Fishery Data Series No. 09-02

Estimation of the Escapement of Chinook Salmon in the Unuk River in 2006

by

Jan L. Weller

and

David G. Evans

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Alaska Department of Fish and Game Divisions of Sport Fish and Commercial Fisheries

Symbols and Abbreviations

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Weights and measures (metric)

centimeter	cm
deciliter	dL
gram	g
hectare	ha
kilogram	kg
kilometer	km
liter	L
meter	m
milliliter	mL
millimeter	mm

Weights and measures (English)

cubic feet per second	ft^3/s
foot	ft
gallon	gal
inch	in
mile	mi
nautical mile	nmi
ounce	oz
pound	lb
quart	qt
yard	yd

Time and temperature

day	d
degrees Celsius	°C
degrees Fahrenheit	°F
degrees kelvin	K
hour	h
minute	min
second	s

Physics and chemistry

all atomic symbols	
alternating current	AC
ampere	A
calorie	cal
direct current	DC
hertz	Hz
horsepower	hp
hydrogen ion activity (negative log of)	pH
parts per million	ppm
parts per thousand	ppt, ‰
volts	V
watts	W

General

Alaska Department of Fish and Game	ADF&G
Alaska Administrative Code	AAC
all commonly accepted abbreviations	e.g., Mr., Mrs., AM, PM, etc.
all commonly accepted professional titles	e.g., Dr., Ph.D., R.N., etc.
at	@
compass directions:	
east	E
north	N
south	S
west	W
copyright	©
corporate suffixes:	
Company	Co.
Corporation	Corp.
Incorporated	Inc.
Limited	Ltd.
District of Columbia	D.C.
et alii (and others)	et al.
et cetera (and so forth)	etc.
exempli gratia (for example)	e.g.
Federal Information Code	FIC
id est (that is)	i.e.
latitude or longitude	lat. or long.
monetary symbols (U.S.)	$, ¢
months (tables and figures): first three letters	Jan,...,Dec
registered trademark	®
trademark	™
United States (adjective)	U.S.
United States of America (noun)	USA
U.S.C.	United States Code
U.S. state	use two-letter abbreviations (e.g., AK, WA)

Measures (fisheries)

fork length	FL
mideye-to-fork	MEF
mideye-to-tail-fork	METF
standard length	SL
total length	TL

Mathematics, statistics

all standard mathematical signs, symbols and abbreviations	
alternate hypothesis	H_A
base of natural logarithm	*e*
catch per unit effort	CPUE
coefficient of variation	CV
common test statistics	(F, t, χ^2, etc.)
confidence interval	CI
correlation coefficient (multiple)	R
correlation coefficient (simple)	r
covariance	cov
degree (angular)	°
degrees of freedom	df
expected value	*E*
greater than	>
greater than or equal to	≥
harvest per unit effort	HPUE
less than	<
less than or equal to	≤
logarithm (natural)	ln
logarithm (base 10)	log
logarithm (specify base)	$log_{2,}$ etc.
minute (angular)	'
not significant	NS
null hypothesis	H_O
percent	%
probability	P
probability of a type I error (rejection of the null hypothesis when true)	α
probability of a type II error (acceptance of the null hypothesis when false)	β
second (angular)	"
standard deviation	SD
standard error	SE
variance	
population	Var
sample	var

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by
Jan L. Weller
Division of Sport Fish, Ketchikan
and
David G. Evans
Division of Sport Fish, Anchorage

Alaska Department of Fish and Game
Division of Sport Fish, Research and Technical Services
333 Raspberry Road, Anchorage, Alaska, 99518-1599

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Jan L. Weller,[a]
Alaska Department of Fish and Game, Division of Sport Fish, Region I
2030 Sealevel Dr., Suite 205, Ketchikan, AK 99901, USA

and
David G. Evans,
Alaska Department of Fish and Game, Division of Sport Fish, Region III
333 Raspberry Road, Anchorage, AK 99518-1599, USA

[a] *Author to whom all correspondence should be addressed: red.weller@alaska.gov*

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ABSTRACT

A two-event mark–recapture experiment was used to estimate the abundance of Chinook salmon *Oncorhynchus tshawytscha* that returned to spawn in the Unuk River in 2006. Biological data were collected during both events. Fish were captured during event 1 in the lower Unuk River using set gillnets from 11 June through 3 August. Each apparently healthy fish was marked with a numbered solid-core spaghetti tag sewn through its back and two secondary batch marks in the form of an upper-left operculum punch and removal of the left axillary appendage. In event 2, fish were examined on the spawning grounds from 4 through 24 August to estimate the fraction of the population that had been marked. Abundance of large Chinook salmon (≥660 mm MEF) was estimated to be 5,645 (SE = 476). The estimate was made from 853 marked and 102 recaptured fish out of 680 examined upstream. Abundance of medium-sized fish (545–659 mm MEF) was estimated to be 1,767 (SE = 418). The estimate was made from 147 marked and 18 recaptured fish out of 226 examined on the spawning grounds. Using indirect methods, the abundance of small-sized fish (<545 mm MEF) was estimated to be 311 (SE = 58). An estimated 23.7% of the spawning population (fish of all sizes) was sampled during the project. Peak survey counts in August totaled 940 large Chinook salmon, or about 17% of the mark–recapture estimate of large fish, similar to fractions seen in previous years. The mean expansion factor through 2006 is 5.27 (SD = 1.09) for estimating total escapement from survey counts. The estimated spawning population of 7,723 Chinook salmon was composed of 42.2% (SE = 3.4%) age-1.2 fish, 27.8% (SE = 2.0%) age-1.3 fish, 27.2% (SE = 2.1%) age-1.4 fish, and 2.9% (SE = 0.6) age-1.1 fish. Females composed an estimated 31.9% (2,466 fish) of spawners (SE = 2.4%), all of which were age-1.3 and -1.4 fish.

Key words: escapement, Chinook salmon, Unuk River, mark–recapture, set gillnet, spaghetti tag, operculum punch, axillary appendage, peak survey counts, expansion factor

INTRODUCTION

The Unuk, Chickamin, Blossom, and Keta rivers in Southeast Alaska (SEAK) are four of eleven escapement indicator streams for Chinook salmon *Oncorhynchus tshawytscha* (Pahlke 1997). These four systems traverse the Misty Fjords National Monument and flow into Behm Canal, a narrow saltwater passage east of Ketchikan (Figure 1). Peak single-day aerial and foot survey counts of “large” Chinook salmon ≥660 mm MEF have been used as indices of escapement in each of these systems. These indices are roughly dome-shaped when plotted against time (1975–1999) with peak values occurring between 1987 and 1990 (Pahlke 1997). Since 1999, survey counts and estimated total escapement have increased to levels approaching the former peak values in the Unuk and Chickamin rivers.

Several consecutive low survey counts in the early 1990s generated concern for the health of the Chinook salmon stocks in Behm Canal. In 1992, the Division of Sport Fish of the Alaska Department of Fish and Game (ADF&G) began a research program on the Unuk River, which is the largest Chinook salmon producer in Behm Canal. Goals of the program were to estimate overwinter survival of fingerlings, production and marine survival of smolts, escapement and harvest of adults, total run size, and exploitation rates. These goals are being accomplished with inriver mark–recapture experiments on adults and smolts and with marine catch sampling programs.

The current escapement goal for the Unuk River is 650–1,400 large fish counted in surveys, or an actual escapement of about 3,000–7,000 large fish (McPherson and Carlile 1997). Only large fish are counted in aerial surveys because smaller Chinook salmon are readily mistaken for other salmon species of similar size and color. For our purposes, Chinook salmon ≥660 mm MEF are considered large and are generally fish 3-ocean age (age-.3) or older. Nearly all females in the spawning population are classified as large. Chinook salmon 401–659 mm MEF are usually considered to be medium fish and Chinook salmon ≤400 mm MEF are considered small fish, but we redefined these two size categories for the 2006 analysis. An index of escapement on the Unuk River has been determined annually since 1977 as the peak count of large spawners observed during several aerial and foot surveys of six tributaries: Cripple, Genes Lake, Kerr, Clear, and Lake creeks plus the Eulachon River (Pahlke 1997; Figure 2). The tributary supporting the

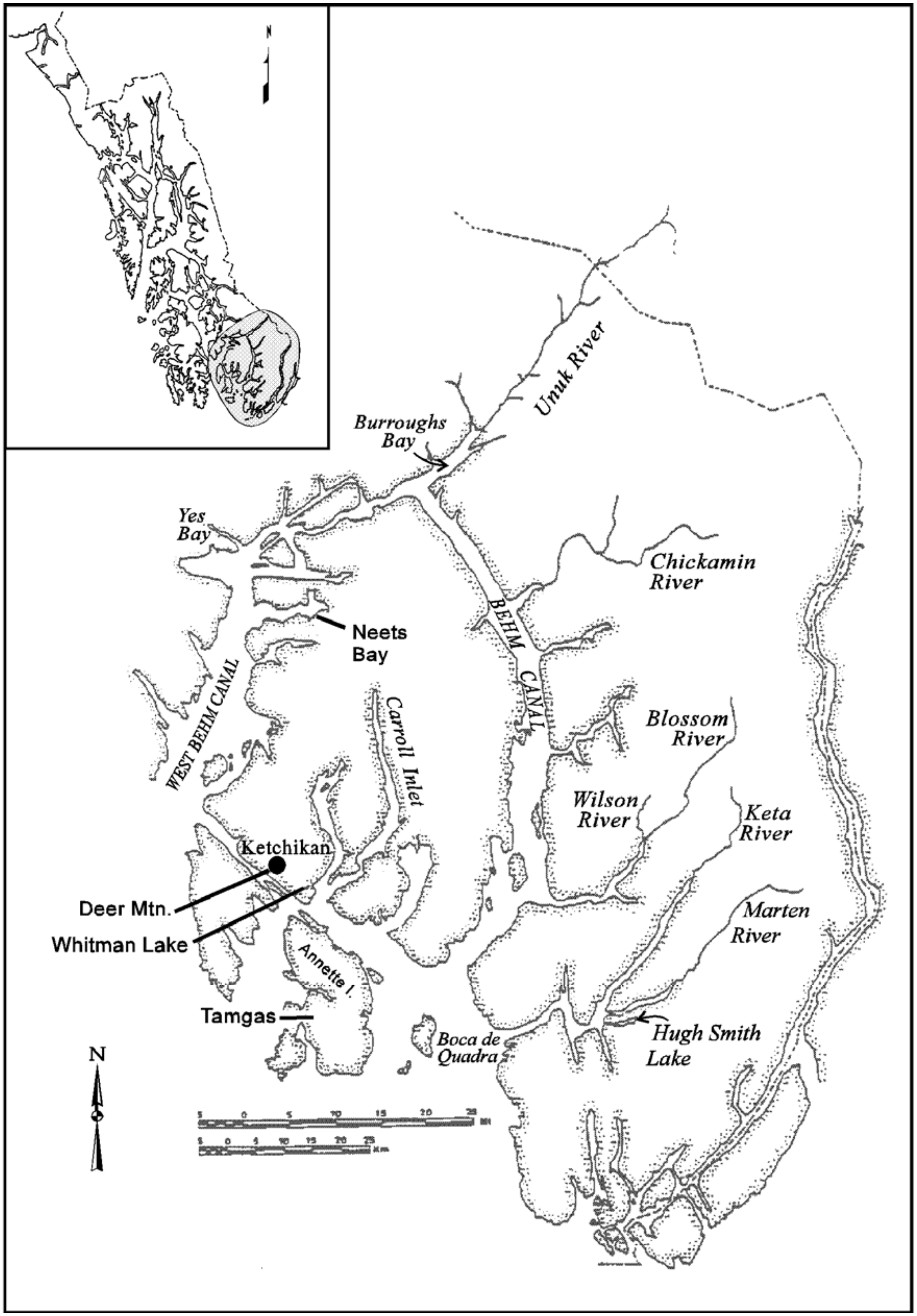

Figure 1.–Behm Canal area in Southeast Alaska and location of selected Chinook salmon systems and hatcheries.

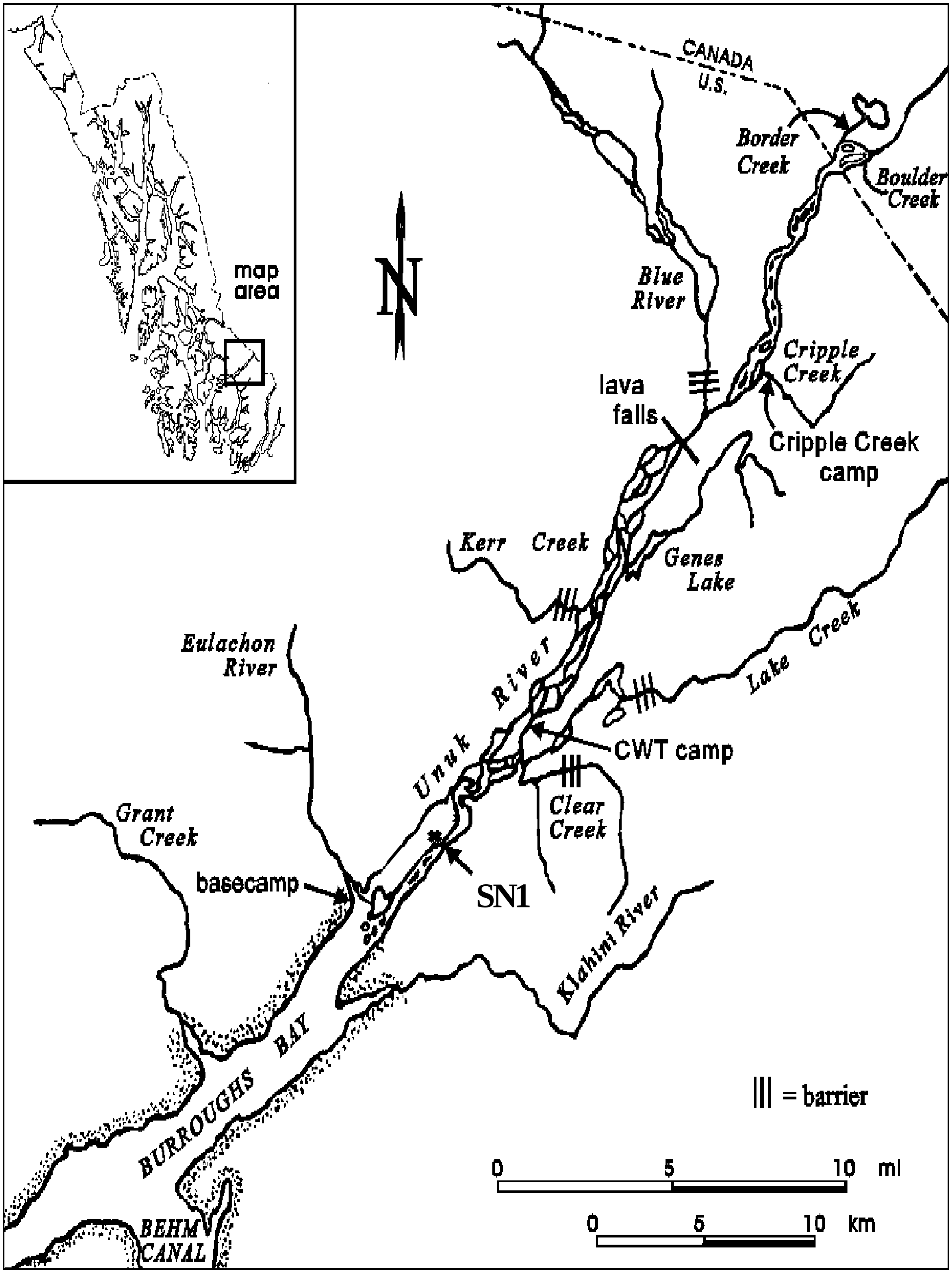

Figure 2.–Unuk River area in Southeast Alaska, showing major tributaries, barriers to Chinook salmon migration, and location of ADF&G research sites.

largest known spawning population to be excluded from the index is Boundary Creek (also known as Border creek). Surveys of Boundary Creek didn't commence until 1991; difficulties in accessing this tributary have resulted in surveys being conducted sporadically since 1991, and consequently this tributary is not included in the index.

Mark–recapture and radiotelemetry studies were conducted in 1994 (Pahlke et al. 1996). Mark–recapture studies have also been conducted annually from 1997 through 2005 (Jones III et al. 1998, Jones III and McPherson 1999, 2000, 2002; Weller and McPherson 2003a-b, 2004, 2006a-b). The radiotelemetry study indicated that 83% (SE = 9%) of all spawning occurred in the six tributaries surveyed. Despite being downriver of the Event 1 tagging site, the Eulachon River is included in the mark–recapture study because no significant difference in tag recovery rates between the Eulachon River and upriver spawning locations was found by Pahlke et al. (1996). The 1997–2005 mark–recapture experiments estimated that an average of 5,408 large Chinook salmon entered the river during those years and ranged from 2,970 (1997) to 10,541 (2001; Weller and McPherson 2006b). Indices during those years averaged 1,052 large Chinook salmon, or 19.9% of the mark–recapture estimates, and ranged from 636 (1997) to 2,019 (2001). The highest recorded index of 2,126 large fish occurred in 1986 (Pahlke 1997). From 1977 to 2005, average peak survey counts in the six index tributaries of the Unuk River were distributed as follows: Cripple Creek (412 fish, 37%), Gene's Lake Creek (362 fish, 33%), Eulachon River (162 fish, 15%), Clear Creek (103 fish, 9%), Kerr Creek (40 fish, 4%), and Lake Creek (31 fish, 3%). Cripple Creek and Gene's Lake Creek are not surveyed from the air because of heavy canopy cover; surveys of these areas are made on foot. All other index areas are surveyed by helicopter or on foot (Pahlke 2008). There is a significant correlation between survey count and mark–recapture estimate of large fish ($r = 0.89$; $P < 0.01$).

Other studies on the Unuk River were based on coded wire tags (CWTs) inserted into Chinook salmon juveniles from the 1982–1986 brood years (Pahlke 1995). This research showed that commercial and sport harvest rates on the Unuk River Chinook salmon stock (age-1.1–1.5) ranged from 14% to 24%; however, the precision of the harvest estimates was low, as was confidence in the expansion factor used to estimate escapements (McPherson and Carlile 1997; Pahlke 1995).

Starting in 1993, young-of-the-year (YOY) fingerlings were tagged with CWTs. From 1993 through 2006, 485,719 Chinook (fall) fingerlings have been tagged, at an annual average of 34,694 and a range of 13,789 (1993) to 61,905 (1997; Weller et al. *In Prep*). Tagging of smolt commenced in spring 1994, and 143,860 smolt have been tagged through 2006 at an annual average of 11,066 and a range of 2,642 (1994) to 17,121 (1998; Weller et al. *In Prep*).

The current stock assessment program for adult escapement of Chinook salmon to the Unuk River has three primary objectives: (1) to estimate escapement; (2) to estimate age, sex, and length distribution in the escapement; and (3) to estimate the fraction of fish possessing CWTs by brood year. Meeting this last objective is essential to estimating harvest of this stock in current and future sport and commercial fisheries. Together harvest and escapement data will enable us to estimate run size, exploitation rates and harvest distribution. Marine survival estimates are also possible when these data are combined with smolt abundance estimates.

STUDY AREA

The Unuk River originates in a heavily glaciated area of northern British Columbia and flows for 129 km where it empties into Burroughs Bay, 85 km northeast of Ketchikan, Alaska. The Unuk River drainage encompasses an area of approximately 3,885 km^2 (Pahlke et al. 1996). The lower 39 km of the Unuk River are in Alaska (Figure 2), and in most years, the Unuk River is the fourth or fifth largest producer of Chinook salmon in Southeast Alaska.

METHODS

A two-event mark–recapture experiment for a closed population was used to estimate the number of immigrant medium and large Chinook salmon to the Unuk River in 2006. Fish were captured using set gillnets in the lower river for the first event and were sampled for marks with a variety of gear types on the spawning grounds for the second event.

EVENT 1: SAMPLING IN THE LOWER RIVER

Adult Chinook salmon were captured using set gillnets at the SN1 site (Figure 2) as they immigrated into the lower Unuk River between 11 June and 3 August 2006. The set gillnets were 37 m (120 ft) long by 4 m (14 ft) deep with 18 cm (7¼ in.) stretch mesh and a loose hanging ratio of about 2.2:1. The SN1 site has been used for event 1 fish capture since 1997. This site is located approximately 2 miles upstream of saltwater on the south channel, mainstem of the lower Unuk River well below all known spawning areas except the Eulachon River (Figure 3).

Two back-to-back shifts of personnel fished two set gillnets at SN1 12 hours per day, 6 days per week. Crew shifts were staggered during the week so that at least one shift fished each day of the week whenever possible. One net was set perpendicular to the main flow of the Unuk River; it was attached to shore and ran directly across a small slough to a fixed buoy placed about 3 m downstream of a small island. Another net was attached to the same fixed buoy and trailed downstream along the eddy line formed between the mainstem and the side slough (Figure 4). Fish captured in the set gillnet were immediately and carefully untangled or cut loose and placed in a live tank aboard the set gillnet skiff.

All fish captured, regardless of health, were sampled to estimate the age, sex, and length (ASL) composition of the escapement. Length in MEF was measured to the nearest 5 mm, and sex was determined from external, dimorphic characteristics. Five scales were taken about 1″ apart within the preferred area on the left side of each fish. The preferred area is two to three rows above the lateral line and between the posterior terminus of the dorsal fin and the anterior margin of the anal fin (Welander 1940). Scales were mounted on gum cards that held scales from ten fish, as described in ADF&G (1994). The age of each fish was later determined from the pattern of circuli (Olsen 1995), seen on images of scales impressed into acetate cards magnified 70× (Clutter and Whitesel 1956). The presence or absence of an adipose fin was also noted for each sampled fish. Those fish missing adipose fins and <700 mm MEF (jacks) were sacrificed, and their heads were sent to the ADF&G Commercial Fishery Division's Mark Tag and Age Laboratory (Tag Lab) for detection and decoding of CWTs.

With the exception of fish <700 mm MEF that were missing an adipose fin, all captured fish judged healthy were marked with a uniquely numbered solid-core spaghetti tag sewn through the back, a clip of the left axillary appendage (LAA), and a left upper operculum punch (LUOP) 0.63 cm (¼″) in diameter. The axillary clip and operculum punch enabled detection of tag loss. The spaghetti tag consisted of a 5.71 cm (2¼″) section of laminated Floy tubing shrunk onto a 38 cm (15″) piece of 80-lb-test monofilament fishing line. The monofilament was sewn through the back just behind the dorsal fin and secured by crimping both ends of the monofilament in a line crimp. The excess monofilament was then trimmed off. Each spaghetti tag was individually numbered and stamped with an ADF&G phone number.

EVENT 2: SAMPLING ON THE SPAWNING GROUNDS

Chinook salmon of all sizes were sampled on Boundary Creek (also known as Border Creek); on Clear, Cripple, Genes Lake, Kerr, and Lake creeks; and on the Eulachon River in 2006 (Figure 2). Various methods were used to capture fish including rod and reel, dip nets, gillnets, and carcass surveys. Use of a variety of gear types has been shown to produce unbiased estimates of age, sex, and length composition (Jones III et al. 1998, Jones III and McPherson 1999, 2000, 2002; McPherson et al. 1997). A hole was punched into the left lower operculum (LLOP) of all newly inspected fish to prevent double sampling. Inspected fish were closely examined for a tag, an LUOP, an LLOP, an LAA, a missing adipose fin, and were sampled to obtain ASL data by the same techniques used in the lower river. For Chinook salmon missing adipose fins, all fish <700 mm MEF, as well as spawned-out fish of all sizes, were sacrificed to retrieve CWTs. Heads so collected were sent to the Tag Lab for dissection

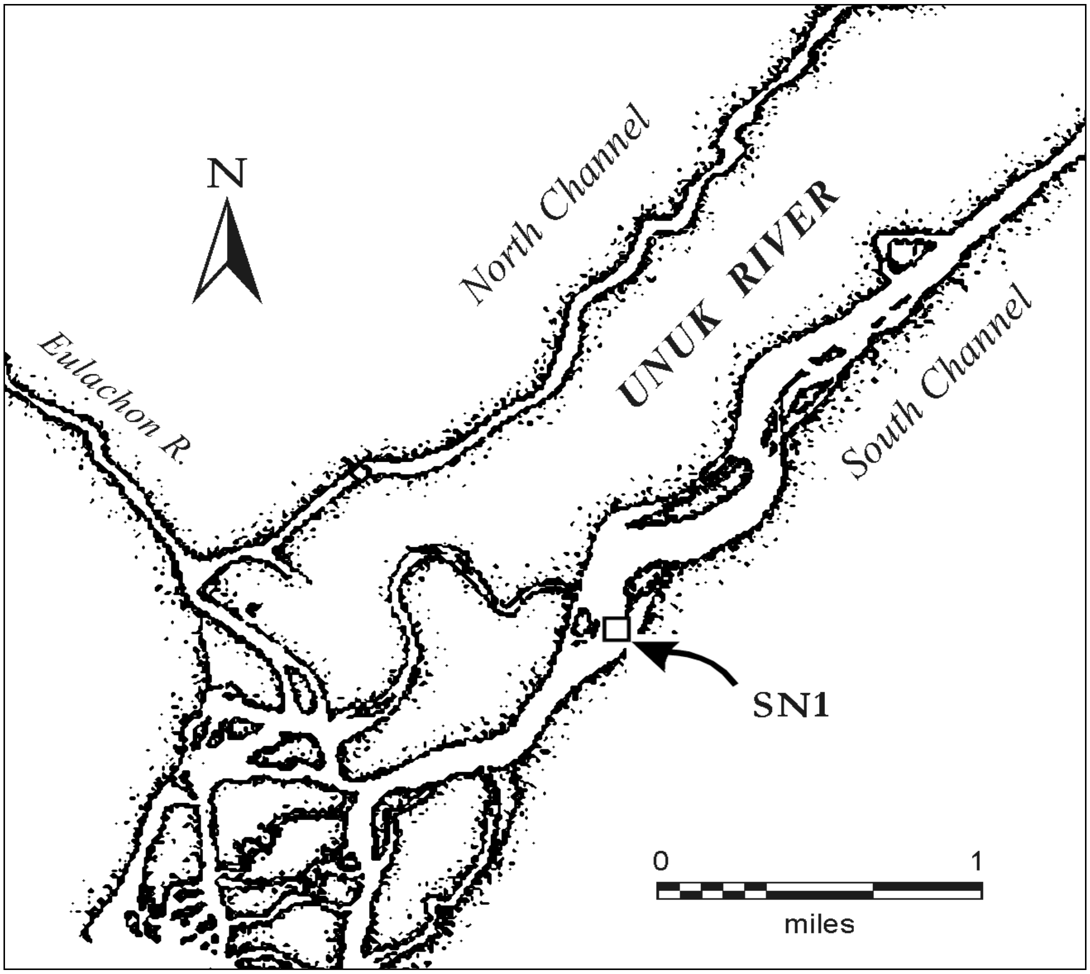

Figure 3.–Location of the set gillnet site (SN1) on the lower Unuk River in 2006.

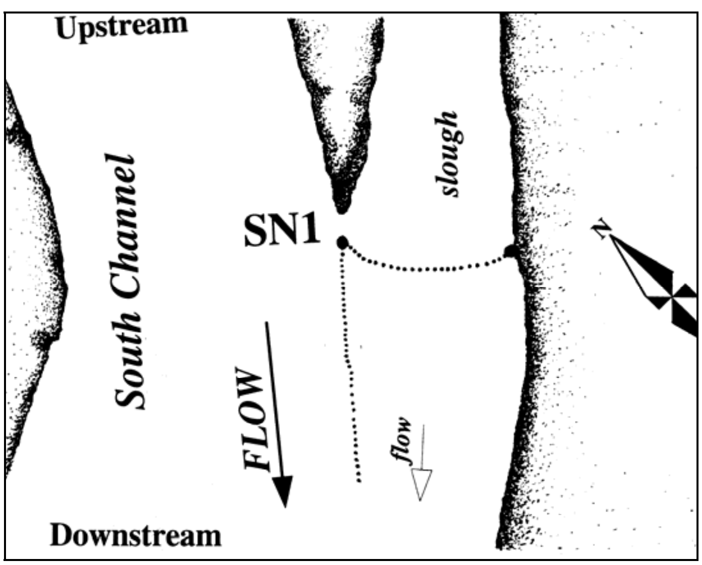

Figure 4.–Net placement used at the set gillnet site (SN1) on the lower Unuk River in 2006.

and decoding of tags. Foot surveys were also conducted on each of the sampled tributaries on at least one occasion. Multiple surveys were spaced approximately one week apart and when possible, a survey was conducted on the historical peak of observed abundance.

ABUNDANCE BY SIZE

Abundance of medium and large fish was estimated separately so that the estimate for large fish $\hat{N}_L$ could be compared to the index. For medium Chinook salmon, no marked fish were recovered smaller than 545mm MEF, so the medium size class was redefined to include only fish 545–659 mm MEF. Using Chapman's modification of the Petersen estimator (Seber 1982), estimated abundance $\left(\hat{N}_i\right)$ for each group was calculated as:

$$\hat{N}_i = \frac{(M_i + 1)(C_i + 1)}{(R_i + 1)} - 1 \quad (1)$$

where M_i is the number of fish of size *i* (medium or large) sampled and marked during event 1, C_i is the number of fish of size *i* inspected for marks during event 2, and R_i is the number of C_i that possessed marks applied during event 1. The general conditions that must hold for $\hat{N}_i$ to be a consistent estimate of abundance are in Seber (1982) and may be cast as follows:

(a) every fish had an equal probability of being marked in the first event, or that every fish had an equal probability of being captured in the second event, or that marked fish mixed completely with unmarked fish;

(b) both recruitment and mortality did not occur between events;

(c) marking did not affect the catchability of a fish;

(d) fish did not lose their marks in the time between the two events;

(e) all marks were reported on recovery in the second event; and,

(f) double sampling did not occur.

Condition (a) may be violated if size- or sex-selective sampling occurs. Kolmogorov-Smirnov (K-S, Conover 1980) two-sample tests were used to test the hypothesis that fish of different lengths were captured with equal probability during both first and second sampling events. These test procedures are described in Appendix A1, as well as corrective measures (stratification) based on diagnostic test results that minimize bias in estimation of abundance and composition parameters. Tests for gender bias were not conducted because of errors detected in gender classification during first event sampling.

Three consistency tests (Appendix A2) described by Seber (1982) and Arnason et al. (1996) were used to test for temporal and/or spatial violations of condition (a). Contingency table analyses were used to test three null hypotheses: 1) for all marked fish recovered during event 2, time of marking is independent of where recovery occurs; 2) the probability that a fish inspected during event 2 is marked is independent of where it was caught during the second event; and 3) the probability that a marked fish is recovered during event 2 is independent of when it was marked. If all three hypotheses were rejected, the "partially" stratified abundance estimator described by Darroch (1961) was necessary to estimate abundance. Failure to reject at least one of these three hypotheses was sufficient to conclude that at least one of assumptions in conditions (a) was satisfied, and a Petersen-type model was appropriate to estimate abundance.

The experiment was assumed closed to recruitment because first event sampling spanned the entire immigration. Marking was assumed to have little effect on behavior of released fish or the catchability of fish on the spawning grounds because only fish in good condition were tagged and released, and because the 1994 radio telemetry study indicated minimal mortality from handling in the marking event for Chinook salmon (Pahlke et al. 1996). The use of multiple marks during event 1, careful inspection of all fish captured during event 2, and additional marking of all fish inspected helped to ensure assumptions (d), (e), and (f) were met.

Variance, bias, and confidence intervals for $\hat{N}_i$ were estimated with modifications of bootstrap procedures in Buckland and Garthwaite (1991). Fish were divided into four capture histories (Table 1).

Table 1.–Capture histories for medium-and large Chinook salmon in the population spawning in the Unuk River in 2006 (notation explained in text).

Capture history	Medium	Large	Source of statistics
Marked and not captured in tributaries	129	751	$M_i - R_i$
Marked and captured in tributaries	18	102	R_i
Not marked, but captured in tributaries	208	578	$C_i - R_i$
Not marked and not captured in tributaries	1,412	4,214	$\hat{N}_i - M_i - C_i + R_i$

A bootstrap sample was built by drawing with replacement a sample of size $\hat{N}_i$ from the empirical distribution defined by the capture histories. A new set of statistics from each bootstrap sample $\{\hat{M}_i^*, \hat{C}_i^*, \hat{R}_i^*\}$ was generated, along with a new estimate for abundance $\hat{N}_i^*$. A thousand such bootstrap samples were drawn, creating the empirical distribution $\hat{F}(\hat{N}_i^*)$, which is an estimate of $F(\hat{N}_i)$. The difference between the average $\hat{N}_i^*$ of bootstrap estimates and $\hat{N}_i$ is an estimate of statistical bias in the latter statistic (Efron and Tibshirani 1993b, Section 10.2). Confidence intervals were estimated from $\hat{F}(\hat{N}_i^*)$ with the percentile method (Efron and Tibshirani 1993b, Section 13.3). Variance was estimated as:

$$\text{var}(\hat{N}_i^*) = (B-1)^{-1}\sum_{b=1}^{B}(\hat{N}_{i(b)}^* - \overline{\hat{N}}_i^*)^2 \qquad (2)$$

where B is the number of bootstrap samples (1,000).

Due to our failure to capture a sufficient number of small-sized fish, redefined as fish <545 mm MEF, the mark–recapture experiment could not be used to directly estimate the abundance of small Chinook salmon. Consequently the abundance of small-sized fish was estimated indirectly by expanding the estimate for large and medium fish by the estimated size composition of the spawning escapement:

$$\hat{N}_S = \hat{N}_{LM}\left(\frac{1}{\hat{\phi}} - 1\right) \qquad (3)$$

where $\hat{N}_S$ is the estimated spawning escapement of small-sized fish, $\hat{N}_{LM}$ is the estimated spawning escapement of large plus medium fish, and $\hat{\phi}$ is the estimated fraction of large- and medium-sized fish in the spawning population of Chinook salmon (McPherson et al. 1997).

The variance of the estimate of the abundance of small fish was estimated:

$$\text{var}(\hat{N}_S) = \text{var}(\hat{N}_{LM})\left[\frac{1}{\phi} - 1\right]^2 + \hat{N}_{LM}^{\,2}\,\text{var}\left(\frac{1}{\hat{\phi}}\right) - \text{var}\left(\frac{1}{\hat{\phi}}\right)\text{var}(\hat{N}_{LM}) \qquad (4)$$

where

$$\text{var}\left(\frac{1}{\hat{\phi}}\right) \approx \left(\frac{1}{\hat{\phi}}\right)^4 \frac{\hat{\phi}(1-\hat{\phi})}{n-1} \qquad (5)$$

where n is the number of fish of all sizes sampled in event 2.

AGE AND SEX COMPOSITION

The proportion of the spawning population composed of a given age within a size class was estimated as a binomial variable:

$$\hat{p}_{ij} = \frac{n_{ij}}{n_i} \qquad (6)$$

$$\text{var}(\hat{p}_{ij}) = \frac{\hat{p}_{ij}(1-\hat{p}_{ij})}{n_i - 1} \qquad (7)$$

where $\hat{p}_{ij}$ is the estimated proportion of the population of age j in size group i, n_{ij} is the number of Chinook salmon of age j of size group i, and n_i is the number of Chinook salmon in the sample n of size group i. Information gathered during event 1 was not used to estimate age or sex composition as some gender misidentification was found to have occurred at SN1. There was a significant difference in the age composition among sampled tributaries. However, as the tributaries supplying the preponderance of samples (Genes Lake and Cripple Creek) had similar proportions, and stratifying escapement by tributary was not feasible, samples gathered at each spawning tributary were pooled for purposes of age composition. Numbers of spawning fish by age were estimated as the sum of the products of estimated age composition and estimated abundance within a size category:

$$\hat{N}_j = \sum_i (\hat{p}_{ij}\hat{N}_i) \tag{8}$$

and

$$\text{var}(\hat{N}_j) = \sum_i \begin{pmatrix} \text{var}(\hat{p}_{ij})\hat{N}_i^2 + \text{var}(\hat{N}_i)\hat{p}_{ij}^2 \\ -\text{var}(\hat{p}_{ij})\,\text{var}(\hat{N}_i) \end{pmatrix} \tag{9}$$

with variance calculated according to procedures in Goodman (1960).

The proportion of the spawning population composed of a given age was estimated as the summed totals across size categories:

$$\hat{p}_j = \frac{\hat{N}_j}{\hat{N}} \tag{10}$$

and

$$\text{var}(\hat{p}_j) = \frac{\sum_i (\text{var}(\hat{p}_{ij})\hat{N}_i^2 + \text{var}(\hat{N}_i)(\hat{p}_{ij} - \hat{p}_j)^2)}{\hat{N}^2} \tag{11}$$

where $\hat{N}$ is the sum of fish of all sizes, and variance is approximated according to procedures in Seber (1982, p. 8–9).

Sex composition and age-sex composition for the entire spawning population and its associated variances were also estimated using the above equations by first redefining the binomial variables in samples to produce estimated proportions by sex $\hat{p}_k$, where k denotes gender (male or female), such that $\sum_k \hat{p}_k = 1$, and by age-sex $\hat{p}_{jk}$, such that $\sum_{jk} \hat{p}_{jk} = 1$.

EXPANSION FACTOR

An expansion factor ($\hat{\pi}$) for Unuk River Chinook salmon in a calendar year is:

$$\hat{\pi}_i = \hat{N}_i / C_i \tag{12}$$

and

$$\text{var}(\hat{\pi}_i) = \text{var}(\hat{N}_i) / C_i^2 \tag{13}$$

where i is the year (with a mark–recapture experiment), $\hat{N}_i$ is the mark–recapture estimate of large Chinook salmon and C_i is the peak aerial survey count.

The expansion factor for a year for which we have no mark–recapture experiment is anticipated as the mean of the $\hat{\pi}_i$ over the k years for which we have mark–recapture experiments (10 for the Unuk River at present, from 1997 to 2006):

$$\bar{\pi} = \sum_{i=1}^{k} \hat{\pi}_i \,/\, k \tag{14}$$

The variance associated with use of $\bar{\pi}$ in a prediction, var (π_p), was estimated:

$$\begin{aligned} v\hat{a}r(\pi_p) &= v\hat{a}r_B(\hat{\pi}) \\ &- \frac{\sum_{i=1}^{k} v\hat{a}r(\hat{\pi}_i)}{k} + v\hat{a}r_B(\bar{\pi}) \end{aligned} \tag{15}$$

where k is the number of years with both counts and M–R estimates and $\hat{\pi}_i$ is the observed expansion factor in year i. The estimate $v\hat{a}r(\pi_p)$ is the appropriate term for predicting a new value of π, and the measurement error within years (i.e., the mark–recapture induced error in escapement estimation) has been removed (See Appendix A3 for details).

The estimator for expanding peak survey counts into estimates of spawning abundance is:

$$\hat{N}_p = \bar{\pi}\, C_p \tag{16}$$

$$\text{var}(\hat{N}_p) = C_p^2\ \text{var}(\pi_p) \tag{17}$$

MIGRATORY TIMING

The mean date of migration for Unuk River stock (Boundary Creek, Clear Creek, Cripple Creek, Genes Lake Creek, Kerr Creek, Lake Creek or the Eulachon River) was calculated as:

$$\bar{d}_w = \frac{\sum_{i=1}^{n_w} d_{wi}}{n_w} \quad (16)$$

where n_w is the number of marked fish recovered at location w and d_{wi} is the day the i^{th} fish was marked at the SN1 gillnet site, with variance estimated as:

$$\text{var}(\bar{d}_w) = \frac{\sum_{i=1}^{n_w} (d_{wi} - \bar{d})^2}{(n_w - 1)n_w} \quad (17)$$

RESULTS

TAGGING, INRIVER RECOVERY AND SPAWNING ABUNDANCE

Between 11 June and 3 August, 1,028 Chinook salmon were sampled in the lower river, of which 1,004 (853 large, 147 medium, and 4 small) were marked and released (Tables 2 and 3).

Approximately 95% of the Chinook salmon marked during the first sampling event were captured between 21 June and 31 July. Fishing effort at the set gillnets was maintained at relatively constant levels, with the exception of 21–27 July when high water negated attempts to operate the set gillnets (Figure 5). A total of 78 fish were missing adipose fins, of which 15 were sacrificed and 1 died prior to marking; the rest were marked and released in good condition. Of the 16 heads recovered during event 1, fourteen had valid CWTs for this stock and two were without CWTs. Among the fish that were missing adipose fins and of those sacrificed, 51% and 100%, respectively, were males. The fish that died prior to marking was a female.

During event 2, 944 fish were inspected (38 small, 226 medium, and 680 large), of which 120 were recaptured fish (18 medium and 102 large; Tables 2 and 3). Two fish had shed their spaghetti tags (1 medium and 1 large) and one spaghetti tag number was misrecorded. Adipose fins were missing on 55 fish sampled during event 2, and 39 of these were sacrificed. Of the 39 adipose-clipped fish sacrificed, 30 carried a valid CWT for this stock and 1 fish carried a CWT from Crystal Lake Hatchery (Anita Bay release site).

Length distributions of large fish that were marked and recaptured were not significantly different (P = 0.515, D = 0.084; Figure 6; M vs. R in Appendix A1). Likewise, no difference was detected in the length distributions of large fish that were marked and inspected (P = 0.937, D = 0.027, Figure 7; M vs. C in Appendix A1) or inspected and recaptured (P = 0.606, D = 0.079, Figure 8; C vs. R in Appendix A1). These results indicate that size-selective sampling did not occur during either event for large-sized fish (Case I, Appendix A1).

There was no evidence of gender selectivity in either sampling event for large fish (χ^2 = 0.640, df = 1, P = 0.424 for M vs. C, χ^2 = 1.558, df = 1, P = 0.212 for M vs. R, and χ^2 = 0.720, df = 1, P = 0.396 for C vs. R; Appendix A1); however 3.9% of large and 5.6% of medium recaptured fish were found to have had gender misdiagnosed during event 1. Consequently only fish sampled on the spawning grounds were used to estimate the length and age composition of the escapement.

Samples of large fish from the spawning grounds had near equal fractions of marked fish regardless of where samples were taken (χ^2 = 2.048, df = 6, P = 0.915; Table 2), satisfying the Equal Proportions Test (Appendix A2); we are also confident that event 2 sampling accessed the majority of spawning areas in the drainage (footnote b Appendix A2).

Results from the diagnostic tests above indicated that the pooled estimator (equation 1) was appropriate for estimating abundance of large Chinook salmon. Estimated abundance of large fish is 5,645 (n_1 = 853; n_2 = 680; m_2 = 102; SE = 476). Statistical bias of the estimate is 0.5% and the 95% confidence interval for the estimated abundance is 4,808 to 6,786 (Table 4).

Table 2.–Numbers of marked large (≥660 mm MEF) Chinook salmon released in the lower Unuk River in 2006, by marking period, and the number inspected for marks and recaptured at each recovery location.

		Recovery location								
Marking dates	Number marked	Boundary Creek	Clear Creek	Cripple Creek	Eulachon River	Genes Lake Creek	Kerr Creek	Lake Creek	Total recovered	Fraction recovered
11 June–4 July	352	1	3	10		16	1	3	34	0.097
5 July–10 July	163	1	1	13		15		3	33	0.202
11 July–3 August	338		5	13	1	14		1	34	0.101
Total/proportion[a]	853	2	9	36	1	46	1	7	102	0.120
Number inspected		17	69	236	8	276	11	63	680	
Fraction marked		0.118	0.130	0.153	0.125	0.167	0.091	0.111	0.150	

[a] Total for Genes Lake Creek includes one recovery that shed its spaghetti tag with consequent unknown marking date.

Table 3.–Numbers of marked medium (545–659 mm MEF) Chinook salmon released in the lower Unuk River in 2006, by marking period, and the number inspected for marks and recaptured at each recovery location.

		Recovery location								
Marking dates	Number marked	Boundary Creek	Clear Creek	Cripple Creek	Eulachon River	Genes Lake Creek	Kerr Creek	Lake Creek	Total recovered	Fraction recovered
11 June–4 July	53			1		3	1		5	0.094
5 July–10 July	12	1		1		1			3	0.250
11 July–3 August	82	1		2		5			8	0.098
Total/proportion[a]	147	2	1	4	0	10	1	0	18	0.122
Number inspected		11	17	82	1	107	2	6	226	
Fraction marked		0.182	0.059	0.049		0.093	0.500		0.080	

[a] Total includes one recovery from Clear Creek with a mis-recorded spaghetti tag number and one recovery from Genes Lake Creek with a shed spaghetti tag, neither of which could be allocated to marking strata.

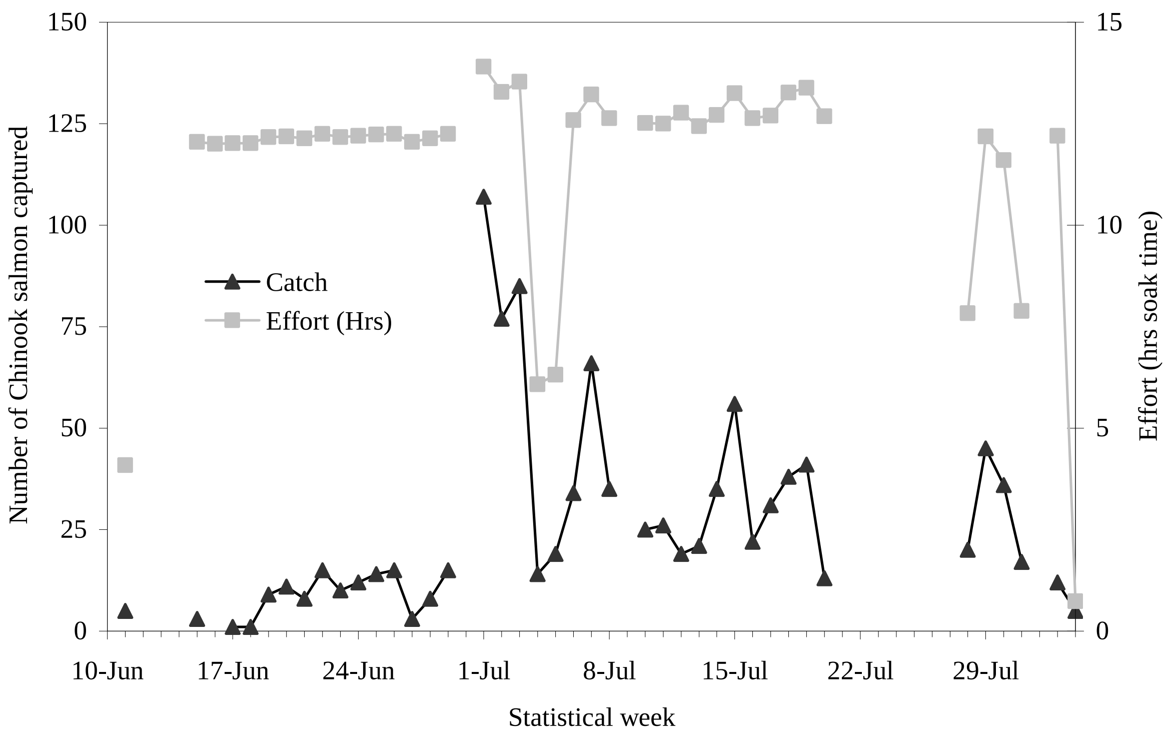

Figure 5.–Effort (in hours of soak time) and catch of Chinook salmon by date at SN1 on the Unuk River, 2006.

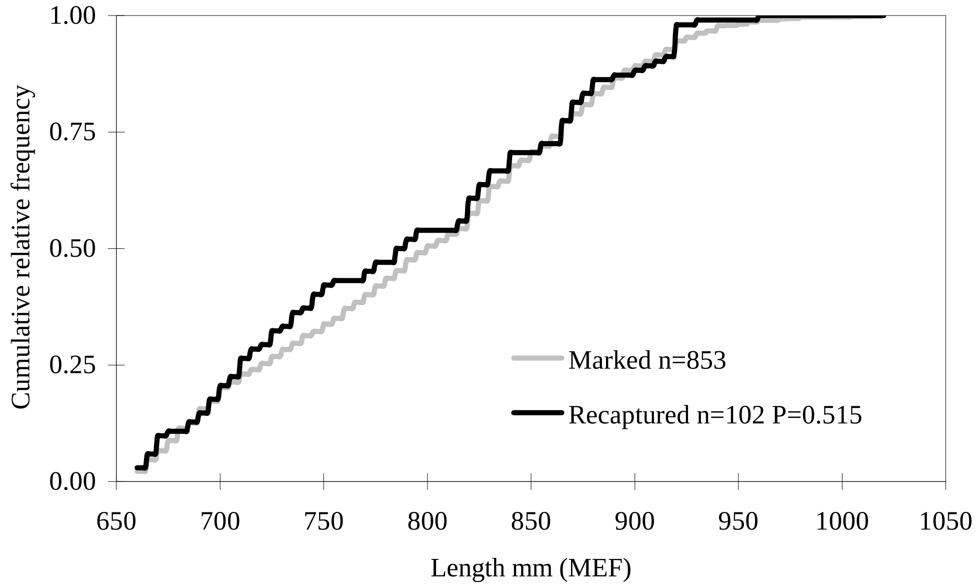

Figure 6.–Cumulative relative frequencies of large Chinook salmon (>659 mm MEF) marked in the lower Unuk River in 2006 compared with those recaptured on the spawning grounds.

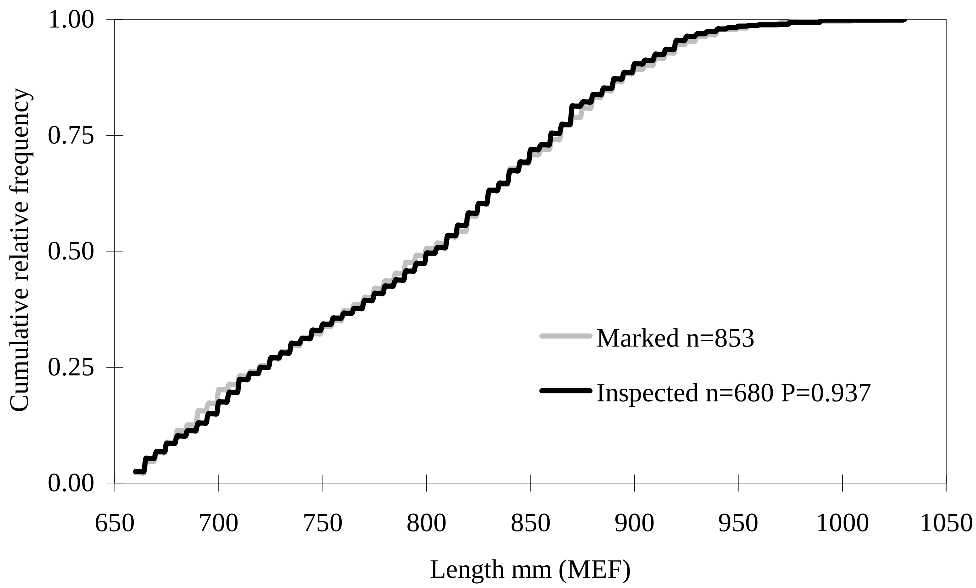

Figure 7.–Cumulative relative frequencies of large Chinook salmon (>659 mm MEF) marked in the lower Unuk River in 2006 compared with those inspected on the spawning grounds.

Length distributions of medium fish that were marked and inspected were significantly different (P = 0.000, D = 0.260; Figure 9; M vs. C in Appendix A1). No difference was detected in the length distributions of medium fish that were marked and recaptured (P = 1.000, D = 0.084, Figure 10; M vs. R in Appendix A1) or inspected and recaptured (P = 0.250, D = 0.242, Figure 11; C vs. R in Appendix A1). These results indicate that further evaluation was required (Appendix A1) to determine if size-selective sampling occurred. Small sample size for recaptured fish, a

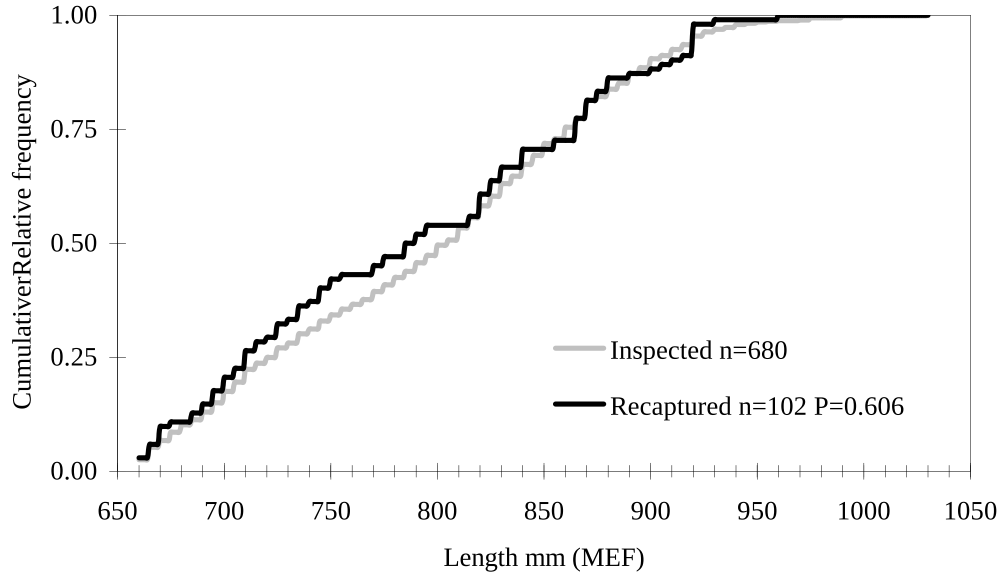

Figure 8.–Cumulative relative frequencies of large Chinook salmon (>659 mm MEF) inspected on the spawning grounds in 2006 compared with those recaptured on the spawning grounds.

small P value for the length distributions of inspected and recaptured fish, and a large P value for the length distributions of marked and recaptured fish suggests that scenario "C" and *Case III* in the evaluation protocol (Appendix A1) would be most appropriate.

Samples of medium fish from the spawning grounds, excluding the Eulachon River and Kerr Creek due to sample size considerations (Table 3), had near equal fractions of marked fish regardless of where samples were taken (χ^2 = 3.64, df = 4, P = 0.457), satisfying the Equal Proportions Test (Appendix A2); we are also confident that event 2 sampling accessed the majority of spawning areas in the drainage (footnote b Appendix A2). Results from the diagnostic tests above indicated that the pooled estimator (equation 1) was appropriate for estimating abundance of medium Chinook salmon. Estimated abundance of medium fish is 1,767 (n_1 = 147; n_2 = 226; m_2 = 18; SE = 418). Statistical bias of the estimate is 3.5% and the 95% confidence interval for the estimated abundance is 1,231 to 2,744 (Table 4).

Estimated abundance of small fish is 311 (SE = 58).

ESTIMATES OF AGE AND SEX COMPOSITION

There was evidence of gender bias during event 1; therefore only event 2 samples were used to estimate the age, sex, and length composition of the spawning population. An estimated 42.2% of the spawning population of Chinook salmon was comprised of age-1.2 fish (Table 5). Since 1997, only the escapement in 2004 has had a larger proportion of the escapement (48.3%: Appendix A4) represented by age-1.2 fish. Age-1.3 comprised 27.8% of the estimated spawning population. From 1997 to 2005, the percentage of age-1.3 fish in the spawning population ranged from 21.2% (2004) to 68.6% (2005), averaging 46.9%. Age-1.4 comprised 27.2% of the estimated spawning population. The percentage of age-1.4 fish in the spawning population ranged from 15.1% (2005) to 38.8% (1997) and averaged 27.1% (Appendix A4, Table 5).

Approximately 32% of the spawning population was female in 2006, in contrast to the previous 9-year average of about 40% (Table 5, Appendix A4). There were an estimated 2,465 (SE = 246) spawning females in 2006 (Table 5). Estimated average lengths by age and sex were similar

Table 4.–Peak survey counts, mark–recapture estimates of abundance, expansion factors, and other statistics for medium (401–659 mm MEF) and large (>659 mm MEF) Chinook salmon in the Unuk River (1997–2006, 1997–2006 average, and 1997–2005 average).

	1997		1998		1999		2000		2001		2002	
	Medium	Large	Medium	Large	Medium	Large	Medium	Large	Medium	Large	Medium	Large
Survey count		636		840		680		1,341		2,019		897
m2	16	78	15	79	13	50	8	69	3	74	9	66
n1	75	307	87	466	125	380	128	570	71	778	148	725
n2	156	761	217	707	251	523	158	719	74	1,014	109	644
Mark–recapture (M–R) estimate	701	2,970	1,198	4,132	2,267	3,914	2,278	5,872	769	10,541	1,638	6,988
SE (M–R)	158	277	290	413	602	490	675	644	124	1,181	690	805
Survey count/ (M–R) (%)		21.4		20.3		17.4		22.8		19.2		12.8
CV (M–R) (%)	22.5	9.3	24.2	10.0	26.6	12.5	29.6	11.0	16.1	11.2	42.1	11.5
95% RP M–R estimate (%)	44.2	18.3	47.4	19.6	52.0	24.5	58.1	21.5	31.6	22.0	82.6	22.6
Expansion factor (EF)		4.67		4.92		5.76		4.38		5.22		7.79
SE (EF)		0.44		0.49		0.72		0.48		0.58		0.90
CV (EF)		9		10		13		11		11		12
95% RP (EF)		18		20		25		21		22		23
M–R lower 95% C.I.	489	2,499	815	3,433	1,506	3,110	1,358	4,848	557	8,705	1,017	5,775
M–R upper 95% C.I.	1,109	3,636	1,903	4,974	3,811	5,071	5,042	7,347	1,068	13,253	3,331	8,845
Estimated bias (%)	2.3	0.1	3.0	0.6	3.4	1.5	9.6	1.1	1.5	0.9	7.5	0.6

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Table 4.–Page 2 of 2.

	2003		2004		2005		2006		Average 1997–2006		Average 1997–2005	
	Medium	Large	Medium	Large	Medium	Large	Medium[b]	Large	Medium	Large	Medium	Large
Survey count		1,121		1,008		929		940		1,041		1,052
m2	2	114	30	105	13	101	18	102	13	84	12	82
n1	52	646	189	501	70	644	147	853	109	587	105	557
n2	124	985	344	836	133	749	226	680	179	762	174	771
Mark–recapture (M–R) estimate	698	5,546	2,114	3,963	679	4,742	1,767	5,645	1,411	5,431	1,371	5,408
SE (M–R)	80	433	339	325	176	396	418	476	355	544	348	552
Survey count/ (M–R) (%)		20.2		25.4		19.6		16.7		19.6		19.9
CV (M–R) (%)	11.5	7.8	16.0	8.2	25.9	8.4	23.7	8.4	23.8	9.8	23.8	10.0
95% RP M–R estimate (%)	22.5	15.3	31.4	16.1	50.8	16.4	46.4	16.5	46.7	19.3	46.7	19.6
Expansion factor (EF)		4.95		3.93		5.10		6.01		5.27		5.19
SE (EF)		0.39		0.32		0.43		0.50		1.09		0.95
CV (EF)		8		8		8		8		21		18
95% RP (EF)		15		16		16		17		41		36
M–R lower 95% C.I.	557	4,814	1,602	3,406	450	4,094	1,231	4,808	715	4,365	689	4,327
M–R upper 95% C.I.	1,068	6,530	2,907	4,684	1,149	5,579	2,744	6,786	2,107	6,498	2,054	6,489
Estimated bias (%)[a]	0.4	0.87	1.4	0.50	3.4	0.5	3.5	0.5	3.6	0.7	3.6	0.7

[a] Estimated bias in 2003 for large fish was previously misreported and has been updated.

[b] Medium fish in 2006 defined as 545–659 mm MEF.

Table 5.–Estimated age and sex composition of the escapement of small (<545 mm MEF), medium (545–659 mm MEF), and large (>659 mm MEF) Chinook salmon in the Unuk River in 2006 as determined from spawning grounds samples.

		Brood year and age class				
		2003	2002	2001	2000	
		1.1	1.2	1.3	1.4	Total
PANEL A: AGE COMPOSITION OF SMALL CHINOOK SALMON						
Males	Sample size	27	11			38
	p_{ijk} x100	71.1	28.9			100.0
	SE(p_{ijk}) x100	7.4	7.4			
	N_{ijk}	221	90			311
	SE(N_{ijk})	47	28			58
Females	Sample size					
	p_{ijk} x100					
	SE(p_{ijk}) x100					
	N_{ijk}					
	SE(N_{ijk})					
Sexes combined	Sample size	27	11			38
	p_{ij} x100	71.1	28.9			100.0
	SE(p_{ij}) x100	7.4	7.4			
	N_{ij}	221	90			311
	SE(N_{ij})	47	28			58
PANEL B: AGE COMPOSITION OF MEDIUM CHINOOK SALMON						
Males	Sample size		217	8		225
	p_{ijk} x100		96.4	3.6		100.0
	SE(p_{ijk}) x100		1.2	1.2		
	N_{ijk}		1,704	63		1,767
	SE(N_{ijk})		403	26		418
Females	Sample size					
	p_{ijk} x100					
	SE(p_{ijk}) x100					
	N_{ijk}					
	SE(N_{ijk})					
Sexes combined	Sample size		217	8		225
	p_{ij} x100		96.4	3.6		100.0
	SE(p_{ij}) x100		1.2	1.2		
	N_{ij}		1,704	63		1,767
	SE(N_{ij})		403	26		418

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Table 5.–Page 2 of 2.

		Brood year and age class				
		2003	2002	2001	2000	
		1.1	1.2	1.3	1.4	Total
PANEL C: AGE COMPOSITION OF LARGE CHINOOK SALMON						
Males	Sample size		169	138	76	383
	p_{ijk} x100		24.9	20.3	11.2	56.3
	SE(p_{ijk}) x100		1.7	1.5	1.2	1.9
	N_{ijk}		1,403	1,146	631	3,180
	SE(N_{ijk})		157	134	88	305
Females	Sample size		7	113	177	297
	p_{ijk} x100		1.0	16.6	26.0	43.7
	SE(p_{ijk}) x100		0.4	1.4	1.7	1.9
	N_{ijk}		58	938	1,469	2,466
	SE(N_{ijk})		22	116	162	246
Sexes combined	Sample size		176	251	253	680
	p_{ij} x100		25.9	36.9	37.2	100.0
	SE(p_{ij}) x100		1.7	1.9	1.9	0.0
	N_{ij}		1,461	2,084	2,100	5,645
	SE(N_{ij})		162	214	215	506
PANEL D: AGE COMPOSITION OF SMALL, MEDIUM, AND LARGE CHINOOK SALMON						
Males	Sample size	27	397	146	76	646
	p_{ik} x100	2.9	41.4	15.6	8.2	68.1
	SE(p_{ik}) x100	0.6	3.4	1.4	1.0	2.4
	N_{jk}	221	3,197	1,209	631	5,258
	SE(N_{jk})	47	434	137	88	520
Females	Sample size		7	113	177	297
	p_{ik} x100		0.8	12.1	19.0	31.9
	SE(p_{ik}) x100		0.3	1.3	1.7	2.4
	N_{jk}		58	938	1,469	2,465
	SE(N_{jk})		22	116	162	246
Sexes combined	Sample size	27	404	259	253	943
	p_j x100	2.9	42.2	27.8	27.2	100.0
	SE(p_j) x100	0.6	3.4	2.0	2.1	
	N_j	221	3,256	2,147	2,100	7,723
	SE(N_j)	47	436	215	215	659

between events 1 and 2 in 2006, although age-1.2 fish were generally larger in event 1 (Table 6). This result is consistent with the K-S test depicted in Figure 9.

PEAK SURVEY COUNTS AND THE EXPANSION FACTOR

The peak survey count of large Chinook salmon in the six index streams of the Unuk River was 940 fish in 2006 (Pahlke 2008; Table 4). Genes Lake Creek accounted for 58.6% of the total peak survey count, the largest contribution since the surveys began in 1977 (minimum 8.8%, maximum 50.7%, mean 33.3%; Figure 12). Cripple and Genes Lake creeks combined accounted for 81% of these fish, in contrast to an average of 70% from 1977 to 2005 (Figure 12; Weller and McPherson 2006b).

Of the estimated 5,645 large Chinook salmon immigrating to the Unuk River in 2006, 16.7% were counted during peak survey counts. This percentage was the third lowest on record (Table 4; Pahlke et al. 1996). Using the 1997–2006 mark–recapture estimates and peak survey counts, the mean expansion factor is 5.27 (SD = 1.09, Table 4).

MIGRATORY TIMING

Migration past SN1 in 2006 was similar to migration in other years. The mean date of migration past SN1 was estimated to be 9 July for

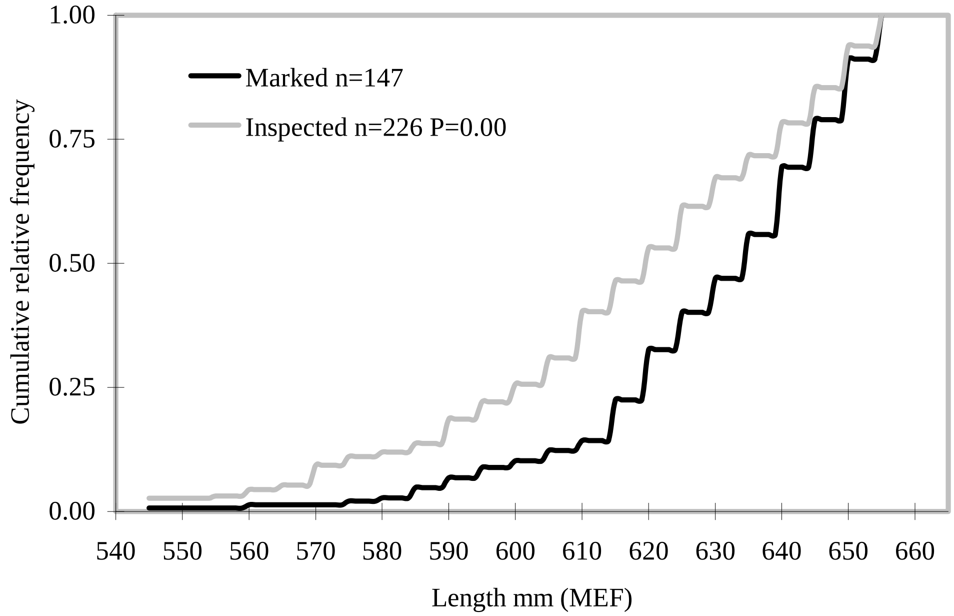

Figure 9.–Cumulative relative frequencies of medium Chinook salmon (545–659 mm MEF) marked in the lower Unuk River in 2006 compared with those inspected on the spawning grounds.

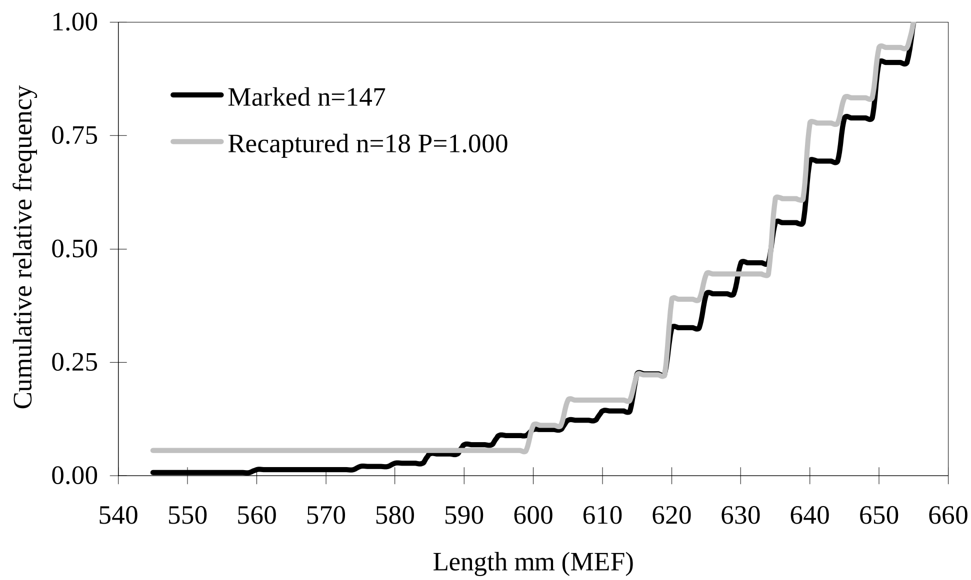

Figure 10.–Cumulative relative frequencies of medium Chinook salmon (545–659 mm MEF) marked in the lower Unuk River in 2006 compared with those recaptured on the spawning grounds.

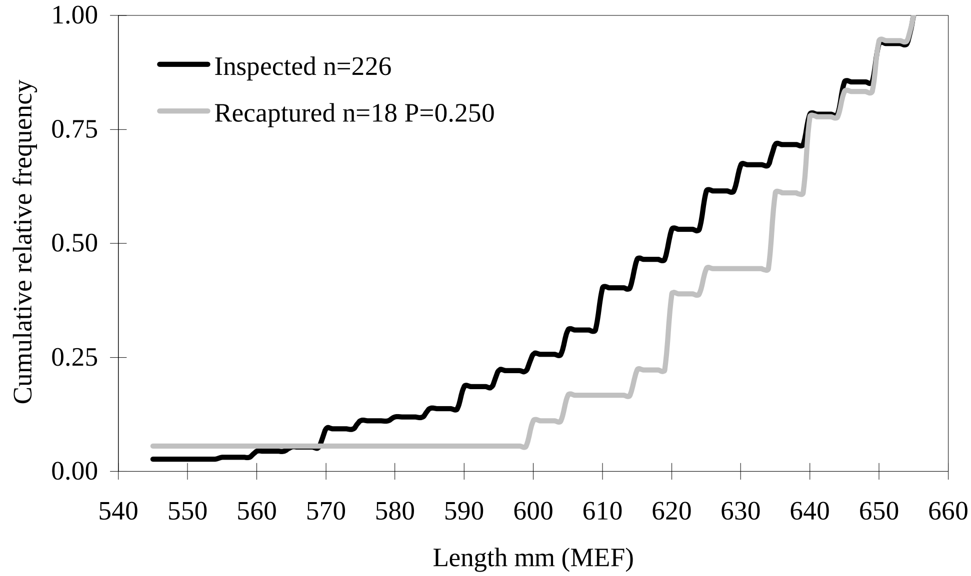

Figure 11.–Cumulative relative frequencies of medium Chinook salmon (545–659 mm MEF) inspected on the spawning grounds in 2006 compared with those recaptured on the spawning grounds.

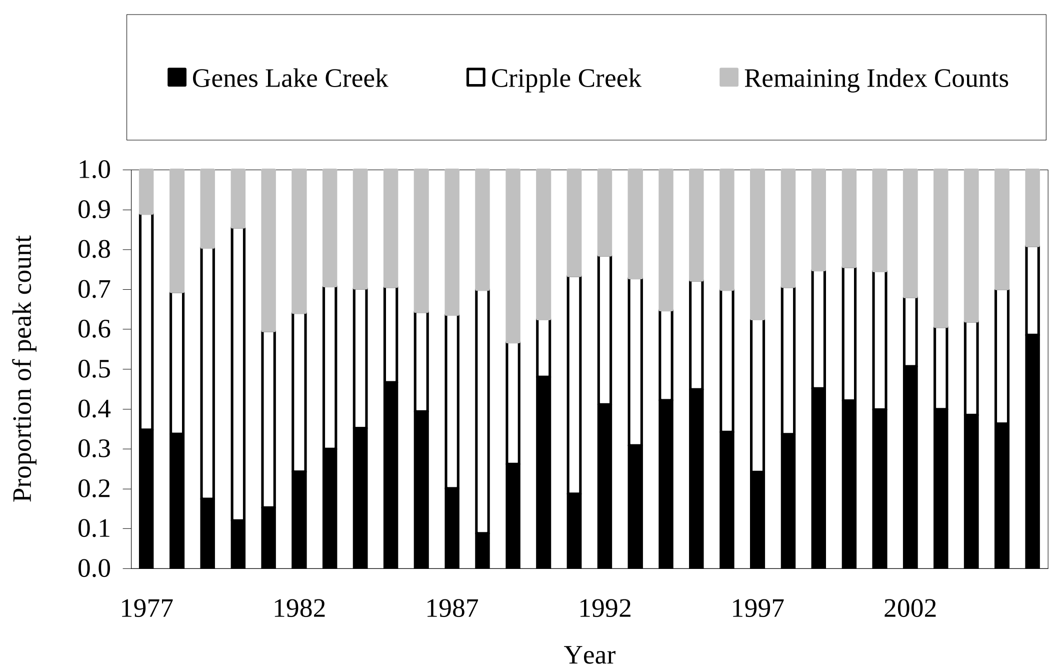

Figure 12.–Proportion of the annual peak count of Chinook salmon in the Unuk River attributed to Genes Lake Creek, Cripple Creek, and the remaining four index streams combined (the Eulachon River and Clear, Lake, and Kerr creeks), 1977–2006.

Table 6.–Estimated average length (MEF in mm) by age, sex, and sampling event of Chinook salmon sampled in the Unuk River in 2006.

		Brood year and age class							
		2003 1.1	2002 1.2	2001 2.2	2001 1.3	2000 2.3	2000 1.4	1999 1.5	Total
PANEL A: EVENT 1, LOWER UNUK RIVER SET GILLNET[a]									
Males	Sample size	1	373	1	184	1	74		634
	Avg. length	460	666	700	780	820	885		725
	SD		46		60		54		93
	SE		2		4		6		93
Females	Sample size		17		175		201	1	394
	Avg. length		692		807		880	915	840
	SD		39		43		41		63
	SE		9		3		3		3
Sexes combined	Sample size	1	390	1	359	1	275	1	1,028
	Avg. length	460	668	700	793	820	882	915	769
	SD		46		54		45		100
	SE		2		3		3		3
PANEL B: EVENT 2, SPAWNING GROUNDS									
Males	Sample size	27	396		146		76		645
	Avg. length	407	648		772		876		693
	SD	41	53		62		63		115
	SE	8	3		5		7		5
Females	Sample size		7		113		177		297
	Avg. length		696		808		868		841
	SD		26		44		40		55
	SE		10		4		3		3
Sexes combined	Sample size	27	403		259		253		942
	Avg. length	407	648		787		870		739
	SD	41	53		58		48		121
	SE	8	3		4		3		4

[a] Includes fish captured but not marked.

those Chinook salmon marked at the set gillnet site and subsequently recovered on the spawning grounds (Table 7). This compares to an average date of 11 July from 1997 through 2005.

DISCUSSION

In previous years of study, Chinook salmon tagged and released during event 1 have shown a "sulking" behavior or a delay in upstream migration (Jones III et al. 1998; Jones III and McPherson 1999, 2000, 2002; Pahlke et al. 1996; Weller and McPherson 2003a-b; Weller and McPherson 2006a-b). In 2006, 81 fish were marked, released, and subsequently recaptured in event 1. Four fish were recaptured twice. For these fish, the average time between release and recapture (i.e., an estimate of the "sulk" rate) was approximately 6 days and 8 hours, with a maximum period of over 20 days and a minimum of 6 minutes (Appendix A5). This phenomenon has been observed in other studies (Bendock and Alexandersdottir 1993; Johnson et al. 1992; Johnson et al. 1993; Milligan et al. 1984) and has been shown to be a benign result of handling-induced behavior (Bernard et al. 1999).

The average rate of primary tag loss from 1997 to 2005 was approximately 6.9%, with a range of 0.0% observed in 2005 to 15% in 2002. In 2006, 118 of the 120 fish recaptured in event 2 retained their primary tags, a tag loss of 1.7%. Tag retention was likely a result of samplers applying greater attention to the amount of pressure exerted with the crimping tool; too much pressure can burn the monofilament leader and decrease its strength, not enough pressure on the crimping tool results in an inadequate crimp. In all cases, secondary marks were clearly visible on recaptured fish once fish were in hand.

Table 7.–Estimated mean date of migration of Chinook salmon stocks past SN1 on the Unuk River from 1997–2006 (Panel A), standard deviation (Panel B), and sample size (Panel C).

PANEL A: ESTIMATED MEAN DATE OF MIGRATION AT SN1									
		Tributary							
Year	SN1	Eulachon River	Clear Creek	Lake Creek	Kerr Creek	Genes Lake Creek	Cripple Creek	Boundary Creek	Tributaries combined
1997	7 July	12 July	6 July		7 July	6 July	9 July		8 July
1998	3 July	10 July	5 July	21 June	29 June	2 July	4 July	3 July	3 July
1999	12 July		11 July		14 July	11 July	13 July		12 July
2000	12 July	16 July	12 July	11 July	15 July	14 July	16 July		14 July
2001	15 July	21 July	16 July	4 July	17 July	15 July	10 July	9 July	13 July
2002	14 July	19 July	11 July	22 July	20 July	17 July	17 July	26 July	17 July
2003	12 July	14 July	13 July	13 July	14 July	9 July	6 July	8 July	11 July
2004	10 July	19 July	9 July	11 July	10 July	8 July	10 July		10 July
2005	8 July	10 July	8 July	3 July	10 July	11 July	6 July	9 July	8 July
2006	9 July	14 July	11 July	5 July	3 July	9 July	11 July	12 July	10 July
97–05 Average	11 July	15 July	10 July	8 July	12 July	10 July	10 July	11 July	11 July
PANEL B: STANDARD DEVIATION (in days)									
1997	0.36	3.59	1.54		1.28	1.36	0.73		0.59
1998	0.44	2.50	2.41		1.71	2.24	1.39		0.94
1999	0.43		1.56		4.01	1.92	1.67		1.02
2000	0.48		2.46	5.11	3.56	2.24	1.50		1.11
2001	0.38	3.84	3.46	6.81	0.33	1.67	1.65	6.67	1.15
2002	0.34	4.89	2.13	6.50	2.27	1.29	1.85	6.00	0.95
2003	0.39	5.50	2.10	2.70	1.70	1.28	2.90	7.37	0.87
2004	0.42	3.40	2.38	2.28	3.24	1.28	1.60		0.84
2005	0.32	0.79	1.11	5.07	3.45	0.98	1.02	0.49	0.61
2006	0.35		3.41	1.85	0.00	1.19	1.65	5.98	0.86
PANEL C: NUMBER OF FISH MARKED AT SN1 AND RECAPTURED ON TRIBUTARIES									
1997	383	5	20		9	18	38		90
1998	550	2	21	1	13	18	37	1	93
1999	504		13		6	11	29		59
2000	697	1	15	7	6	19	18		66
2001	853	3	13	3	3	15	28	3	68
2002	873	5	5	2	5	25	22	2	66
2003	703	2	22	9	21	37	10	4	105
2004	690	9	17	10	13	53	27		129
2005	714	6	18	4	7	26	46	6	113
2006	1,004	1	9	7	2	54	40	4	117

The validity of the abundance estimate rests in part upon the degree to which the second sampling event was devoid of size-selectivity. Size-selective sampling occurred during the spawning grounds surveys prior to 1995, primarily as a result of an over reliance upon sampling carcasses and small sample size (Pahlke et al. 1996). Beginning in 1995, sample sizes were increased and diverse techniques were used to obtain spawning grounds samples to reduce bias in age, gender, and length composition estimates (Jones III et al. 1998; Jones III and McPherson 1999, 2000, 2002; Weller and McPherson 2003a-b, 2004, 2006a-b Appendix A6). The approach apparently worked because there has been no indication of size-selective sampling on the spawning grounds since 1997.

Partial counts of large Chinook salmon have been conducted on the Unuk River since 1977. Using the expansion factor of 5.27 to estimate annual spawning abundance prior to 1997, the estimated abundance of large Chinook salmon on the Unuk River has averaged 5,592 from 1979 to 2005 with a range of 2,970 in 1997 to 11,209 in 1986 (Appendix A7). The 2006 abundance estimate of

5,645 large Chinook salmon represents a near average spawning population.

CONCLUSIONS AND RECOMMENDATIONS

Because this project will be repeated in 2007, we recommend some strategies for continued success. As in previous years, effort should concentrate on maximizing the numbers of fish tagged during event 1 and those sampled for tags in event 2. SN1 should continue to be used as the tagging site because it has yielded adequate sample sizes in this and prior years. Knowledge of run timing gathered in prior years should be used as an indicator of peak spawning abundance and optimum sampling periods. We recommend that survey counts continue in a similar manner as those made in the past and that observers attempt to maintain consistency in counting efficiency from year to year. Finally, the age, sex, and length composition estimates from previous years of study have been relatively unbiased, which can be primarily attributed to the use of multiple gear types during spawning grounds sampling (Appendix A7). We recommend continuing this practice in future years. Data collected have been archived in ADF&G offices in Ketchikan, Douglas, and Anchorage (Appendix A8).

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APPENDIX A

Appendix A1.–Detection of size- and/or sex-selective sampling during a two-sample mark–recapture experiment and its effects on estimation of population size and population composition

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Size selective sampling: The Kolmogorov-Smirnov two sample test (Conover 1980) is used to detect significant evidence that size selective sampling occurred during the first and/or second sampling events. The second sampling event is evaluated by comparing the length frequency distribution of all fish marked during the first event (M) with that of marked fish recaptured during the second event (R) by using the null test hypothesis of no difference. The first sampling event is evaluated by comparing the length frequency distribution of all fish inspected for marks during the second event (C) with that of R. A third test that compares M and C is then conducted and used to evaluate the results of the first two tests when sample sizes are small. Guidelines for small sample sizes are <30 for R and <100 for M or C.

Sex selective sampling: Contingency table analysis (Chi^2-test) is generally used to detect significant evidence that sex selective sampling occurred during the first and/or second sampling events. The counts of observed males to females are compared between M&R, C&R, and M&C using the null hypothesis that the probability that a sampled fish is male or female is independent of sample. If the proportions by gender are estimated for a sample (usually C), rather an observed for all fish in the sample, contingency table analysis is not appropriate and the proportions of females (or males) are then compared between samples using a two sample test (e.g. Student's t-test).

M vs. R	**C vs. R**	**M vs. C**
Case I:		
Fail to reject H_o	Fail to reject H_o	Fail to reject H_o

There is no size/sex selectivity detected during either sampling event.

Case II:

Reject H_o	Fail to reject H_o	Reject H_o

There is no size/sex selectivity detected during the first event but there is during the second event sampling.

Case III:

Fail to reject H_o	Reject H_o	Reject H_o

There is no size/sex selectivity detected during the second event but there is during the first event sampling.

Case IV:

Reject H_o	Reject H_o	Either result possible

There is size/sex selectivity detected during both the first and second sampling events.

-continued-

Evaluation Required:

Fail to reject H_o Fail to reject H_o Reject H_o

Sample sizes and powers of tests must be considered:

A. If sample sizes for M vs. R and C vs. R tests are not small and sample sizes for M vs. C test are very large, the M vs. C test is likely detecting small differences which have little potential to result in bias during estimation. *Case I* is appropriate.

B. If a) sample sizes for M vs. R are small, b) the M vs. R p-value is not large (~0.20 or less), and c) the C vs. R sample sizes are not small and/or the C vs. R p-value is fairly large (~0.30 or more), the rejection of the null in the M vs. C test was likely the result of size/sex selectivity during the second event which the M vs. R test was not powerful enough to detect. *Case I* may be considered but *Case II* is the recommended, conservative interpretation.

C. If a) sample sizes for C vs. R are small, b) the C vs. R p-value is not large (~0.20 or less), and c) the M vs. R sample sizes are not small and/or the M vs. R p-value is fairly large (~0.30 or more), the rejection of the null in the M vs. C test was likely the result of size/sex selectivity during the first event which the C vs. R test was not powerful enough to detect. *Case I* may be considered but *Case III* is the recommended, conservative interpretation.

D. If a) sample sizes for C vs. R and M vs. R are both small, and b) both the C vs. R and M vs. R p-values are not large (~0.20 or less), the rejection of the null in the M vs. C test may be the result of size/sex selectivity during both events which the C vs. R and M vs. R tests were not powerful enough to detect. *Cases I, II, or III* may be considered but *Case IV* is the recommended, conservative interpretation

Case I. Abundance is calculated using a Petersen-type model from the entire data set without stratification. Composition parameters may be estimated after pooling length, sex, and age data from both sampling events.

Case II. Abundance is calculated using a Petersen-type model from the entire data set without stratification. Composition parameters may be estimated using length, sex, and age data from the first sampling event without stratification. If composition is estimated from second event data or after pooling both sampling events, data must first be stratified to eliminate variability in capture probability (detected by the M vs. R test) within strata. Composition parameters are estimated within strata, and abundance for each stratum needs to be estimated using a Petersen-type formula. Overall composition parameters are estimated by combining stratum estimates weighted by estimated stratum abundance according to the formulae below.

Case III. Abundance is calculated using a Petersen-type model from the entire data set without stratification. Composition parameters may be estimated using length, sex, and age data from the second sampling event without stratification. If composition is estimated from first event data or after pooling both sampling events, data must first be stratified to eliminate variability in capture probability (detected by the C vs. R test) within strata. Composition parameters are estimated within strata, and abundance for each stratum needs to be estimated using a Petersen-type type formula. Overall composition parameters are estimated by combining stratum estimates weighted by estimated stratum abundance according to the formulae below.

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Case IV. Data must be stratified to eliminate variability in capture probability within strata for at least one or both sampling events. Abundance is calculated using a Petersen-type model for each stratum, and estimates are summed across strata to estimate overall abundance. Composition parameters may be estimated within the strata as determined above, but only using data from sampling events where stratification has eliminated variability in capture probabilities within strata. If data from both sampling events are to be used, further stratification may be necessary to meet the condition of capture homogeneity within strata for both events. Overall composition parameters are estimated by combining stratum estimates weighted by estimated stratum abundance.

If stratification by sex or length is necessary prior to estimating composition parameters, then an overall composition parameters (p_k) is estimated by combining within stratum composition estimates using:

$$\hat{p}_k = \sum_{i=1}^{j} \frac{\hat{N}_i}{\hat{N}_\Sigma} \hat{p}_{ik} \quad (1)$$

$$\hat{V}[\hat{p}_k] \approx \frac{1}{\hat{N}_\Sigma^2} \left(\sum_{i=1}^{j} \hat{N}_i^2 \hat{V}[\hat{p}_{ik}] + (\hat{p}_{ik} - \hat{p}_k)^2 \hat{V}[\hat{N}_i] \right). \quad (2)$$

where: j = the number of sex/size strata;
$\hat{p}_{ik}$ = the estimated proportion of fish that were age or size k among fish in stratum i;
$\hat{N}_i$ = the estimated abundance in stratum i; and,
$\hat{N}_\Sigma$ = sum of the $\hat{N}_i$ across strata.

Appendix A2.–Tests of consistency for the Petersen estimator (from Seber 1982, page 438).

Tests of consistency for Petersen estimator

Of the following conditions, at least one must be fulfilled to meet assumptions of a Petersen estimator:

1. Marked fish mix completely with unmarked fish between events;
2. Every fish has an equal probability of being captured and marked during event 1; or,
3. Every fish has an equal probability of being captured and examined during event 2.

To evaluate these three assumptions, the chi-square statistic will be used to examine the following contingency tables as recommended by Seber (1982). At least one null hypothesis needs to be accepted for assumptions of the Petersen model (Bailey 1951, 1952; Chapman 1951) to be valid. If all three tests are rejected, a temporally or geographically stratified estimator (Darroch 1961) should be used to estimate abundance.

I.–Mixing Test[a]

Area/time	Time/area where recaptured				Not recaptured
where marked	1	2	…	t	(n_1-m_2)
1					
2					
…					
s					

II.–Equal Proportions Test (SPAS terminology)[b]

	Area/time where examined			
	1	2	…	t
Marked (m_2)				
Unmarked (n_2-m_2)				

III.–Complete Mixing Test (SPAS terminology)[c]

	Area/time where marked			
	1	2	…	s
Recaptured (m_2)				
Not Recaptured (n_1-m_2)				

[a] This tests the hypothesis that movement probabilities (θ) from time or area i (i = 1, 2, s) to section j (j = 1, 2, t) are the same among sections: H_0: $\theta_{ij} = \theta_j$.

[b] This tests the hypothesis of homogeneity on the columns of the 2-by-t contingency table with respect to the marked to unmarked ratio among time or area designations: H_0: $\Sigma_i a_i \theta_{ij} = kU_j$, where k = total marks released/total unmarked in the population, U_j = total unmarked fish in stratum j at the time of sampling, and a_i = number of marked fish released in stratum i. Note that failure to reject H_0 means the Pooled Petersen estimator can be considered consistent only if the degree of closure among tagging strata is constant ($\Sigma_j \theta_{ij} = \lambda$,) (Schwarz and Taylor 1998). One way this may be achieved is to sample all or the large majority of spawning areas.

[c] This tests the hypothesis of homogeneity on the columns of this 2-by-s contingency table with respect to recapture probabilities among time or area designations: H_0: $\Sigma_j \theta_{ij} p_j = d$, where p_j is the probability of capturing a fish in section j during the second event, and d is a constant.

Appendix A3.–Predicting escapement from index counts using an expansion factor.

The expansion factor provides a means of predicting escapement in years where only an index count of the escapement is available, i.e. no weir counts or mark–recapture experiments were conducted. The expansion factor is the average over several years of the ratio of the escapement estimate (or weir count) to the index count.

Systems where escapement is known

On systems where escapement can be completely enumerated with weirs or other complete counting methods, the expansion factor is an estimate of the expected value of the "population" of annual expansion factors (π's) for that system:

$$\overline{\pi} = \frac{\sum_{y=1}^{k} \pi_y}{k} \qquad (1)$$

where $\pi_y = N_y / C_y$ is the observed expansion factor in year y, N_y is the known escapement in year y, C_y is the index count in year y, and k is the number of years for which these data are available to calculate an annual expansion factor.

The estimated variance for expansion of index counts needs to reflect two sources of uncertainty for any predicted value of π, (π_p). First is an estimate of the process error ($var(\pi)$-the variation across years in the π's, reflecting, for example, weather or observer-induced effects on how many fish are counted in a survey for a given escapement), and second is the sampling variance of $\overline{\pi}$ ($var(\overline{\pi})$), which will decline as we collect more data pairs.

The variance for prediction will be estimated (Neter et al. 1990):

$$v\hat{a}r(\pi_p) = v\hat{a}r(\pi) + v\hat{a}r(\overline{\pi}) \qquad (2)$$

where

$$v\hat{a}r(\pi) = \frac{\sum_{y=1}^{k} (\pi_y - \overline{\pi})^2}{k-1} \qquad (3)$$

and

$$v\hat{a}r(\overline{\pi}) = \frac{\sum_{y=1}^{k} (\pi_y - \overline{\pi})^2}{k(k-1)} \qquad (4)$$

such that

$$v\hat{a}r(\pi_p) = \frac{\sum_{y=1}^{k} (\pi_y - \overline{\pi})^2}{k-1} + \frac{\sum_{y=1}^{k} (\pi_y - \overline{\pi})^2}{k(k-1)} \qquad (5)$$

-continued-

Systems where escapement is estimated

On systems where escapement is estimated, the expansion factor is an estimate of the expected value of the "population" of annual expansion factors (π 's) for that system:

$$\overline{\pi} = \frac{\sum_{y=1}^{k} \hat{\pi}_y}{k} \qquad (6)$$

where $\hat{\pi}_y = \hat{N}_y / C_y$ is the estimate of the expansion factor in year *y*, $\hat{N}_y$ is the estimated escapement in year *y*, and other terms are as described above.

The variance for prediction will again be estimated:

$$v\hat{a}r(\pi_p) = v\hat{a}r(\pi) + v\hat{a}r(\overline{\pi}) \qquad (7)$$

The estimate of *var* (π) should again reflect only process error. Variation in $\hat{\pi}$ across years, however, represents process error **plus** measurement error within years (e.g. the mark–recapture induced error in escapement estimation) and is described by the relationship (Mood et al. 1974):

$$V(\hat{\pi}) = V[E(\hat{\pi})] + E[V(\hat{\pi})] \qquad (8)$$

This relationship can be rearranged to isolate process error, that is:

$$V[E(\hat{\pi})] = V[\hat{\pi}] - E[V(\hat{\pi})] \qquad (9)$$

An estimate of *var* (π) representing only process error therefore is:

$$v\hat{a}r(\pi) = v\hat{a}r(\hat{\pi}) - \frac{\sum_{y=1}^{k} v\hat{a}r(\hat{\pi}_y)}{k} \qquad (10)$$

where $v\hat{a}r(\hat{\pi}_y) = v\hat{a}r(\hat{N}_y) / C_y^2$ and $v\hat{a}r(\hat{N}_y)$ is obtained during the experiment when N_y is estimated.

We can calculate:

$$v\hat{a}r(\hat{\pi}) = \frac{\sum_{y=1}^{k} (\hat{\pi}_y - \overline{\pi})^2}{k-1} \qquad (11)$$

and we can estimate $var(\overline{\pi})$ similarly to as we did above:

-continued-

$$v\hat{a}r(\overline{\pi}) = \frac{\sum_{y=1}^{k}(\hat{\pi}_y - \overline{\pi})^2}{k(k-1)} \qquad (12)$$

where both process and measurement errors need to be included.

For large *k* (*k* > 30), equations (11) and (12) provide reasonable parameter estimates, however for small *k* the estimates are imprecise and may result in negative estimates of variance when the results are applied as in equation (7).

Because *k* is typically < 10, we will estimate $var(\hat{\pi})$ and $var(\overline{\pi})$ using parametric bootstrap techniques Efron and Tibshirani 1993a. The sampling distributions for each of the $\hat{\pi}_y$ are modeled using Normal distributions with means $\hat{\pi}_y$ and variances $v\hat{a}r(\hat{\pi}_y)$. At each bootstrap iteration, a bootstrap value $\hat{\pi}_{y(b)}$ is drawn from each of these Normal distributions and the bootstrap value $\hat{\pi}_{(b)}$ is randomly chosen from the *k* values of $\hat{\pi}_{y(b)}$. Then, a bootstrap sample of size *k* is drawn from the *k* values of $\hat{\pi}_{y(b)}$ by sampling with replacement, and the mean of this bootstrap is the bootstrap value $\overline{\pi}_{(b)}$. This procedure is repeated *B* = 1,000,000 times. We can then estimate $var(\hat{\pi})$ using:

$$v\hat{a}r_B(\hat{\pi}) = \frac{\sum_{b=1}^{B}(\hat{\pi}_{(b)} - \overline{\hat{\pi}_{(b)}})^2}{B-1} \qquad (13)$$

where

$$\overline{\hat{\pi}_{(b)}} = \frac{\sum_{b=1}^{B}\hat{\pi}_{(b)}}{B} \qquad (14)$$

and we can calculate $var_B(\overline{\pi})$ using equations (13) and (14) with appropriate substitutions. The variance for prediction is then estimated:

$$v\hat{a}r(\pi_p) = v\hat{a}r_B(\hat{\pi}) - \frac{\sum_{y=1}^{k}\mathrm{v\hat{a}r}(\hat{\pi}_y)}{k} + v\hat{a}r_B(\overline{\pi}) \qquad (15)$$

As the true sampling distributions for the $\hat{\pi}_y$ are typically skewed right, using a Normal distribution to approximate these distributions in the bootstrap process will result in estimates of $var(\hat{\pi})$ and $var(\overline{\pi})$ that are biased slightly high, but simulation studies using values similar to those realized for this application indicated that the bias in equation (15) is < 1%.

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Predicting Escapement

In years when an index count (C_p) is available but escapement (N_p) is not known, it can be predicted:

$$\hat{N}_p = \bar{\pi}\, C_p \qquad (16)$$

and

$$v\hat{a}r(\hat{N}_p) = C_p^2 v\hat{a}r(\pi_p) \qquad (17)$$

Appendix A4.–Estimated annual escapement of Chinook salmon in the Unuk River by age class and gender, 1997–2006.

		Age Class									
Year	Gender	1.1	1.2	0.4	1.3	2.2	1.4	2.3	1.5	2.4	Total
	Male	46	881		724	5	323		14		1,992
1997	%	1.3	24.0		19.7	0.1	8.8		0.4		54.3
estimated	Female		5		526		1,102		46		1,679
escapement	%		0.1		14.3		30.0		1.3		45.7
	Total	46	885		1,250	5	1,425		60		3,671
	%	1.3	24.1		34.0	0.1	38.8		1.6		100.0
	Male	232	1,299		1,392	6	325		6		3,259
1998	%	4.4	24.4		26.1	0.1	6.1		0.1		61.2
estimated	Female				1,172		870		29		2,071
escapement	%				22.0		16.3		0.5		38.8
	Total	232	1,299		2,564	6	1,195		35		5,330
	%	4.4	24.4		48.1	0.1	22.4		0.7		100.0
	Male	211	2,189		1,134		492		9		4,036
1999	%	3.4	35.4		18.3		8.0		0.1		65.3
estimated	Female		26		914		1,196		9		2,145
escapement	%		0.4		14.8		19.3		0.1		34.7
	Total	211	2,216		2,049		1,688		18		6,181
	%	3.4	35.8		33.1		27.3		0.3		100.0
	Male	9	2,444		2,312		517		19		5,302
2000	%	0.1	30.0		28.4		6.3		0.2		65.1
estimated	Female		47		1,636		1,128		38		2,848
escapement	%		0.6		20.1		13.8		0.5		34.9
	Total	9	2,491		3,948		1,645		56		8,150
	%	0.1	30.6		48.4		20.2		0.7		100.0
	Male	83	936		3,680		894		21		5,613
2001	%	0.7	8.3		32.5		7.9		0.2		49.6
estimated	Female		10		3,243		2,443				5,697
escapement	%		0.1		28.7		21.6				50.4
	Total	83	946		6,923		3,337		21		11,310
	%	0.7	8.4		61.2		29.5		0.2		100.0
	Male		2,437		1,675		1,146		22		5,280
2002	%		28.3		19.4		13.3		0.3		61.2
estimated	Female		48		1,212		2,042		33	11	3,346
escapement	%		0.6		14.1		23.7		0.4	0.1	38.8
	Total		2,485		2,887		3,188		55	11	8,626
	%		28.8		33.5		37.0		0.6	0.1	100.0
	Male	192	580	6	2,135		447		11		3,371
2003	%	3.1	9.3	0.1	34.2		7.2		0.2		54.0
estimated	Female		11		1,795	6	1,027		34		2,874
escapement	%		0.2		28.7	0.1	16.4		0.5		46.0
	Total	192	592	6	3,930	6	1,474		46		6,244
	%	3.1	9.5	0.1	62.9	0.1	23.6		0.7		100.0
	Male	75	2,909		912		523				4,419
2004	%	1.2	47.9		15.0		8.6				72.7
estimated	Female		27		377		1,234		19		1,658
escapement	%		0.4		6.2		20.3		0.3		27.3
	Total	75	2,936		1,289		1,756		19		6,077
	%	1.2	48.3		21.2		28.9		0.3		

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Year	Gender	Age Class									Total
		1.1	1.2	0.4	1.3	2.2	1.4	2.3	1.5	2.4	
2005 estimated escapement	Male	368	507		2,454	5	247		6		3,587
	%	6.6	9.1		44.3	0.1	4.5		0.1		64.7
	Female		6		1,348		589	6	6		1,956
	%		0.1		24.3		10.6	0.1	0.1		35.3
	Total	368	513		3,802	5	836	6	12		5,543
	%	6.6	9.3		68.6	0.1	15.1	0.1	0.2		
2006 estimated escapement	Male	221	3,197		1,209		631				5,258
	%	2.9	41.4		15.7		8.2				68.1
	Female		58		938		1,469				2,465
	%		0.8		12.1		19.0				31.9
	Total	221	3,255		2,147		2,100				7,723
	%	2.9	42.2		27.8		27.2				
1997–2005 mean annual estimated escapement	Male	135	1,576	1	1,824	2	546		12		4,096
	%	2.0	23.2	< 0.1	26.9	< 0.1	8.0		0.2		60.3
	Female		20		1,358	1	1,292	1	24	1	2,697
	%		0.3		20.0	< 0.1	19.0	< 0.1	0.3	< 0.1	39.7
	Total	135	1,596	1	3,182	2	1,838	1	36	1	6,792
	%	2.0	23.5	< 0.1	46.9	< 0.1	27.1	< 0.1	0.5	< 0.1	

Appendix A5.–Elapsed time between release and recapture (sulking period) of Chinook salmon at SN1 in the lower Unuk River in 2006.

			Sulking period		
Spaghetti tag no.	Release date/time	Recapture date/time	Days	Hours	Minutes
1027	06/20/06 13:46	06/29/06 12:05	8	22	29
1063	06/23/06 16:50	07/13/06 17:45	19	0	55
1107	06/27/06 08:24	07/01/06 08:40	4	0	16
1127	06/29/06 15:56	07/12/06 17:25	13	1	29
1153	07/01/06 08:06	07/10/06 15:10	9	7	4
1154	07/01/06 08:10	07/07/06 10:43	6	2	33
1176	07/01/06 11:54	07/01/06 15:06		3	12
1184	07/01/06 12:50	07/20/06 11:45	18	22	55
1195	07/01/06 15:05	07/15/06 11:00	13	19	55
1241	07/02/06 06:04	07/03/06 16:30	1	10	26
1242	07/02/06 06:05	07/11/06 12:51	9	6	46
1254	07/02/06 08:11	07/08/06 13:06	6	4	55
1256	07/02/06 09:05	07/07/06 18:20	5	9	15
1290	07/02/06 15:51	07/02/06 16:50			59
1294	07/02/06 16:11	07/17/06 17:45	15	1	34
1297	07/02/06 16:36	07/12/06 17:15	10	0	39
1298	07/02/06 16:51	07/12/06 10:04	9	17	13
1304	07/02/06 17:40	07/10/06 16:06	7	22	26
1313	07/03/06 05:50	07/15/06 06:54	12	1	4
1315	07/03/06 06:00	07/14/06 15:06	11	9	6
1318	07/03/06 06:20	07/14/06 17:34	11	11	14
1326	07/03/06 08:00	07/03/06 09:15		1	15
1327	07/03/06 08:07	07/03/06 08:25			18
1331	07/03/06 08:54	07/18/06 12:48	15	3	54
1345	07/03/06 12:01	07/03/06 15:52		3	51
1352	07/03/06 13:02	07/13/06 13:20	10	0	18
1354	07/03/06 13:36	07/15/06 18:15	12	4	39
1368	07/03/06 15:25	07/14/06 17:59	11	2	34
1391	07/03/06 17:58	07/19/06 10:45	15	16	47
1394	07/03/06 18:40	07/15/06 09:58	12	15	18
1395	07/03/06 18:52	07/18/06 15:24	14	20	32
1400	07/04/06 06:07	07/15/06 15:17	11	9	10
1405	07/04/06 08:39	07/04/06 11:00		2	21
1406	07/04/06 11:45	07/18/06 12:51	14	1	6
1417	07/05/06 15:15	07/17/06 08:43	11	17	28
1434	07/06/06 13:42	07/16/06 15:48	10	2	6
1460	07/06/06 18:04	07/18/06 07:40	11	13	36
1464	07/07/06 07:31	07/07/06 15:57		8	26
1501	07/07/06 14:59	07/07/06 16:22		1	23
1501	07/07/06 16:22	07/11/06 15:44	3	23	22
1527	07/08/06 06:04	07/28/06 10:15	20	4	11
1532	07/08/06 07:58	07/08/06 09:12		1	14
1540	07/08/06 10:09	07/10/06 09:55	1	22	46
1545	07/08/06 11:48	07/17/06 15:40	9	3	52
1553	07/08/06 14:51	07/18/06 14:28	9	23	37
1555	07/08/06 15:30	07/18/06 13:24	10	2	6
1559	07/10/06 06:30	07/13/06 14:00	3	7	30
1569	07/10/06 12:30	07/14/06 13:23	4	0	53
1570	07/10/06 12:47	07/18/06 12:17	7	23	30

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Spaghetti tag no.	Release date/time	Recapture date/time	Sulking period		
			Days	Hours	Minutes
1572	07/10/06 13:11	07/19/06 16:10	9	2	59
1574	07/10/06 13:40	07/14/06 13:43	4	0	3
1580	07/10/06 16:09	07/11/06 13:40		21	31
1582	07/10/06 17:07	07/10/06 17:13			6
1582	07/10/06 17:13	07/28/06 11:00	17	17	47
1583	07/10/06 17:45	07/14/06 16:28	3	22	30
1593	07/11/06 10:40	07/12/06 13:50	1	1	10
1604	07/11/06 15:04	07/17/06 13:00	5	21	56
1628	07/13/06 06:05	07/13/06 12:45		6	40
1642	07/13/06 15:00	07/14/06 13:42		22	42
1654	07/14/06 09:40	07/14/06 15:59		6	19
1659	07/14/06 12:25	07/14/06 17:07		4	42
1669	07/14/06 14:24	08/02/06 15:06	19	0	42
1690	07/15/06 07:25	07/19/06 18:28	4	11	3
1701	07/15/06 10:39	07/15/06 13:10		2	31
1737	07/16/06 06:17	07/19/06 11:49	3	5	32
1752	07/16/06 15:23	07/19/06 08:45	2	17	12
1772	07/17/06 10:45	07/17/06 12:20		1	35
1772	07/17/06 12:20	07/29/06 14:46	12	2	26
1792	07/18/06 06:30	07/30/06 12:19	12	5	49
1799	07/18/06 08:03	07/19/06 17:38	1	9	35
1811	07/18/06 14:44	07/18/06 15:12			28
1555	07/18/06 13:24	07/18/06 13:33			9
1813	07/18/06 15:34	07/19/06 07:48		16	14
1825	07/19/06 06:12	07/19/06 13:45		7	33
1841	07/19/06 12:11	07/19/06 13:17		1	6
1841	07/19/06 13:17	07/19/06 13:25			8
1859	07/19/06 16:45	07/28/06 08:49	8	16	4
1861	07/19/06 17:03	07/19/06 18:09		1	6
1871	07/20/06 09:01	07/30/06 15:45	10	6	44
1882	07/28/06 06:20	07/30/06 15:23	2	9	3
1892	07/28/06 10:17	07/28/06 11:03			46
1909	07/29/06 08:09	07/29/06 17:06		8	57
1931	07/29/06 14:23	07/29/06 14:50			27
1934	07/29/06 15:18	07/30/06 13:40		22	22
1992	07/31/06 13:49	08/02/06 16:33	2	2	44

Average = 6 days, 8 hours, and 43 minutes; maximum = 20 days, 4 hours, and 11 minutes; minimum = 6 minutes.

Appendix A6.–Numbers by gender and age for Chinook salmon sampled on the Unuk River spawning grounds in 2006 by location (Panel A) and gear (Panel B), and by size group (Panel C), in the lower river gillnet samples. Results were not stratified by size class; for the age composition of the escapement, see Table 5.

			Brood year and age class							
			2003	2002	2001	2001	2000	2000	1999	
			1.1	1.2	2.2	1.3	2.3	1.4	1.5	Total
PANEL A: EVENT 2 SAMPLES BY LOCATION										
	Males	n	1	15		7				23
		%	3.4	51.7		24.1				79.3
Boundary Creek	Females	n		1		3		2		6
		%		3.4		10.3		6.9		20.7
	Total	n	1	16		10		2		29
		%	3.4	55.2		34.5		6.9		100.0
	Males	n	2	31		8		10		51
		%	2.2	34.8		9.0		11.2		57.3
Clear Creek	Females	n				8		30		38
		%				9.0		33.7		42.7
	Total	n	2	31		16		40		89
		%	2.2	34.8		18.0		44.9		100.0
	Males	n	2	131		58		22		213
		%	0.6	39.9		17.7		6.7		64.9
Cripple Creek	Females	n		5		53		57		115
		%		1.5		16.2		17.4		35.1
	Total	n	2	136		111		79		328
		%	0.6	41.5		33.8		24.1		100.0
	Males	n	1	2		2		3		8
		%	10.0	20.0		20.0		30.0		80.0
Eulachon River	Females	n				2				2
		%				20.0				20.0
	Total	n	1	2		4		3		10
		%	10.0	20.0		40.0		30.0		100.0
	Males	n	20	205		65		17		307
		%	4.9	50.4		16.0		4.2		75.4
Genes Lake Creek	Females	n		1		43		56		100
		%		0.2		10.6		13.8		24.6
	Total	n	20	206		108		73		407
		%	4.9	50.6		26.5		17.9		100.0
	Males	n		2		1		5		8
		%		15.4		7.7		38.5		61.5
Kerr Creek	Females	n						5		5
		%						38.5		38.5
	Total	n		2		1		10		13
		%		15.4		7.7		76.9		100.0
	Males	n	1	11		7		20		39
		%	1.4	15.7		10.0		28.6		55.7
Lake Creek	Females	n				4		27		31
		%				5.7		38.6		44.3
	Total	n	1	11		11		47		70
		%	1.4	15.7		15.7		67.1		100.0

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			Brood year and age class							
			2003	2002	2001	2001	2000	2000	1999	
			1.1	1.2	2.2	1.3	2.3	1.4	1.5	Total
PANEL B: EVENT 2 SAMPLES BY GEAR										
	Males	n								
		%								
Carcass	Females	n				1				1
		%				100.0				100.0
	Total	n				1				1
		%				100.0				100.0
	Males	n								
		%								
Dip net	Females	n				1				1
		%				100.0				100.0
	Total	n				1				1
		%				100.0				100.0
	Males	n		6		2		1		9
		%		60.0		20.0		10.0		90.0
Rod and reel lure	Females	n				1				1
		%				10.0				10.0
	Total	n		6		3		1		10
		%		60.0		30.0		10.0		100.0
	Males	n	25	294		102		68		489
		%	3.4	40.3		14.0		9.3		67.1
Rod and reel snag	Females	n		6		86		148		240
		%		0.8		11.8		20.3		32.9
	Total	n	25	300		188		216		729
		%	3.4	41.2		25.8		29.6		100.0
	Males	n	1	97		42		10		150
		%	0.5	47.8		20.7		4.9		73.9
Gillnet	Females	n		1		24		28		53
		%		0.5		11.8		13.8		26.1
	Total	n	1	98		66		38		203
		%	0.5	48.3		32.5		18.7		100.0
	Males	n	1							1
		%	50.0							50.0
Other/unknown	Females	n						1		1
		%						50.0		50.0
	Total	n						1		2
		%						50.0		100.0

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			Brood year and age class							
			2003 1.1	2002 1.2	2001 2.2	2001 1.3	2000 2.3	2000 1.4	1999 1.5	Total
PANEL C: EVENT 1-LOWER UNUK RIVER SET GILLNET SAMPLES										
Small-sized	Males	n	1	3						4
		%	0.6	1.9						2.5
	Females	n								
		%								
	Total	n	1	3						4
		%	0.6	1.9						2.5
Medium-sized	Males	n		153		4				157
		%		96.2		2.5				98.7
	Females	n		2						2
		%		1.3						1.3
	Total	n		155		4				159
		%		97.5		2.5				100.0
Large-sized	Males	n		217	1	180	1	74		473
		%		25.1	0.1	20.8	0.1	8.6		54.7
	Females	n		15		175		200	1	391
		%		1.7		20.3		23.1	0.1	45.3
	Total	n		232	1	355	1	274	1	864
		%		26.9	0.1	41.1	0.1	31.7	0.1	100.0
Total	Males	n	1	373	1	184	1	74		634
		%	0.1	36.3	0.1	17.9	0.1	7.2		61.7
	Females	n		17		175		200	1	393
		%		1.7		17.0		19.5	0.1	38.3
	Total	n	1	390	1	359	1	274	1	1,027
		%	0.1	38.0	0.1	35.0	0.1	26.7	0.1	100.0

Appendix A7.–Estimated abundance of the spawning population of large (>659 mm MEF) Chinook salmon in the Unuk River, 1977–2006. The mean expansion factor is 5.27 (SD = 1.09). The expansion factor was calculated from m–r experiment and survey results, 1997–2006.

		Abundance estimated from expanded count		Abundance estimated from m–r experiment		Preferred abundance estimate	
Year	Peak count from surveys	$\hat{N}$	$SE(\hat{N})$	$\hat{N}$	$SE(\hat{N})$	$\hat{N}$	$SE(\hat{N})$
1977	974	5,135	1,062			5,135	1,062
1978	1,106	5,831	1,206			5,831	1,206
1979	576	3,037	628			3,037	628
1980	1,016	5,357	1,108			5,357	1,108
1981	731	3,854	797			3,854	797
1982	1,351	7,123	1,473			7,123	1,473
1983	1,125	5,931	1,227			5,931	1,227
1984	1,837	9,685	2,003			9,685	2,003
1985	1,184	6,243	1,291			6,243	1,291
1986	2,126	11,209	2,318			11,209	2,318
1987	1,973	10,402	2,151			10,402	2,151
1988	1,746	9,206	1,904			9,206	1,904
1989	1,149	6,058	1,253			6,058	1,253
1990	591	3,116	644			3,116	644
1991	655	3,453	714			3,453	714
1992	874	4,608	953			4,608	953
1993	1,068	5,631	1,165			5,631	1,165
1994	711	3,749	775	4,623	1,266	3,749	775
1995	772	4,070	842			4,070	842
1996	1,167	6,153	1,273			6,153	1,273
1997	636	3,353	694	2,970	277	2,970	277
1998	840	4,429	916	4,132	413	4,132	413
1999	680	3,585	741	3,914	490	3,914	490
2000	1,341	7,070	1,462	5,872	644	5,872	644
2001	2,019	10,645	2,202	10,541	1,181	10,541	1,181
2002	897	4,729	978	6,988	805	6,988	805
2003	1,121	5,910	1,222	5,546	433	5,546	433
2004	1,008	5,315	1,099	3,963	325	3,963	325
2005	929	4,898	1,013	4,742	396	4,742	396
2006	940	4,956	1,025	5,645	476	5,645	476

Appendix A8.–Computer files used to estimate the spawning abundance of Chinook salmon in the Unuk River in 2006.

File name	Description
06unk41a.xls	Spreadsheet containing Tables 1–6, Figure 5, Appendices A5-A7, and bootstrap results.
KS FIG6.xls	Spreadsheet containing Figures 6.
KS FIG7.xls	Spreadsheet containing Figures 7.
KS FIG8.xls	Spreadsheet containing Figures 8.
KS FIG9.xls	Spreadsheet containing Figures 9.
KS FIG10.xls	Spreadsheet containing Figures 10.
KS FIG11.xls	Spreadsheet containing Figures 11.
U41migratory06.xls	Spreadsheet containing Table 7.
06Unuk41ASL.xls	Spreadsheet containing mark–recapture data.