, sIDHP-1,2, sMDH-A1,2, sMDH-B1,2) are mean frequencies computed over both loci of the pair. Data for the individual loci sIDHP-1 and sIDHP-2 are also given in Appendix III due to our current ability to distinguish variation

expressed at each locus (Shaklee and Phelps 1992). Frequencies for sIDHP-1,2 will be useful for comparison with data from older electrophoretic studies in which data were collected without the knowledge of how to score the loci independently. The frequencies for GPIr and sMEP-2 are genotype frequencies. Only homozygous phenotypes for the common or variant alleles at these two loci are scored because heterozygotes are not reliably distinguished.

As reported for previous Idaho chinook collections (Marshall 1992 and 1993), uncommon or rare variation was seen at several loci, specifically, the sAAT-3*113 allele, the sIDHP-2*66 allele, the sMDH-B1,2*126 allele, the PEPA*81 allele, and the mSOD*142 allele. Two other rare variants, the sAAT-1,2*105 allele and the LDH-C*84 allele, were not observed in any 1993-4 collections, although they had been previously. Interestingly, the mAAT-2*125 allele (which rarely has been observed in any upper Columbia/Snake basin chinook populations) was present only in the Lemhi River collection, as had been the case for the previous two years of sampling.

Many of the 1993-94 collections had relatively high frequencies of the mMDH-2*200 allele, the sMEP-1*92 allele, the sIDHP-1*74 allele, and the TPI-4*104 allele, as did previous collections. The variation observed at IDDH-1 and IDDH-2 was scored as reported for the 1991-92 samples. Although last year it was reported that the variant allele at IDDH-1 in the Idaho populations was different from a similar one present in Canadian chinook collections, rerunning samples side-by-side this year did not support that interpretation. However the model for the variability of the IDDH system remains the same, and the NMFS-Seattle genetics labs score the loci in the same way.

Resolving mAH-1 and mAH-2 was difficult again this year, relative to the amount of heart tissue available. Weak or no activity for mAH-1 was found in most collections. The mAH-2 locus appeared to be variable (mAH-2*83 allele) in the fish that were scorable. Variation was seen in six of the nine collections, however four collections had no or a very low percentage of reliable mAH-2 scores. Allele frequencies for mAH-2 are not presented in Appendix III. Another locus resolved only in heart, sSOD-2, was also screened, but was difficult to score in many samples. The sSOD-2*120 allele was observed in one wild chinook collection (N.F. Salmon) and in both hatchery collections. Allele frequencies are not reported however due to problems with reliability.

Two loci, ALAT and bGLUA, added experimentally to the electrophoretic protocol, were scored for all the 1993-94 collections. No variation was observed for ALAT, but two collections, N.F. Salmon and E.F. Salmon at Sawtooth Hatchery, appeared to have the bGLUA*60 allele at low frequency ($\leq$ 0.02). Changing screening conditions, such as using a different gel buffer system, may improve resolution for bGLUA if we continue to try to resolve it in the future. We should also obtain mobility standards for the bGLUA variant from the NMFS-Seattle labs to verify our scoring. Only one collection, Dworshak Hatchery, showed variation at ADH; it had a frequency of 0.005 for the ADH*-52 allele.

Genetic Variability Analysis

Only the collections having a sample size of 40 or larger were used to test for Hardy-Weinberg proportions in the variable loci. The variable isoloci sAAT-1,2 and sMDH-B1,2 were not included in these tests because we can not distinguish which locus of the pair is variable. sMEP-2 was not included because heterozygotes were not scorable. For the seven large collections, 118 tests were made and 7 showed significant ($p<0.05$) departures from expected genotypic frequencies. Overall, this is a low rate (6%) of significance since 5% of the tests would be expected to be significant by chance alone. Of the seven tests out of Hardy-Weinberg equilibrium, four involved sAAT-4 genotype scores showing a deficit of heterozygotes. I believe this is a result of scoring problems typical of this locus when enzyme expression is weak. The small amount of liver tissue available from some of the juveniles likely reduced the scorability of sAAT-4. Under these conditions, heterozygotes are the most difficult phenotypes to score reliably, and may be given "zero" or questioned scores and thus not used in computing allele frequencies or in genotype counts.

Over all collections, variation was found at 31 of the 53 loci resolved (excluding sAH-2, ALAT, and bGLUA). Several measures of genetic variability were calculated over 43 loci for the seven large collections and are presented in Table 2. Loci and isoloci not included in these calculations were GPIr, sMEP-2, sAAT-1,2, sMDH-A1,2, and sMDH-B1,2. Note that two of the isoloci were variable (Appendix III). The percentage of loci polymorphic at the .99 level (common allele frequency $\leq$ .99 in at least one collection) ranged from 27.9% to 48.8% per collection. Average observed heterozygosity values (average percent of heterozygous loci per fish) at 43 loci for the seven collections are also shown in Table 2. They ranged from .044 to .068.

Genetic Relationships Among 1993-94 Collections

Results of the G-tests done for all possible pairs of the seven large collections (29 variable loci) showed all comparisons to be significantly different at $p < 0.01$. Cluster analyses based on genetic distances were not done for the 1993-94 collections because only seven had a large enough sample size, and previous results using only one year's collections have not been particularly informative. The 1993-94 data were used in combination with earlier data to analyze relationships among populations.

COMPARATIVE ANALYSIS AMONG ALL COLLECTIONS, 1991-1994

Six collection sites had large enough sample sizes for two or three years to test for differences in allele frequencies between or among years. Three locations with small 1993 sample sizes had their genetic data combined among years without testing, in order to provide a profile for comparisons among locations. Despite three years' sampling, the total sample size for Brushy Fork Creek (N=45) is still rather small. The data for populations

not sampled in 1993-94 were also used in the comparative geographic analysis. Table 3 presents a summary of all the samples used and how they were combined.

Temporal Comparisons

Two wild populations, Bear Valley Creek and Lemhi River, and the two hatchery populations, Dworshak and East Fork Salmon, were tested for differences in allele frequencies among three years' samples. Two other wild populations, Red River and North Fork Salmon River, were tested for temporal differences between two samples. All temporal comparisons within the same location or hatchery were significantly different at $p < 0.05$. All of these except one, Lemhi 93 versus Lemhi 92, were significantly different at $p < 0.01$. The largest temporal allele frequency differences were observed among the hatchery samples.

Geographic Comparisons

To provide single population genetic profiles, I combined the data among years for each of the six locations described above, despite the temporal differences in allele frequencies. Combining data for consecutive brood years should provide a better profile of population allele frequencies, especially for populations like these with low numbers of adult spawners returning at different ages. Data for eight other locations, also resulting from combining multiple year samples, and from the single year South Fork Salmon River sample, were used with these six to analyze genetic relationships among locations. The total samples from the fifteen locations will henceforth be referred to as population samples. Allele frequencies at 29 loci for all populations are presented in Appendix IV.

Genetic heterogeneity among the 15 populations was analyzed using G-tests (29 loci). All G-test results for paired comparisons between all populations were significantly different ($p < 0.01$). Genetic distances were calculated among all possible pairs using both the Nei (1978) and the Cavalli-Sforza and Edwards (1967) methods. These values were used in cluster analyses to produce the dendrograms shown in Figures 1 and 2. Different relationships among the 15 populations were found using the two different statistics. Neither showed any clear separation of Clearwater River basin and Salmon River basin populations.

In the Nei dendrogram (Figure 1), all the Clearwater populations except Dworshak Hatchery clustered together, but have a Salmon River tributary, West Fork Yankee Fork, grouped with them. Most of the Salmon River populations clustered together, except for two relative outliers, Herd Creek and East Fork Salmon River. The fact that the East Fork Salmon River population is not closely associated with the East Fork Salmon Hatchery population (which is maintained by wild E.F. Salmon R. spawners) is apparently an artifact of the clustering process. The genetic distance between the E.F. Salmon River and Hatchery baselines was relatively small compared to distances between E.F. Salmon River and the other populations. However, because genetic distances were smaller between the E.F. Salmon Hatchery and over half of the other 13 populations, the Hatchery population clustered first with these, and E.F. Salmon River became a relative outlier.

Table 2. Genetic variability in seven 1993-94 Idaho Chinook collections - 43 loci (sAAT-1,2, sMDH-A1,2, sMDH-B1,2, GPIr, & sMEP-2 not included); standard errors in parentheses.

COLLECTION	MEAN SAMPLE SIZE PER LOCUS	MEAN NO. ALLELES/ LOCUS	PERCENTAGE OF LOCI POLYMORPHIC*	MEAN HETEROZYGOSITY	
				DIRECT-COUNT	HDYWBG# EXPECTED
LEMHI R 93	53.3 (0.4)	1.5 (0.1)	39.5	0.061 (0.016)	0.064 (0.017)
RED R 93	48.9 (0.4)	1.5 (0.1)	46.5	0.068 (0.017)	0.066 (0.016)
NF SALMON R 93	49.5 (0.2)	1.3 (0.1)	30.2	0.060 (0.024)	0.051 (0.019)
BEAR VALLEY 93	48.9 (0.3)	1.5 (0.1)	46.5	0.058 (0.015)	0.055 (0.014)
LOLO CR 93	39.7 (0.2)	1.3 (0.1)	27.9	0.044 (0.014)	0.040 (0.012)
DWORSHAK HAT 94	99.4 (0.4)	1.5 (0.1)	48.8	0.061 (0.015)	0.064 (0.015)
EF SALMON HAT 94	99.2 (0.4)	1.4 (0.1)	37.2	0.057 (0.016)	0.057 (0.016)

* A locus is considered polymorphic if the frequency of the most common allele does not exceed 0.99

\# Unbiased estimate based on Hardy-Weinberg equilibrium (see Nei 1978)

Table 3. Summary of 1991-1994 Idaho chinook baseline collections and their use in temporal comparative analyses. N = sample size.

YEAR AND LOCATION	N	COMBINED TOTAL N
Samples tested for between year differences prior to combining data		
1993 Bear Valley Creek	50	
1992 " " "	75	
1991 " " "	50	175
1993 N.F. Salmon River	50	
1992 " " "	56	
(1991 " " "	30)*	136
1993 Red River	50	
1991-2 " "	61	111
1993 Lemhi River	54	
1992 " "	74	
1991 " "	50	178
1994 Dworshak Hatchery	100	
1993 " "	100	
1992 " "	102	302
1994 EF Salmon/Saw. Hat.	100	
1993 " " " "	100	
1992 " " " "	90	290
Samples combined without testing due to sample size		
1993 Pahsimeroi River	29	
1992 " "	39	
1991 " "	50	118
1993 Brushy Fork Creek	13	
1992 " " "	19	
1991 " " "	13	45
1993 Lolo Creek	40	
1992 " "	23	
1991 " "	36	99
Samples previously tested and combined		
1992 W.F. Yankee Fork	55	
1991 " " "	50	105
1992 Herd Creek	53	
1991 " "	50	103
1992 Camas Creek	56	
1991 " "	50	106
1992 Crooked Fork Cr.	52	
1991 " " "	50	102
Samples previously combined without testing		
1992 E.F. Salmon R.	54	
1991 " " "	20	74
Location with single year sample		
1991 S.F. Salmon R.	51	

*This sample was not used for the temporal comparisons, but was eventually combined with the data from the other two years for geographic comparisons.

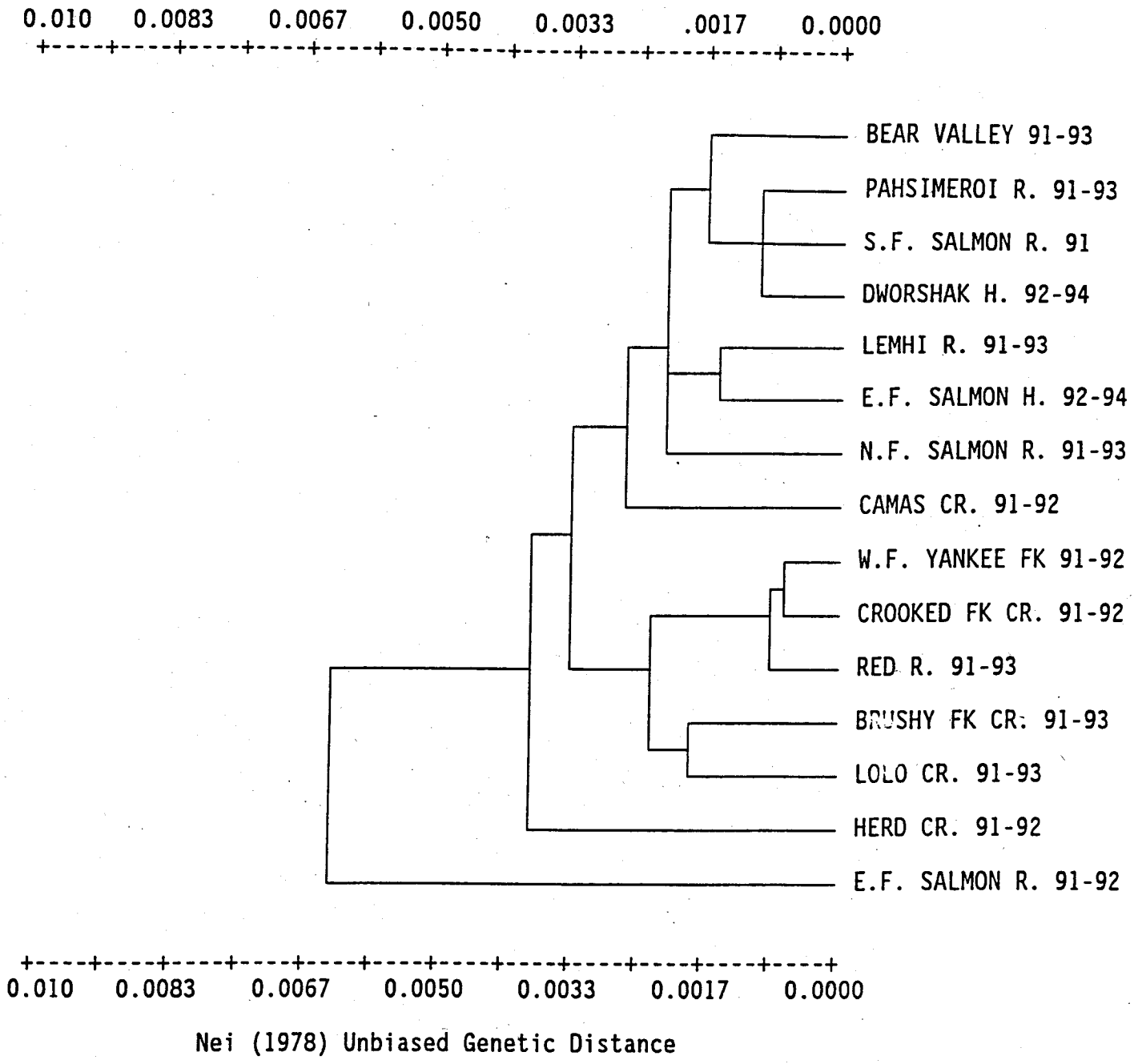

Figure 1. Dendrogram resulting from cluster analysis (unweighted pair group method) of genetic distance values (Nei 1978) computed using 29 polymorphic loci for 15 Idaho spring chinook populations. Data were combined between or among years for populations sampled in 2 or 3 years.

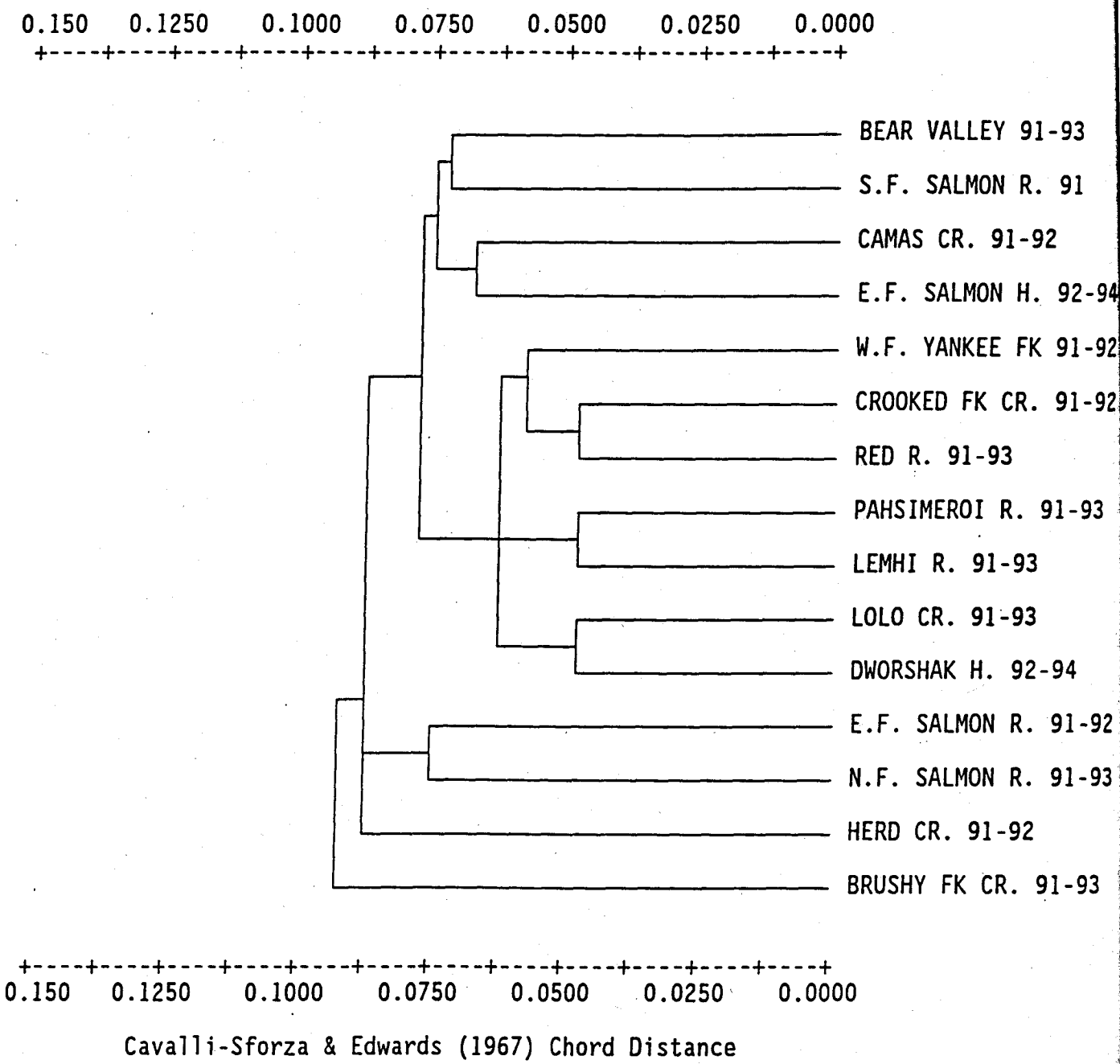

Figure 2. Dendrogram resulting from cluster analysis (unweighted pair group method) of genetic distance values (Cavalli-Sforza and Edwards 1967) computed using 29 polymorphic loci for 15 Idaho spring chinook populations. Data were combined between or among years for populations sampled in 2 or 3 years.

In the Cavalli-Sforza and Edwards dendrogram (Figure 2), all the Clearwater populations except Brushy Fork Creek were found in a central cluster along with three Salmon River populations. Herd Creek again appeared as a relative outlier, but E.F. Salmon River did not. Similar to the Nei cluster analysis, the E.F. Salmon River and Hatchery populations had a relatively small genetic distance, but distances between the wild population and other Salmon River populations were relatively large. One grouping that persisted between the two dendrograms included the West Fork Yankee Fork, Crooked Fork Creek, and Red River populations.

There were quite a few similarities in clustering patterns between the Nei and Cavalli-Sforza and Edwards dendrograms produced for the same 15 populations characterized by two years of data (Marshall 1993) and these two new dendrograms.

COMPARATIVE ANALYSIS WITH OTHER SNAKE RIVER BASIN POPULATIONS

A description of the twelve Snake River basin spring and summer-run chinook populations used for a more comprehensive comparative analysis appears in Table 4. Not all loci and/or alleles were shared in common between this NMFS baseline allele frequency data set and the data of this study. Of the 29 polymorphic loci (Appendix IV) used in comparative analyses for this study, four loci (mAAT-2, GPI-B2, IDDH-1, and mSOD) were removed, and one locus, GR, was added, due to variability in the NMFS samples. Thus, allele frequencies for 26 loci were used for the comparative analyses of all 27 baseline populations. Allele pooling was done for sIDHP-1 (*66 allele with *83 allele), sMDH-B1,2 (*121 allele with *126 allele), sMEP-1 (*86 allele with *92 allele), and PEPA (*86 allele with *81 allele). Note that this different data set will change the values of genetic distance statistics computed among the 15 populations of this study.

G-tests comparing all possible pairs of the 27 baselines showed all populations to have significantly different ($p < 0.01$) allele frequencies. Nei (1978) and Cavalli-Sforza and Edwards (1967) genetic distance values were used in cluster analyses to produce the dendrograms shown in Figures 3 and 4. A clear separation between nearly all the Salmon River basin populations and those from other basins (Clearwater, Imnaha and Grande Ronde) was evident in the Nei dendrogram (Figure 3). Grande Ronde populations appeared to be more closely related to Clearwater populations than to those of the Salmon River basin. As shown in Figures 1 and 2, the West Fork Yankee Fork population continued to cluster with Clearwater populations. The Cavalli-Sforza and Edwards dendrogram (Figure 4) showed a different clustering of the Salmon River populations, and that several of them were relative outliers. This dendrogram also had Clearwater and Grande Ronde populations grouping together, but had one Clearwater population, Brushy Fork Creek, as the most distant outlier of all the baselines.

Table 4. Chinook salmon populations from the NMFS 1989-90 baseline data set used for basin-wide comparative analyses.

Population	Run-timing	Sample size	Drainage
Upper Salmon River	spring	160	Salmon
Valley Creek	"	198	"
Sawtooth Hatchery	"	200	"
Marsh Creek	"	180	"
Johnson Creek	summer	180	Salmon
Secech River	"	174	"
McCall Hatchery	"	200	"
Imnaha River & Hatchery	"	380	Imnaha
Minam River	spring	100	Grande Ronde
Lostine River	"	199	"
Catherine Creek	"	100	"
Rapid River & Lookingglass Hatcheries	"	200	"

DISCUSSION AND CONCLUSIONS

Rare allelic variants at several loci, and relatively high frequencies of certain alleles at other loci were found for the third year in the 1993-94 Idaho chinook baseline samples. Measures of genetic variability, such as mean heterozygosity, were similar to or higher than those calculated for previous years' collections. Thus, it appears that genetic diversity and variability, and the distinctive allelic profiles that characterize these chinook populations have persisted in spite of recent declining population sizes.

Heterogeneity in allele frequencies between years was high for the six populations with two or three years of samples that were tested. Temporal heterogeneity was generally greater than that measured in large wild and hatchery chinook populations sampled in Washington and Canada (Marshall, unpublished data). This result was similar to findings from the previous analysis (Marshall 1993). These between-year frequency differences could be due to sampling error, genetic drift due to small spawner populations, and the juveniles being the product of a unique group of adult spawners annually. Also, straying between populations or planting of fish from different populations can destabilize allele frequencies.

Again, the two hatchery populations showed larger between-year frequency differences than the wild populations, except for one comparison. The Dworshak 1994 (brood year 1992) and Dworshak 1992 (brood year 1990) samples had a level of temporal variability more like that of the wild populations. The large temporal variability between all comparisons for the three years' of samples from the East Fork Salmon hatchery population is most likely a reflection of the small number of spawners that have been taken into the hatchery (Hassemer, 1993).

The genetic differences found between years within the populations suggest that a baseline profile, even one produced by combining all years' samples, may have limited utility for monitoring changes occurring in a population due to the supplementation study. Persistence of rare or low frequency alleles could be used as an indicator of change, but these, due to their rarity, can be lost simply by chance events (genetic drift) in a small population. There is the possibility, however, that allele frequencies could become temporally stable if the size of a population increases due to supplementation. This is an effect that could be measured against the baseline condition.

The baseline profiles resulting from multi-year data do show a large amount of heterogeneity among the populations. For the Salmon River basin populations that have not been planted with non-local hatchery fish, their genetic distinctness may be due as much to reproductive isolation and local adaptation as to higher rates of genetic drift due to their small population size. It seems obvious, based on the history of hatcheries and outplanting reported by Bowles and Leitzinger (1991), that the recently re-established Clearwater populations show heterogeneity among themselves due to the variety of source populations, as well as from factors associated with small population size. The significance of this heterogeneity among populations, in terms of its reflection of important adaptive differences among populations, needs to be evaluated within the context of the experimental design of the supplementation study.

LITERATURE CITED

Bowles, E. and E. Leitzinger. 1991. Salmon supplementation studies in Idaho rivers - Experimental design. Report to Bonneville Power Administration, Portland, OR. DOE/BP-01466-1.

Cavalli-Sforza, L.L., and A.W.F. Edwards. 1967. Phylogenetic analysis: models and estimation procedures. Evolution 21: 550-570.

Hassemer, P.F. 1993. Salmon spawning ground surveys, 1989-1992. Idaho Department of Fish and Game Fishery Research Report. Project No.F-73-R-15.

Marshall, Anne R. 1992. Genetic analysis of 1991 Idaho chinook salmon baseline collections. Attachment B in Leitzinger, E. J., K. Plaster, and E. Bowles. 1993. Idaho supplementation studies. Annual report, 1991-1992, to Bonneville Power Administration, Portland, OR. DOE/BP-01466-2.

Marshall, Anne R. 1993. Genetic analysis of 1992-93 Idaho chinook salmon baseline collections, and a comparative analysis with 1991 collections. A report to Idaho Fish and Game. 16 pp. and appendices.

Nei, M. 1978. Estimation of average heterozygosity and genetic distance from a small number of individuals. Genetics 89: 583-590.

Shaklee, J.B. and S. Phelps. 1992. Chinook salmon $NADP^+$-dependent cytosolic isocitrate dehydrogenase: electrophoretic and genetic dissection of a complex isozyme system and geographic patterns of variation. Biochemical Genetics 30:455-489.

Sneath, P.H.A., and R.R. Sokal. 1973. Numerical taxonomy. W.H. Freeman, San Francisco, CA.

Swofford, D.L. and R.B. Selander. 1981. BIOSYS-1: a FORTRAN program for the comprehensive analysis of electrophoretic data in population genetics and systematics. J. Heredity 72:281-283.

Waples, R.S., O.W. Johnson, P.B. Aebersold, C.K. Shiflett, D.M. VanDoornik, D.J. Teel, A.E. Cook. 1993. A genetic monitoring and evaluation program for supplemented populations of salmon and steelhead in the Snake River basin. Annual Report of Research to Bonneville Power Administration, Portland, OR.

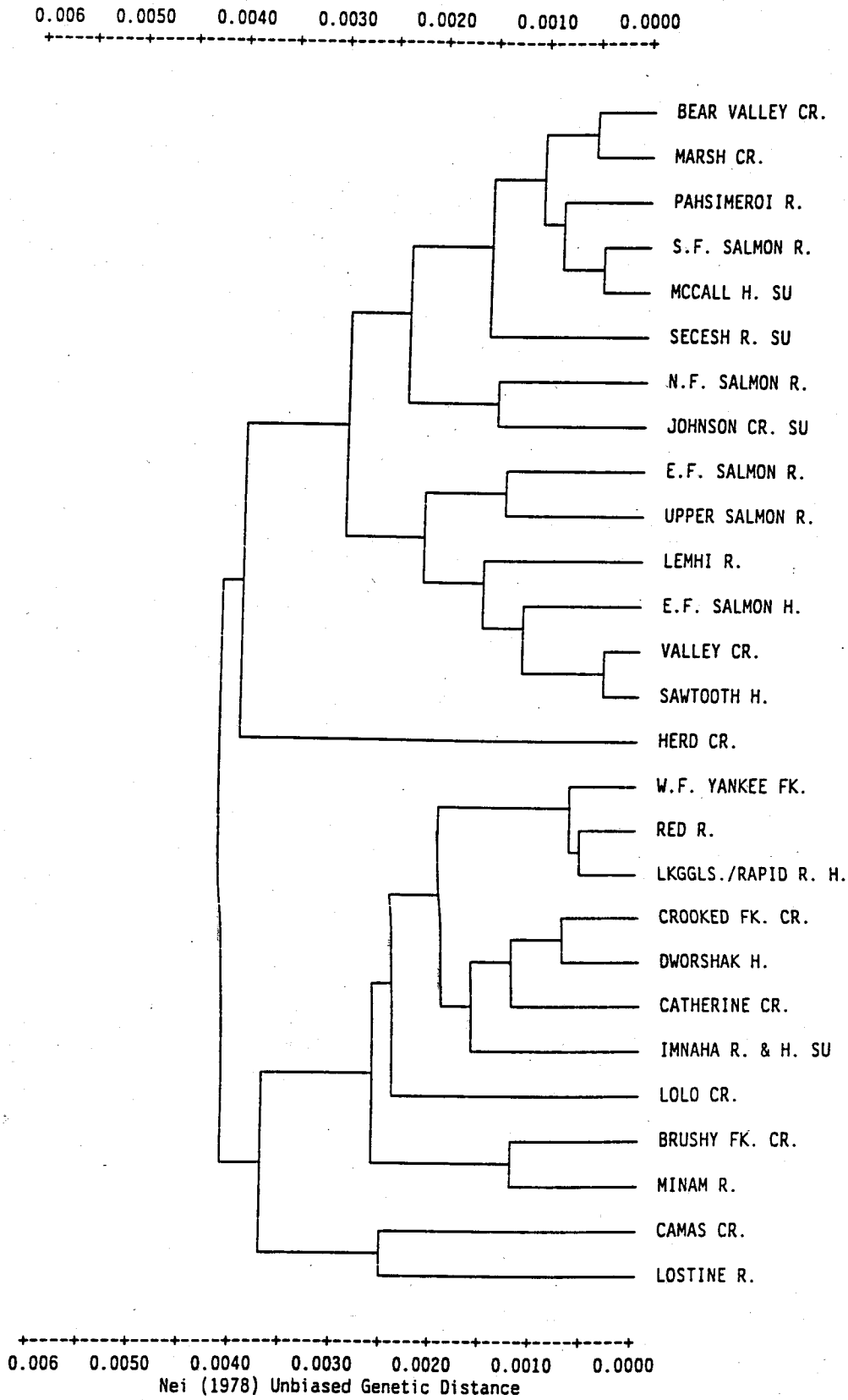

Figure 3. Dendrogram resulting from cluster analysis (unweighted pair group method) of genetic distance values (Nei 1978) computed using 26 polymorphic loci for 27 Idaho chinook populations. Data for 12 populations from the National Marine Fisheries Service.

Appendix A. Continued

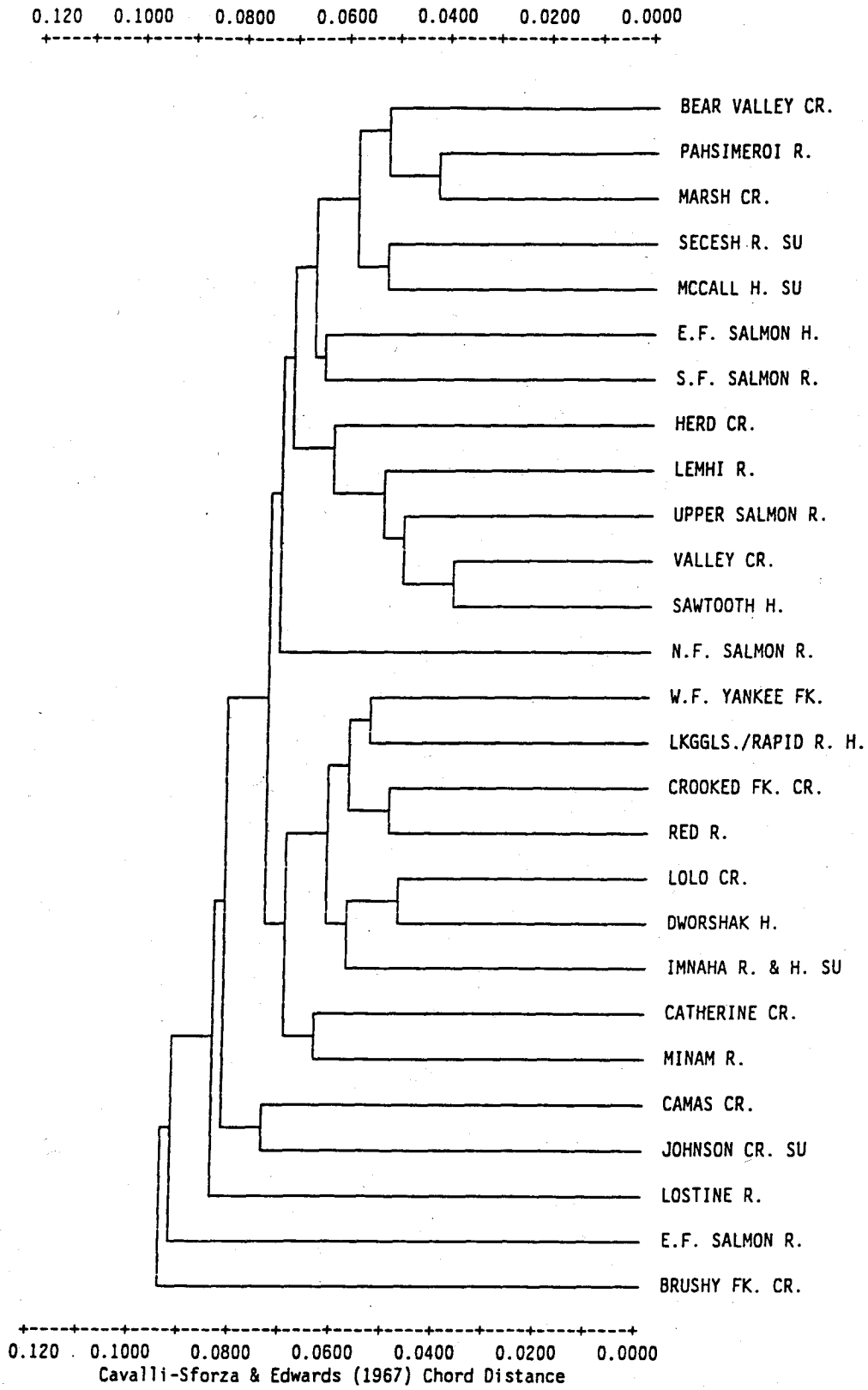

Figure 4. Dendrogram resulting from cluster analysis (unweighted pair group method) of genetic distance values (Cavalli-Sforza & Edwards 1967) computed using 26 polymorphic loci for 27 Idaho chinook populations. Data for 12 populations from the National Marine Fisheries Service.

Appendix I. Electrophoretic screening protocol for 1993-94 Idaho juvenile chinook baseline samples.

HEART

TRIS-GLY (35mm origin) 5 hrs @ 550V (max. 75 mA) LKB THIN GEL

PEPB (PEPB-1=PEPB-H & -2)
PGM (PGM-1 & 2) score quickly
HAGH
SOD (sSOD-1) **c only, from middle**
MPI
ADA (ADA-1 & 2)

CAMEN 6.8 (35mm origin) 5 1/4 hrs @ 250V (max. 75 mA) THIN GEL
ADD 15mg NAD/100ml gel buffer immediately before degassing
(Trays need 30mg NAD/100ml electrode buffer)

G3PDH (G3PDH-3)
AH (mAH-1, 2, 3, & 4)
MDH (sMDH-A1,2 & B1,2 & mMDH-1, 2, & 3) **a + c**
AAT (mAAT-1 & 2) **c only from middle**
PEPD (PEPD-2)
GAPDH (GAPDH-2 & 3)

TC-4 (40mm origin) 5 hrs @ 90 mA (max. 250V) LKB **THICK GEL**
[use of Heathkit may reguire longer run]

PEPB (PEPB-1=PEPB-L) **a + c**
AAT (sAAT-1,2 & mAAT-1 & 2) **a + c**
MEP (sMEP-1 & 2) (use 15mg oxaloacetate)
SOD (sSOD-1 & 2 & mSOD) **a + c**
GR
IDHP (sIDHP-1,2T)

EYE

TRIS-GLY (35mm origin) 5 hrs @ 550V (max. 75 mA) LKB THIN GEL

LDH (LDH-B1, B2, & C)
AAT (sAAT-3)
TPI (TPI-3 & 4)
PEPA (PEPA-1) score quickly
HAGH

CAME 6.8 (35mm origin) 5 hrs @ 250V (max. 75 mA) THIN GEL

AAT (sAAT-3)
IDHP + PGDH (IDHP-1,2C + PGDH)
PGK (PGK-2) score quickly
GR
LDH (LDH-B1, B2, & C)

Appendix I. Idaho juvenile chinook baseline protocol, cont.

MUSCLE

TRIS-GLY (35 mm origin) 5 hrs @600V (max. 90 mA) **LKB** **THICK GEL**

PEPB (PEPB-1=PEPB-H)
PGM + MPI (PGM-1 & 2) **cut anode in 2 pieces (lower half ~2.5 cm) & stain separately* score PGM quickly
GPI (GPI-B1, B2, A & r) score very quickly
SOD (sSOD-1) **c only from middle**
PEP-LT (PEPA-1 & PEP-LT)
TPI (TPI-1, 2, 3, & 4)
ADA (ADA-1 & 2)
ALAT

CAME 6.8 (35mm origin) 5 hrs @ 250V (max. 90 mA) **THICK GEL**

AH (mAH-3 & 4)
PGK (PGK-2) score quickly
MDH (sMDH-A1,2 & B1,2 & mMDH-2, & 3) **a + c**
AAT (sAAT-1,2 & mAAT-1 & 2) **a + c**
IDHP + PGDH (mIDHP-1, 2 & sIDHP-1,2C + PGDH)
G3PDH (G3PDH-4)

TC-4 (40mm origin) 5 hrs @ 90 mA (max. 250V) **LKB** **THICK GEL**
[use of Heathkit may reguire longer run]

PEP-LT + PEPB (PEP-LT + PEPB-L) **a + c**
AAT (mAAT-1 & 2) **c only, from middle**
IDHP (sIDHP-1,2T)
MEP (sMEP-1 & 2) use 15mg oxaloacetate
GR
PEPD (PEPD-2)
ADA (ADA-2)

LIVER

CAME 6.8 (35 mm origin) 5 hrs @ 250V (max. 80 mA) THIN GEL

LDH (LDH-B2)
AAT (sAAT-4)
AH (sAH)
IDHP (sIDHP-1,2C)
MDH (sMDH-A1,2)
ADH **c only, from middle**

LIOH-RW (40mm origin) 80 mA (max. 400V) **LKB** THIN GEL
run until buffer front is 1 cm from end of gel

IDDH (IDDH-1 & 2) **a + c**
AAT (sAAT-4)
AH (sAH)
SOD (sSOD-1) **a + c**
bGLUA
ADH **c only, from middle**

Appendix II. Chinook variable loci and alleles - 1993-94

WDF ALLELE CODES & STANDARD RELATIVE MOBILITIES

LOCUS	1	2	3	4	5	6	7	8	9	10	TISSUE
sAAT-1,2	100	85	105	(91*)							M,H
sAAT-3	100	90	113	95*	71*						E
sAAT-4	100	130	63								L
mAAT-1	-100	-77	-104	XX	(-119)*						M,H
mAAT-2#	-100	[-125]	[-90]								M,H
mAAT-3#	100	-450									H
ADA-1	100	83	(69*)	96*	f*						M,E,H
ADA-2	100	105	96*	85*	["3" & "4" on TC-4 buffer]						M,E,H
ADH	100	-52	-170	[on hi pH]							L
sAH	100	86	112	108@	69	118*					L
mAH-1	100	65	130*								H
mAH-2#	100	83									H
mAH-3	100	126	74								M,H
mAH-4	100	119	112	109*	(136*)						M,H
CK-A1#	100	-450									M
CK-A2#	100	s?									M
CK-C1#	100	[s]									E
CK-C2#	100	[105]	[95]								E
CK-B#	100	96									E
GAPDH-2#	100	22									H
GAPDH-3#	100	123									H,M
GPI-B1#	100	XX	(175)								M
GPI-B2	100	60	135	24							M
GPI-A	100	105	93	85*							M,E,H
GPI-r	100	{%}									M
GR	100	85	110	89*	117*	71*	(vf*)				M,E,H,L
G3PDH-3#	100	[112]	[90]								H
G3PDH-4#	100	s?									M
IAGH	100	143	131*	65*	28*						M,H,L
IDDH-1#	100	0									L
IDDH-2#	100	61									L
IDHP-1#	100	147	30	178							M,E
IDHP-2	100	154	50*	f/TC4*	122*						M,E
IDHP-1,2	100	127	74	142	50	94	83	129	136*	92* &&	M,H,E,L
IDHP-1	100		74	142		94	(83)	129	136*	92* &&	M,H,E,L
IDH-2	100	127			50		83			&&	H,E,L
DH-1#	100	~60									E,L
DH-B2	100	112	134	71	56*						E,L
DH-C	100	90	84								E
MDH-A1,2	100	120	27	-45	(160*) (27 measures 50 on CAME6.8)						M,H,E
MDH-B1,2	100	121	70	83	126* null/f* null/s*						M,H,L
MDH-1	-100	-900									M,H
MDH-2	100	200	~180*								M,H
MDH-3#	100	190									M,H
MEP-1	100	92	105	86*							M,H
MEP-2	100	{78}									M,H
MEP-1#	100	150	~50								H
PI	100	109	95	113	103*	ms*	vs*				M,H,E
PPA	100	90	86	81*	XX	(~111*) (86 comigrates with 100 on TC-4)					M,E,H,L

(cont.)

Appendix II. Chinook variable loci - (cont.)

WDF ALLELE CODES & STANDARD RELATIVE MOBILITIES

LOCUS	1	2	3	4	5	6	7	8	9	10	TISSU
PEPB-1	100	130	-350	(s* = old 45 or 68?)							M,E,H,
PEPB-2	100	108									M,H
PEPD-2	100	107	83*								M,H
PEP-LT	100	110	(120*)	88* (120 on TC-4 only)							M,H
PGDH	100	90	85	(95*)	(109*)						M,E,H
PGK-2	100	90	74*	(ms*)							M,E,L
PGM-1	100	210	165*	50*							M,H
PGM-2	100	166	136	(~145*)	63*						M,H,L
PGM-3,4#	100	96	90	108	86						H,L
sSOD-1	-100	-260	580	1260	-175*	(~-160*)					M,H,E
sSOD-2#	100	[120]									H
mSOD	100	142	141$*	~70*							M,H
TPI-1#	100	(-155?)									M,E,H
TPI-2#	100	-400									M,E,H
TPI-3#	100	[104]	[106]	[91]							M,E,H
TPI-4	100	[104]	[75*]	[96*]	[102*]	[101*]					M,E,H

* = allele is not currently recognized in the coast-wide baseline
( ) = allele has only been seen in mixed-stock fishery samples
\# = locus is not currently supported by the coast-wide baseline
[ ] = scoring of variant & mobility of allele determined from heterodi
@ = mobility standards are necessary to distinguish the 108 and 112 alleles, or run side-by-side; measure on CAME 6.8
{ } = allele does not generate an isozyme of different mobility and is only scored reliably in the homozygous state
% = allele represents the absence of the GPI 1/3 heterodimer
$ = allele has approximately the same mobility as the "142" (on high buffers, but not on TC-4) and has greatly reduced activity, therefore the phenotypes are distinguishable
&& = the "11" allele is 66* and is from IDH-4
the "12" allele is ~126* and is from IDH-3
the "13" allele is 72* (TC-4) and is from IDH-3 (="74" on CAME6.8)
the "14" allele is ~132* and is from IDH-3; on TC-4 looks like a 129/100 or 127/127, on CAME6.8 looks like a 136/100.

Appendix A. Continued

Appendix III. Allele frequencies at 51 loci in 9 1993-94 Idaho chinook baseline collections. N = number of fish scored per locus.

COLLECTIONS 1 THROUGH 9

LOCUS/ALLELE	PAHSIMEROI	LEMHI	RED RIVER	NF SALMON	BEAR VAL	BRUSHY FK	LOLO	DWORSHAK H	EF SALM H
sAAT-1,2									
(N)	29	54	50	50	50	13	40	100	100
100	0.991	0.986	1.000	1.000	1.000	1.000	1.000	0.995	0.917
85	0.008	0.014	0.000	0.000	0.000	0.000	0.000	0.005	0.082
105	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
sAAT-3									
(N)	29	54	50	50	50	13	40	100	100
100	1.000	0.991	1.000	1.000	0.990	1.000	1.000	1.000	1.000
90	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
113	0.000	0.009	0.000	0.000	0.010	0.000	0.000	0.000	0.000
sAAT-4									
(N)	29	51	48	50	45	11	34	81	87
100	1.000	0.853	0.885	0.980	0.967	1.000	1.000	0.969	0.937
130	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
63	0.000	0.147	0.115	0.020	0.033	0.000	0.000	0.031	0.063
mAAT-1									
(N)	29	54	45	48	47	13	40	100	100
-100	1.000	1.000	0.978	1.000	1.000	1.000	1.000	1.000	1.000
-77	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
-104	0.000	0.000	0.022	0.000	0.000	0.000	0.000	0.000	0.000
mAAT-2									
(N)	29	48	39	44	44	9	38	99	92
-100	0.983	0.969	0.859	0.977	0.977	1.000	1.000	0.909	1.000
-125	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000
-90	0.017	0.021	0.141	0.023	0.023	0.000	0.000	0.091	0.000
ADA-1									
(N)	29	54	50	50	50	13	40	100	100
100	0.914	0.963	0.980	1.000	0.960	1.000	1.000	0.990	0.920
83	0.086	0.037	0.020	0.000	0.040	0.000	0.000	0.010	0.080
ADA-2									
(N)	29	54	50	50	50	13	40	100	100
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
sAH									
(N)	29	54	50	50	50	13	40	100	100
100	1.000	1.000	0.990	1.000	1.000	1.000	1.000	0.995	0.965
86	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.005	0.035
112	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

(continued)

Appendix III. 1993-94 Idaho chinook collections (cont.)

COLLECTIONS 1 THROUGH 9

LOCUS/ALLELE	PAHSIMEROI	LEMHI	RED RIVER	NF SALMON	BEAR VAL	BRUSHY FK	LOLO	DWORSHAK H	EF SALM H
mAH-3									
(N)	29	54	47	50	49	12	40	100	100
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
mAH-4									
(N)	29	54	40	43	48	13	40	100	100
100	1.000	1.000	0.975	1.000	1.000	1.000	1.000	1.000	1.000
119	0.000	0.000	0.025	0.000	0.000	0.000	0.000	0.000	0.000
GAPDH-2									
(N)	29	54	47	48	42	11	40	100	100
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
GAPDH-3									
(N)	29	54	47	48	42	11	40	100	100
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
123	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
GPI-B1									
(N)	29	54	50	50	50	13	40	100	100
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
GPI-B2									
(N)	29	54	50	50	50	13	40	99	100
100	1.000	0.991	0.990	1.000	0.950	1.000	0.987	0.985	0.945
60	0.000	0.009	0.010	0.000	0.050	0.000	0.012	0.015	0.055
GPI-A									
(N)	29	54	50	50	50	13	40	100	100
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
GPIr									
(N)	29	54	50	50	50	13	40	100	100
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
GR									
(N)	29	54	50	50	50	13	40	100	100
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.995	1.000
85	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000
HAGH									
(N)	29	54	50	50	50	13	40	100	100
100	0.948	0.926	0.930	0.800	0.940	0.885	0.862	0.925	0.925
143	0.052	0.074	0.070	0.200	0.060	0.115	0.137	0.075	0.075

(continued)

Appendix III. 1993-94 Idaho chinook collections (cont.)

COLLECTIONS 1 THROUGH 9

LOCUS/ALLELE	PAHSIMEROI	LEMHI	RED RIVER	NF SALMON	BEAR VAL	BRUSHY FK	LOLO	DWORSHAK H	EF SALM H
IDDH-1									
(N)	27	43	47	49	45	11	38	99	93
100	0.963	0.953	0.936	1.000	0.822	1.000	0.987	0.919	0.973
0	0.037	0.047	0.064	0.000	0.178	0.000	0.013	0.081	0.027
IDDH-2									
(N)	26	44	47	49	45	11	38	100	95
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
mIDHP-1									
(N)	29	54	50	50	50	13	39	100	100
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
mIDHP-2									
(N)	29	54	50	49	50	9	39	100	100
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.995	1.000
154	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
50	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000
sIDHP-1,2									
(N)	29	54	50	50	50	13	40	100	100
100	0.845	0.903	0.945	0.810	0.945	0.962	0.962	0.932	0.902
127	0.000	0.005	0.000	0.010	0.005	0.000	0.000	0.000	0.000
74	0.155	0.088	0.040	0.155	0.040	0.038	0.031	0.063	0.040
142	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
50	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
94	0.000	0.005	0.015	0.025	0.010	0.000	0.006	0.005	0.047
83	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
129	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
136	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
92	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
66	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010
sIDHP-1									
(N)	29	54	50	50	50	13	40	100	100
100	0.690	0.815	0.890	0.640	0.900	0.923	0.925	0.865	0.825
74	0.310	0.176	0.080	0.310	0.080	0.077	0.062	0.125	0.080
142	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
94	0.000	0.009	0.030	0.050	0.020	0.000	0.012	0.010	0.095
129	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
136	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
92	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

(continued)

Appendix III. 1993-94 Idaho chinook collections (cont.)

COLLECTIONS 1 THROUGH 9

LOCUS/ALLELE	PAHSIMEROI	LEMHI	RED RIVER	NF SALMON	BEAR VAL	BRUSHY FK	LOLO	DWORSHAK H	EF SALM H
sIDHP-2									
(N)	29	54	50	50	50	13	40	100	100
100	1.000	0.991	1.000	0.980	0.990	1.000	1.000	1.000	0.980
127	0.000	0.009	0.000	0.020	0.010	0.000	0.000	0.000	0.000
50	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
83	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
66	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.020
LDH-B1									
(N)	29	54	50	50	50	13	40	100	100
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
LDH-B2									
(N)	29	54	50	50	50	13	40	100	100
100	1.000	1.000	1.000	1.000	0.960	1.000	1.000	0.995	1.000
112	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.005	0.000
LDH-C									
(N)	29	54	50	50	50	13	40	100	100
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
90	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
84	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
sMDH-A1,2									
(N)	29	54	50	50	50	13	40	100	100
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
sMDH-B1,2									
(N)	29	54	50	50	50	13	40	100	100
100	1.000	0.990	0.990	0.940	0.970	1.000	0.987	0.987	1.000
121	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
70	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
83	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
126	0.000	0.009	0.010	0.060	0.030	0.000	0.012	0.012	0.000
mMDH-2									
(N)	29	54	49	50	49	13	40	100	100
100	0.534	0.389	0.755	0.540	0.724	0.692	0.912	0.750	0.585
200	0.466	0.611	0.245	0.460	0.276	0.308	0.087	0.250	0.415
mMDH-3									
(N)	29	54	50	50	50	13	40	100	100
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000

(continued)

Appendix III. 1993-94 Idaho chinook collections (cont.)

COLLECTIONS 1 THROUGH 9

LOCUS/ALLELE	PAHSIMEROI	LEMHI	RED RIVER	NF SALMON	BEAR VAL	BRUSHY FK	LOLO	DWORSHAK H	EF SALM H
sMEP-1									
(N)	29	54	49	50	49	13	40	98	100
100	0.103	0.065	0.041	0.110	0.031	0.000	0.125	0.056	0.025
92	0.897	0.935	0.959	0.890	0.969	1.000	0.875	0.944	0.975
86	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
sMEP-2									
(N)	29	54	50	50	49	13	39	100	100
100	1.000	1.000	1.000	1.000	1.000	1.000	0.949	1.000	1.000
78	0.000	0.000	0.000	0.000	0.000	0.000	0.051	0.000	0.000
MPI									
(N)	29	54	50	50	50	13	40	100	100
100	1.000	0.963	0.950	0.990	0.900	1.000	0.850	0.875	0.925
109	0.000	0.037	0.050	0.010	0.100	0.000	0.150	0.125	0.075
PGDH									
(N)	29	54	50	50	50	13	40	100	100
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
PGM-1									
(N)	29	54	50	49	50	13	40	100	100
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
PGM-2									
(N)	29	54	50	50	50	13	40	100	100
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
PGK-2									
(N)	29	54	50	50	50	13	40	100	100
100	0.241	0.157	0.060	0.210	0.040	0.192	0.062	0.205	0.125
90	0.759	0.843	0.940	0.790	0.960	0.808	0.937	0.795	0.875
PEPA									
(N)	29	54	50	50	50	13	40	100	100
100	1.000	1.000	0.980	1.000	1.000	1.000	1.000	0.990	1.000
90	0.000	0.000	0.020	0.000	0.000	0.000	0.000	0.000	0.000
86	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
81	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000
PEPB-1									
(N)	29	54	50	50	50	12	40	100	100
100	0.914	0.824	0.750	0.970	0.890	0.917	0.875	0.900	0.910
130	0.052	0.148	0.120	0.020	0.110	0.000	0.125	0.060	0.055
-350	0.034	0.028	0.130	0.010	0.000	0.083	0.000	0.040	0.035

(continued)

Appendix III. 1993-94 Idaho chinook collections (cont.)

COLLECTIONS 1 THROUGH 9

LOCUS/ALLELE	PAHSIMEROI	LEMHI	RED RIVER	NF SALMON	BEAR VAL	BRUSHY FK	LOLO	DWORSHAK H	EF SALM H
PEPD-2									
(N)	29	54	50	50	50	13	40	100	100
100	1.000	1.000	0.990	1.000	0.990	1.000	1.000	0.970	1.000
107	0.000	0.000	0.010	0.000	0.010	0.000	0.000	0.030	0.000
PEP-LT									
(N)	29	54	50	50	50	13	40	98	100
100	0.897	0.944	0.880	0.980	0.880	1.000	0.975	0.903	0.970
110	0.103	0.056	0.120	0.020	0.120	0.000	0.025	0.097	0.030
sSOD-1									
(N)	29	54	50	50	50	13	40	100	100
-100	0.948	0.880	0.890	0.990	0.990	0.885	0.862	0.845	0.950
-260	0.052	0.120	0.110	0.010	0.010	0.115	0.137	0.155	0.050
mSOD									
(N)	29	54	48	50	49	11	40	100	100
100	1.000	1.000	1.000	1.000	0.980	1.000	1.000	1.000	1.000
142	0.000	0.000	0.000	0.000	0.020	0.000	0.000	0.000	0.000
TPI-1									
(N)	29	54	50	50	50	13	40	100	100
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
TPI-2									
(N)	29	54	50	50	50	13	40	100	100
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
TPI-3									
(N)	29	54	50	50	50	13	40	100	100
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
TPI-4									
(N)	29	54	50	50	50	13	40	100	100
100	0.948	0.889	0.880	0.970	0.910	1.000	0.987	0.905	0.840
104	0.052	0.111	0.120	0.030	0.090	0.000	0.012	0.095	0.160

Appendix IV. Allele frequencies at 29 loci in 15 Idaho chinook populations. Data for 1991, 1992, 1993, and 1994 collections combined where available. N = number of fish scored per locus.

POPULATIONS 1 THROUGH 9

LOCUS/ALLELE	BEAR VAL	WF YANKEE	EF SALMON	HERD CR	PAHSIMEROI	CAMAS	NF SALMON	BRUSHY FK	CROOKED FK
sAAT-1,2									
(N)	175	104	74	103	118	106	136	45	102
100	0.998	0.974	0.936	0.980	0.993	0.979	0.967	1.000	1.000
85	0.002	0.017	0.061	0.020	0.007	0.021	0.033	0.000	0.000
105	0.000	0.009	0.004	0.000	0.000	0.000	0.000	0.000	0.000
sAAT-3									
(N)	175	105	74	103	118	106	136	45	102
100	0.960	1.000	0.953	1.000	1.000	1.000	1.000	1.000	1.000
90	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
113	0.040	0.000	0.047	0.000	0.000	0.000	0.000	0.000	0.000
sAAT-4									
(N)	161	93	73	93	112	82	131	40	91
100	0.950	0.995	0.979	0.995	0.964	0.835	0.989	1.000	0.940
130	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
63	0.050	0.005	0.021	0.005	0.036	0.165	0.011	0.000	0.060
mAAT-1									
(N)	171	103	74	102	118	103	134	44	89
-100	0.988	1.000	1.000	1.000	1.000	0.990	1.000	1.000	1.000
-77	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
-104	0.012	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000
mAAT-2									
(N)	168	98	71	96	114	91	130	40	85
-100	0.991	0.821	0.986	1.000	0.943	0.984	0.985	0.950	0.847
-125	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
-90	0.009	0.179	0.014	0.000	0.057	0.016	0.015	0.050	0.153
ADA-1									
(N)	175	105	74	103	118	106	136	45	102
100	0.949	0.967	0.946	0.971	0.898	0.910	0.996	1.000	0.980
83	0.051	0.033	0.054	0.029	0.102	0.090	0.004	0.000	0.020
sAH									
(N)	175	104	74	102	117	106	136	45	101
100	1.000	1.000	0.986	0.995	0.996	1.000	1.000	1.000	0.990
86	0.000	0.000	0.014	0.000	0.000	0.000	0.000	0.000	0.010
112	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000
108	0.000	0.000	0.000	0.000	0.004	0.000	0.000	0.000	0.000

(continued)

Appendix IV. 15 Idaho chinook populations, 1991-1994 (cont.)

POPULATIONS 1 THROUGH 9

LOCUS/ALLELE	BEAR VAL	WF YANKEE	EF SALMON	HERD CR	PAHSIMEROI	CAMAS	NF SALMON	BRUSHY FK	CROOKED FK
mAH-4									
(N)	173	105	74	103	118	106	129	45	102
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.900	0.956
119	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.100	0.044
GPI-B2									
(N)	173	104	74	103	118	105	135	45	102
100	0.962	1.000	1.000	1.000	0.996	0.971	1.000	1.000	1.000
60	0.038	0.000	0.000	0.000	0.004	0.029	0.000	0.000	0.000
HAGH									
(N)	175	105	74	103	118	106	136	45	102
100	0.949	0.890	0.946	0.976	0.949	0.962	0.904	0.878	0.951
143	0.051	0.110	0.054	0.024	0.051	0.038	0.096	0.122	0.049
IDDH-1									
(N)	153	103	72	97	113	88	133	43	92
100	0.905	0.990	0.958	0.918	0.978	0.943	1.000	0.988	0.967
0	0.095	0.010	0.042	0.082	0.022	0.057	0.000	0.012	0.033
sIDHP-1									
(N)	175	105	74	103	118	103	135	45	102
100	0.751	0.900	0.743	0.874	0.758	0.908	0.744	0.822	0.838
74	0.243	0.057	0.189	0.097	0.212	0.068	0.230	0.122	0.132
142	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
94	0.006	0.043	0.068	0.029	0.030	0.024	0.026	0.056	0.029
129	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
136	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
92	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
sIDHP-2									
(N)	175	105	74	103	118	106	136	45	102
100	0.991	0.962	0.980	0.825	1.000	1.000	0.993	0.944	0.961
127	0.009	0.029	0.014	0.150	0.000	0.000	0.007	0.056	0.034
50	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
83	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
66	0.000	0.010	0.007	0.024	0.000	0.000	0.000	0.000	0.005
LDH-B2									
(N)	175	105	74	103	118	106	136	45	102
100	0.966	0.990	1.000	0.995	1.000	0.981	1.000	0.989	0.990
112	0.034	0.010	0.000	0.005	0.000	0.019	0.000	0.011	0.010

(continued)

Appendix IV. 15 Idaho chinook populations, 1991-1994 (cont.)

POPULATIONS 1 THROUGH 9

LOCUS/ALLELE	BEAR VAL	WF YANKEE	EF SALMON	HERD CR	PAHSIMEROI	CAMAS	NF SALMON	BRUSHY FK	CROOKED FK
LDH-C									
(N)	175	105	74	103	118	106	136	45	102
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.995
90	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
84	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005
sMDH-B1,2									
(N)	173	105	74	103	118	106	136	45	102
100	0.981	0.990	0.936	0.988	0.989	1.000	0.978	1.000	0.990
121	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
70	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
83	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
126	0.019	0.009	0.064	0.012	0.010	0.000	0.022	0.000	0.010
mMDH-2									
(N)	174	104	74	103	117	106	135	45	101
100	0.667	0.731	0.392	0.641	0.637	0.689	0.552	0.733	0.767
200	0.333	0.269	0.608	0.359	0.363	0.311	0.448	0.267	0.233
sMEP-1									
(N)	174	103	72	102	117	106	136	45	101
100	0.060	0.044	0.007	0.005	0.077	0.132	0.136	0.022	0.030
92	0.940	0.956	0.993	0.995	0.923	0.868	0.864	0.978	0.970
105	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
86	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
MPI									
(N)	175	105	74	103	118	106	136	45	102
100	0.954	0.938	0.899	0.835	0.928	0.934	0.982	0.989	0.922
109	0.046	0.062	0.101	0.165	0.072	0.066	0.018	0.011	0.078
PGK-2									
(N)	175	105	74	103	118	106	136	45	102
100	0.051	0.186	0.155	0.184	0.178	0.009	0.099	0.111	0.240
90	0.949	0.814	0.845	0.816	0.822	0.991	0.901	0.889	0.760
PEPA									
(N)	175	105	74	103	118	106	136	45	102
100	1.000	0.995	1.000	1.000	0.996	1.000	1.000	1.000	0.985
90	0.000	0.005	0.000	0.000	0.004	0.000	0.000	0.000	0.010
86	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
81	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005

(continued)

Appendix IV. 15 Idaho chinook populations, 1991-1994 (cont.)

POPULATIONS 1 THROUGH 9

LOCUS/ALLELE	BEAR VAL	WF YANKEE	EF SALMON	HERD CR	PAHSIMEROI	CAMAS	NF SALMON	BRUSHY FK	CROOKED FK
PEPB-1									
(N)	175	105	74	103	118	106	136	44	102
100	0.937	0.757	0.959	0.820	0.886	0.958	0.930	0.920	0.848
130	0.063	0.110	0.007	0.150	0.093	0.024	0.051	0.011	0.078
-350	0.000	0.133	0.034	0.029	0.021	0.019	0.018	0.068	0.074
PEPD-2									
(N)	175	105	74	103	118	106	136	45	102
100	0.994	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
107	0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
PEP-LT									
(N)	175	105	74	103	118	106	136	45	102
100	0.843	0.952	0.966	0.942	0.903	0.962	0.967	0.989	0.931
110	0.157	0.048	0.034	0.058	0.097	0.038	0.033	0.011	0.069
sSOD-1									
(N)	175	103	74	103	118	106	136	45	102
-100	0.983	0.956	1.000	0.956	0.949	0.901	0.974	0.833	0.922
-260	0.017	0.044	0.000	0.044	0.051	0.099	0.026	0.167	0.078
mSOD									
(N)	173	103	74	103	118	106	135	43	102
100	0.965	1.000	1.000	1.000	1.000	0.995	1.000	1.000	1.000
142	0.035	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000
TPI-4									
(N)	175	105	74	103	118	106	136	45	102
100	0.940	0.914	0.939	0.811	0.911	0.896	0.941	0.967	0.931
104	0.057	0.086	0.061	0.189	0.089	0.104	0.059	0.033	0.069
75	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
96	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
102	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

(continued)

Appendix IV. Allele frequencies at 29 loci in 15 Idaho chinook populations, data combined between years (1991-1994) - cont.

POPULATIONS 10 THROUGH 15

LOCUS/ALLELE	RED R	LOLO CR	LEMHI	DWORSHAK H	E FORK H	SF SALMON
sAAT-1,2						
(N)	110	99	178	302	290	51
100	1.000	0.997	0.990	0.998	0.954	0.995
85	0.000	0.003	0.010	0.002	0.044	0.005
105	0.000	0.000	0.000	0.000	0.002	0.000
sAAT-3						
(N)	111	99	178	302	290	51
100	1.000	1.000	0.997	1.000	0.991	1.000
90	0.000	0.000	0.000	0.000	0.000	0.000
113	0.000	0.000	0.003	0.000	0.009	0.000
sAAT-4						
(N)	96	81	164	261	247	38
100	0.927	0.938	0.905	0.966	0.907	0.934
130	0.000	0.000	0.000	0.002	0.000	0.000
63	0.073	0.062	0.095	0.033	0.093	0.066
mAAT-1						
(N)	98	98	175	301	290	48
-100	0.990	1.000	1.000	1.000	1.000	1.000
-77	0.000	0.000	0.000	0.000	0.000	0.000
-104	0.010	0.000	0.000	0.000	0.000	0.000
mAAT-2						
(N)	92	84	164	289	253	41
-100	0.908	0.970	0.924	0.926	0.994	0.988
-125	0.000	0.000	0.012	0.000	0.000	0.000
-90	0.092	0.030	0.064	0.074	0.006	0.012
ADA-1						
(N)	110	99	178	302	290	51
100	0.968	0.995	0.958	0.978	0.936	0.922
83	0.032	0.005	0.042	0.022	0.064	0.078
sAH						
(N)	111	99	178	302	289	50
100	0.995	1.000	1.000	0.998	0.964	1.000
86	0.005	0.000	0.000	0.002	0.036	0.000
112	0.000	0.000	0.000	0.000	0.000	0.000
108	0.000	0.000	0.000	0.000	0.000	0.000

(continued)

Appendix IV. 15 Idaho chinook populations, 1991-1994 - cont.

POPULATIONS 10 THROUGH 15

LOCUS/ALLELE	RED R	LOLO CR	LEMHI	DWORSHAK H	E FORK H	SF SALMON
mAH-4						
(N)	101	99	178	302	290	50
100	0.990	1.000	1.000	0.993	1.000	0.990
119	0.010	0.000	0.000	0.007	0.000	0.010
GPI-B2						
(N)	111	98	178	298	290	51
100	0.995	0.985	0.992	0.953	0.974	0.922
60	0.005	0.015	0.008	0.047	0.026	0.078
HAGH						
(N)	111	99	178	302	290	51
100	0.955	0.904	0.958	0.934	0.916	0.922
143	0.045	0.096	0.042	0.066	0.084	0.078
IDDH-1						
(N)	102	88	159	292	270	42
100	0.961	0.960	0.937	0.937	0.924	0.988
0	0.039	0.040	0.063	0.063	0.076	0.012
sIDHP-1						
(N)	110	98	178	302	290	47
100	0.900	0.862	0.826	0.828	0.824	0.787
74	0.059	0.107	0.140	0.156	0.109	0.117
142	0.000	0.000	0.000	0.000	0.000	0.000
94	0.041	0.031	0.034	0.017	0.067	0.096
129	0.000	0.000	0.000	0.000	0.000	0.000
136	0.000	0.000	0.000	0.000	0.000	0.000
92	0.000	0.000	0.000	0.000	0.000	0.000
sIDHP-2						
(N)	111	99	178	302	290	51
100	1.000	1.000	0.980	1.000	0.993	0.990
127	0.000	0.000	0.020	0.000	0.000	0.010
50	0.000	0.000	0.000	0.000	0.000	0.000
83	0.000	0.000	0.000	0.000	0.000	0.000
66	0.000	0.000	0.000	0.000	0.007	0.000
LDH-B2						
(N)	111	99	178	302	290	51
100	0.995	0.970	0.992	0.970	0.995	1.000
112	0.005	0.030	0.008	0.030	0.005	0.000

(continued)

Appendix IV. 15 Idaho chinook populations, 1991-1994 - cont.

POPULATIONS 10 THROUGH 15

LOCUS/ALLELE	RED R	LOLO CR	LEMHI	DWORSHAK H	E FORK H	SF SALMON
LDH-C						
(N)	111	99	178	302	290	51
100	1.000	1.000	1.000	0.993	1.000	1.000
90	0.000	0.000	0.000	0.007	0.000	0.000
84	0.000	0.000	0.000	0.000	0.000	0.000
sMDH-B1,2						
(N)	111	99	178	302	290	51
100	0.995	0.977	0.984	0.990	0.998	0.990
121	0.000	0.000	0.000	0.000	0.000	0.000
70	0.000	0.000	0.000	0.000	0.000	0.000
83	0.000	0.000	0.000	0.000	0.000	0.000
126	0.005	0.022	0.015	0.010	0.002	0.010
mMDH-2						
(N)	109	99	174	302	290	51
100	0.798	0.864	0.517	0.732	0.576	0.735
200	0.202	0.136	0.483	0.268	0.424	0.265
sMEP-1						
(N)	110	99	176	300	290	51
100	0.055	0.131	0.045	0.088	0.010	0.020
92	0.945	0.869	0.952	0.912	0.990	0.980
105	0.000	0.000	0.000	0.000	0.000	0.000
86	0.000	0.000	0.003	0.000	0.000	0.000
MPI						
(N)	110	94	178	302	290	51
100	0.932	0.904	0.938	0.914	0.917	0.912
109	0.068	0.096	0.062	0.086	0.083	0.088
PGK-2						
(N)	111	99	178	302	290	51
100	0.122	0.076	0.132	0.162	0.114	0.137
90	0.878	0.924	0.868	0.838	0.886	0.863
PEPA						
(N)	111	99	178	302	290	51
100	0.991	1.000	0.994	0.995	1.000	1.000
90	0.009	0.000	0.006	0.002	0.000	0.000
86	0.000	0.000	0.000	0.000	0.000	0.000
81	0.000	0.000	0.000	0.003	0.000	0.000

(continued)

Appendix IV. 15 Idaho chinook populations, 1991-1994 - cont.

POPULATIONS 10 THROUGH 15

LOCUS/ALLELE	RED R	LOLO CR	LEMHI	DWORSHAK H	E FORK H	SF SALMON
PEPB-1						
(N)	110	99	178	302	290	51
100	0.755	0.838	0.798	0.897	0.916	0.971
130	0.136	0.081	0.146	0.051	0.053	0.020
-350	0.109	0.081	0.056	0.051	0.031	0.010
PEPD-2						
(N)	111	99	178	298	290	51
100	0.995	0.995	1.000	0.980	1.000	0.931
107	0.005	0.005	0.000	0.020	0.000	0.069
PEP-LT						
(N)	111	99	178	300	290	51
100	0.905	0.980	0.952	0.942	0.862	0.892
110	0.095	0.020	0.048	0.058	0.138	0.108
sSOD-1						
(N)	111	99	178	302	290	51
-100	0.932	0.803	0.896	0.863	0.928	0.961
-260	0.068	0.197	0.104	0.137	0.072	0.039
mSOD						
(N)	109	99	178	302	290	51
100	1.000	1.000	0.997	1.000	1.000	0.971
142	0.000	0.000	0.003	0.000	0.000	0.029
TPI-4						
(N)	111	99	178	302	290	51
100	0.932	0.960	0.938	0.911	0.860	0.892
104	0.068	0.040	0.062	0.089	0.140	0.108
75	0.000	0.000	0.000	0.000	0.000	0.000
96	0.000	0.000	0.000	0.000	0.000	0.000
102	0.000	0.000	0.000	0.000	0.000	0.000

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