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Feasibility of Estimating the 2011 Terminal Run Sizes for Chinook Salmon Driver Stocks Harvested in Southeast Alaska Troll and Sport Fisheries

by

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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 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)

Mathematics, statistics	
all standard mathematical signs, symbols and abbreviations	
alternate hypothesis	H_A
base of natural logarithm	*e*
harvest 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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FEASIBILITY OF ESTIMATING THE 2011 TERMINAL RUN SIZES FOR CHINOOK SALMON DRIVER STOCKS HARVESTED IN SOUTHEAST ALASKA TROLL AND SPORT FISHERIES

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ABSTRACT

We investigated using genetic analysis and coded wire tags to estimate terminal run size of Chinook salmon in 2011 from four large stock groups that are major contributors to Southeast Alaska troll and sport fisheries—West Coast Vancouver Island (WCVI), Washington Coast (WAC), North Oregon Coast (NOC), and Upper Columbia River Falls (UCF). The *driver stock method* uses harvest, genetic stock identification, age-length, and coded-wire tag information. A diagnostic algorithm was developed to test a core assumption of the method, which is that a driver stock experiences the same catch and maturation rates as its associated indicator stocks. CVs of terminal run size estimates ranged from 9% to 42%, which improved to 7% to 31% with 3-year-olds excluded. For the UCF driver stock, a direct comparison between the driver stock method and an independent estimate based on counts past Bonneville Dam showed that the driver stock estimate was 13% lower; however, the diagnostic algorithm for the UCF stock indicated that the driver stock method was accurate. On a scale of 0–98 percentage points with 0 being complete accuracy, the score for the UCF stock was 2 points. No independent estimates of terminal run size were available for NOC and WAC stocks; their diagnostic scores were 7 and 13 points, respectively. Higher scores for the NOC and WAC driver stocks were posited to partially reflect the uncertainty in independently estimated relative age distributions in their terminal runs. Independent estimates of relative age distribution for terminal runs showed that the driver stock method gave reasonable estimates for partially recruited 3-year-olds from UCF, WAC, and NOC stocks but not for the WCVI stock. Imprecision in estimates of 6-year-old Chinook salmon in terminal runs due to their low frequency had no appreciable effect on the combined estimate for 3- to 6-year-old fish.

Key words: Chinook salmon, *Oncorhynchus tshawytscha*, terminal run size estimates, CWT, genetic stock identification, otolith, West Coast Vancouver Island, Washington coast, Oregon coast, Upper Columbia River, driver stock method, gorilla assumption, Southeast Alaska fisheries

INTRODUCTION

In autumn, stocks of Chinook salmon (*Oncorhynchus tshawytscha*) spawn in streams and are spawned in hatcheries on the West Coast of Vancouver Island (WCVI), along the Washington (WAC) and north Oregon coasts (NOC), and in the Upper Columbia River[1] (UCF). Collectively these four aggregate stocks comprise a large proportion of all Chinook salmon annually harvested in Southeast Alaska (SEAK) fisheries and thus are important stocks that help drive catch allocations under the Pacific Salmon Treaty (PST; CTC 2012). The standard method for indirectly estimating the harvest size (landed catch) from these and other driver stocks in SEAK and from other ocean fisheries under management through the PST is as follows:

- Estimate terminal run size for the driver stock.
- Estimate exploitation rates for a tagged *indicator stock*, which is a stock selected to have the same exploitation and maturation rates as the driver stock.
- Calculate harvest from the driver stock as a function of its terminal run size and exploitation rates from the indicator stock (run size multiplied by exploitation rate).

However, there are problems with the standard method, primarily with estimating terminal run size for the driver stock. Accurately and precisely estimating spawning abundance, a significant component of terminal run size, for a single population of Chinook salmon through field sampling is expensive, prohibitively so for estimating spawning abundance of all populations in a driver stock complex. In many cases imprecise indices are used as proxies to estimate escapement, thereby adding uncertainty to the estimates of terminal run size and subsequently to estimated catches.

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[1] All fall Chinook salmon transiting Bonneville Dam from August 1 through November 15, 2011, destined for areas above McNary Dam and the Deschutes River.

Recent advances in genetic stock identification (GSI) provide accurate and precise harvest estimates of driver stocks by sampling landed catches in SEAK fisheries (Gilk-Baumer et al. 2013). Direct estimation of harvest of each driver stock in SEAK fisheries has the added benefit of providing a means to invert the standard method and use harvest to indirectly estimate terminal run size. Such indirect estimation can be accomplished through the following steps:

- Estimate harvests of the driver stock in SEAK fisheries using GSI.
- Estimate harvest in SEAK fisheries and terminal run size for a tagged indicator stock selected to share the same exploitation and maturation rates as the driver stock.
- Calculate terminal run size for the driver stock as a function of harvests from the driver and indicator stocks and the terminal run size of the indicator stock.

Collectively these three steps are referred to as the *driver stock method*. A core assumption of this method, also known as the *gorilla assumption*, is that the chosen indicator stocks can be surrogates for each driver stock because they experience the same maturation and exploitation rates. The same assumption is also made in the standard method.

Our goal was to test the feasibility of using the driver stock method to estimate terminal run sizes of four driver stocks of Chinook salmon—WCVI, WAC, NOC, and UCF. Our tests consisted of estimating hatchery-origin (hatchery) and natural-origin (natural)[2] terminal run sizes for each driver stock. We used data from 2011 to calculate these estimates. We also developed a diagnostic test to detect possible violation of the gorilla assumption.

BACKGROUND

SEAK FISHERIES

Six fisheries in SEAK were involved in our study, including five troll fisheries and one sport fishery in two quadrants (Figure 1). The northern outside (NO) troll quadrant was the location of four fisheries:

- spring commercial troll fishery from April through June (Spring)
- first retention commercial troll fishery from July 1–12 (NO-1)
- second retention commercial troll fishery from August 15–17 (NO-2)
- Sitka sport fishery from May 15 through September (Sitka Sport)

The other two fisheries occurred in the southern outside (SO) quadrant:

- first retention commercial troll fishery from July 1–12 (SO-1)
- second retention commercial troll fishery from August 15–17 (SO-2)

Fisheries within inside quadrants (Figure 1) were not included in our analysis because exploitation of the four driver stocks in these quadrants was negligible in 2011.

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[2] We define a *natural* population as a group of Chinook salmon that were spawned in the wild.

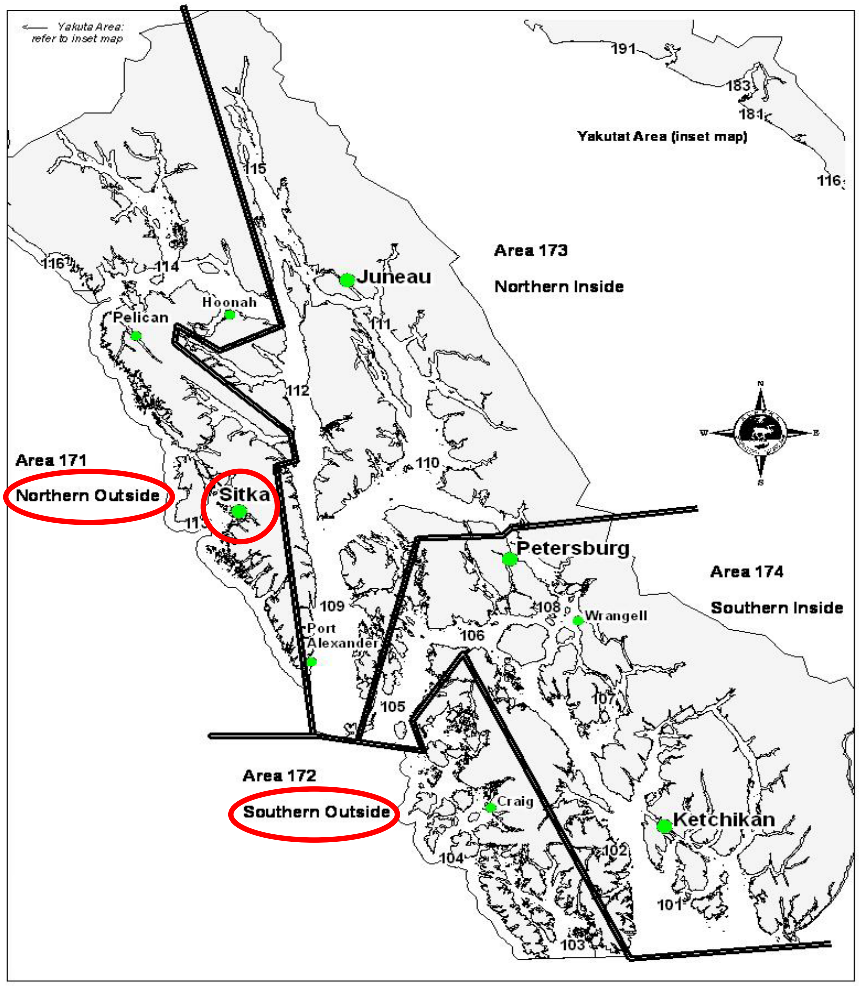

Figure 1.– Locations of fishing grounds for commercial troll fisheries (Northern Outside, Southern Outside) and the home port for the Sitka sport fishery.

DRIVER STOCKS

The driver stocks involved in this feasibility study are WCVI, WAC, NOC, and UCF stocks. Although there are seven driver stocks to SEAK fisheries, not all were included in this study. Chinook salmon spawning in the South Thompson River, a tributary to the Fraser River, contributed an estimated 13% of the landed catch in SEAK in 2011; however, a version of the driver stock method has already been applied to this stock since 2010 by the Canadian Department of Fisheries and Oceans with success using GSI on landed catches from ocean fisheries in Northern British Columbia (Korman et al. 2012). The four driver stocks in our feasibility study were chosen because they were four of the major contributors to the SEAK fisheries examined (Gilk-Baumer et al. 2013).

Terminal areas were defined for each of the designated driver stocks as follows:

- WCVI – estuaries, spawning grounds, waters immediately offshore, and hatcheries releasing juveniles along the western coastline of Vancouver Island

- WAC – estuaries, spawning grounds, waters immediately offshore, and hatcheries releasing juveniles into the aforementioned areas along the western coastline of Washington State including the western coastline inside the Strait of Juan de Fuca
- NOC – estuaries, spawning grounds, and hatcheries releasing juveniles into the aforementioned areas along the western coastline of Oregon State from the Siuslaw River north to, but not including, the Columbia River
- UCF – spawning grounds and hatcheries releasing juveniles into waters upstream of Bonneville Dam on the Columbia River

Driver stocks represent fall runs of ocean-type Chinook salmon. While there are spring, summer, and fall runs of Chinook salmon along the Washington coast, only the fall runs contribute significantly to SEAK fisheries. Similarly, although there are spring and summer runs of Chinook salmon in the Columbia River, the upriver bright fall run is the more important contributor from the Columbia stocks to SEAK fisheries, so we excluded consideration of the earlier runs in our analysis. All populations in the NOC and WCVI driver stocks are fall runs.[3]

The individual populations and runs of Chinook salmon are too numerous to list in this report; for example, Chinook salmon are known to spawn in over 100 streams along the WCVI alone. However, the list of streams and hatcheries that make up the genetic baseline is indicative of the coverage in this report (Table 1). As long as members of unsampled populations genetically classify as members of the appropriate driver stock, estimates of terminal run size from the driver stock method will correspond to all populations in the driver stock.

Table 1.–Populations included in the genetic baseline for the WCVI, WAC, NOC, and UCF driver stocks. Only fall runs are listed for the WCVI, NOC, and UCF driver stocks. Unless otherwise noted, listed populations for the WAC driver stock are also fall runs. Further detail regarding samples from these populations is in Appendix B1.

WCVI	WAC	NOC	UCF
SPAWNING GROUNDS			
Burman River	Hoh River	Alsea River	Clearwater River
Gold River	Hoh River (Spr/Sum)	Kilchis River	Deschutes River
Kennedy River	Queets River	Nehalem River	Hanford Reach
Nahmint River	Quillayute River	Salmon River	Klickitat River
San Juan River	Quinault River	Siletz River	Marion Drain
Tahsis River		Trask River	Yakima River
Thornton Creek		Wilson River	
Tlupana River		Yaquina River	
Toquart River		Siuslaw River	
Tranquil Creek			
Zeballos River			
HATCHERIES			
Conuma River	Forks Creek	Necanicum River	Little White Salmon
Marble River	Hoko	Nestucca River	Lyons Ferry
Nitinat River	Humptulips	Salmon River	Nez Perce Tribal
Robertson Creek	Makah		Priest Rapids
Sarita River	Quinault		Umatilla
	Sol Duc (Spr)		

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[3] There are a few Chinook salmon that return to the NOC each year that arguably could be considered a summer run, but because their numbers are negligible relative to the fall run the summer run was not considered in this report.

Three types of estimates of terminal run size were calculated depending on the driver stock: hatchery run, natural run, and combined hatchery/natural run. Because hatchery broodstock has been selected from natural populations within the same driver stock, hatchery-produced and natural Chinook salmon within the same driver stock are genetically indistinguishable. For that reason hatchery-produced Chinook salmon are marked so they can be distinguished from their natural counterparts. Marks consisted of coded wire tags (CWTs), excised adipose fins of the NOC, WAC, and UCF driver stocks, and thermally coded otoliths of the WCVI driver stock.

INDICATOR STOCKS

Indicator stocks chosen to represent each driver stock in this analysis (Table 2) are essentially the same as those used by the Chinook Technical Committee (CTC) of the Pacific Salmon Commission in their annual exploitation rate and calibration analyses (CTC 2012). All indicator stocks are distinguished by batch-identifiable CWTs and excised adipose fins as an external, secondary mark. All indicator stocks are hatchery releases or a collection of hatchery releases with one exception: the indicator stock for UCF contains natural Chinook salmon captured in rearing areas of the Hanford Reach of the Columbia River and released with CWTs.

Table 2.–Indicator stocks for each of the Chinook salmon driver stocks included in this study and their terminal fisheries.

WCVI	WAC	NOC	UCF
INDICATOR STOCKS			
Robertson Creek Hatchery	Queets River Hatchery	Salmon River Hatchery	Ringold Springs Hatchery
	Hoko River Falls Hatchery		Priest Rapids Hatchery
	Makah National Fish Hatchery on Sooes River		Lyons Ferry Hatchery
	Salmon River Fish Culture on Salmon River (feeds into Queets River)		Hanford Wilds
TERMINAL FISHERIES			
Alberni Inlet Gillnet	Queets Coastal Gillnet	Salmon River Sport	All fisheries above the Bonneville Dam on the Columbia River
Alberni Inlet Sport		Siletz River Sport	
Barkley Sound Sport		Tillamook Estuary Sport	
First Nations Alberni Inlet Net			
First Nations Somass River Net			

Statistics for indicator stocks are calculated from sampling fishery catches and expansion of those numbers across catches. The estimated numbers of CWTs in landed catches in SEAK fisheries and in the various terminal fisheries were calculated as the number of tags recovered expanded by the fraction of the catch sampled with corrections for the number of heads lost before reaching a lab and unreadable tags. CWTs recovered on spawning grounds and at hatcheries were expanded in a like manner. Batch-identifiable codes for CWTs defining indicator stocks are listed in Appendix A.

METHODS

TERMINAL RUN SIZE ESTIMATION

Terminal run size $M_{term(D)}$ for driver stock *D* of natural origin was estimated as

$$\hat{M}_{term,nat(D)} = \sum_a \sum_f \hat{\pi}_{a(I)} \hat{p}_{f,a,nat(D)} \hat{H}_f \quad , \tag{1}$$

where *a* signifies salmon age and *f* signifies the SEAK fishery. All calculations were stratified by age to reduce differences in maturation rates between the indicator and driver stocks.[4] The variable $\hat{p}_{f,a,nat(D)}$ is the estimated harvest fraction from fishery *f* by age *a* for driver stock *D* of natural origin. Estimating terminal run size for driver stock *D* of hatchery origin ($\hat{M}_{term,hat(D)}$) would have $\hat{p}_{f,a,hat(D)} \to \hat{p}_{f,a,nat(D)}$ in Equation (1); estimating terminal run size for combined natural and hatchery-origin salmon ($\hat{M}_{term,\bullet(D)}$) would have $\hat{p}_{f,a,\bullet(D)} \to \hat{p}_{f,a,nat(D)}$. The ratio $\pi_{a(I)}$ of the number of salmon belonging to indicator stock *I* in the terminal area of indicator stock *I* ($n_{term,a(I)}$) to the number of salmon from indicator stock *I* landed in SEAK fisheries ($\Sigma_f n_{f,a(I)}$) was estimated as

$$\hat{\pi}_{a(I)} = \frac{\hat{n}_{term,a(I)}}{\sum_f \hat{n}_{f,a(I)}} \quad . \tag{2}$$

If exploitation and maturation rates were the same for the indicator and the driver stocks, the gorilla assumption holds, making $\pi_{a(I)} = \pi_{a(D)}$ and $\mathrm{E}[\hat{M}_{term(D)}] = M_{term(D)}$. Estimated harvest in fishery *f* ($\hat{H}_f$) represents estimated harvest regardless of origin.

Estimating $\pi_{a(I)}$ required information from several independent, established sampling programs in ocean and terminal fisheries, at hatcheries, and on spawning grounds. Large fractions of landed catches in SEAK and other fisheries were inspected for external marks indicating the presence of a CWT in marked salmon. Salmon encountered with such marks were collected, dissected to recover tags, and the recovered CWTs were read to determine origin. Rack returns and spawning escapement were similarly sampled. Numbers of CWTs in terminal areas ($n_{term,a(I)}$) and landed catches ($n_{f,a(I)}$) were estimated by dividing the number of CWTs recovered by the fraction of catch sampled, fraction of rack returns sampled, and in the case of the Hanford Wilds,[5] the fraction of estimated escapement sampled when appropriate. Expanded numbers of recovered CWTs for the four indicator stocks were obtained from the database used by the CTC for their annual exploitation rate analysis (CTC 2012). Information on fishery and

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[4] Chinook salmon of different ages in the same population have different maturation rates. Because age composition in the terminal run for a hatchery-produced indicator stock is in part a function of the size of releases years before, the relative age distribution of an indicator stock based on hatchery-produced fish is expected to differ from the natural stock or other hatchery stocks.

[5] A component of the UCF driver stock.

hatchery recoveries in the CTC database was downloaded from the coastwide Regional Mark Information System (RMIS) database (http://www.rmpc.org/). Information on spawning ground recoveries was entered directly into the CTC database by the agencies that sampled those spawning populations.

Estimating harvest size relied on retrieving recorded information with little uncertainty from the established commercial fish ticket system for SEAK troll fisheries (ADF&G 2013) or relied on statistics from an established, annual postal survey of licensed recreational fishermen that fished in Alaska in 2011 (ADF&G 2012), including those that landed catches at the port of Sitka (Figure 1). Sitka sport fishery harvest was estimated with uncertainty and a measure of this uncertainty was available for analysis.

Estimating fractions $p_{f,a,nat(D)}$ and $p_{f,a,hat(D)}$ of the landed catch began with genetic samples independently drawn from each fishery (Figure 2). Sampling protocols were used that would produce samples representative of the landed catch (see Appendix B). In addition to sampling the axillary process for genotyping, each fish was also sampled for scales, and the head was collected. After genotyping, if an individual was identified as originating from one of the driver stocks, scales were used to determine age and otoliths were examined for hatchery marks. Each sample was first treated as a mixture from which the fraction $P_{f(D)}$ of the landed catch composed of Chinook salmon belonging to driver stock *D* was estimated; such fractions for all driver stocks were estimated simultaneously from the same sample (see Appendix B for details on genetic methods). Estimates $\hat{P}_{f(D)}$ were derived with a Bayesian mixture analysis for each fishery. Corrections $\beta_{f(D)}$ for misclassification error in the mixture analysis were estimated from the genetic baseline following methods outlined in Anderson et al. (2008) and initial estimates of $P_{f(D)}$.

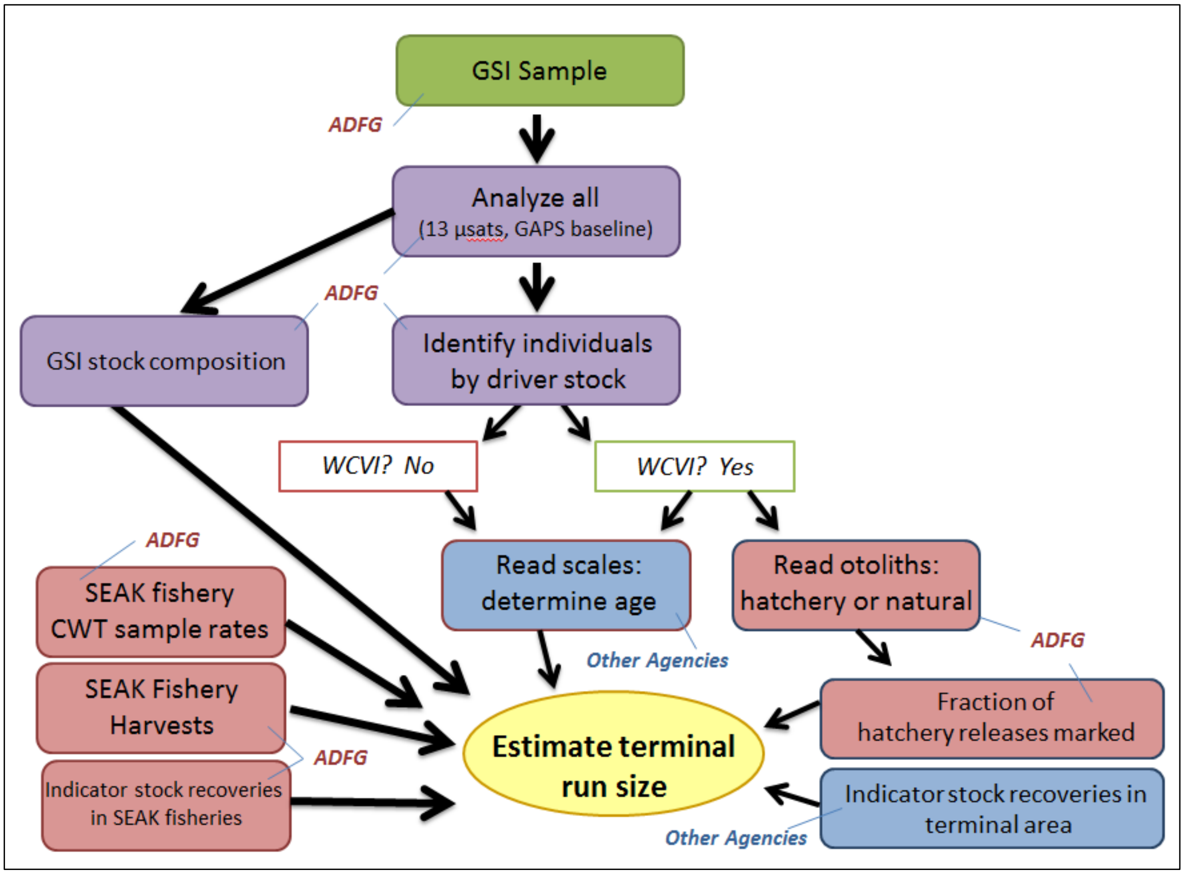

Figure 2.–Graphic outlining the steps used to estimate terminal run size with genetic, tag, scale, and otolith information from sampled catches in SEAK fisheries and with tag information for indicator stocks taken from their terminal areas. Responsible agencies are noted.

In a second genetic analysis involving the same samples, individual salmon were identified to stock of origin. Mark status was determined for each salmon in the sample identified as being from WCVI, NOC, UCF, or WAC driver stocks through the absence of an adipose fin, or for the WCVI driver stock through the presence of a thermally banded otolith. Age for marked individuals in a sample was determined from the mark itself, CWT or thermally banded otolith, at the ADF&G Mark, Tag and Age Lab. Age of unmarked individuals in the sample was determined from scales by agencies with jurisdiction over the region where the stocks originated (WCVI by Canadian Department of Fisheries and Oceans [CDFO], WAC by Washington Department of Fish and Wildlife [WDFW], NOC by Oregon Department of Fish and Wildlife [ODFW], and UCF by Columbia River Inter-Tribal Fish Commission). Fractions of the harvest in fishery f of driver stock D that were unmarked $q_{f,a,u(D)}$ and marked $q_{f,a,m(D)}$ by age were estimated as

$$\hat{q}_{f,a,m(D)} = \hat{P}_{f(D)}\hat{\beta}_{f(D)} \frac{S_{f,a,m(D)}}{\sum_b [S_{f,b,m(D)} + S_{f,b,u(D)}]} \quad \text{and} \tag{3}$$

$$\hat{q}_{f,a,u(D)} = \hat{P}_{f(D)}\hat{\beta}_{f(D)} \frac{S_{f,a,u(D)}}{\sum_b [S_{f,b,m(D)} + S_{f,b,u(D)}]} \; , \tag{4}$$

where $s_{f,a,m(D)}$ is the number of Chinook salmon in the GSI sample from the driver stock that were marked with a CWT or a thermally banded otolith for which an age was determined, $s_{f,a,u(D)}$ is the number in that sample not marked for which an age was determined, $\hat{\beta}_{f(D)}$ is the estimated correction for misclassification, and *b* designates fish age for summations. Equations to estimate fractions $p_{f,a,nat(D)}$ and $p_{f,a,hat(D)}$ for potential use in Equation (1) are

$$\hat{p}_{f,a,nat(D)} = \hat{q}_{f,a,u(D)} - \hat{q}_{f,a,m(D)} \left[\frac{1-\lambda_{a(D)}}{\lambda_{a(D)}} \right] \quad \text{and} \tag{5}$$

$$\hat{p}_{f,a,hat(D)} = \frac{\hat{q}_{f,a,m(D)}}{\lambda_{a(D)}}, \tag{6}$$

where $\lambda_{a(D)}$ is the fraction of hatchery Chinook salmon in the driver stock released with marks in year 2011– *a* + 1. The $\lambda_{a(D)}$ for the WAC and NOC hatchery driver stocks were computed from data on numbers released and numbers in releases with CWTs downloaded from the RMIS database. The $\lambda_{a(D)}$ for the WCVI hatchery driver stock was obtained from CDFO (Chuck Parken, Salmon and Freshwater Ecosystems Division Habitat Assessment Biologist, Fisheries and Oceans Canada, Nanaimo; November 30, 2012, e-mail). For the UCF driver stock in which the terminal run is comprised of both hatchery and natural-origin fish,

$$\hat{p}_{f,a,\bullet(D)} = \hat{P}_{f(D)} \hat{\beta}_{f(D)} \frac{s_{f,a,m(D)} + s_{f,a,u(D)}}{\sum_b [s_{f,b,m(D)} + s_{f,b,u(D)}]} \tag{7}$$

was used in Equation (1). Variances of terminal run size estimates for a driver stock were approximated as described in Appendix C.

ASSUMPTION DIAGNOSTICS

Direct Comparison

At the core of the driver stock method is the gorilla assumption, which is that the indicator stock experiences the same exploitation rate in all nonterminal fisheries and has the same maturation rate as the driver stock. The best method to test of this assumption would be to compare an estimate of terminal run size from the driver stock method to a known value or independent estimate with little uncertainty. Unfortunately, such a comparison for one driver stock provides no information as to meeting the gorilla assumption for another driver stock. Each comparison is independent of other comparisons, with its outcome depending on the specific indicator stock and how well it actually represents the associated driver stock.

A direct comparison was only possible for the UCF driver stock. The comparable estimate was the count of adults past Bonneville Dam of fall Chinook salmon[6] from August 1 through

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[6] Counting protocols at Bonneville Dam can be found at http://www.nwd-wc.usace.army.mil/tmt/documents/fpp/2012/index.html

November 15, 2011.[7] Adults were defined as Chinook salmon ≥558 mm total length (22 inches). Length-at-age statistics for 2011 were reported by Fryer et al. (2013) in their Table 15.

Relative Age Distribution and Bias

Although the best test of the core assumption behind the driver stock method is not available for three of the driver stocks (WCVI, WAC, and NOC), we tested the results for the WAC, NOC, and UCF driver stocks with estimates of relative age distributions of Chinook salmon using a simple algorithm. The relative age distributions are listed below:

- landed catch of the driver stock in SEAK fisheries
- landed catch of the indicator stock in SEAK fisheries
- terminal run of the indicator stock in its terminal area
- terminal run of the driver stock in its terminal areas

Relative age distributions were restricted to 4-year-old and 5-year-old fish because estimates of these ages were the most consistent, nontrivial, fully recruited age groups in all populations. The diagnostic algorithm described below could not be applied to the WCVI driver stock because catch from this stock was comprised almost entirely of 4-year-old salmon.

Estimates of the first three types of relative age distributions were generated when estimating terminal run size for driver stocks with the driver stock method; the last type of distribution was obtained from field sampling and field surveys by local management agencies and tribes. The algorithm is described below:

> STEP 1: Insert the relative age distribution for the driver stock in terminal areas [age distribution (4) from above] into the back end of a set of standard catch/maturation equations.
>
> STEP 2: Alter the catch and maturation rates on the driver stock until the relative age distribution of the projected catches match the relative age distribution of landed catches in SEAK fisheries [age distribution (1)].
>
> STEP 3: Insert the relative age distribution for the indicator stock in its terminal area [age distribution (3)] into the back end of a second set of standard catch/maturation equations.
>
> STEP 4: Insert the final maturation and catch rates from the first set of catch/maturation equation into the second.
>
> STEP 5: Compare the projected relative age distribution of catches from the second catch/maturation equation with the relative age distribution for landed catch of the indicator stock in SEAK fisheries [age distribution (2)].

Having the two relative age distributions match in STEP 5 is consistent with having met the necessary condition for the gorilla assumption; that is, the assumption may be valid. Having the two relative age distributions in STEP 5 differ, at least beyond plausible uncertainty in estimates of age distributions, indicates the gorilla assumption is not valid. The greater the difference in percentage points between age 4 (or age 5) in the relative age distributions, the more likely the gorilla assumption was violated. Figure 3 provides a schematic of the algorithm.

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[7] http://www.cbr.washington.edu/dart/query/adult_daily

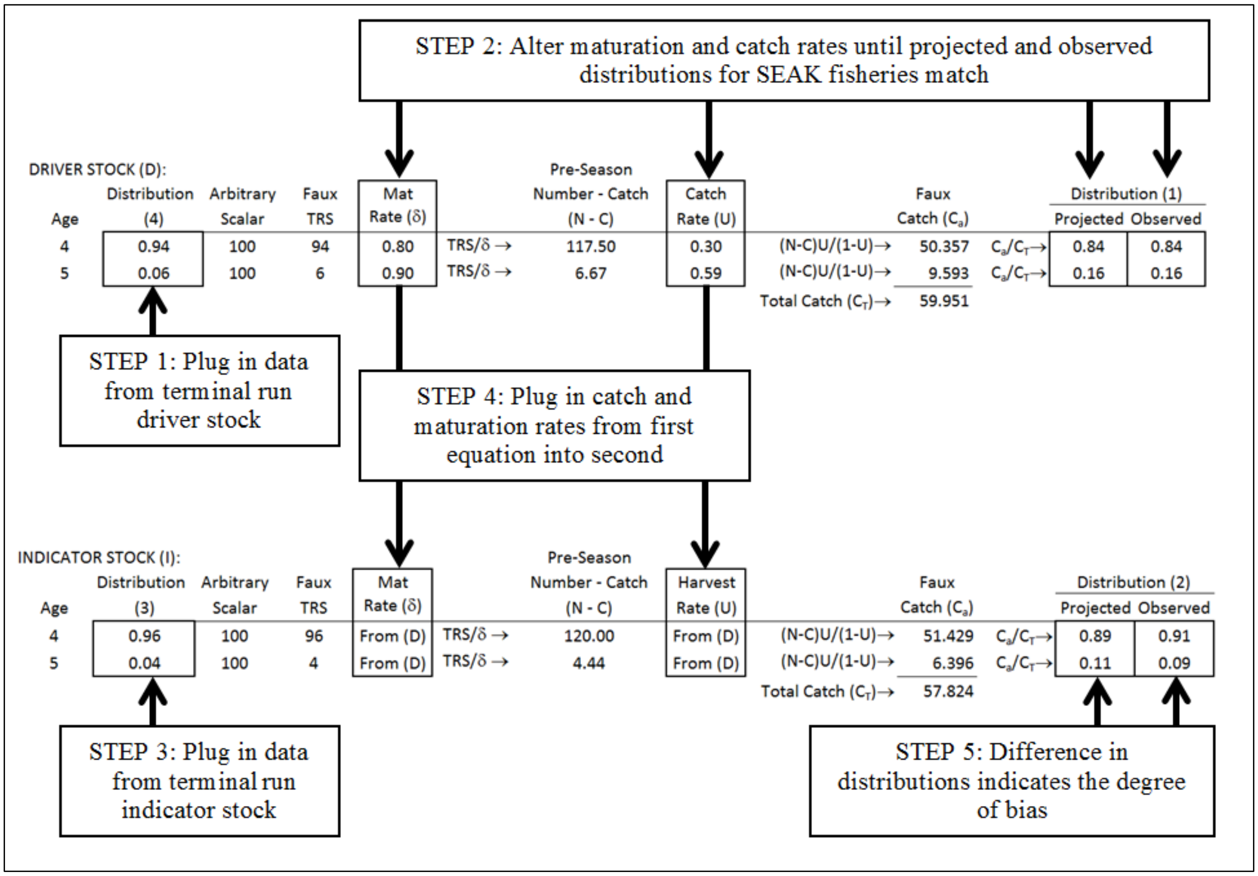

Figure 3.–Schematic of the algorithm used to detect bias in estimates of terminal run size for driver stocks from potentially violating the gorilla assumption (driver and indicator stocks experience the same maturation and exploitation rates). Numbers in the schematic and the comparative results from STEP 5 are for the UCF natural/hatchery driver stock in 2011.

RESULTS

TERMINAL RUN SIZE ESTIMATES

Estimates of terminal run size for the driver stocks in this study had precision based on CVs that ranged from approximately 9% to 42% for ages 3 to 6 combined (see Table 3). Precision improved to a range of 7% to 31% when 3-year-olds were excluded from the estimates of terminal run size. Precision was highest for larger driver stocks—CVs of 7% to 9% for the combined hatchery and natural stocks for WAC and UCF stocks of all ages; 10% to 11% for the natural NOC stock of all ages; and 10% for the WCVI hatchery stock comprised of 4-year-olds (Table 3). Precision was low for small driver stocks (hatchery NOC stock of all ages and WCVI natural stock of all ages).

Few CWTs were recovered in SEAK fisheries for some age groups and indicator stocks in 2011 (Table 4). Only one CWT was recovered from a 3-year-old Chinook salmon from the WCVI indicator stock in a SEAK fishery, even though this cohort represented about a fourth of the recoveries in the terminal area. Few to no CWTs were recovered for 5- and 6-year-old Chinook salmon in some indicator stocks as well. Lack of recoveries of 6-year-olds for the WCVI and UCF indicator stocks in SEAK fisheries and in terminal areas is evidence that few salmon of this age were in these driver stocks in 2011 (Table 4).

Table 3.–Estimates of terminal run size, standard errors, and coefficients of variation in 2011 for WCVI, WAC, NOC, and UCF hatchery and natural driver stocks using the driver stock method applied to landed catches in SEAK fisheries.

		Hatchery			Natural			Natural/Hatchery Combined		
Stock	Age	Point	SE	CV	Point	SE	CV	Point	SE	CV
WCVI	3									
	4	61,919	6,316	10%	14,267	2,745	19%			
	5									
	6									
	3–6	61,919	6,316	10%	28,466	9,243	32%			
	4–6	61,919	6,316	10%	14,267	2,745	19%			
WAC[a]	3							3,816	1,836	48%
	4							41,627	4,184	10%
	5							30,980	4,866	15%
	6							19,494	7,200	37%
	3–6							95,917	8,574	9%
	4–6							92,101	8,475	9%
NOC	3	2,173	2,215	102%	15,805	6,953	44%			
	4	2,662	930	35%	38,778	5,047	13%			
	5	1,223	796	63%	25,014	4,989	20%			
	6	0	0	0	781	481	63%			
	3–6	6,058	2,520	42%	80,373	9,001	11%			
	4–6	3,885	1,221	31%	64,001	6,448	10%			
UCF	3							77,447	24,924	32%
	4							254,379	18,783	7%
	5							17,279	5,669	33%
	6							-	-	-
	3–6							349,105	29,888	9%
	4–6							271,658	18,783	7%

[a] Fall run only. No CWTs from the spring run of Chinook salmon and only one CWT from the summer run made estimates of terminal run size of these WAC runs impossible or impractical.

Table 4.–Expanded number of Chinook salmon with CWTs recovered in SEAK fisheries and terminal areas in 2011 from indicator stocks representing driver stocks WCVI, WAC, NOC, and UCF. Shaded areas are instances where one or fewer CWTs were recovered.

		$\hat{n}_{f,a(I)}$									$\hat{n}_{term,a(I)}$
Driver Stock	Age	NO-1	NO-2	SO-1	SO-2	Spring	Sitka Sport	Total	Terminal Fisheries	Spawning Numbers[b]	Total
$\phi_f =$		0.30[a]	0.47	0.24	0.35	0.38	0.44				
WCVI	3	3.4	0	0	0	0	0	3.4	117.56	238.01	355.57
	4	88.2	17.2	21.15	2.94	72.19	21.86	223.54	447.73	460.91	908.64
	5	0	0	0	0	0	0	0	5.45	10.58	16.03
	6	0	0	0	0	0	0	0	0	0	0
WAC[c]	3	10.2	10.75	0	5.88	0	0	26.83	0	205.9	205.9
	4	244.8	40.85	160.74	44.1	9.38	68.82	568.69	69.86	1582.12	1,651.98
	5	68	21.5	16.92	5.88	6.86	24.59	143.75	117.04	287.45	404.49
	6	10.2	2.15	8.46	2.94	0	0	23.75	148.59	320.32	468.91
NOC	3	17	15.05	0	8.82	0	1.92	42.79	761.16	751.65	1,512.81
	4	207.4	40.85	46.53	23.52	0	18.24	336.54	513.37	1044.45	1,557.82
	5	61.2	8.6	12.69	8.82	0	9.28	100.59	134.67	174.8	309.47
	6	3.4	0	0	0	0	0	3.4	1.8	10.92	12.72
UCF	3	0	8.6	0	0	0	0	8.6	137.4	233.44	370.86
	4	153	36.55	63.45	17.64	24.76	16.95	312.35	987.3	813.58	1,800.85
	5	13.6	0	12.69	2.94	1.9	0	31.13	47.95	18.06	66.01
	6	3.4	0	0	0	0	0	3.4	0	0	0

[a] Fraction of the catch inspected for CWTs.

[b] Spawning numbers include returns to the hatchery.

[c] Fall run only.

Results of genetic analyses and hatchery release information used to estimate terminal run size are in Appendices B and D.

While our intention was the estimation of terminal run size for hatchery and natural WAC stocks separately, our attempts to do so resulted in negative estimates for naturally spawned salmon. The problem arose because WAC fish identified in genetic samples (Table 5) had a higher fraction (0.28) of marked fish than the original releases (0.14–0.18; Table 6). The marked fraction in genetic samples needs to be lower, not higher than the marked fraction of hatchery releases to account for the presence of unmarked, natural production. Therefore we limited our estimate of terminal run size for the WAC stock to all production regardless of origin.

Table 5.–Fraction of genetic samples taken in 2011 from each SEAK fishery identified as WAC Chinook salmon that were marked at WAC hatcheries. The weighted fraction over all SEAK fisheries is 28%. Estimated catch of WAC fish in SEAK fisheries from GSI were used in the weighting.

	NO-1	NO-2	SO-1	SO-2	Spring	Sitka
Estimated WAC Catch	12,213	2,767	3,078	1,462	526	4,098
No. WAC Salmon in GSI Samples	133	51	22	28	11	148
Number Marked:	34	14	7	7	0	58
Fraction Marked:	0.256	0.275	0.318	0.250	0.000	0.392

Table 6.–Number of Chinook salmon released from WAC hatcheries for brood years (BY) 2006–2009 that contributed to the 2011 terminal run and the number and fraction of these releases marked. List of the hatcheries involved is given in Appendix D1.

	Age 6 BY 2005	Age 5 BY 2006	Age 4 BY 2007	Age 3 BY 2008
Released	10,904,202	13,465,904	9,587,982	9,982,339
Marked	2,005,945	1,855,940	1,440,315	1,625,219
Fraction Marked	0.184	0.138	0.150	0.163

DIAGNOSTICS

Direct Comparison

The estimate of terminal run size for 3-year-old and older Chinook salmon from the UCF hatchery/natural driver stock in 2011 (349,105) was 13% lower than a comparable, independent estimate of counts of adults past Bonneville Dam (401,576). Length-at-age statistics reported by Fryer et al. (2013) for fall Chinook salmon represented all 6-, 5-, 4-, and 3-year-olds past Bonneville Dam except for about 12,000 smaller stream-type 3-year-olds (age 1.1 in European notation). The 13% difference between the driver-stock estimate and the count is within expectations given a CV of 9%.

Independent estimates of terminal run size with little uncertainty, expressed or not, were not available for the other driver stocks in our study.

Relative Age Distribution and Bias

Results from the algorithm involving estimates of relative age distribution from four different groups for each driver stock (driver and indicator stocks in catches from SEAK fisheries and driver and indicator stocks in terminal areas) were consistent with the direct comparison of estimates for the UCF driver stock (Figure 3, Table 7). Relative age distributions for the UCF stock was off by two points; that difference was associated with a 13% difference estimated from a direct measurement of terminal run size for the UCF driver stock at Bonneville Dam. The estimated relative age distributions for 3- to 6-year-olds for the UCF driver and indicator stocks and for all the others can be found in Table 8. The relative age distributions for 4- and 5-year-olds are graphically presented in Figure 4 for the UCF, NOC, and WAC stocks. Except for WCVI, the fractions of each driver stock terminal run composed of 3-year-olds as estimated with the driver stock method and through direct estimation (from Table 7) are given in Table 9.

Comparisons of projected and observed relative age distributions for NOC and WAC indicator stocks in SEAK fisheries indicate possible violations of the gorilla assumption (Table 7). While the difference between projected and observed distributions was two points for the UCF stock, the difference was 7 points for the NOC stock and 13 points for the WAC stock. Standard catch and maturation equations, as described in Figure 3 for the UCF stock, are provided in Appendix E for the WAC, NOC, and UCF stocks.

Table 7.–Projected and observed relative age distributions for UCF, NOC, and WAC indicator stocks in 2011. Differences in projected and observed distributions are a measure of bias due to violating the assumption that driver stocks experience the same catch rates and maturation rates as their indicator stocks.

	UCF Indicator Stock SEAK Fisheries		NOC Indicator Stock SEAK Fisheries		WAC Indicator Stock SEAK Fisheries	
Age	Projected	Observed	Projected	Observed	Projected	Observed
4-year-old	0.89	0.91	0.70	0.77	0.67	0.80
5-year-old	0.11	0.09	0.30	0.23	0.33	0.20
Actual Difference	13%		NA[a]		NA[a]	

[a] A direct comparison was not possible for the NOC and WAC.

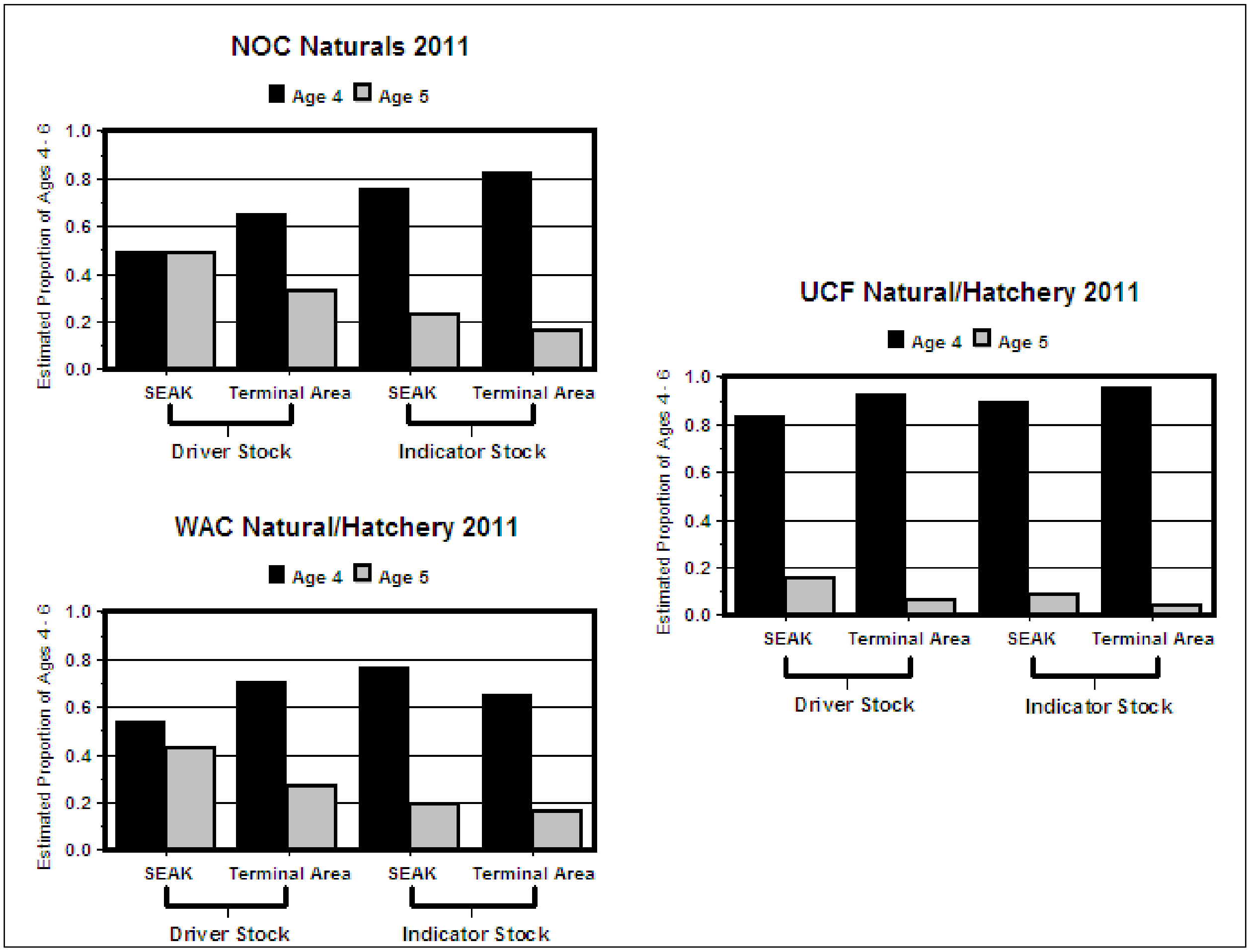

Figure 4.–Estimated relative age distributions for driver and indicator stocks in SEAK fisheries and in terminal areas for the NOC natural stock and the WAC and UCF natural/hatchery stocks in 2011.

Table 8.–Estimated relative age distributions for catches in SEAK fisheries and of the terminal run of driver (D) and indicator (I) stocks for WAC, NOC, and UCF stocks in 2011. Details on calculations are given in Appendix E.

Stock	Age 3	Age 4	Age 5	Age 6	Source
WAC					
SEAK Fish (*D*)	0.018	0.529	0.417	0.036	Appendix B4
Terminal Area (*D*)	0.114	0.628	0.239	0.019	PFMC (2013) and WDFW[a]
SEAK Fish (*I*)	0.035	0.745	0.188	0.031	Table 4
Terminal Area (*I*)	0.075	0.605	0.148	0.172	Table 4
NOC					
SEAK Fish (*D*)	0.026	0.486	0.477	0.012	Appendix B4
Terminal Area (*D*)	0.152	0.564	0.278	0.006	ODFW[b]
SEAK Fish (*I*)	0.089	0.696	0.208	0.007	Table 4
Terminal Area (*I*)	0.446	0.459	0.091	0.004	Table 4
UCF					
SEAK Fish (*D*)	0.033	0.810	0.149	0.007	Appendix B4
Terminal Area (*D*)	0.280	0.667	0.046	0.006	Fryer et al. (2013, Table 12)
SEAK Fish (*I*)	0.024	0.879	0.088	0.010	Table 4
Terminal Area (*I*)	0.169	0.797	0.035	0.000	Table 4

[a] Information obtained from Ethan Clemons, Fish and Fisheries Biologist, Oregon Department of Fish and Wildlife, Newport; November 8, 2013, e-mail.

[b] Information obtained from Peter McHugh, Salmon Policy Analyst, Washington Department of Fish and Wildlife, Olympia; September 9, 2013, e-mail.

Table 9.–Proportions of 3-year-old fall Chinook salmon in the terminal runs of the WAC and UCF combined natural and hatchery and the NOC natural driver stocks in 2011 as estimated with the driver stock method and from independent field sampling.

	WAC	NOC	UCF
Estimated thru sampling (from Table 7)	0.11	0.15	0.28
Estimated w/ driver stock method	0.05	0.20	0.23

DISCUSSION

DETECTING BIAS

The diagnostic algorithm to detect violations of the gorilla assumption in the driver stock method gave promising results. Results from this test were arguably consistent with a single direct comparison of terminal run size for the UCF combined natural and hatchery driver stock for data collected in 2011. Still, there may be concern that catch and maturation rates were selected in an arbitrary manner, but this concern is debatable. Varying the catch and maturation equations with different sets of catch rates and maturation rates (STEP 2) shows that there are several, if not many, sets of potential solutions demonstrating a match between projected and observed relative age distributions for a given driver stock. Plugging any of these solutions into the catch and maturation rate equations for the indicator stock (STEP 4) will produce the exact same result in

STEP 5. Another concern is that the catch and maturation rate equations are too simplistic. Indeed the equations are simple, but more importantly, they are comprehensive. The equations cover all fisheries, all maturation rates, and all natural mortality that occurs in the SEAK fishery and on through other fisheries to the terminal areas. Any difference between a driver stock and its indicator stock in terms of mortality rates or maturation rates anywhere and anytime will be encompassed by the estimated relative age distributions used in this test. In addition, there may be concerns that relative age distributions are estimated with some degree of uncertainty. While this uncertainty is considered in the estimates of terminal run size, it is not considered in the diagnostic algorithm applied here.

Our diagnostic algorithm results demonstrated the problem of uncertainty in relative age distributions. Estimates of terminal run size for UCF combined natural and hatchery, NOC natural, and WAC combined natural and hatchery stocks all have similar CVs (9–11%), which indicated uncertainty in the sampling. Uncertainty in relative age distribution estimates in a terminal area may differ across the three driver stocks because of the sampling used. Relative age distribution in each of the terminal areas was estimated as follows:

- for the UCF driver stock, relative age distribution was estimated by sampling 1,258 fall Chinook salmon in 2011 in a semi-proportional, self-weighting fashion throughout the run at a fish trap at Bonneville Dam (Fryer et al. 2013);
- for the NOC driver stock, relative age distribution was estimated by sampling more than 5,000 fall Chinook salmon in 2011 in an opportunistic fashion on the spawning grounds of seven streams with results weighted by expanded estimates of habitat for each stream; and
- for the WAC driver stock, relative age distribution was estimated by sampling seven streams, but included summer Chinook salmon in some of those samples, taking some samples exclusively at weirs on some streams, taking some samples exclusively from fisheries using size-selective gear on other populations, and using weights generated from counting redds.

Systematic sampling at Bonneville Dam as described above was most likely to have produced an accurate (unbiased) and precise estimate of relative age composition[8] (Thompson 1992). In contrast, the estimate of relative age composition for the NOC driver stock was more precise than that for the UCF estimates because of greater sample sizes, but potentially less accurate because older, larger Chinook salmon are more likely to be encountered on spawning grounds as carcasses (Zhou 2002). Accuracy in the estimate of relative age composition of the WAC driver stock was most likely the least accurate because of substitution of populations in the sampling. Given this sampling history, one might expect estimated relative age distribution in a terminal area to be most certain for the UCF driver stock, less so for the NOC driver stock, and least certain for the WAC driver stock. This order of uncertainty follows the same order as the diagnostic algorithm results: 2 points difference for the UCF driver stock, 7 points for the NOC driver stock, and 13 for the WAC driver stock. Such a result was consistent with differences in relative age distributions in the diagnostic algorithm that were caused by uncertainty in estimates of relative age distributions and not from violating the gorilla assumption.

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[8] We say most likely because we have knowledge of the overall sampling plan, but no specific knowledge of how samples were actually drawn.

One last consideration concerning the diagnostic algorithm is that it is a test for meeting necessary conditions. Dissimilarity between relative age distributions from projection and sampling indicated that the gorilla assumption had not been met; however, similarity does not prove that it had been met. For any set of relative age distributions 1, 3, and 4 above, there were several combinations of maturation and exploitation rates that would produce age distribution 2, some of which involve different rates between driver and indicator stocks. There were no such instances where dissimilarity between age distribution 2 and its projection from age distributions 1, 3, and 4 can occur when the gorilla assumption had been met.

LIMITED REPRESENTATION OF AGE GROUPS

Selectivity in fisheries limits the utility of the driver stock method for some stocks, as demonstrated by the WCVI driver stock. Only one CWT from a 3-year-old in the WCVI indicator stock was recovered in SEAK fisheries in 2011 and no CWTs were recovered from 5- and 6-year-olds. Estimates cannot be generated without data, so an estimate of terminal run size was only possible for 4-year-olds with the driver stock method in 2011 for WCVI. Similarly, we were not able to estimate terminal run size for WAC spring or summer runs because of a lack of information; no CWTs from the indicator stock for the spring run, and only one CWT for the summer run were recovered.

Reasonably good estimates of terminal run size of 3-year-old Chinook salmon can be obtained with the driver stock method when 3-year-old Chinook salmon are recruited to SEAK fisheries and some information is available from catch sampling. Inspection of Appendix B4 shows that some information is available for 3-year-olds for UCF, NOC, and WAC driver stocks in 2011. The resulting estimates of terminal run age distribution from the driver stock method for ages 3–6 (Table 3) can be normalized and the result compared with independent estimates from field sampling (appropriate rows in Table 7). These comparisons are reported in Table 9 for 3-year-old salmon. A difference of only 5–6 percentage points for these stocks corroborates that the driver stock method provided reasonably accurate estimates of terminal run size of 3-year-old Chinook salmon so long as 3-year olds from that stock are caught in SEAK fisheries.

Few CWTs were recovered from 6-year-olds belonging to indicator stocks WAC, NOC, and UCF in 2011. The reason was not selectivity of 6-year-olds in SEAK fisheries, but the low frequency of these older Chinook salmon in any fishery and in terminal runs. Fortunately, this low frequency means that 6-year-olds can be considered along with the other age groups in the analysis without meaningfully affecting the precision or accuracy of estimated total terminal run size.

Limited information on age distribution for the WCVI driver stock is an example of another problem that can occur with the driver stock method. The diagnostic algorithm requires two large age groups in the driver stock population. For fall Chinook salmon those age groups are usually 4- and 5-year-old fish. With only a few 5-year-old salmon in the WC`VI driver stock in 2011, application of the diagnostic algorithm to test meeting the gorilla assumption was impossible.

PROBLEMS PROCURING SAMPLES

In 2011, ADF&G samplers encountered difficulties acquiring the heads of Chinook salmon along with scale and genetic samples from commercial fisheries in SEAK. Removal of the head of troll caught Chinook salmon greatly reduces the exvessel price of fish. Such difficulty was not a problem of the driver stock method per se, so long as a marked fish from a hatchery can be determined by visual inspection alone, or there was no need for such a determination. The first instance was germane to the NOC stock in 2011 where only the indicator stock was of hatchery origin. The second instance was germane to the UCF driver stock where estimates are for natural and hatchery-origin salmon combined. Heads were required from all sampled salmon, not just marked ones because the batch mark defining a WCVI hatchery fish was a thermally banded otolith. The need for the otolith could not be determined until the origin of the sample had been determined through genetic analysis.

An unusually high number of heads from Chinook salmon were collected for CWT sampling in 2011 because ADF&G was not set up to do electronic sampling for CWTs, and in order to support mark-select fisheries in the southern U.S., many Chinook salmon had their adipose fin clipped even though they were not tagged with a CWT (Anne Reynolds, Commercial Fisheries Biologist IV, Alaska Department of Fish and Game, Juneau; January 2012, telephone conversation). In some cases, sampling goals were moved among ports and fisheries to lessen the burden on any one processor while still achieving the overall sample goal.

Sampling only the Sitka Sport fishery would reduce the problem of taking heads, but at a cost to accuracy and precision of estimates. Participants in the sport fishery proved generally amenable to volunteering heads from their landed catch. Restricting sampling to only the Sitka Sport fishery in 2011 would have reduced the sampled harvest from 185,582 to 27,877. Most catch in the sport fishery occurred at different times than the troll fishery, thereby increasing the chance that the final estimates of terminal run size would be less accurate if only the sport fishery were sampled. It is likely that natural-origin and hatchery-origin WCVI Chinook salmon have similar ocean distributions. If so, samples to collect otoliths need only come from the Sitka Sport fishery and the samples of hatchery or natural-origin salmon in that fishery can be applied to samples from commercial fisheries in SEAK with a lesser reduction in precision.

IMPOSSIBLE ALLOCATION

Estimating hatchery and natural production separately in the WAC terminal run was not possible because genetic samples in 2011 had a higher percentage of marked WAC salmon than possible considering the fraction of hatchery releases and likely catches of unmarked, naturally produced WAC salmon.[9] Inconsistencies in the RMIS database, confusion over what is and what is not a marked salmon in genetic samples, unrepresentative genetic sampling of SEAK catches, or nonrandom genetic misclassification were all possible causes for the discrepancy. This discrepancy had no effect on the accuracy of the terminal run size estimate for the WAC combined hatchery and natural stocks.

GENETIC BASELINE

One potential problem identified with estimating WAC terminal run size of Chinook salmon was the genetic baseline populations for the Washington Coast contained samples from spring, summer, and fall runs. Thus, if Washington Coast spring and summer stocks of Chinook salmon were caught in the SEAK fisheries, the WAC estimate of catch in the SEAK fisheries would include fish that returned in the spring and summer along with those that returned in the fall.

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[9] Unlike percentages for 2011, percentage of marked WAC salmon in genetic samples taken from SEAK catches in 2012 (7%) were lower than the marked percentage of the relevant hatchery releases (14–16%)—as they should be.

Such a scenario was not likely in 2011. Downloads from the RMIS database showed that only one of 859 CWTs from WAC stocks recovered in SEAK fisheries in 2011 was not a fall Chinook salmon. This indicates that the genetic catch estimates for WAC in the SEAK fisheries in 2011 essentially represented fall Chinook salmon only.

Another potential problem with the baseline for the fall Chinook salmon lies in including fish that may be of a summer run in the UCF baseline. A quick inspection of Appendix B1 shows that 65% of baseline samples representing the UCF are from a population that may be part of the summer run or may be part of the fall run.

PRECISION

Not all of the estimates of terminal run size meet the CTC bilateral standards for precision in estimates of spawning abundance (CV ≤ 15%; CTC 2013, Appendix C). Estimates of terminal run size for the UCF hatchery/natural, NOC natural, WCVI hatchery, and perhaps the WAC hatchery driver stocks have CVs low enough to possibly attain the CTC precision standard once discounted for terminal catch to produce an estimate of spawning abundance.

Of interest here is that the terminal run size estimates presented in this report were generated with only catches from the SEAK fisheries. Precision of estimates from the driver stock program is directly related to the relative size of catches in fisheries. One way to improve the precision of estimates in the future would be to increase the size of catches—not by increasing exploitation rates in SEAK fisheries—but by including catches in other fisheries in the analysis. Fisheries in Northern British Columbia would be prime candidates for inclusion because approximately the same stocks are exploited there as in SEAK fisheries.

Not all of the uncertainty in estimates from the driver stock method is expressed in our analysis. The correction for misclassification β has some unexpressed uncertainty. Variances for this error correction can be calculated, but were not available at the time of this writing. We also ignored uncertainty in ϕ in our calculations, but selected an expansion for CWTs recovered in terminal areas that would make precision of our estimates conservative. Also, the fraction λ of hatchery production with marks was based on releases; a better measure would have been based on returns. We believe that these sources of uncertainty when considered together had inconsequential effect on the estimated precision of our results.

CONCLUSIONS AND RECOMMENDATIONS

Feasibility of using the driver stock method to estimate terminal run size and spawning escapement of Chinook salmon was measured according to the accuracy and precision of those estimates. Because the driver stock method is a mathematical construct, its accuracy depends upon the relevance of the central assumption (gorilla assumption) and the accuracy of data used as inputs. Relevance of the central assumption and the accuracy of data vary from driver stock to driver stock and potentially from year to year. Just because the method is verified as dependable for one driver stock says nothing about the feasibility of using the method for another driver stock. Also, because data can be improved and indicator stocks changed, the driver stock method might be judged not reasonable under current circumstances but realistic later if those circumstances change.

Feasibility of the driver stock method is stock- and time-specific, so our conclusions about the driver stock method are presented by driver stock. Our recommendations consider those ways that the feasibility of the driver stock method might be realized or improved upon in the future.

UPPER COLUMBIA FALLS

Estimated terminal run size of the UCF past Bonneville Dam in 2011 as calculated with the driver stock method based on SEAK catches is an accurate estimate that met precision standards. On this basis we conclude that the driver stock method is a feasible means of estimating terminal run size for the UCF driver stock. Although there may be a potential problem with the UCF genetic baseline, this problem was evidently not enough to cause an inaccurate estimate. No evidence was produced with the diagnostic algorithm to suggest that the indicator stock for the UCF was not representative of the driver stock in general.

The UCF driver stock will be dropped from our study for 2012. The terminal run size for the UCF is estimated annually with counts at Bonneville Dam, making estimates from the driver stock method redundant.

WEST COAST VANCOUVER ISLAND

We conclude that the driver stock method based on SEAK catches was a reasonable approach to estimate the age-4 terminal run but not a feasible means to estimate the total WCVI terminal run size for 2011 because

- age-3 Chinook salmon comprised a significant portion of the WCVI terminal run but were not well represented in SEAK catches; and
- lack of age-5 Chinook salmon in the terminal run prevented testing the gorilla assumption through comparing relative age distributions with the diagnostic algorithm.

The lack of age-5 fish will probably not persist into future years, while the lack of age-3 fish probably will. In the latter case the driver stock method must be augmented with field sampling and catch monitoring in the terminal areas to expand estimates to cover age-3 salmon. Fortunately, genetic misclassification of catch samples from SEAK fisheries is negligible for the WCVI stock. Our recommendations to make the driver stock method feasible for the WCVI driver stock in the future are

- field and catch sampling and/or test fishing to estimate relative age distributions and the fraction of hatchery-produced fish in the terminal run, and
- comparing recovery rates of Chinook salmon produced in the major hatcheries of WCVI (Robertson Creek, Nitinat, and Conuma) to determine the best indicator stock.

The recommended sampling changes would provide an expansion to estimate the number of age-3 fish in the terminal run and provide information to run the diagnostic algorithm, and to better allocate terminal run into hatchery and natural production. We will include the WCVI stock in our 2012 report and funding for additional sampling as per our recommendations is pending for 2015.

WASHINGTON COAST

We conclude that the driver stock method based on SEAK catches was not a feasible approach to estimate WAC terminal run size for 2011 because

- the number of CWTs recovered from SEAK catches were insufficient to estimate terminal run size for spring and summer runs,
- the WAC genetic baseline for the fall-run has a high rate of misclassification,
- there is a potentially poor selection of the fall-run indicator stock, and
- there is a potential sampling error (bias) in estimates of relative age distributions for the fall run.

The number of CWTs recovered was probably a result of timing differences between migration and the scheduling of SEAK fishery, neither of which can realistically be changed. The genetic baseline, potentially poor selection, and sampling error problems can perhaps be solved and the driver stock method made feasible, at least to the point there is

- evidence the GSI analysis provides accurate estimates of catch by stock,
- evidence that the current or yet-to-be-determined indicator stock is a good representative of the WAC stock, and
- sufficient information to precisely use the diagnostic algorithm.

We will include the fall-run WAC stock in our study for 2012. Our recommendations to address genetic misclassification, selection of an appropriate indicator stock, and sampling error are to

- reduce genetic misclassification error by
    - removing the significant number of summer-run fish currently in the fall-run WAC genetic baseline,
    - assessing the relevance of the Hoko stock to the WAC aggregate, and
    - increasing the number of markers in the genetic analysis sufficient to identify stock origin for individual Chinook salmon in lieu of using mixture analysis;
- apply the diagnostic algorithm to various combinations of stocks to find the set that appears to be the most representative of the aggregate WAC stock; and
- improve field and catch sampling programs along with improving reporting.

At the time of this writing, we know of no new projects to improve field and catch sampling programs for the WAC fall-run aggregate.

NORTH OREGON COAST

We conclude that the driver stock method based on SEAK catches was an arguably feasible approach to estimate NOC terminal run size in 2011 because

- estimates of terminal run size met precision standards, and
- results of the diagnostic algorithm were consistent with there being an arguably small bias.

Information on the NOC driver stock was best of the four stocks in our feasibility study. Estimates of relative age compositions were based on large sample sizes in terminal fisheries and spawning grounds and estimates were appropriately weighted. The indicator stock was well tagged with a distinct terminal area. All age groups in the terminal areas were represented in SEAK catches. The genetic misclassification error was not quite as good as with the WCVI stock, but was better than the error for WAC and UCF. Results from the diagnostic algorithm were ambiguous at best. Our recommendation for analyzing data for 2012 is to

- increase the number of markers in the genetic analysis sufficient to identify stock origin for individual Chinook salmon in lieu of using mixture analysis, and
- compare estimates of terminal run size from the driver stock method to estimates generated from mark-recapture and creel studies on individual stocks along the NOC.

We will include the NOC stock in our study for 2012 with these recommendations in mind.

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APPENDIX A: CODED WIRE TAG CODES USED FOR INDICATOR STOCKS

Appendix A1.–List of codes on CWTs used to distinguish each indicator stock in 2011 for the four driver stocks used in our study.

Driver Stock	Indicator Stock	Tag Codes				
WCVI	Robertson Creek Hatchery	185257	185823	186302	180391	180388
		185258	185825	186344	180387	180390
		185259	185826	186301	180392	180883
		185260	185827	186134	180393	186306
		185948	185828	186305	180685	180394
		185824	185950	180389	180884	185961
		185821	185949	180885	186343	185951
		185962	185822	180881	180386	186304
		185960	186303	180882		
WAC	Queets River Hatchery	210679	210738	210791	210843	
	Hoko River Hatchery	210678	210739	210786	210841	
	Sooes River Hatchery	052888	053394	054376	054694	053393
		052890	053392	054378	054692	054375
		052889	053391	054377	054691	054693
		052887				
NOC	Salmon River Hatchery	094428	094525	094645	094701	
UCF	Ringold Spring Hatchery	094504	094663			
	Priest Rapids Hatchery	633173	633894	634391	634799	
	Hanford wild	610411	610413	610415	610420	610417
		610412	610414	610408	610416	610419
		610424	610428	610418	610425	610422
		610421	610423	610431	610430	610429
	Lyons Ferry Hatchery	633582	633986	634672	634671	634995

APPENDIX B: GENETIC METHODS AND RESULTS

Sampling SEAK Fisheries

Chinook salmon were collected from landings at fish processors (for commercial fisheries) and from landings at the dock (for the sport fishery) in SEAK for the following fisheries: northern outside (NO) and southern outside (SO) summer troll retention periods 1 (July 1–12) and 2 (August 15–17), NO spring troll (April–June), and the Sitka sport fishery (Figure 1). In the troll fisheries, Chinook salmon were selected for sampling without regard to size, sex, presence of an adipose fin, or position in the hold or tote, and sampling was as representative as possible of that fishery's harvest. The numbers of Chinook salmon sampled from each delivery were limited to ensure the sampling was spread throughout the fishery. Samples taken from tender deliveries were taken from the beginning, middle, and end of the delivery. In the sport fishery, sampling took place at major boat harbors and boat ramps in Sitka, and the sample survey was designed to be representative of the majority of exiting boats accessing the fishery (e.g., Bingham et al. 2013). The days of the week and time periods sampled in the Sitka sport fishery were restricted to those days and time periods (known from historic sampling) when the majority of boats exit the fishery.

The axillary process (for genetic analysis), three to four scales from the preferred area[10] (Clutter and Whitesel 1956), and the head (for otoliths and CWTs) were collected from each sampled Chinook salmon in a manner that allowed specimens to be tracked to individual sample. The presence or absence of an adipose fin was also recorded for each Chinook salmon sampled. The axillary processes were shipped to the Alaska Gene Conservation Laboratory in Anchorage, and heads were sent to the Alaska Mark, Tag, and Age Laboratory in Juneau. Scales were pressed onto acetate cards and stored until individual stock assignment was completed for each sample.

Laboratory Analysis

Tissue samples from the axillary processes were assayed for DNA loci developed by the Genetic Analysis of Pacific Salmon (GAPS) consortium for use in Treaty fisheries (Seeb et al. 2007). DNA was extracted from axillary process tissue using DNeasy®, 96-tissue kits (QIAGEN® Valencia CA). Polymerase chain reaction (PCR) was carried out in 10 ul reaction volumes (10 mM Tris-HCl, 50 mM KCl, 0.2 mM each dNTP, 0.5 units Taq DNA polymerase [Promega, Madison, WI]) using an Applied Biosystems (AB, Foster City CA) thermocycler. Primer concentrations, $MgCl_2$ concentrations and the corresponding annealing temperature for each primer are available in Seeb et al. (2007). PCR fragment analysis was done on an AB 3730 capillary DNA sequencer. A 96-well reaction plate was loaded with 0.5 ul PCR product along with 0.5 ul of GS500LIZ (AB) internal lane size standard and 9.0 ul of Hi-Di (AB). PCR bands were visualized and separated into bin sets using AB GeneMapper software v4.0. All laboratory analyses followed protocols accepted by the Pacific Salmon Commission (PSC) Chinook Technical Committee (CTC) similar to Seeb et al. (2007).

Genetic data were collected as individual multilocus genotypes for the 13 microsatellite loci currently included in the CTC standardized baseline. According to the convention implemented by the CTC, at each locus, a standardized allele is one that has a recognized holotype specimen from which the standardized allele can be reproduced using commonly applied fragment analysis techniques. By the process of sizing the alleles from the holotype specimens, any individual

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[10] Scales just dorsal of the lateral line on the ventral end of a diagonal line of scales on the right side of the salmon with its dorsal terminus as the posterior insertion of the dorsal fin and its ventral terminus at the anterior insertion of the anal fin.

laboratory should be able to convert allele sizes obtained in the laboratory to standardized allele names. Genotype data were stored as GeneMapper (*.fsa) files on a network drive that was backed up nightly. Long-term storage of the data was in an *Oracle* database (*LOKI*) on a network drive maintained by ADF&G computer services.

Several measures were implemented to insure the quality of data produced. Handling of individual samples in the lab followed a strict protocol. First, each individual tissue sample was assigned a unique identification number when the tissue was obtained. At the time DNA was extracted or analyzed from each sample, a sample sheet was created that linked each individual salmon to a specific well number in a uniquely numbered 96-well plate. This sample sheet then followed the sample through all phases of the project, minimizing the risk of misidentification of samples through human-induced errors. Second, genotypes were assigned to individual salmon using a system in which two technicians score the genotype data independently. Discrepancies between the two sets of scores were then resolved with one of two possible outcomes: (1) one score was accepted and the other rejected, or (2) both scores were rejected and the score was blanked. Last, approximately 8% of individuals—eight samples from each 96-well DNA extraction plate—were reanalyzed for all loci to insure that data were reproducible and to correct any errors created from the processing of individual plates.

Genotypes were retrieved from LOKI and imported into *R* (R Development Core Team 2010). All subsequent analyses were performed in R unless otherwise noted. Prior to mixed stock analysis or individual assignment, two statistical quality control analyses were conducted to ensure that only quality genotypic data was included in the estimation of stock compositions. First, individuals missing substantial genotypic data were removed from further analyses. Individuals missing genotypes for 20% or more of loci were excluded, because these individuals likely have poor quality DNA. The inclusion of individuals with poor quality DNA could introduce genotyping errors and reduce accuracy and precision of subsequent analyses. Second, individuals with duplicate genotypes were identified and removed from further analyses. Duplicate genotypes can occur as a result of sampling or extracting the same individual twice, and were defined as pairs of individuals sharing the same genotype in 95% of markers screened. The individual with the most missing data from each duplicate pair was removed from further analysis. Final sample sizes after removing individuals with missing or duplicate genotypes are indicated as m_f.

Mixed Stock Analysis

Proportions $P_{f(D)}$ of landed catches in SEAK fisheries comprised of driver stock *D* and other stocks were estimated with a mixed stock analysis (MSA) based on the program BAYES (Pella and Masuda 2001) and five pieces of information: (1) a baseline of allele frequencies for each population, (2) the grouping of populations into stocks desired for MSA, (3) prior information about the stock proportions of the fishery, (4) the genotypes of Chinook salmon sampled from the fishery, and (5) misclassification of salmon within the baseline. The baseline of allele frequencies for Chinook salmon populations was obtained from Version 3 of the GAPS baseline database (Appendix B1). A standardized baseline was first available during the summer of 2005 (Seeb et al. 2007). This baseline has continued to be improved with the addition of more genetic markers and more populations. Version 3 of the GAPS baseline contains allele frequencies from 356 populations ranging from the Situk River in Alaska to the Central Valley of California. In earlier versions of the baseline, results indicated that 44 stocks could be identified in mixtures with acceptable accuracy and precision (Seeb et al. 2007). For this study, these 44 stocks have been combined into 27 stocks.

Appendix B1.–Location and collection details (where available) for each population of Chinook salmon included in the coastwide Genetic Analysis of Pacific Salmon (GAPS) baseline of microsatellite data for the four driver stocks in this study. Details for the other 23 stocks and 305 populations in the baseline are listed in Seeb et al. (2007).

Driver Stock	Population	N[a]	Run[b]	Origin[c]	Stage	Collection Year
West Coast Vancouver Island	Burman River	218			Adult	1985,1989–1992,2000,2002,2003
	Conuma River	140	F	H	Adult	1997
	Gold River	258			Adult	1983, 1985–1987, 1992, 2002
	Kennedy River (Lower)	320			Adult	2005, 2007, 2008
	Marble River	136	F	H	Adult	1996, 1999, 2000
	Nahmint River	43			Adult	2002, 2003
	Nitinat River	125	F	H	Adult	1996
	Robertson Creek	120	F	H	Adult	1996, 2003
	San Juan River	175			Adult	2001, 2002
	Sarita River	137	F	H	Adult	1997, 2001
	Tahsis River	174	F	W	Adult	1996, 2002, 2003
	Thornton Creek	158			Adult	2001
	Tlupana River	58			Adult	2002, 2003
	Toquart River	68			Adult	1999, 2000
	Tranquil Creek	227	F	W	Adult	1996, 1999, 2004
	Zeballos River	148			Adult	2002, 2005– 2008
Washington Coast	Forks Creek Hatchery	140	F	H	Adult	2005
	Hoh River	115	F	W	Adult	2004, 2005
	Hoh River	138	Sp/Su	W	Adult	1995–1998, 2005, 2006
	Hoko Hatchery	73	F	H,W	Adult	2004, 2006
	Humptulips Hatchery	60	F	H	Adult	1990
	Makah Hatchery	128	F	H	Adult	2001, 2003
	Queets River	53	F	W	Adult	1996, 1997
	Quillayute River	52	F	W	Adult	1995, 1996
	Quinault River	54	F	W	Adult	1995, 1997, 1998
	Quinault Hatchery	82	F	H	Adult	2001, 2006
	Sol Duc Hatchery	94	Sp	H	Adult	2003
Upper Columbia Falls	Hanford Reach	163	Su/F	W		1999, 2000, 2001
	Klickitat River	149	Su/F	W	Adult	1994, 2005
	Little White Salmon Hatchery	94	Su/F	H	Juvenile	2006
	Marion Drain	131	Su/F	W	Adult	1989, 1992
	Priest Rapids Hatchery	181	Su/F	H	Juvenile	1998–2001
	Priest Rapids Hatchery	67	Su/F	H	Adult	1998
	Umatilla Hatchery	90	F	H	Adult	2006
	Umatilla Hatchery	94	Su/F	H	Adult	2003
	Yakima River (Lower)	102	Su/F	W	Adult	1990, 1993, 1998
	Deschutes River (Lower)	101	F	W		1999, 2001, 2002
	Deschutes River (Upper)	128	Su/F	W	Juvenile	1998, 1999, 2002
	Clearwater River	88	F	W	Adult	2000, 2001, 2002
	Lyons Ferry	185	F	H	Adult	2002, 2003
	Nez Perce Tribal Hatchery	123	F	H	Adult	2003, 2004
North Oregon Coast	Alsea River	108	F	W	Adult	2004
	Kilchis River	44	F	Unk	Adult	2000, 2005
	Necanicum Hatchery	50	F	H,W	Adult	2005
	Nehalem River	131	F	W	Adult	2000, 2002
	Nestucca Hatchery	119	F	H	Adult	2004, 2005
	Salmon River	83	F	H	Adult	2003
	Siletz River	107	F	W	Adult	2000
	Trask River	123	F	W	Adult	2005
	Wilson River	120	F	W	Adult	2005
	Yaquina River	113	F	W	Adult	2005
	Siuslaw River	105	F	W	Adult	2001

[a] Sample size

[b] F = fall, Sp = spring, Su = summer

[c] H = spawned in a hatchery, W = spawned in the wild, Unk = unknown

In a Bayesian MSA, the choice of prior information about stock proportions in a fishery (the prior probability distribution hereafter referred to as the prior) can influence the outcome of the MSA (Habicht et al. 2012). In our analysis, posterior distributions for stock proportions from a 2010 MSA were used as prior distributions for the 2011 MSA. The prior information about stock proportions was incorporated in the form of a Dirichlet probability distribution. The sum of all prior parameters was set to 1 (prior weight), which is equivalent to adding 1 fish to each mixture (Pella and Masuda 2001).

Five independent Markov Chain Monte Carlo chains of 40,000 iterations, each with different starting values, were run for each of the SEAK fisheries, with the first 20,000 iterations discarded to remove the influence of the initial values. Gelman-Rubin shrink factors were computed for all stock groups in BAYES (Gelman and Rubin 1992) to assess the among-chain convergence. If a shrink factor for any stock group in a mixture was greater than 1.2, the mixture was considered nonconvergent and reanalyzed with 80,000 iterations. Estimates of the mean, standard deviation, and 90% credibility intervals for stock proportions $P_{f(D)}$ in the mixture were generated from the posterior probability distributions for each variable as tabulated from the combined set of the second half of the five chains (Appendix B2).

Appendix B2.–Statistics for posterior distributions for the fractions of the landed catches H_f of Chinook salmon from four driver stocks in SEAK fisheries in 2011 as determined in a mixed stock analysis of m_f genetic samples taken from each SEAK fishery.

	$\hat{P}_{f(D)}$		90% CI		$\hat{P}_{f(D)}$		90% CI	
Driver Stock	Mean	SD	5%	95%	Mean	SD	5%	95%
	NO-1 (m_f = 1,360; H_f = 79,826)				NO-2 (m_f = 441; H_f = 16,372)			
WCVI	0.085	0.008	0.073	0.098	0.063	0.012	0.045	0.083
WAC	0.153	0.010	0.136	0.170	0.169	0.019	0.139	0.201
NOC	0.130	0.010	0.114	0.147	0.097	0.016	0.072	0.124
UCF	0.242	0.013	0.221	0.263	0.342	0.024	0.303	0.383
	SO-1 (m_f = 426; H_f = 33,461)				SO-2 (m_f = 291; H_f = 10,515)			
WCVI	0.088	0.014	0.066	0.112	0.024	0.009	0.011	0.040
WAC	0.092	0.015	0.068	0.118	0.139	0.022	0.105	0.176
NOC	0.032	0.010	0.017	0.051	0.167	0.025	0.127	0.209
UCF	0.229	0.022	0.193	0.266	0.362	0.031	0.311	0.413
	Spring (m_f = 681; H_f = 17,531)				Sitka Sport (m_f = 1,678; $\hat{H}_f$ = 27,877)			
WCVI	0.229	0.016	0.203	0.256	0.185	0.010	0.170	0.202
WAC	0.030	0.007	0.019	0.042	0.147	0.010	0.132	0.163
NOC	0.002	0.002	0.000	0.007	0.079	0.008	0.067	0.092
UCF	0.058	0.010	0.042	0.076	0.213	0.011	0.196	0.231

Stock proportions from the Bayesian analysis were subject to misclassification error—incorrectly classifying a salmon from driver stock *D* to another stock, or incorrectly classifying a salmon from another stock as being from driver stock *D*. Adjustments for genetic misclassification were derived from a confusion matrix $\boldsymbol{\phi}$ using the 27-stock baseline built with an iterative, leave-one-out process similar to the method in Anderson et al. (2008). Each individual salmon in the baseline was removed from the baseline, baseline frequencies were recalculated, and the relative probability that the excluded individual originated from each baseline population was estimated based solely on the individual multi-locus genotype. Once all individuals in the baseline had been so processed, the sum of the assignment probabilities of each individual across the populations in a stock was calculated. The assignment rate for each population to each stock was then estimated as the mean of the probabilities across individuals from each population to produce the confusion matrix. Each row of this 27×27 matrix represented the assignment rate of a specific stock across all stock groups with the diagonal elements representing the correct, and the off-diagonal elements the incorrect, assignments.

Adjustment factors $\beta_{f(D)}$ for misclassification error were estimated from the confusion matrix with the following relationship $\hat{\mathbf{P}} = \boldsymbol{\phi}\mathbf{P}$ where $\hat{\mathbf{P}}$ is the 27×1 vector of unadjusted assignment rates for a SEAK fishery (means of posterior distributions from the Bayesian analysis), $\mathbf{P}$ is the 27×1 vector of adjusted assignment rates, and $\boldsymbol{\phi}$ the 27×27 matrix of actual misclassification error. The relationship was inverted such that $\mathbf{P} = \boldsymbol{\phi}^{-1}\hat{\mathbf{P}}$ and solved for $\mathbf{P}$ for each fishery using the calculated confusion matrix as a proxy for $\boldsymbol{\phi}$. Because most off diagonal elements of the confusion matrix were either zero or near zero, the proxy matrix for $\boldsymbol{\phi}$ was composed of only two to three stocks—the driver stock and the one or two stocks most involved with misclassification. Those stocks were the upper Columbia River Summers for the UCF, the NOC and Mid Oregon Coast stocks for the WAC, and the Mid Oregon Coast stock for the NOCs. The estimated adjustment factor was calculated as $\hat{\beta}_{f(D)} = P_{f(D)} \big/ \hat{P}_{f(D)}$ for each fishery and driver stock. Because misclassification error for the WCVI was negligible, all $\hat{\beta}_{f(D)} \leftarrow 1$ for that stock. Estimated adjustment factors can be found in Appendix B3.

Appendix B3.–Estimated adjustments $\hat{\beta}_{f(D)}$ for misclassification error in the Bayesian mixture analysis. The expected misclassification matrices ($\boldsymbol{\varepsilon}$) are below.

	NO-1	NO-2	SO-1	SO-2	Spring	Sitka
WCVI	1	1	1	1	1	1
WAC	1.118	1.164	1.167	1.046	1.213	1.172
NOC	1.071	1.088	0.949	1.040	0.991	1.100
UCF	1.278	1.243	1.190	1.301	1.211	1.275

NOC (ε)		WAC (ε)		UCF (ε)	
NOC to NOC (0.87)	MOC to NOC (0.10)	WAC to WAC (0.81)	NOC to WAC/MOC (0.06)	UCF to UCF (0.82)	UCS to UCF (0.34)
NOC to MOC (0.05)	MOC to MOC (0.69)	WAC to NOC/MOC (0.06)	NOC to NOC (0.78)	UCF to UCS (0.09)	UCS to UCS (0.58)

Individual Stock Assignment

Each Chinook salmon sampled was assigned to a driver stock using the ONCOR[11] software. In this program individuals in a mixture sample are assigned to the baseline population that would have the highest probability of producing the given genotype in a mixture, using the method of Rannala and Mountain (1997). Individuals assigned to the WCVI, WAC, NOC, or UCF driver stocks with a cumulative probability of at least 0.95 of having originated from their representative populations (Table 1; Appendix B1) in the baseline were used in the analysis. Results of individual assignments were used to identify individuals for otolith and age analysis (Appendix B4).

Appendix B4.– Marked and unmarked numbers by age of individual Chinook salmon in genetic samples identified to be members of the four driver stocks in 2011 from harvests in six SEAK fisheries.

		NO-1		NO-2		SO-1		SO-2		Spring		Sitka Sport	
Driver Stock	Age	mrk[a]	un[b]	mrk	un	mrk	un	mrk	un	mrk	un	mrk	un
WCVI	3	2	1	1	1	0	0	1	0	0	0	3	1
	4	56	26	16	1	19	12	1	0	71	13	142	46
	5	2	0	0	0	0	1	0	1	3	5	7	3
	6	0	0	0	0	0	0	0	0	0	1	0	0
$\hat{S}_{f,u(D)}+\hat{S}_{f,m(D)}$		87		19		32		3		93		202	
WAC	3	3	0	1	2	0	0	0	0	0	0	0	0
	4	27	41	9	26	4	8	5	6	0	4	33	46
	5	4	54	4	8	3	5	2	14	0	7	24	41
	6	0	4	0	1	0	2	0	1	0	0	1	3
$\hat{S}_{f,u(D)}+\hat{S}_{f,m(D)}$		133		51		22		28		11		148	
NOC	3	0	3	1	2	0	0	0	1	0	0	0	0
	4	3	56	1	14	0	2	2	17	0	0	4	34
	5	0	59	0	10	1	2	1	15	0	0	1	32
	6	0	1	0	0	0	0	0	1	0	0	0	2
$\hat{S}_{f,u(D)}+\hat{S}_{f,m(D)}$		122		28		5		37		0		73	
UCF	3	0	5	3	6	0	3	1	0	0	0	1	2
	4	21	145	19	76	12	37	15	42	1	9	45	150
	5	0	41	0	4	0	5	0	6	3	7	6	35
	6	1	0	0	1	0	1	0	0	0	0	0	2
$\hat{S}_{f,u(D)}+\hat{S}_{f,m(D)}$		213		109		58		64		20		241	

[a] Numbers under the column mrk correspond to $\hat{S}_{f,a,m(D)}$

[b] Numbers under the column un correspond to $\hat{S}_{f,a,u(D)}$.

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[11] ONCOR. Software for genetic stock identification. 2008 Available for download from http://www.montana.edu/kalinowski/Software/ONCOR.htm

APPENDIX C: VARIANCE EQUATIONS FOR DRIVER STOCK TERMINAL RUN ESTIMATES

Estimated Variance

With most of the notation as defined in the text, and as per procedures described in Goodman (1960) for estimating the variance for the product of three variables,

$$v(\hat{M}_{term(D)}) =$$

$$\sum_a \sum_f \left[\begin{array}{l} v(\hat{\pi}_{a(I)})\hat{H}_f^2 \hat{p}_{f,a(D)}^2 + v(\hat{H}_f)\hat{\pi}_{a(I)}^2 \hat{p}_{f,a(D)}^2 + v(\hat{p}_{f,a(D)})\hat{H}_f^2 \hat{\pi}_{a(I)}^2 - v(\hat{\pi}_{a(I)})v(\hat{H}_f)\hat{p}_{f,a(D)}^2 - \\ v(\hat{\pi}_{a(I)})v(\hat{p}_{f,a(D)})\hat{H}_f^2 - v(\hat{H}_f)v(\hat{p}_{f,a(D)})\hat{\pi}_{a(I)}^2 + v(\hat{\pi}_{a(I)})v(\hat{H}_f)v(\hat{p}_{f,a(D)}) + \\ 2\sum_{b>a} \hat{\pi}_{a(I)}\hat{\pi}_{b(I)}\hat{H}_f^2 \operatorname{cov}(\hat{p}_{f,a(D)}, \hat{p}_{f,b(D)}) \end{array} \right], \qquad \text{(C1)}$$

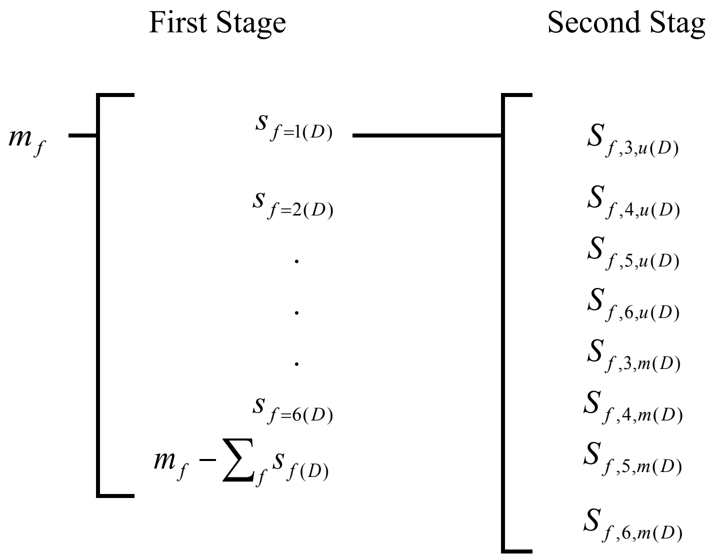
where $\hat{H}_f$, $\hat{p}_{f,a(D)}$, and $\hat{\pi}_{a(I)}$ are the three variables in the product expressed in Equation (1). Note the subscripts *nat*, *hat*, and • designating driver stocks of natural, hatchery, or combined-origin were dropped in Equation (C1) to simplify the expression of the equation. The subscript *b* designates an age other than *a*. Only one covariance is expressed in Equation (C1) because estimated harvest, ratio of CWT recoveries, and estimated GSI fractions are products of three independent programs. Although $\hat{\pi}_{a(I)}$ and $\hat{\pi}_{b(I)}$ from two cohorts are calculated with recoveries of CWTs from the same sampling program, their covariance is so small that it can be ignored with essentially no consequence (Bernard and Clark 1996) and is not represented in Equation (C1). Estimated variance for the estimated ratio $\hat{\pi}_{a(I)}$ was approximated as

$$v(\hat{\pi}_{a(I)}) \cong \frac{\hat{\pi}_{a(I)}^4}{\hat{n}_{term,a}^2} \sum_f \frac{\hat{n}_{fa}}{\phi_f} + \frac{\hat{\pi}_{a(I)}^2}{\phi_{term} \hat{n}_{term,a}}, \qquad \text{(C2)}$$

where ϕ_f represents the fraction of harvest in SEAK fishery *f* inspected for CWTs, and ϕ_{term} represents fraction of the terminal run inspected for CWTs. Derivation of Equation (C2) can be found in the latter half of this appendix. While values for ϕ_f were readily available for all SEAK fisheries, values for fraction inspected for ϕ_{term} were not. For that reason, ϕ_{term} was set to a conservative 0.10 for all indicator stocks.

Variances for $\hat{p}_{f,a(D)}$ were estimated through parametric simulations of landed catch from a driver stock in SEAK fisheries based on posterior probability distributions and on age distributions from GSI on individual fish. Steps in the calculations were as follows:

> STEP 1: 1000 values of the fraction of landed catch from a stock were generated for each combination of driver stock and fishery. The mean and standard deviation of each reported posterior distribution in the mixed stock analyses were used to define a beta distribution from which the 1000 simulated values $\tilde{P}_{f(D)}$ were drawn.
>
> STEP 2: 1000 values for GSI samples were generated for each combination of driver stock and fishery from assignment of individuals to specific stocks. For each fishery and driver stock combination the original sample was divided as follows:



where $s_{f(D)}$ is the number of individuals in the GSI sample of size m_f for which a driver stock could be identified genetically. In the first stage of generating each simulated sample, $\tilde{s}_{f(D)}$ was generated with a binomial distribution using original observations to obtain the probability of identifying a member of driver stock *D* in the sample; the original observed GSI sample size m_f was used as the number of trials. In the second stage the eight simulated variates $\tilde{S}_{f,3,u(D)}$ through $\tilde{S}_{f,6,m(D)}$ were generated with a multinomial distribution based on original observations to obtain probabilities, but with $\tilde{s}_{f(D)}$ as the number of trials.

STEP 3: Simulated variates were substituted for observed variates $[\tilde{P}_{f(D)} \rightarrow \hat{P}_{f(D)}$, $\tilde{S}_{f,a,u(D)} \rightarrow S_{f,a,u(D)}$, and $\tilde{S}_{f,a,m(D)} \rightarrow S_{f,a,m(D)}]$ in Equations (3–7) for each simulated sample to produce simulated fractions for natural ($\tilde{p}_{f,a,nat(D)}$), hatchery ($\tilde{p}_{f,a,hat(D)}$), and combined-origin ($\tilde{p}_{f,a,\bullet(D)}$) driver stocks. Values of $\lambda_{a(D)}$ and $\hat{\beta}_{f(D)}$ were fixed.

STEP 4: Estimated variance for a simulated fraction $\tilde{p}_{f,a(D)}$ was calculated for all 1000 simulated samples for each driver stock, fishery, and age combination:

$$v(\tilde{p}_{f,a(D)}) = \frac{\sum_{k=1}^{1000} ([\tilde{p}_{f,a(D)}]_k - [\bar{\tilde{p}}_{f,a,(D)}]_k)^2}{999} \tag{C3}$$

Estimated variances were then substituted into Equation (C1) – $v(\tilde{p}_{f,a(D)}) \rightarrow v(\hat{p}_{f,a(D)})$.

The final calculation involves estimating the covariance in Equation (C1):

$$\operatorname{cov}(\hat{p}_{f,a(D)}, \hat{p}_{f,b(D)}) = -\frac{\hat{p}_{f,a(D)} \hat{p}_{f,b(D)}}{s_{f(D)}}. \tag{C4}$$

Derivation of Estimated Variance for $\hat{\pi}$

The ratio $\hat{\pi}_{a(I)}$ is a function of the numbers $r_{f,a(I)}$ and $r_{term,a(I)}$ of CWTs recovered from samples in nonterminal fisheries and terminal areas, expanded by fraction ϕ_f of catches sampled, or by fraction of ϕ_{term} terminal run sampled:

$$\hat{\pi}_{a(I)} = \frac{\hat{n}_{term,a(I)}}{\sum_f \hat{n}_{f,a(I)}} = \frac{r_{term,a} / \phi_{term,a(I)}}{\sum_f r_{f,a(I)} / \phi_f}. \tag{C5}$$

Applying the delta method to Equation (C5) produces the approximation to $v(\hat{\pi}_a)$:

$$v(\hat{\pi}) \cong \sum_f \left[v(r_f)\left(\frac{\partial \hat{\pi}}{\partial r_f}\right)^2 + 2\sum_{j>f} \operatorname{cov}(r_f, r_j)\left(\frac{\partial \hat{\pi}}{\partial r_f}\right)\left(\frac{\partial \hat{\pi}}{\partial r_j}\right)\right] +$$

$$v(r_{term})\left(\frac{\partial \hat{\pi}}{\partial r_{term}}\right)^2 + 2\sum_f \operatorname{cov}(r_f, r_{term})\left(\frac{\partial \hat{\pi}}{\partial r_f}\right)\left(\frac{\partial \hat{\pi}}{\partial r_{term}}\right). \tag{C6}$$

Note that subscripts *a* and *I* were dropped in Equation (C6) to simplify notation; the derivation holds for any age, and all variables are for the indicator stock. The subscript *j* denotes a preterminal fishery other than fishery *f* and that $\operatorname{cov}(r_f, r_{term})$ here is for recoveries from the same cohort (the same age implied) across two fisheries.

The *N* salmon in a tagged cohort extant at the beginning of the year suffer by the end of the year one of a series of fates. Some are taken in preterminal fisheries and their CWTs recovered during sampling; some evade being caught and subsequently mature; some evade being caught but do not mature; some are caught but are not landed; some are caught, landed, but not sampled; etc. The numbers of tagged salmon grouped by fate follow a multinomial distribution where τ_i is the probability that a fish suffers fate *i*. The maximum likelihood estimate for the probability that a CWT is recovered by sampling a fishery is $\hat{\tau}_f = r_f / N$; $\hat{\tau}_{term} = r_{term} / N$ is the maximum likelihood estimate for probability of recovery in the terminal area. Estimated variances for the r_f, r_{term}, and their two covariances are $N\hat{\tau}_f(1-\hat{\tau}_f)$, $N\hat{\tau}_{term}(1-\hat{\tau}_{term})$, $-N\hat{\tau}_f\hat{\tau}_j$, and $-N\hat{\tau}_f\hat{\tau}_{term}$, respectively. Partial derivatives are:

$$\frac{\partial \hat{\pi}}{\partial r_f} = \frac{-\hat{\pi}^2}{\phi_f \hat{n}_{term}} \text{ and } \frac{\partial \hat{\pi}}{\partial r_{term}} = \frac{\hat{\pi}}{\phi_{term} \hat{n}_{term}}.$$

Substituting these variances, covariances, and derivatives into Equation (C6) produces the approximation

$$v(\hat{\pi}) \cong \sum_f \left[N\hat{\tau}_f(1-\hat{\tau}_f)\frac{\hat{\pi}^4}{\phi_f^2 \hat{n}_{term}^2} + 2\sum_{j>f} - N\hat{\tau}_f\hat{\tau}_j \frac{\hat{\pi}^4}{\phi_f \phi_j \hat{n}_{term}^2}\right] +$$

$$\left[N\hat{\tau}_{term}(1-\hat{\tau}_{term})\frac{\hat{\pi}^2}{\phi_{term}^2\hat{n}_{term}^2}\right]+2\sum_f\left[-N\hat{\tau}_f\hat{\tau}_{term}\frac{-\hat{\pi}^3}{\phi_f\phi_{term}\hat{n}_{term}^2}\right]. \tag{C7}$$

Remembering that $\hat{\tau}_f = r_f / N$ and that $r_f = \hat{n}_f\phi_f$, Equation (C7) can be modified to become

$$v(\hat{\pi}) \cong \frac{\hat{\pi}^4}{n_{term}^2}\sum_f\left[\frac{\hat{n}_f}{\phi_f}-\frac{\hat{n}_f^2}{N}-2\sum_{j>f}\frac{\hat{n}_f\hat{n}_j}{N}\right]+\hat{\pi}^2\left[\frac{1}{\phi_{term}n_{term}}-\frac{1}{N}\right]+2\frac{\hat{\pi}^3}{\hat{n}_{term}}\left[\sum_f\frac{\hat{n}_f}{N}\right]. \tag{C8}$$

Substituting the relationship $\hat{\pi} = \hat{n}_{term} / \Sigma\hat{n}_f$ into Equation (C8) and collecting terms gives

$$v(\hat{\pi}) \cong \frac{\hat{\pi}^4}{\hat{n}_{term}^2}\sum_f\frac{\hat{n}_f}{\phi_f}+\frac{\hat{\pi}^2}{\phi_{term}\hat{n}_{term}}+\frac{\hat{\pi}^2}{N}\left(1-\frac{\sum_f\hat{n}_f^2}{(\sum_f\hat{n}_f)^2}-2\frac{\sum_f\sum_{j>f}\hat{n}_f\hat{n}_j}{(\sum_f\hat{n}_f)^2}\right). \tag{C9}$$

The term in brackets in Equation (C9) equals zero, which means that knowledge of cohort size is unnecessary to approximating variance and that the approximation is

$$v(\hat{\pi}) \cong \frac{\hat{\pi}^4}{\hat{n}_{term}^2}\sum_f\frac{\hat{n}_f}{\phi_f}+\frac{\hat{\pi}^2}{\phi_{term}\hat{n}_{term}}, \tag{C10}$$

which is the same as Equation (C2) when implied subscripts *a* and *I* are considered. Relative precision in $\hat{\pi}$,

$$cv(\hat{\pi}) \cong \sqrt{\frac{\sum_f\hat{n}_f/\phi_f}{(\sum_f n_f)^2}+\frac{1}{\phi_{term}\hat{n}_{term}}}, \tag{C11}$$

improves with more recoveries (larger numbers tagged in the indicator stock, more and larger fisheries sampled for GSI and CWTs, and higher sampling fractions in the CWT programs).

The expansion factors ϕ_f and ϕ_{term} in Equation (C11) are supposedly known without error. In reality ϕ_f for the Sitka recreational fishery is an estimate because harvest is estimated with a mail survey and therefore has uncertainty; and ϕ_{term} is an estimate whenever the number of spawners is estimated through sampling of terminal recreational fisheries or sampling on the spawning grounds and therefore also has uncertainty. For these reasons (among others) variances expressed in Equation (C10) are truly approximations.

APPENDIX D: HATCHERY RELEASE INFORMATION

Appendix D1.–Hatcheries, lake pens, and sea pens whose releases were used to determine the proportion of hatchery Chinook salmon marked at release for brood years 2005–2008 for each driver stock.

WCVI	WAC	NOC	UCF
Goldstream River	Bingham Creek Hatchery	Nehalem River	Little White Salmon
Gold River	Forks Creek Hatchery	Salmon River	Spring Creek
Conuma River	Humptulips Hatchery	Trask River	Klickitat
Marble River	Lake Aberdeen Hatchery	Trask River Ponds	Lyons Ferry
Tahsis River	Makah NFH (Sooes River)		Ringold Springs
Zeballos River	Mayr Brothers Rearing Ponds		Priest Rapids
VI North School District	Naselle Hatchery		Prosser
Colonial River	Nemah Hatchery		Oxbow
San Juan Estuary Sea Pens	Quinault Lake Hatchery		Nez Perce Tribal
Cordy Creek	Quinault NFH (Cook Creek)		Bonneville
San Juan River	Salmon River Fish Culture Ponds		Irrigon
Kennedy River	Satsop Springs Ponds		Umatilla
Robertson Creek			
Nitinat River			
Thornton Creek			
Nitinat Lake Pens			
Sooke River			
Tofino			
Henderson Lake			
Omega Pacific			
Moutcha Bay Sea Pens			
Tahsis Inlet Sea Pens			
Quatsino Sound Sea Pens			
Sucwoa Estuary Sea Pens			
Tlupana Estuary Sea Pens			
Gold Estuary Sea Pens			
Burman Estuary Sea Pens			
Nahmint Estuary Sea Pens			
Poett Nook Sea Pens			
Esquimalt Harbour Sea Pens			
Sooke Harbour Sea Pens			

Appendix D2.–Number of Chinook salmon released from hatcheries for brood years (BY) 2006–2009 that in 2011 contributed to the terminal run for a driver stock along with the number and fraction of these releases marked. List of the hatcheries involved is given in Appendix D1.

Driver Stock		Age 6 Brood Year 2005	Age 5 Brood Year 2006	Age 4 Brood Year 2007	Age 3 Brood Year 2008
WCVI	Released	13,364,374	15,736,540	12,566,656	15,219,875
	Marked	12,248,319	14,536,224	11,361,826	14,136,481
	Fraction Marked ($\lambda_{a(D)}$)	0.916	0.924	0.904	0.929
WAC	Released	10,904,202	13,465,904	9,587,982	9,982,339
	Marked	2,005,945	1,855,940	1,440,315	1,625,219
	Fraction Marked ($\lambda_{a(D)}$)	0.184	0.138	0.150	0.163
NOC	Released	388,406	400,914	323,295	273,487
	Marked	287,920	284,484	320,574	271,987
	Fraction Marked ($\lambda_{a(D)}$)	0.741	0.710	0.992	0.995
UCF	Number Released	28,846,035	24,560,961	23,636,927	28,163,397
	Number Marked	24,047,422	20,155,278	19,455,684	22,740,147
	Fraction Marked ($\lambda_{a(D)}$)	0.834	0.821	0.823	0.807

APPENDIX E: EQUATIONS FOR ESTIMATING RELATIVE AGE DISTRIBUTION

Appendix E1.–Equations used to estimate relative age distributions for driver and indicator stocks in landed catches by SEAK fisheries and in terminal runs. Notation is defined in the body of the report except for the following: *C* is catch, *b* is an age for salmon, θ_a is a proportion of a population, N_a is the number on the spawning grounds, *i* and *j* are streams, and *W* is a weight (redds for WAC and counts on foot surveys for NOC).

Driver Stock	
NOC Naturals SEAK	$\hat{C}_{f,a,u(D)} = \hat{P}_{f(D)}\hat{H}_f \frac{S_{f,a,u(D)}}{\sum_b [S_{f,b,m(D)} + S_{f,b,u(D)}]}$ $\hat{\theta}_{SEAK,a(D)} = \frac{\sum_f \hat{C}_{f,a,u(D)}}{\sum_b \sum_f \hat{C}_{f,b,u(D)}}$
NOC Naturals Terminal Area[a]	$\hat{W}_{i,a(D)} = \frac{\hat{N}_{i,a(D)}}{\sum_j \hat{N}_{j,a(D)}}$ $\hat{\theta}_{term,a(D)} = \sum_i \hat{W}_{i,a(D)} \hat{\theta}_{i,a(D)}$
WAC Natural/Hatchery Terminal Area[b]	$\hat{\theta}_{term,a(D)} = \frac{\sum_i \hat{N}_{i,a(D)}}{\sum_b \sum_i \hat{N}_{i,b(D)}}$
WAC and UCF Natural/Hatchery SEAK	$\hat{C}_{f,a(D)} = \hat{P}_{f(D)}\hat{H}_f \frac{S_{f,a,u(D)} + S_{f,a,m(D)}}{\sum_b [S_{f,b,m(D)} + S_{f,b,u(D)}]}$ $\hat{\theta}_{SEAK,a(D)} = \frac{\sum_f \hat{C}_{f,a(D)}}{\sum_b \sum_f \hat{C}_{f,b(D)}}$
UCF Natural/Hatchery Terminal Area	From Table 12 of Fryer et al. (2013) adjusted so the population included all fall Chinook salmon three years old and older except for half of those with age 1.1.
Indicator Stock	
WAC, NOC, and UCF SEAK	$\hat{\theta}_{SEAK,a(I)} = \frac{\sum_f \hat{n}_{f,a(D)}}{\sum_b \sum_f \hat{n}_{f,b(D)}}$
WAC, NOC, and UCF Terminal Area	$\hat{\theta}_{term,a(I)} = \frac{\hat{n}_{term,a(I)}}{\sum_b \hat{n}_{term,b(I)}}$

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[a] Information obtained from Ethan Clemons, Fish and Fisheries Biologist, Oregon Department of Fish and Wildlife, Newport; November 8, 2013, e-mail.

[b] Information obtained from Peter McHugh, Salmon Policy Analyst, Washington Department of Fish and Wildlife, Olympia; September 9, 2013, e-mail.