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An Evaluation of the Selectivity of Fish Wheels used to Apportion Sonar Counts to Species on the Yentna River, Alaska

by

T. Mark Willette

Robert D. DeCino

Andy W. Barclay

and

Xinxian Zhang

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

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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*
catch per unit effort	CPUE
coefficient of variation	CV
common test statistics	(F, t, χ^2, etc.)
confidence interval	CI
correlation coefficient (multiple)	R
correlation coefficient (simple)	r
covariance	cov
degree (angular)	°
degrees of freedom	df
expected value	*E*
greater than	>
greater than or equal to	≥
harvest per unit effort	HPUE
less than	<
less than or equal to	≤
logarithm (natural)	ln
logarithm (base 10)	log
logarithm (specify base)	$\log_2$, etc.
minute (angular)	'
not significant	NS
null hypothesis	H_O
percent	%
probability	P
probability of a type I error (rejection of the null hypothesis when true)	α
probability of a type II error (acceptance of the null hypothesis when false)	β
second (angular)	"
standard deviation	SD
standard error	SE
variance	
population	Var
sample	var

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AN EVALUATION OF THE SELECTIVITY OF FISH WHEELS USED TO APPORTION SONAR COUNTS TO SPECIES ON THE YENTNA RIVER, ALASKA

by
T. Mark Willette, Robert D. DeCino, Xinxian Zhang
Alaska Department of Fish and Game, Division of Commercial Fisheries, Soldotna

and

Andy W. Barclay
Alaska Department of Fish and Game, Gene Conservation Laboratory, Anchorage

Alaska Department of Fish and Game
Division of Sport Fish, Research and Technical Services
333 Raspberry Road, Anchorage, Alaska, 99518-1565

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T. Mark Willette, Robert D. DeCino
Alaska Department of Fish and Game, Division of Commercial Fisheries,
43961 Kalifornsky Beach Rd., Ste B, Soldotna, Alaska 99669, USA

Andy W. Barclay
Alaska Department of Fish and Game, Gene Conservation Laboratory,
333 Raspberry Rd, Anchorage, Alaska 99518

and

Xinxian Zhang
Alaska Department of Fish and Game, Division of Commercial Fisheries,
333 Raspberry Rd, Anchorage, Alaska 99518, USA

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ABSTRACT

This study estimated the selectivity of fish wheels used to apportion sonar counts to species at the Yentna River sonar site. The selectivity of fish wheels were estimated from tag–recapture probabilities that were estimated from recaptures of dart tags applied to sockeye (*Oncorhynchus nerka*), coho (*O. kistusch*), pink (*O. gorbuscha*), and chum (*O. keta*) salmon from 2009 to 2012. Logistic regression analyses were conducted for each species separately to model the relationships among tag–recapture probabilities and fish length, water level, and total salmon abundance. Logistic-regression models were then used to calculate historical sonar estimates of sockeye salmon abundance adjusted for fish wheel selectivity. Genetic-based mark–recapture studies were conducted from 2008 to 2012 to estimate sockeye salmon abundance at the Yentna sonar site. Tissue samples for genetic analysis were collected from sockeye salmon captured in fish wheels that operated on both banks at the Yentna site to estimate the proportion of the population migrating along each bank originating from Judd and Chelatna lakes. These data were used in conjunction with weir counts of sockeye salmon at these 2 lakes to estimate the abundance of sockeye salmon passing the Yentna site. Genetic mark–recapture estimates of sockeye salmon abundances were 233,677 (90% CI: 204,400–271,500) in 2008; 139,168 (CI: 123,160–158,340) in 2009; 151,774 (CI: 135,260–171,580) in 2010; 290,801 (CI: 253,500–334,400) in 2011; and 109,981 (CI: 95,290–129,080) in 2012. Genetic mark–recapture and adjusted-sonar estimates of sockeye salmon abundance were not significantly different in 5 of 7 years (2006–2012). The adjusted-sonar sockeye salmon abundance estimate in 2011 was clearly biased low, apparently because the total sonar estimate was biased. When the 2011 data were omitted, genetic mark–recapture and adjusted-sonar estimates of sockeye salmon abundances were highly correlated (R2 = 0.997, $P < 0.001$).

Key words: Sockeye salmon (*Oncorhynchus nerka*), pink salmon (*O. gorbuscha*), coho salmon (*O. kistusch*), chum salmon (*O. keta*), inriver abundance estimation, sonar, species apportionment, fish wheel, gear selectivity, genetic mark–recapture, Yentna River

INTRODUCTION

In 1979, the Alaska Department of Fish and Game (ADF&G) set a biological escapement goal (BEG) of 200,000 spawners for the Susitna River sockeye salmon (*Oncorhynchus nerka*) (Fried 1994). From 1981 to 2008, the ADF&G managed harvests of Susitna River sockeye salmon to achieve escapements into the Yentna River (a major tributary of the Susitna River). Based on a 5-year comparison of sockeye salmon escapements into the Yentna River and Susitna mainstem (above the confluence with the Yentna River), ADF&G determined that an escapement of 100,000–150,000 sockeye salmon into the Yentna River would result in an escapement of 200,000 sockeye salmon into the entire Susitna River drainage (Fried 1994). In 2001, ADF&G determined that it would be more appropriate to set a sustainable escapement goal (SEG) of 90,000–160,000 based upon empirical estimates of Yentna River sockeye salmon escapement obtained using a fish wheel apportioned Bendix sonar system[1]. However, deficiencies in the Bendix sonar system and species apportionment process became apparent during 2006–2008 when Bendix estimates of sockeye salmon escapement were lower than aggregate estimates of escapement from upstream weir counts, mark–recapture, and dual-frequency identification sonar (DIDSON; Maxwell et al. 2011; Yanusz et al. 2007, 2011a, 2011b).

The Alaska Board of Fisheries designated Susitna River sockeye salmon as a stock of yield concern at the February 2008 meeting, and ADF&G committed to improve management of this stock. In 2009, ADF&G replaced the sonar-based Yentna River sockeye salmon SEG with 3 SEGs for Chelatna (20,000–65,000), Judd (25,000–55,000) and Larson (15,000–50,000) lakes (Fair et al. 2009). Subsequently, ADF&G obtained funding through the Alaska Sustainable Salmon Fund (AKSSF) for 3 projects (*Yentna sonar error estimation*, *Yentna fish wheel*

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[1] Product names used in this report are included for scientific completeness but do not constitute product endorsement.

selectivity, and *Susitna sockeye salmon production*) that focused on improving sockeye salmon escapement estimation and our understanding of sockeye salmon production in the Susitna River watershed. This report describes the results from the *Yentna fish wheel selectivity* project.

Since 1981, fish wheels have been used to apportion total sonar salmon passage estimates to species at the ADF&G sonar site located at river kilometer (rkm) 5 on the Yentna River (Westerman and Willette 2013). Sonars and fish wheels have been operated on each bank of the river from approximately July 7 until daily sockeye salmon passage estimates reach <1% of the season total estimate for 3 consecutive days (usually in early August). From 2006 to 2008, Maxwell et al. (2011) conducted studies to compare Bendix and DIDSON sonar total salmon passage estimates at the Yentna site. Beginning in 2009, DIDSON replaced Bendix sonars at this site, but the procedure for apportioning total salmon passage estimates to species did not change. Use of fish wheels to apportion total salmon passage estimates to species is based on the assumption that catchabilities are equal among all species. However, a previous study on the Taku River found that this assumption was violated, and that fish wheels tended to select for pink salmon (*O. gorbuscha*) and smaller Chinook salmon (*O. tshawytscha*) (Meehan 1961). Subsequent studies on the Susitna River at Talkeetna and Curry stations (ADF&G 1983) concluded that fish wheels selected for pink salmon and less for chum (*O. keta*) and Chinook salmon with no apparent selection for coho (*O. kistusch*) or sockeye salmon. Because these studies suggested that fish wheel selectivity are probably dependent on environmental conditions and site characteristics, we determined that correcting for fish wheel selectivity would require estimating selectivity at the Yentna site and modeling selectivity in relation to biological and environmental conditions at this site.

OBJECTIVES

This project estimated the selectivity of fish wheels used to apportion sonar estimates to species using tagging methods. The project also calculated fish wheel selectivity-corrected sonar abundance estimates and compared them to genetic mark–recapture estimates of sockeye salmon abundance passing the Yentna sonar site. The project objectives were to:

1. Estimate tag–recapture probabilities for sockeye, pink, coho, and chum salmon in fish wheels at the Yentna sonar site;
2. Model tag–recapture probabilities in relation to biological and environmental factors;
3. Adjust sonar estimates of sockeye salmon abundances during 2009–2012 using estimated tag–recapture probabilities to adjust for fish wheel selectivity;
4. Adjust sonar estimates of sockeye salmon abundances during 1986–2012 using modelled tag–recapture probabilities to correct for fish wheel selectivity;
5. Estimate sockeye salmon abundances during 2008–2012 using genetic mark–recapture methods; and
6. Compare adjusted-sonar and genetic mark–recapture sockeye salmon abundance estimates.

STUDY AREA

The Susitna drainage comprises 49,210 km^2 and originates in the Alaska Range north of Anchorage (Figure 1). It flows generally south from the Alaska Range for approximately 400 km before entering Cook Inlet west of Anchorage. The largest tributaries are the Yentna, Chulitna, and Talkeetna rivers, and there are numerous sockeye salmon nursery lakes. Most of the sockeye salmon produced within the Talkeetna drainage are thought to come from Larson and Stephan lakes. Many small lakes contribute to sockeye salmon production in the Chulitna drainage, but Byers and Swan lakes are thought to have the greatest production potential. The Yentna drainage has at least 12 lakes known to support sockeye salmon, of which Chelatna, Shell, Hewitt, and Judd lakes are thought to provide the most production potential (King and Walker 1997).

METHODS

STUDY DESIGN

This project used tagging methods to estimate the selectivity of fish wheels used to apportion sonar counts to species at the ADF&G Yentna sonar site. Sockeye, pink, chum, and coho salmon were marked with dart tags at Flathorn station located 10 km downstream of the Yentna sonar site on the mainstem Susitna River from 2009 to 2012 (Figure 1). Species selectivity of the Yentna fish wheels were estimated from dart tag–recapture probabilities for each species in the Yentna fish wheels. Radio tags were also applied to each species using esophageal implant to estimate the fraction of all tagged fish that migrated up the Yentna River and past the ADF&G sonar site. Tag–recapture probabilities were used to develop models to correct for species selectivity of the fish wheels and develop adjusted species-apportioned sonar estimates of the abundance of sockeye salmon passing the Yentna sonar site.

The abundance of sockeye salmon passing the Yentna sonar site was also estimated using genetic mark–recapture methods (Hamazaki and DeCovich 2014). Genetic mark–recapture estimates are not affected by handling effects, tag loss, or tag detection that can bias conventional mark–recapture estimates. Mixed-stock analyses (MSA; Barclay et al. 2010a) using genetic data were used to estimate the proportion of the sockeye salmon population passing Yentna that originated from Judd and Chelatna lakes located upstream of the Yentna site (Figure 1). Tissue samples were collected for genetic analysis from sockeye salmon captured in the Yentna fish wheels. The abundance of sockeye salmon passing the Yentna site was then estimated from counts of sockeye salmon passing Judd and Chelatna lakes weirs and MSA estimates of stock proportions in fish wheel catches (Hamazaki and DeCovich 2014).

Genetic mark–recapture abundance estimates were then compared to adjusted species-apportioned sonar estimates to evaluate whether corrections for fish wheel selectivity improved the accuracy of sockeye salmon abundance estimates.

FISH WHEEL SELECTIVITY

Marking Event Dart Tags

During each year of the study, approximately 17,000 dart tags (Model FT-1-94, Floy Tag and Manufacturing Inc.) were applied to sockeye, pink, chum, and coho salmon captured in a fish wheel operated on the west bank of the west channel at Flathorn station on the lower Susitna River (Fish Wheel #1, Figure 2). Each year, dart tags were applied during the period of Yentna sonar operations (approximately July 6 through early August). Dart tags were used in this study because they are uniquely numbered, inexpensive, and quick to apply. The same color (yellow) dart tag was used on all species to avoid any differences in tag detection among species and unique tag numbers were used to identify individual fish.

Two 3-person crews applied dart tags to sockeye, pink, chum, and coho salmon captured in the west bank fish wheel at Flathorn. Initially, dart tags were applied to every sockeye, pink, chum, and coho salmon captured, and the tagging rate for sockeye and pink salmon was reduced when high catch rates prohibited tagging every fish.

Crews worked on a rotating schedule to insure that fish were tagged throughout the 24-hour day. Each crew worked 9 hours each day with 1 hour off for meals in the middle of the shift resulting in 2 tagging sessions that lasted 4 to 5 hours. Previous studies have shown that coho salmon tagged close to saltwater are very vulnerable to handling stress, and that mortality for all salmon species increases the longer the fish are in the livebox (Carlon and Evans 2007). Therefore, every effort was made to tag fish taken directly out of the fish wheel basket. This required manning the fish wheel during the entire 9-hour shift. The fish wheel was turned on at the beginning of each shift, turned off during the meal break, and then turned off again at the end of the shift. All tagged salmon were quickly processed to reduce handling time and associated stress. Fish that were severely injured were not tagged. Fish were tagged in a tote partially filled with water. A padded plastic cradle device was slipped around the fish to restrain it during tagging. Dart tags were applied on the left (port) side of the fish near the posterior end of the dorsal fin below the dorsal line at a 45° angle using a hollow canula (Floy Tag and Manufacturing Inc.). Dart tags were sequentially numbered and applied in order. The crew measured length (MEFL, from the mid eye to the fork of tail) to the nearest 1 mm using a tape. One crew member input the species, sex, and length of dart-tagged fish into a handheld computer using a custom data entry program. The program automatically recorded the date, time, and sequential dart tag number into a data file. The program automatically displayed the sequential dart tag number, but this number could be changed if tags were lost, etc. A new data file was created by the program each day.

Marking Event Radio Tags

Approximately 100 esophageal radio tags were applied to each of the 4 salmon species to estimate the fraction of dart-tagged fish of each species that migrated up the Yentna River and past the ADF&G sonar site versus up the mainstem Susitna River. Yanusz et al. (2007) found that 98% of radiotagged sockeye salmon captured in Fish Wheel #1 at Flathorn station migrated up the Yentna River (Figure 2). A radio tag application schedule was developed in collaboration with Sport Fish Division (SFD) for each salmon species based upon historical average run timing. We collaborated with SFD because they were applying radio tags to chum and coho salmon captured in 3 other fish wheels at Flathorn station, and radio tags applied to fish captured in Fish Wheel #1 were also used in their study. In an attempt to apply tags as close as possible to relative abundance each year, the deployment schedule was adjusted to slide ahead or back in time. The first day of the tagging schedule for chum or coho salmon began when any 1 of 3 criteria were met for a given species: (1) 4 consecutive days with a total daily catch in all 4 fish wheels of >0 fish, (2) total daily catch in all 4 fish wheels of ≥10 fish, or (3) 20 July. The SFD crew leader informed our crew leader when to begin following the tagging schedule. The first day of the tagging schedule for sockeye and pink salmon began when any 1 of 2 criteria were met for a given species: (1) 4 consecutive days with a total daily catch in Fish Wheel #1 of >0 fish, (2) total daily catch in Fish Wheel #1 of ≥10 fish, or (3) 20 July (sockeye salmon) or 25 July (pink salmon). For each species, the deployment schedule was rigidly adhered to once it was initiated.

Based upon the tagging schedule, the morning-shift crew leader determined the number of radio tags to apply to each species each day. If more than 1 tag was to be applied to a species in a day, the tags were evenly split between the morning and evening shifts. If only 1 tag was to be applied to a species, it was applied by the morning crew. To minimize handling stress, only fish that came directly from the fish wheel basket while a crew member was present were radiotagged. During each shift, the first *n* healthy salmon caught of each species were radiotagged. If an insufficient number of salmon were caught to meet the schedule, then the radio tags not applied were added to the goal for the next day. Each radio tag was assigned a unique sequential number (1–100 for chum salmon, 101–200 for coho salmon, 201–300 for sockeye salmon, 301–400 for pink salmon). Model F1840B and F1835B radio transmitters manufactured by Advanced Telemetry Systems, Inc. (ATS) operating on 12 frequencies within the 151.033–151.634 MHz range were used in this study. Within each frequency, several different transmitting patterns or *pulse codes* were used, resulting in 400 uniquely identifiable transmitters. Each transmitter was equipped with a mortality indicator code that activated when the tag was motionless for approximately 24 hours. The F1840B transmitters were 56 mm long, 17 mm in diameter, with a weight of 22 g in air, a 30 cm external whip antenna, and a warranty life of at least 63 days. The F1835B transmitters were 48 mm long, 17 mm in diameter, with a weight of 16 g in air, a 30 cm external whip antenna, and a warranty life of at least 48 days.

Radio tags were applied to fish in a tote that was partially filled with water. A padded, plastic cradle device was slipped around the fish to restrain it during tagging. One person restrained the fish and the other inserted the radio tag through the esophagus and into the upper stomach of the fish using an approximately 25 cm polyvinyl chloride tube with a diameter nearly equal to that of the radio tag. The radio transmitter was seated on the end of the tube. The antenna was threaded through the tube and gripped to hold the tag in place. The radio transmitter was then pushed through the esophagus and seated such that only the antenna was visible coming out of the esophagus. The crew measured MEFL to the nearest 1 mm, determined the fish’s sex, and removed and preserved the left axillary process (coho and chum salmon only) for later genetic analysis. Salmon <400 mm MEFL (5.2% of all dart-tagged salmon) were not radiotagged, to minimize mortality. The 42 smaller F1835B radio tags were applied to smaller pink salmon in the range of 400–420 mm MEFL. The frequency and pulse code of each radiotagged fish, sex, MEFL, and genetic vial number (chum and coho only) were entered into a handheld computer using a custom data entry program. All tagged salmon were released into the river adjacent to the fish wheel immediately after data was recorded. At the end of each tagging session, the date; session begin and end times; crew; and the number of sockeye, pink, chum, and coho salmon dart- and radio-tagged were recorded onto a hard copy data form. In addition, the start and stop times for the fish wheel, as well as revolutions per minute, water depth at the axle (at about noon each day), and any other information relevant to maintaining fish wheel efficiency were recorded onto a hard copy data form. The crew leader was responsible for error checking electronic and hardcopy data, and downloading electronic data files to a laptop computer each day.

Recapture Event Dart Tags

Two 2-person crews scanned all sockeye, pink, chum and coho salmon captured in both fish wheels at the Yentna sonar site for the presence of a dart tag. Each crew worked 9-hour shifts with an hour off for meal breaks (Crew 1: 0400–0830, 0930–1400; Crew 2: 1400–1830, 1930–2400). When catches were low, fish wheels were operated continuously and the crew alternated between fish wheels, scanning all fish as they were dipnetted out of the livebox. When catch rates exceeded the crew’s ability to scan all fish caught, fish wheels were turned off until all captured fish had been scanned.

To ensure that all fish were carefully scanned for tags, only a few fish were dipped from the livebox at a time. Lights were mounted in the boat for nighttime operations, to maintain high tag detection rates. When tagged fish were recaptured, the tag was clipped off of the fish and placed in small ziplock bags (one for each species). The bags were labeled with the date, bank, and species. The date, time, species, and unique tag number of the fish were recorded on a hard copy data form. Total catch by species were recorded on the data forms normally used by the sonar crew (Westerman and Willette 2013).

Recapture Event Radio Tags

Because SFD was simultaneously conducting a radiotelemetry study to determine spawning distribution of chum and coho salmon radiotagged at Flathorn station, we relied on SFD to relocate all radio tags applied in our study. Merizon et al. (2010) provided a detailed description of these radio tag relocation methods.

The conceptual design of the radio tag relocation project involved tracking movements of radiotagged fish using a combination of stationary radio receivers and aerial surveys. One stationary receiver was placed 5.0 km above the Flathorn fish wheels and below the Yentna River confluence. Radiotagged fish passing this ‘gateway’ receiver were considered to have entered the experiment. Two receivers were placed downstream of the Flathorn fish wheels to detect tagged fish that dropped downstream. Six stationary receivers were also placed upstream of the Yentna sonar fish wheels, and 4 were placed upstream of the Yentna River confluence on the Susitna River mainstem (Figure 2). Two antennas were deployed at each fixed station with 1 oriented in a downstream direction and the other in an upstream direction. The receivers continually scanned the frequencies of all transmitters 24 hours per day. Radiotagged fish within detection range of the stations are identified and electronically recorded in a data file.

Fixed-wing aircraft were used to conduct aerial surveys to relocate radiotagged fish throughout the Susitna watershed and to identify potential spawning sites. Tracking flights were made approximately weekly from 1 August through 15 October, weather permitting. Two Yagi antennas were mounted, with one on each side of the plane, to maximize tag detection and enable more accurate determination of tag location using a global positioning system.

The relocation data from all fixed stations and aerial surveys was assembled into a database to construct a history of movement for each radiotagged fish and identify its potential spawning site based on the highest upstream movement in the watershed.

Sonar Adjustment Using Estimated Tag–recapture Probabilities

We first estimated uncorrected tag–recapture probabilities (P_u) for each species (x) from the number of dart-tagged salmon recaptured (m_2) in both Yentna sonar site fish wheels combined divided by the number of dart-tagged salmon released from Fish Wheel #1 at Flathorn (N_x), i.e.,

$$Pu_x = \frac{m_2}{N_x}. \tag{1}$$

Radio tag relocation data was then used to estimate the fraction of dart-tagged salmon of each species that migrated upstream past the Yentna sonar site versus those that remained in the mainstem Susitna River, i.e.,

$$Py_x = \frac{Ryt_x}{Rt_x}, \tag{2}$$

where Rt_x was the total number of radiotagged salmon of each species released from Flathorn Fish Wheel #1, and Ryt_x was the number of radiotagged salmon of each species later relocated above the Yentna sonar site. Tag–recapture probabilities corrected for the fraction of dart-tagged salmon that did not migrate past the Yentna sonar site were then given by:

$$Pc_x = Pu_x \cdot \frac{1}{Py_x}. \tag{3}$$

We estimated tag–recapture probabilities separately for each species and then relied on both length and temporal stratification to reduce the bias of recapture probabilities applied to correct for fish wheel selectivity. Following Clark (1991), we used maximally selected chi-square values to determine cut points for strata. Because fish cannot move between length categories, we first applied this method to identify length strata. The split was made among length groups if the maximum chi-square was significant ($\alpha = 0.05$). Only 2 length strata were constructed to maintain the sample size within each stratum. The process was then repeated within the small and large length strata to identify temporal strata. Temporal strata were determined by lagging the cut point dates by the average travel time between Flathorn and the Yentna sonar site (1 day).

Recapture probabilities were then applied within length and/or temporal strata to correct daily fish wheel catches for species selectivity and estimate the proportion of the total salmon stock passing the sonar site that was sockeye (red) salmon ($PROP_r$), i.e.,

$$PROP_r = \frac{\left(C_r \middle/ Pc_r \right)}{\left[\left(C_r \middle/ Pc_r \right) + \left(C_s \middle/ Pc_s \right) + \left(C_p \middle/ Pc_p \right) + \left(C_c \middle/ Pc_c \right) \right]}, \tag{4}$$

where C_r was the catch of sockeye salmon, Pc_r was the tag–recapture probability for sockeye salmon, C_s was the catch of coho salmon, Pc_s was the tag–recapture probability for coho salmon, C_p was the catch of pink salmon, Pc_p was the tag–recapture probability for pink salmon, C_c was the catch of chum salmon, and Pc_c was the tag–recapture probability for chum salmon. Equation 4 was applied to apportion the daily sonar counts on each bank separately, because this has been the standard method used at this sonar site (Westerman and Willette 2013).

A simulation model was used to estimate the mean and variance of the annual fish wheel apportioned sonar estimates of sockeye salmon abundance. The model estimated stratum recapture probabilities over 10,000 iterations using the RAND function in SAS (SAS Institute, Cary, NC) with a hypergeometric distribution. Equation 4 was then applied to estimate sockeye salmon abundances over all iterations. The mean and variance of the simulated sockeye salmon abundances was then estimated, and 90% confidence intervals were approximated using the 5th and 95th percentiles of the distribution of abundance estimates.

Sonar Adjustment Using Modelled Tag–recapture Probabilities

For each species, separate logistic maximum-likelihood regression analyses were conducted to model recapture probabilities using all available data (2009–2012). The dependent variable in the analyses was the logit-transformed probability that a tagged fish was recaptured (event) in either fish wheel at the Yentna sonar site. The independent variables in the analyses were MEFL of tagged salmon, water level measured at the Yentna sonar site, the abundance of all salmon estimated using sonar (DIDSON units), and their pairwise interaction terms. DIDSON estimates of salmon abundance were used for 2009–2012. Prior to 2009, Bendix sonar estimates of salmon abundance were converted to DIDSON units using data collected by Maxwell et al. (2011). Daily Bendix sonar estimates were converted to DIDSON units using regression analyses with no intercept for each bank separately (regression slopes: 1.847 south bank, 1.561 north bank).

Dart-tagged fish that were not recaptured in fish wheels were randomly censored from the dataset to correct for the fraction of dart-tagged fish that did not migrate past the Yentna sonar site based upon radio tags. Observations with similar values of independent variables were regarded as coming from the same subpopulation (i.e., not independent) and were therefore grouped. This was done to satisfy the model assumption of independence of observations, to avoid expected cell frequencies <5, and to reduce noise in estimated probabilities (Harrell 2001). Lengths were grouped in 5 cm intervals, water levels were grouped in 0.2 m intervals, and DIDSON salmon abundances were grouped in 10,000-fish intervals. A backward-selection procedure ($\alpha = 0.05$) was used to identify independent variables that were significantly correlated with recapture probability. The Hosmer and Lemeshow (H-L) statistic was used to test for goodness-of-fit, because more than 30% of the groups had sample sizes <10 (Hosmer and Lemeshow 2000). The ability of model predictions to discriminate between cases with and without a recapture event was assessed using the *c*-statistic (Steyerberg et al. 2010). The *c*-statistic can be interpreted as the rank correlation between the predicted probabilities of tag–recapture events and the observed outcome.

A simulation model was also used to estimate the mean and variance of annual fish wheel apportioned sonar estimates (1986–2012) of sockeye salmon abundance derived using the logistic regression equations for each species. The model estimated daily recapture probabilities over 10,000 iterations incorporating uncertainty using the standard error of the regression coefficients. Mean annual MEFL for sockeye salmon was used as a model input from 1986 to 2012. But for the other salmon species, MEFL data were not available prior to 2009, so the mean MEFL for each species (2009–2012) was used as a model input for all years. Water level measurements at the Yentna sonar site were not available for 1987, 1988, and 1990, so the mean water level for all other years combined was used as a model input in these years. Equation 4 was then applied to estimate sockeye salmon abundance over all iterations. The model incorporated uncertainty in converting Bendix sonar estimates of salmon abundance to DIDSON units (1986–2008) as described by Maxwell et al. (2011), and uncertainty in DIDSON estimates (2009–2012) resulted from the 10-minute subsampling procedure used at the Yentna sonar site (Westerman and Willette 2013). Xie and Martens (2014) estimated that a 10-minute subsampling procedure every hour resulted in a 5.5% coefficient of variation in salmon abundance estimates.

The mean and variance of the simulated sockeye salmon abundances was then estimated by bank and for both banks combined, and 90% confidence intervals were approximated using the 5th and 95th percentiles of the distribution of abundance estimates.

GENETIC MARK–RECAPTURE ESTIMATES

A genetic mark–recapture method was used to estimate the abundance (N) of sockeye salmon passing the Yentna sonar site in 2008–2012, i.e.,

$$N = \frac{E_m}{p_m}, \tag{5}$$

where E_m was the escapement of genetic-marked stock m at an upriver tributary and p_m was the proportion of stock m estimated from tissue samples collected at the Yentna sonar site (Hamazaki and DeCovich 2014). Two genetic-marked sockeye salmon stocks originating from Chelatna and Judd lakes were used in the study. Estimates of E_m were obtained from weirs operated below the outlet of each lake. Previous radiotelemetry studies had shown that these 2 stocks account for 31–50% of the total sockeye salmon run passing the Yentna sonar site with Judd fish mostly migrating along the south bank and Chelatna fish migrating along both banks (Yanusz et al. 2007, 2011a, 2011b).

Tissue Sampling

Because it is not possible to stratify a genetic mark–recapture experiment by time, due to lack of unique individual marks, it was necessary to collect tissue samples for genetic analysis approximately in proportion to sockeye salmon abundance over time on each river bank. Tissue samples were collected using fish wheels operated each river bank during three 2 hour periods between 0600–1200, 1200–1800, and 1800–2400 hours each day during the run. Before the beginning of each genetic sampling period, the livebox was emptied of all fish to allow for separate enumeration of the catch during the genetic sampling period. To collect samples in proportion to abundance, both fish wheels were operated continuously during these three 2-hour periods throughout the run, with genetic tissue samples collected from every *n*th sockeye salmon during these periods. Due to differences in catch rates between banks (Westerman and Willette 2013), tissue samples were taken from every sockeye salmon captured on the north bank and every 6th sockeye salmon captured on the south bank, without regard to size, sex, or condition. These sampling rates were established to achieve a sample size of approximately 400 sockeye salmon for each bank, based on historical catch rates. An axillary process was excised from each fish for genetic analysis and placed in a single 2 ml plastic vial containing ethanol. For data continuity, tissue samples were paired with age, sex, and length information collected from each fish. These data were collated and archived by ADF&G staff in Soldotna, and all tissue samples were sent to the ADF&G Gene Conservation Laboratory for later analysis. Yanusz et al. (2011b) collected the genetic tissue samples in 2008 using the same sampling design.

To evaluate whether genetic samples were collected in proportion to abundance, the cumulative proportion of the number of genetic samples collected each day was plotted along with the cumulative proportion of the daily catch per hour (CPUE) in fish wheels. Kolmogorov-Smirnov (K-S) tests were then conducted to test whether the 2 distributions were different.

Assaying Genotypes and Quality Control

Genomic DNA was extracted following the methods of Barclay and Habicht (2012) using DNeasy 96 Tissue Kits by QIAGEN (Valencia, CA). All baseline and fish wheel samples, except for the 2009 samples, were screened for 96 sockeye salmon SNP markers (3 mitochondrial and 93 nuclear DNA) following the methods of Barclay and Habicht (2012). The 2009 samples were screened for 45 sockeye salmon SNP markers (3 mitochondrial and 42 nuclear DNA) following methods of Barclay et al. (2010a).

Genotyping failure rate calculations and quality control measures follow those reported in Barclay et al. (2010a), where they report results for a representative set of baseline collections. Briefly, 8% of all individuals were re-extracted and genotyped from all collections. Here we report on the failure rates and quality control measures for the 2008–2012 Yentna fish wheel samples.

Baseline Marker sets and Reporting Groups

Since 2007, two sets of SNP markers have been used for MSA of sockeye salmon within Cook Inlet. From 2007 to 2009, the Cook Inlet baseline included 45 sockeye salmon SNP markers. During this period, mixtures were also screened for the same set of markers (Habicht et al. 2007; Barclay et al. 2010a; Barclay et al. 2010b). In 2010, additional SNP markers became available and a baseline was developed for MSA within Cook Inlet that used 96 SNP markers. Some of these markers overlapped with the original 45 SNP marker set (Barclay and Habicht 2012). When this new baseline was developed, the 2008 Yentna River sample was reanalyzed with the additional SNP markers to evaluate the relative performance of the 96 SNP baseline for MSA (Barclay and Habicht 2012). As a result, for this report, the Yentna River fish wheel samples from 2009 were screened for 45 SNPs and the 2008 and 2010–2012 samples were screened for 96 SNPs.

The current sockeye salmon baseline in Cook Inlet contains 69 populations representing 10,001 fish screened for 96 SNP loci (Barclay and Habicht 2012). For the purpose of analyzing mixtures of fish within the Yentna River, a subset of 13 Yentna River populations from the Barclay and Habicht (2012) baseline were used. Reporting groups were defined based on 1 or more of the following criteria: 1) the genetic similarity among populations, 2) the expectation that proportional harvest would be greater than 5%, or 3) the applicability to answer fishery management questions. Populations were assigned into the following 3 reporting groups (stocks) for MSA of sockeye salmon captured by the Yentna River fish wheels: 1) the major sockeye salmon producing lake monitored with a weir in the Skwentna River drainage, Judd Lake, 2) the major sockeye salmon producing lake monitored with a weir in the Lake Creek drainage, Chelatna Lake, and 3) the remaining Yentna River populations (Yentna Other).

Baseline Evaluation for Mixed Stock Analysis

Proof tests were used to evaluate how the baseline performed for MSA using methods described by Eskelin et al. (2013). Markers found to be invariant (i.e., without variation) among Yentna River baseline populations were excluded from the analysis. In addition, markers from the 45 SNP marker set that were not included in the 96 SNP marker set were excluded from the analysis. Proof tests were repeated 10 times for each reporting group for both 45 and 96 SNP marker sets. These tests provided an indication of the power of the baseline for MSA, assuming that all populations were represented in the baseline.

Data Retrieval and Quality Control

Methods for data retrieval and quality control were reported in Barclay et al. (2010a). In that report, a threshold of 80% scorable markers per individual was established and all individuals that did not meet this threshold were excluded from MSA. This rule (referred to as the "80% rule") was used to filter samples with poor quality DNA and missing data from analyses to decrease errors and reduce estimate variances. We applied this same rule to the Yentna River fish wheel mixture individuals. Baseline development methods are reported in Barclay and Habicht (2012) and included tests for Hardy-Weinberg equilibrium and linkage disequilibrium, methods for combining or excluding linked markers, pooling collections into populations, testing for temporal stability, and visualizing population structure.

Mixed Stock Analysis and Abundance Estimation

Because fish wheel selectivity studies indicated that capture probabilities were sometimes length dependent, we tested whether fish wheel capture probabilities differed by length class, and then conducted separate abundance estimates for each length class, if necessary.

To evaluate length-dependent fish wheel capture probabilities, we first used MSA to estimate the stock composition of all Yentna River fish wheel mixtures by bank. We used the same BAYES protocol as reported in Barclay and Habicht (2012) for the baseline evaluation tests except for defining the informative Dirichlet priors. Informative Dirichlet priors were defined using a similar "step-wise" prior protocol as reported in Barclay et al. (2010a), except for the 2008 mixtures, where the prior was based upon the best approximation of stock composition of the sockeye salmon passing the Yentna River fish wheels (Judd, 0.2; Chelatna, 0.2; Yentna Other 0.6).

We assessed the within- and among-chain convergence of these estimates using the Raftery-Lewis (within-chain) and Gelman-Rubin (among-chain) shrink factor. These compare variation of estimates among iterations within a chain (Raftery and Lewis 1996) and within-chain variation to the total variation among chains (Gelman and Rubin 1992). If a shrink factor for any stock group estimate was greater than 1.2 and Raftery-Lewis estimate suggested a chain had not converged to stable estimates, then we reanalyzed the mixture with 80,000-iteration chains following the same protocol. If the chains still failed to converge, we did not report the estimates.

We then estimated fish wheel capture probabilities (p_2) as:

$$p_2 = \frac{m_1}{n_2}, \tag{6}$$

where m_1 were estimated numbers of sockeye salmon in 1 cm length classes captured in the fish wheels that were genetically identified as originating from Chelatna and Judd lakes combined, and n_2 were counts of salmon in the same length classes sampled at the 2 weirs combined. Following Clark (1991), we used maximally selected chi-square values to determine cut points for length strata. The split was made between length groups if the maximum chi-square was significant ($\alpha = 0.05$). Only 2 length strata were constructed to maintain the sample size within each stratum.

If chi-square tests indicated that length stratification was required, we then estimated the stock composition of Yentna River fish wheel mixtures within each bank and length class using the same BAYES protocol as described above. For the 2009 mixtures, the priors for both length class mixtures from each fish wheel were defined as the posterior means (i.e., the stock composition estimates) of the mixture from the same fish wheel from 2008. For the analysis of subsequent years, the priors were the posterior means of the same length class mixture from the same fish wheel from the previous year.

A stratified-Petersen estimator was used to estimate sockeye salmon abundance passing the Yentna sonar site (Schwarz and Taylor 1998). Stocks originated from Judd and Chelatna lakes were considered as genetic marks. Two fish wheels located on each river bank were the recovery sites. Fish moved to either bank and could be captured or recaptured (if marked) in the fish wheels. The likelihood is specified as being the product of 2 multinomial distributions with respect to Judd and Chelatna lake stocks. The cell probabilities are products of capture probabilities and movement probabilities. We applied a Bayesian approach to the parameter estimation, because the Bayesian procedure provided a convenient framework to include uncertainties of stock proportions estimated from genetic MSA. Having obtained the likelihood for the model, we needed the prior distributions for model parameters. To have minimal effect on the posteriors, we chose non-informative independent beta priors for capture probabilities and movement probabilities. Given stock compositions and their standard errors estimated from genetic MSA, we assumed stock compositions were normally distributed with their own estimates and standard errors. The Bayesian approach was implemented in Winbugs (Lunn et al. 2000). Markov Chain Monte Carlo (MCMC) samples were drawn from the posterior distribution with 15,000 simulations kept for each of 1,000 data sets. These samples were used to calculate the mean, variance, and 90% credibility intervals for the abundance estimates by bank and for both banks combined. We used the *Z-test* statistic (Springhall 2003) to test whether our genetic mark–recapture estimates of sockeye salmon abundance were significantly different between banks.

COMPARISON OF ADJUSTED-SONAR AND GENETIC MARK–RECAPTURE ESTIMATES

We also used the *Z-test* statistic to test whether our genetic mark–recapture and adjusted-sonar estimates (calculated using modelled tag–recapture probabilities) of sockeye salmon abundance were significantly different. These tests were initially conducted by river bank and then with both banks combined. Mark–recapture abundance estimates from radiotelemetry studies conducted in 2006 and 2007 (Yanusz et al. 2007, 2011a) were included in the analysis with both banks combined. Finally, we conducted linear regression analyses to examine the correlation between the estimates (2006–2012) and test whether the regression slope was different from 1.

RESULTS

FISH WHEEL SELECTIVITY

Sonar Adjustment Using Estimated Tag–recapture Probabilities

Tag–recapture probabilities were significantly different among species during all 4 years of the study (Table 1). Aggregate tag–recapture probabilities ranged from 0.009 for chum salmon in 2012 to 0.087 for pink salmon in 2009. With the exception of chum salmon in 2012, tag–recapture probabilities for sockeye salmon tended to be lower than for the other species and tag–recapture probabilities for pink salmon tended to be higher.

Tag–recapture probabilities were also significantly different among years for sockeye ($P < 0.0001$), pink ($P < 0.0001$) and chum ($P < 0.0001$) but not coho ($P = 0.4112$) salmon. When data were aggregated across all 4 years, the tag–recapture probability for coho salmon was 0.054.

Tag–recapture probabilities were significantly lower for larger salmon in 8 of 16 tests conducted (Table 2). In the remaining 8 tests, recapture probabilities were lower for larger salmon in all but 1 case (chum salmon in 2009).

Tag–recapture probabilities were significantly different between date periods (within length classes) in 14 of 24 tests conducted (Table 3). Four tests in 2009 and 2012 indicated a decline, and 10 tests in 2010–2012 indicated an increase in recapture probabilities during the season.

Fish wheel apportioned sonar estimates of sockeye salmon abundance corrected for fish wheel selectivity using estimated tag–recapture probabilities were 80,705 (90% CI: 78,496–82,950) in 2009; 125,137 (90% CI: 122,216–128,058) in 2010; 143,798 (90% CI: 141,413–146,241) in 2011; and 48,324 (90% CI: 43,361–52,024) in 2012.

Sonar Adjustment Using Modelled Tag–recapture Probabilities

Logistic regression analysis indicated that recapture probabilities for tagged sockeye salmon were significantly correlated ($P < 0.0001$) with fish length and water level (Table 4). The c-statistic was 0.630, and the H-L goodness-of-fit statistic indicated that model-predicted probabilities were not different ($P = 0.9517$) from observed probabilities (Table 5). Predicted probabilities declined with length from 0.06 at 32 cm to 0.01 at 67 cm and increased with water level from 0.02 at 4.7 m to 0.07 at 6.1 m (Figure 3). Predicted probabilities exhibited serial correlation with greater variability within years than among years (Figure 4).

Recapture probabilities for tagged coho salmon were only significantly correlated ($P = 0.0001$) with length (Table 4). The c-statistic was only 0.539 (Table 5), but the H-L statistic indicated that model-predicted and observed probabilities were not different ($P = 0.5597$). Predicted probabilities declined with length from 0.09 at 32 cm to 0.03 at 67 cm (Figure 3). Predicted probabilities exhibited little variability within or among years (Figure 4).

Recapture probabilities for tagged pink salmon were significantly correlated with length and salmon abundance with a significant interaction between water level and salmon abundance (Table 4). The c-statistic was 0.562 (Table 5), and the H-L statistic indicated that model predicted and observed probabilities were not different ($P = 0.3348$). Predicted probabilities declined with length from 0.10 at 32 cm to 0.04 at 57 cm, and they declined with salmon abundance from 0.09 at <10,000 salmon to 0.04 at 80,000 salmon (Figure 3). Predicted probabilities exhibited serial correlation with greater variability within years than among years (Figure 4).

An initial logistic regression analysis using the backward-selection procedure ($\alpha = 0.05$) indicated that recapture probabilities for tagged chum salmon were significantly correlated with length, water level and salmon abundance, but the H-L statistic indicated that model-predicted and observed probabilities were significantly different ($P = 0.0077$). When an interaction term between length and salmon abundance was included (Table 4), the H-L statistic indicated that model-predicted and observed probabilities were not different ($P = 0.1098$) and the c-statistic was 0.587 (Table 5). Predicted probabilities declined with length from 0.15 at 37 cm to 0.03 at 67 cm, declined with water level from 0.07 at 4.7 m to 0.05 at 6.1 m, and declined with salmon abundance from 0.06 at <10,000 salmon to 0.02 at 80,000 salmon (Figure 3). Predicted probabilities exhibited serial correlation with greater intra-annual variability in 2009 and 2012 (Figure 4).

Annual fish wheel apportioned sonar estimates (1986–2012) of sockeye salmon abundance derived using logistic regression estimates of recapture probabilities for each species averaged 1.4 times greater than sonar estimates (range: 0.64–2.38) that were not adjusted for fish wheel selectivity (Table 6). The mean absolute percent error on the fish wheel selectivity-adjusted sonar estimates was 27%.

GENETIC MARK–RECAPTURE ESTIMATES

Tissue Sampling

Tissues suitable for genetic analysis were sampled from a total of 353 (2008), 796 (2009), 1,045 (2010), 715 (2011), and 440 (2012) sockeye salmon from the Yentna River fish wheels. K-S tests indicated no differences ($\alpha = 0.05$) between the cumulative proportion of the number of genetic samples collected each day and the cumulative proportion of the daily CPUE in the fish wheels, indicating genetic samples were collected in proportion to CPUE in all years (Appendix A1).

Laboratory Failure Rates and Quality Control

All sampled fish were genotyped from the 2008–2012 Yentna fish wheel collections. Failure rates among collections ranged from 0.26% to 2.95%. Discrepancy rates were uniformly low and ranged from 0.03% to 0.68%. Assuming equal error rates in the original and the quality-control analyses, estimated error rates in the samples is half of the discrepancy rate (0.02–0.34%).

Baseline Evaluation for Mixed Stock Analysis

In the analysis of proof test mixtures, all repeated test mixtures assigned to their correct reporting group at greater than 95% correct allocation (Figure 5). Among all SNP markers, a total of 3 SNPs were found be invariant among Yentna River populations and were excluded from the analysis (Appendix A2). After excluding invariant markers, 6 SNPs were excluded from the 45 SNP marker set because they did not overlap with the 96 SNP marker set. One marker, *One_GPDH2-187*, which was included in both markers sets, was excluded from the analyses using the 96 SNP marker set because it was found to be linked with *One_GPDH-201* in the development of the 96 SNP baseline (Barclay and Habicht 2012). However, *One_GPDH2-187* was included in the 45 SNP maker set because it was not found to be linked during the development of the 45 SNP baseline (Habicht et al. 2007).

Data Retrieval and Quality Control

Data retrieval and quality control results for the baseline collections are reported in Barclay and Habicht (2012). Based upon the 80% scorable marker rule, 0.72% of samples were removed from the fish wheel collections before stock composition estimates were calculated. Based on the 95%-of-loci criterion for detecting duplicate individuals, 0.06% of samples were removed from collections.

Mixed Stock Analysis and Abundance Estimation

Fish wheel capture probabilities (p_2) were significantly lower for larger fish in 2009–2012 but not in 2008 (Table 7). The cut points for the length strata ranged from 49 cm to 56 cm in 2009–2012, and the capture probabilities for fish in the larger length strata averaged 0.50 less than in the smaller length strata. Length data from the weirs were used to estimate the proportion of the total escapement at Chelatna and Judd lakes in each length class (Table 7), and MSA estimated the proportions (and their standard deviations) of fish wheel catches on each bank and in each length class that were fish originating from Chelatna and Judd lakes (Table 8). These data and weir counts of sockeye salmon from Chelatna and Judd lakes (Table 7) were used as inputs to genetic mark–recapture analyses.

Darroch-model abundance estimates were calculated for each length stratum separately in 2009–2012 but not in 2008. Total sockeye salmon abundance estimates (over all lengths) were not significantly different between banks in 2009 and 2011–2012 ($P > 0.35$), but the south bank abundance was significantly lower ($P < 0.0001$) than the north bank estimate in 2010 (Table 9). Total sockeye salmon abundance estimates (over all lengths) were 233,677 (90% CI: 204,400–271,500) in 2008; 139,168 (CI: 123,160–158,340) in 2009; 151,774 (CI: 135,260–171,580) in 2010; 290,801 (CI: 253,500–334,400) in 2011; and 109,981 (CI: 95,290–129,080) in 2012 (Table 10). The absolute error on these abundance estimates ranged from 5.7% in 2009 to 15.4% in 2012.

COMPARISON OF ADJUSTED-SONAR AND GENETIC MARK–RECAPTURE ESTIMATES

We initially compared genetic mark–recapture and sonar estimates of sockeye salmon abundance adjusted for fish wheel selectivity by bank. Mark–recapture and adjusted-sonar abundance estimates were significantly different on the north bank in 2009–2011 and on the south bank in 2010 (Table 9). In all 3 cases, mark–recapture estimates were significantly greater than adjusted-sonar estimates on the north bank, averaging 4.4 times greater in these 3 years. In 2010, the mark–recapture estimate was about one third of the adjusted-sonar estimate on the south bank. The adjusted-sonar abundance estimates were significantly lower ($P < 0.05$) on the north bank compared to the south bank in all years.

We next compared genetic mark–recapture and adjusted-sonar estimates of sockeye salmon abundance with both banks combined, 2006–2012. Mark–recapture and adjusted-sonar estimates were not significantly different in 5 of 7 years; however, in 2011–2012 mark–recapture estimates were significantly greater than adjusted-sonar estimates of sockeye salmon abundance (Table 10). Regression analysis indicated that mark–recapture and adjusted-sonar abundance estimates were significantly correlated ($R^2 = 0.566$, $P = 0.051$), but the 2011 estimate was clearly an outlier (Figure 6a). When 2011 data were omitted from the analysis (Figure 6b), the correlation increased considerably ($R^2 = 0.997$, $P < 0.0001$), and the slope of the regression was not different from 1 ($P = 0.557$), but the intercept was significantly greater than 0 ($P = 0.001$). The historic time series of mark–recapture and adjusted-sonar estimates of sockeye salmon abundance at the Yentna sonar site exhibited a declining trend beginning in 2007 (Figure 7).

DISCUSSION

Tag–recapture probabilities aggregated across all 4 years of this study were highest for pink salmon (0.070), lowest for sockeye salmon (0.030), and intermediate for coho (0.054) and chum salmon (0.049); but for each species there were significant differences across years, within years, and between length classes (Tables 1–3). Logistic regression analyses indicated that changes in recapture probabilities likely resulted from changes in the length distributions of the 4 salmon species, water level and total salmon abundance. However, other factors not measured in this study probably also affected fish wheel selectivity.

For example, the significant effect of water level on tag–recapture probabilities in our regression analysis likely resulted from physical changes in water level and current speed but also from unknown variations in the fish wheel and weir configuration. Water level changes at the Yentna sonar site require that fish wheels be moved to keep the fish wheel baskets sweeping near the bottom. Each time the fish wheels are moved, the crew reinstalls the fish wheel and weir that directs fish into the fish wheel basket. However, due to slight changes in bottom slope and current patterns, it is not possible to duplicate the way the fish wheel interacts with salmon each time the wheels are moved.

The behavioral responses of each salmon species that caused the observed relationships between recapture probabilities and the 3 independent variables in our logistic regression analyses were not always clear. The effect of salmon length on recapture probability was expected because gill netting offshore at the Yentna sonar site has shown that larger salmon are captured offshore of the fish wheels (Westerman and Willette 2012). Thus, the selectivity of the fish wheels for smaller salmon likely resulted in part because larger salmon are migrating offshore of the fish wheels. Our higher overall recapture probability for pink salmon (0.070) compared to sockeye salmon (0.030) was consistent with Xie's et al. (1997) conclusion that sockeye salmon migrated further from shore than pink salmon in the Fraser River. However, we also found the smallest differences in recapture probabilities among species and the lowest recapture probabilities overall among larger fish (Figure 3a), suggesting that larger salmon migrate further from shore regardless of species. Our results may also be explained in part if larger salmon are better able to escape from the fish wheel basket when it is encountered. We attempted to use DIDSON to observe how salmon interact with the fish wheel basket when it is encountered, but the images were obscured by bubbles and turbulence created by the moving basket.

Our study demonstrated that fish wheel selectivity is very dynamic and complex. Daily estimates of the proportion of sockeye salmon in the sonar beam (Equation 4) are affected by changing species composition and how the species-specific selectivity of the fish wheels are affected by the length distribution of each species, and the differing effects of water level and total salmon abundance on the selectivity for each species (Table 4). These interacting effects cause recapture probabilities for each species to change daily (Figure 4), deviating by a factor of 2–3 times the aggregate mean for each species.

Our tag–recapture probabilities may have been biased high, because we used a fish wheel to capture fish for tagging. In 2010, we operated a DIDSON sonar for a few hours immediately below the Flathorn fish wheel used to capture fish for tagging. The sonar data indicated that some salmon were migrating offshore beyond the fish wheel. We attempted to deploy a floating weir to direct these fish into the fish wheel, but this effort was unsuccessful due to the strong current in the area. We recognized that we could improve our study design if we obtained a more representative sample of all salmon migrating into the Yentna River, but other capture methods (gillnets, seines, etc.) would have created unknown handling effects and were too labor intensive. This source of bias may not have severely affected our estimates of the proportion of sockeye salmon in the sonar beam (Equation 4), because these estimates are affected by the relative differences in recapture probabilities among species rather than the absolute value of the probabilities.

Our logistic regression equations and predicted recapture probabilities may be used to adjust for fish wheel selectivity in the future. The most accurate predicted recapture probabilities will probably be obtained in the future if the location and configuration of the fish wheels and weirs are not changed, water levels are measured inseason and salmon lengths are measured for all species. However, even if these actions are taken, the accuracy of predicted recapture probabilities obtained from our regression equations will likely decline over time as the river channel and flow patterns change.

Comparisons between our genetic mark–recapture and adjusted-sonar estimates of sockeye salmon abundance indicated that the adjusted-sonar estimates averaged 26% lower than the mark–recapture estimates (Table 10). It appeared that consistently lower adjusted-sonar estimates on the north bank probably accounted in part for the lower overall adjusted-sonar estimates (Table 9). Adjusted-sonar estimates on the north bank were significantly lower than on the south bank in all years ($P < 0.0001$), but mark–recapture estimates were not significantly different ($P > 0.35$) between banks except in 2010. It is likely that fish wheel selectivity differed between banks. However, our study design did not allow for estimation of fish wheel selectivity for each bank separately, because we did not estimate the number of tagged salmon of each species migrating along each bank. A study design using acoustic tags could estimate the fraction of all tagged salmon within each species migrating along each bank, but the cost would be very high and results may be unclear due to complexity in migration behaviors. Higher proportional catches of pink salmon on the north bank compared to the south bank (Westerman and Willette 2012) have suggested that this fish wheel selected more for pink salmon than the south-bank fish wheel. Nevertheless, the high correlation (Figure 6b) between our genetic mark–recapture and adjusted-sonar abundance estimates (excluding the 2011 outlier) suggested that our correction for fish wheel selectivity with both fish wheels pooled was adequate for this application.

Differences between our genetic mark–recapture and adjusted-sonar estimates may have also resulted from bias in the mark–recapture estimates. Sources of bias in the mark–recapture estimates included: (1) genetic misclassification in MSA, (2) not collecting genetic-tissue samples in proportion to abundance over time at the Yentna sonar site, and (3) interactions between fish wheel size selectivity and the size distributions of the ‘Chelatna’, ‘Judd’ and ‘Yentna Other’ stocks. We evaluated genetic-misclassification errors using proof tests, and all repeated test mixtures assigned to their correct reporting group at greater than 95% correct allocation (Figure 5), so genetic misclassification likely was not a major source of error in our abundance estimates. We evaluated whether genetic-tissue samples were collected in proportion to abundance over time using K-S tests, and there were no differences ($\alpha = 0.05$) between the cumulative proportion of the number of genetic samples collected each day and the cumulative proportion of daily CPUE in the fish wheels (Appendix A1). Although the K-S tests indicated that genetic samples were collected in proportion to CPUE, a bias could have been introduced if fish wheel catchability for sockeye salmon changed over time. Because tag–recapture probabilities for sockeye salmon changed over time (Table 3), this source of error may have introduced an unknown bias into our mark–recapture abundance estimates. Finally, we attempted to correct for the fish wheel size selectivity by testing for size-dependent fish wheel capture probabilities and then stratifying our abundance estimates by length when necessary (2009–2012). In future years, we will also collect genetic tissues samples using gillnets fished offshore of the fish wheels. Comparison of size-stratified genetic mark–recapture estimates calculated using samples collected with different gear types will be used to evaluate whether size stratification adequately corrects for the size selectivity of different gears.

It is possible that the 2011 mark–recapture abundance estimate was biased, but it was consistent with other estimates of Susitna sockeye salmon abundance. The genetic estimate of the 2011 commercial harvest of Susitna sockeye salmon was the second highest since genetic sampling began in 2006 (Table 11). This was consistent with the 2011 mark–recapture abundance estimate, which was the third highest since 2006. Furthermore, regression analysis indicated a strong relationship ($R^2 = 0.941$, $P < 0.001$) between drift-gillnet effort (boat-hours) in July and drift-gillnet harvest rate (total annual drift-gillnet harvest/total run) for Susitna sockeye salmon (Figure 8). Using the 2011 adjusted-sonar estimate of sockeye salmon abundance, the harvest rate was much higher than the regression analysis would predict based upon data collected in the other 6 years.

It appeared that the 2011 data was an outlier in the relationship between genetic mark–recapture and adjusted-sonar abundance estimates (Figure 6a), because the 2011 adjusted-sonar estimate was biased low. In 2011, the aggregate sockeye salmon weir count at Judd and Chelatna lakes was 110,350, while the adjusted-sonar estimate was only 114,652. If the sonar estimate were accurate, the data indicate that 96% of the Yentna sockeye salmon run migrated to Judd and Chelatna lakes. Two years of radiotelemetry studies (2007–2008) showed that approximately 52% of the sockeye salmon in the Yentna drainage migrate to small lake, tributary, and slough spawning habitats (Yanusz et al. 2011a, 2011b). Our genetic mark–recapture estimates (2008–2012) were consistent with these data. If the 2011 adjusted-sonar estimate were accurate, only 4% of the Yentna sockeye salmon run would have spawned in these small lake, tributary, and slough habitats. Because these stocks are composed of more than 4 age classes, it is nearly impossible that this happened in 2011 but not 2010 and 2012.

It appears that the low 2011 adjusted-sonar estimate was due to a low total sonar estimate (all species) of only 341,886 rather than problems with fish wheel selectivity. If both the mark–recapture sockeye salmon estimate (290,801) and total sonar estimate (all species) were accurate, the data indicate that 85% of the total salmon run was composed of sockeye salmon. However, sockeye salmon made up only 14% of the total fish wheel catch of 40,870 salmon in 2011. It is very unlikely that this disparity can be explained by fish wheel selectivity, and we have never seen this high of a proportion of sockeye salmon (i.e., 85%) in the total annual Yentna fish wheel catch (Westerman and Willette 2012).

It is not clear why the 2011 Yentna total sonar estimate was biased low. In 2011, there was a 4-day period of very high water from August 3 to August 6 (Westerman and Willette 2012), during which the total sonar estimate dropped considerably on the south bank and north bank sonar operations were discontinued (August 4–6). The difference between the mark–recapture and adjusted-sonar estimates was 176,000 sockeye salmon in 2011. It seems unlikely that this number of sockeye salmon could have passed the sonars undetected during this short period. Maxwell et al. (2013) estimated that the actual 2011 total salmon passage at the Yentna sonar site was about 1.4 times greater than the total sonar estimate due to fish swimming beyond and above the sonar beams. However, this adjustment is not sufficient to account for the disparity between our mark–recapture and adjusted-sonar estimates (factor 2.5). The most likely explanation for the bias in the 2011 adjusted-sonar estimate is a combination of under-counting as described by Maxwell et al. (2013) throughout the season and perhaps more severe under-counting during the high-water period in early August. Westerman and Willette (2007a, 2007b) found that Yentna total sonar estimates declined and fish wheel CPUE increased during periods of high water. It appears that salmon migrate closer to shore during high-water events, because current velocities are lower nearshore. This behavior may result in more fish passing above the sonar beam near the transducer where the beam is very narrow.

When the 2011 data were omitted, the correlation between our sockeye salmon mark–recapture and adjusted-sonar abundance estimates (Figure 6b) was very high ($R^2 = 0.997$, $P < 0.001$), indicating that adjusted historical sonar estimates (Figure 7) may be sufficiently accurate for escapement goal analyses. However, we do not know if total DIDSON-adjusted sonar estimates in some earlier years were biased as in 2011. Total sonar abundance estimates were more likely to be biased in years when water levels were high. Also, our predicted recapture probabilities (Table 4) may not accurately adjust for fish wheel selectivity in earlier years, because fish wheel configurations may have been different than during the years of our study, river channel and flow patterns may have changed, and salmon length data were not available for all species prior to 2009. For example, after 1997 a weir was installed on the inside of the fish wheel floats to direct salmon into the area where the baskets sweep near the bottom. This modification clearly increased total fish wheel catch, but we do not know if it also somehow affected fish wheel selectivity. Finally, the historic ranges of daily DIDSON abundances and water levels were greater than those available for our regression analyses. The range of DIDSON abundances were 0–80,000 (2009–2012) and 0–220,000 (1986–2008), and the range of water levels were 4.6–6.2 m (2009–2012) and 4.0–7.7 m (1986–2008).

In future years, we will compare our historical adjusted-sonar sockeye salmon abundance estimates (Table 6) to estimates obtained from a run reconstruction model. Genetic stock identification methods will be applied to archived scales to estimate the historical commercial harvest of Susitna sockeye salmon. Estimates of the drift gillnet harvest of Susitna sockeye salmon and a harvest-rate model (Figure 8) will be used to estimate the total Susitna sockeye salmon run and escapement. Comparisons between these estimates and those obtained in the present study will be used to further evaluate whether our historical sockeye salmon escapement estimates are sufficiently accurate for escapement goal analyses.

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TABLES AND FIGURES

Table 1.–Results of chi-square tests for differences in tag–recapture probabilities (Pc_x) among species, 2009–2012.

									Chi-Square
Year	Species	N_x	Rt_x	Ryt_x	Py_x	n_1	m_2	Pc_x	*P*-value
2009	Sockeye	1,845	100	96	0.960	1,771	73	0.041	<0.0001
	Coho	2,766	95	75	0.789	2,184	130	0.060	
	Pink	10,957	100	95	0.950	10,409	906	0.087	
	Chum	735	92	75	0.815	599	33	0.055	
2010	Sockeye	6,593	99	99	1.000	6,593	247	0.037	0.0441
	Coho	3,080	94	81	0.862	2,654	138	0.052	
	Pink	4,063	100	92	0.920	3,738	259	0.069	
	Chum	3,205	98	75	0.765	2,453	119	0.049	
2011	Sockeye	5,823	100	90	0.900	5,241	108	0.021	<0.0001
	Coho	4,295	83	72	0.867	3,726	207	0.056	
	Pink	3,261	100	83	0.830	2,707	210	0.078	
	Chum	5,608	87	61	0.701	3,932	328	0.083	
2012	Sockeye	4,333	100	92	0.920	3,986	86	0.022	<0.0001
	Coho	3,569	97	79	0.814	2,907	142	0.049	
	Pink	9,237	101	86	0.851	7,865	372	0.047	
	Chum	559	89	73	0.820	459	4	0.009	

Note: N_x is the number of dart-tagged salmon released from Fish Wheel #1 at Flathorn. Rt_x is the total number of radiotagged salmon of each species released from Fish Wheel #1 at Flathorn. Ryt_x is the number of radiotagged salmon of each species later relocated above the Yentna sonar site. Py_x is the estimated fraction of dart-tagged salmon of each species that migrated upstream past the Yentna sonar site. n_1 is the number of dart-tagged salmon released at Flathorn corrected for the proportion of radiotagged salmon that did not migrate past the Yentna sonar site. *m2* is the number of dart-tagged salmon recaptured in both Yentna sonar site fish wheels combined. Pc_x is the tag–recapture probability corrected for the fraction of dart-tagged salmon that did not migrate past the Yentna sonar site.

Table 2.–Results of chi-square tests for differences in tag–recapture probabilities (Pc_x) among length classes within species, 2009–2012.

Year	Species	Length class (cm)	n_1	m_2	Pc_x	Chi-square *P*-value
2009	Sockeye	30–47	683	32	0.047	0.3422
		48–62	1,088	41	0.038	
	Coho	32–51	1,108	79	0.071	0.0182
		52–63	1,076	51	0.047	
	Pink	31–40	2,617	244	0.093	0.1944
		41–58	7,792	662	0.085	
	Chum	39–56	372	18	0.048	0.3524
		57–65	227	15	0.066	
2010	Sockeye	31–43	1,377	69	0.050	0.0055
		44–63	5,216	178	0.034	
	Coho	35–54	1,488	89	0.060	0.0410
		55–66	1,166	49	0.042	
	Pink	34–44	1,167	95	0.081	0.0489
		45–59	2,571	164	0.064	
	Chum	36–54	1,030	60	0.058	0.0563
		55–68	1,423	59	0.041	
2011	Sockeye	31–50	1,009	37	0.037	<0.0001
		51–66	4,232	71	0.017	
	Coho	34–47	1,438	103	0.072	0.0007
		48–62	2,288	104	0.045	
	Pink	31–42	1,809	148	0.082	0.2456
		43–60	898	62	0.069	
	Chum	35–56	3,063	268	0.088	0.0823
		57–65	869	60	0.069	
2012	Sockeye	36–52	1,194	40	0.033	0.0007
		53–66	2,792	46	0.016	
	Coho	35–47	982	55	0.056	0.2025
		48–66	1,925	87	0.045	
	Pink	35–49	7,422	360	0.049	0.0396
		50–60	443	12	0.027	
	Chum	44–59	219	3	0.014	0.2734
		60–69	240	1	0.004	

Note: N_x is the number of dart-tagged salmon released from Fish Wheel #1 at Flathorn. Rt_x is the total number of radiotagged salmon of each species released from Fish Wheel #1 at Flathorn. Ryt_x is the number of radiotagged salmon of each species later relocated above the Yentna sonar site. Py_x is the estimated fraction of dart-tagged salmon of each species that migrated upstream past the Yentna sonar site. n_1 is the number of dart-tagged salmon released at Flathorn corrected for the proportion of radiotagged salmon that did not migrate past the Yentna sonar site. *m2* is the number of dart-tagged salmon recaptured in both Yentna sonar site fish wheels combined. Pc_x is the tag–recapture probability corrected for the fraction of dart-tagged salmon that did not migrate past the Yentna sonar site.

Table 3.–Results of chi-square tests for differences in tag–recapture probabilities (Pc_x) among date periods within length classes and species, 2009–2012.

Year	Species	Length class	Date period	n_1	m_2	Pc_x	Chi-square P-value
2009	Sockeye	30–62	7/14–7/26	730	23	0.032	0.0860
			7/27–8/07	1,041	50	0.048	
	Coho	32–51	7/15–8/03	686	42	0.061	0.0957
			8/04–8/07	422	37	0.088	
		52–63	7/14–7/30	324	23	0.071	0.0172
			7/31–8/07	752	28	0.037	
	Pink	31–58	7/14–8/01	7,847	742	0.095	<0.0001
			8/02–8/07	2,562	164	0.064	
	Chum	39–65	7/15–8/04	289	12	0.042	0.1628
			8/05–8/07	310	21	0.068	
2010	Sockeye	31–43	7/06–7/29	949	35	0.037	0.0008
			7/30–8/11	428	34	0.079	
		44–63	7/06–7/24	2,754	54	0.020	<0.0001
			7/25–8/11	2,462	124	0.050	
	Coho	35–54	7/06–7/18	510	18	0.035	0.0040
			7/19–8/11	978	71	0.073	
		55–66	7/06–7/22	422	13	0.031	0.1530
			7/23–8/11	744	36	0.048	
	Pink	34–44	7/13–7/21	259	16	0.062	0.1868
			7/22–8/11	908	79	0.087	
		45–59	7/11–7/19	442	16	0.036	0.0092
			7/20–8/10	2,129	148	0.070	
	Chum	36–68	7/07–7/31	1,447	48	0.033	<0.0001
			8/01–8/11	1,006	71	0.071	
2011	Sockeye	31–50	7/07–7/29	728	21	0.029	0.0333
			7/30–8/11	281	16	0.057	
		51–66	7/06–7/30	3,588	45	0.013	<0.0001
			7/31–8/11	644	26	0.040	
	Coho	34–47	7/09–7/24	401	35	0.087	0.1480
			7/25–8/11	1,037	68	0.066	
		48–62	7/10–7/27	863	31	0.036	0.0886
			7/28–8/11	1,425	73	0.051	
	Pink	31–60	7/06–8/02	2,341	172	0.073	0.0423
			8/03–8/11	366	38	0.104	
	Chum	35–65	7/11–7/29	1,310	71	0.054	<0.0001
			7/30–8/11	2,622	257	0.098	

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Table 3.–Page 2 of 2.

Year	Species	Length class	Date period	n_1	m_2	Pc_x	Chi-square *P*-value
2012	Sockeye	36–52	7/06–7/30	1,045	32	0.031	0.1437
			7/31–8/14	149	8	0.054	
		53–66	7/06–7/18	1,619	31	0.019	0.1929
			7/19–8/14	1,173	15	0.013	
	Coho	35–66	7/08–7/30	1,960	83	0.042	0.0197
			7/31–8/14	947	59	0.062	
	Pink	35–49	7/10–7/25	2,857	165	0.058	0.0034
			7/26–8/14	4,565	195	0.043	
		50–60	7/15–7/25	148	9	0.061	0.0020
			7/26–8/13	295	3	0.010	
	Chum	44–69	7/12–7/27	243	4	0.016	0.1260
			7/28–8/14	216	0	0.000	

Note: N_x is the number of dart-tagged salmon released from Fish Wheel #1 at Flathorn. Rt_x is the total number of radiotagged salmon of each species released from Fish Wheel #1 at Flathorn. Ryt_x is the number of radiotagged salmon of each species later relocated above the Yentna sonar site. Py_x is the estimated fraction of dart-tagged salmon of each species that migrated upstream past the Yentna sonar site. n_1 is the number of dart-tagged salmon released at Flathorn corrected for the proportion of radiotagged salmon that did not migrate past the Yentna sonar site. *m2* is the number of dart-tagged salmon recaptured in both Yentna sonar site fish wheels combined. Pc_x is the tag–recapture probability corrected for the fraction of dart-tagged salmon that did not migrate past the Yentna sonar site.

Table 4.–Parameters estimated from logistic-regression models with tag–recapture probabilities as the dependent variable for sockeye, coho, pink, and chum salmon.

Species	Independent variable	Estimate	Standard error	*P*-value
Sockeye	Intercept	-7.2448	0.8261	<0.0001
	Length	-0.0318	0.0081	<0.0001
	Water Level	1.0219	0.1246	<0.0001
Coho	Intercept	-1.4201	0.3843	0.0002
	Length	-0.0298	0.0078	0.0001
Pink	Intercept	0.3206	0.8005	0.6906
	Length	-0.0414	0.0078	<0.0001
	Water Level	-0.1663	0.1480	0.2613
	DIDSON	-0.8115	0.3355	0.0156
	DIDSON x Water Level	0.1385	0.0649	0.0328
Chum	Intercept	5.1063	1.3858	0.0002
	Length	-0.0918	0.0205	<0.0001
	Water Level	-0.4895	0.1256	<0.0001
	DIDSON	-1.3422	0.6380	0.0354
	DIDSON x Length	0.0211	0.0115	0.0672

Table 5.–Hosmer and Lemeshow (H-L) goodness-of-fit and concordance statistics for logistic-regression models with tag–recapture probabilities as the dependent variable for sockeye, coho, pink, and chum salmon.

Species	Percent concordant	Percent discordant	Tied	*c*-statistic	H-L Test Chi-square	df	*P*-value
Sockeye	60.1	34.0	5.8	0.630	2.70	8	0.9517
Coho	41.3	33.5	25.2	0.539	2.60	3	0.5597
Pink	53.2	40.8	6.0	0.562	9.09	8	0.3348
Chum	55.7	38.4	5.9	0.587	11.73	7	0.1098

Table 6.–Fish wheel apportioned sonar estimates (1986–2012) of sockeye salmon abundance adjusted for fish wheel selectivity using logistic-regression estimates of tag–recapture probabilities for each species, 1986–2012.

Year	Adjusted sonar	90% Confidence interval Lower	Upper	Absolute % error	Standard sonar	Ratio
1986	249,421	75,680	483,379	0.82	157,300	1.59
1987	166,050	131,197	200,476	0.21	120,572	1.38
1988	128,018	86,176	174,370	0.34	94,120	1.36
1989	265,109	199,744	331,641	0.25	176,056	1.51
1990	279,805	187,456	377,371	0.34	239,586	1.17
1991	275,366	234,139	316,247	0.15	200,852	1.37
1992	236,259	160,158	320,765	0.33	121,027	1.95
1993	295,442	214,383	376,598	0.27	261,982	1.13
1994	273,436	225,985	318,168	0.17	234,034	1.17
1995	323,810	256,347	389,441	0.20	215,121	1.51
1996	192,855	145,364	235,881	0.23	161,898	1.19
1997	312,208	286,999	333,375	0.07	286,929	1.09
1998	130,325	88,682	175,328	0.33	203,902	0.64
1999	228,073	198,596	255,516	0.13	177,796	1.28
2000	302,083	240,780	364,077	0.20	275,309	1.10
2001	175,383	121,233	235,284	0.33	146,301	1.20
2002	218,994	148,808	298,596	0.34	152,841	1.43
2003	282,785	203,560	363,923	0.29	325,479	0.87
2004	216,296	158,063	278,112	0.28	131,384	1.65
2005	133,789	112,310	156,094	0.16	66,482	2.01
2006	279,316	200,467	364,101	0.30	171,559	1.63
2007	199,868	171,980	226,785	0.14	145,430	1.37
2008	200,132	161,865	238,660	0.19	162,267	1.23
2009	108,295	74,442	148,864	0.34	45,484	2.38
2010	118,263	91,472	146,738	0.23	88,333	1.34
2011	114,652	86,790	142,026	0.24	80,964	1.42
2012	69,704	45,763	101,692	0.40	35,363	1.97
MAPE				0.27		1.40

Note: MAPE is the mean absolute percent error.

Table 7.–Size-dependent capture probabilities (*p2*) for sockeye salmon captured in fish wheels at the Yentna sonar site, the proportion of total sockeye salmon escapement at Judd and Chelatna lakes within each length stratum, and the total sockeye salmon escapement at Judd and Chelatna lakes, 2008–2012.

	Length (cm)				Chi-square	Escapement proportion		Standard deviation		Escapement	
Year	strata	n_1	m_2	p_2	P-value	Judd	Chelatna	Judd	Chelatna	Judd	Chelatna
2008	29–55	534	82	0.1536	0.2361	0.2859	0.5415	0.0183	0.0193	54,304	73,469
	56–68	741	94	0.1269		0.7141	0.4585				
2009	31–51	256	134	0.5234	<0.0001	0.2128	0.1506	0.0105	0.0115	43,153	17,865
	52–64	945	182	0.1926		0.7872	0.8494				
2010	29–49	435	107	0.2460	<0.0001	0.0485	0.3060	0.0059	0.0133	18,361	37,784
	50–65	2,114	258	0.1220		0.9515	0.6940				
2011	29–56	623	145	0.2327	<0.0001	0.4318	0.3705	0.0156	0.0216	39,997	70,353
	57–65	891	117	0.1313		0.5682	0.6295				
2012	29–51	161	47	0.2919	0.0041	0.1061	0.1958	0.0131	0.0174	18,303	36,577
	52–66	916	157	0.1714		0.8939	0.8042				

Table 8.–Genetic stock proportions for Judd and Chelatna lake sockeye salmon captured in fish wheels on each bank at the Yentna sonar site, 2008–2012.

		Genetic stock proportions						Standard deviation			
	Length (cm)	South Bank			North Bank			South Bank		North Bank	
Year	strata	*n*	Judd	Chelatna	*n*	Judd	Chelatna	Judd	Chelatna	Judd	Chelatna
2008	29–68	263	0.3119	0.2520	82	0.1392	0.3824	0.0302	0.0254	0.0407	0.0541
2009	31–51	249	0.3767	0.0041	164	0.2430	0.0925	0.0403	0.0068	0.0359	0.0242
	52–64	181	0.4009	0.0971	181	0.1854	0.2269	0.0370	0.0213	0.0353	0.0371
2010	29–49	158	0.1190	0.0838	339	0.0260	0.1792	0.0270	0.0224	0.0096	0.0213
	50–65	263	0.4113	0.0899	276	0.0785	0.3882	0.0317	0.0181	0.0167	0.0296
2011	29–56	161	0.2309	0.1840	218	0.0666	0.2889	0.0341	0.0309	0.0182	0.0311
	57–65	147	0.1680	0.2314	179	0.0463	0.2848	0.0320	0.0348	0.0172	0.0337
2012	29–51	50	0.1029	0.1807	114	0.0103	0.2703	0.0430	0.0536	0.0098	0.0420
	52–66	85	0.2796	0.3048	185	0.1007	0.4830	0.0492	0.0495	0.0235	0.0369

Table 9.–Bank-specific comparisons of genetic mark–recapture and sonar estimates of sockeye salmon abundance adjusted for fish wheel selectivity using logistic regression estimates of tag–recapture probabilities for each species at the Yentna sonar site, 2008–2012.

		M-R		90% Credibility interval		Absolute	Adjusted sonar		90% Confidence Interval		Absolute	*Z-test*	
Year	Bank	estimate	Var(n)	Lower	Upper	% error	estimate	Var(n)	Lower	Upper	% error	*P*-value	Ratio
2008	South	115,117	2.28E+09	29,760	191,900	0.704	164,559	3.36E+08	134,074	194,522	0.184	0.327	0.70
	North	118,567	2.92E+09	42,480	219,000	0.744	35,574	3.58E+07	26,154	45,860	0.277	0.125	3.33
2009	South	74,909	2.96E+08	47,310	103,260	0.373	88,544	3.35E+08	61,372	120,468	0.334	0.576	0.85
	North	64,265	4.26E+08	34,605	100,660	0.514	19,750	3.71E+07	11,317	30,885	0.495	0.038	3.25
2010	South	32,944	1.09E+08	22,289	43,802	0.327	95,810	1.83E+08	73,929	118,778	0.234	0.000	0.34
	North	118,838	2.36E+08	97,950	143,320	0.191	22,454	1.51E+07	16,501	29,222	0.283	0.000	5.29
2011	South	172,575	1.91E+09	104,970	247,430	0.413	89,171	1.54E+08	67,799	108,911	0.231	0.065	1.94
	North	118,241	2.13E+09	49,410	198,900	0.632	25,481	2.54E+07	17,474	34,158	0.327	0.045	4.64
2012	South	63,611	4.00E+08	35,280	99,560	0.505	50,185	2.15E+08	29,940	77,527	0.474	0.576	1.27
	North	46,380	2.88E+08	18,818	74,660	0.602	19,520	9.08E+06	15,000	24,840	0.252	0.117	2.38

Note: *Z*-test statistics indicate tests for differences between genetic mark–recapture and adjusted-sonar abundance estimates. The ratio of the mark–recapture and the adjusted-sonar estimates is indicated for comparison.

Table 10.–Comparisons of genetic mark–recapture and sonar estimates of total sockeye salmon abundance adjusted for fish wheel selectivity using logistic regression estimates of recapture probabilities for each species at the Yentna sonar site, 2008–2012.

	M-R		90% Credibility interval		Absolute	Adjusted sonar		90% Confidence interval		Absolute	*Z-test*	
Year	estimate	Var(n)	Lower	Upper	% error	estimate	Var(n)	Lower	Upper	% error	*P*-value	Ratio
2006	311,197	1.3E+09	251,568	391,264	0.224	279,316	2.5E+09	200,467	364,101	0.293	0.591	0.90
2007	239,849	3.0E+08	205,955	273,743	0.109	199,868	2.8E+08	171,980	226,785	0.137	0.094	0.83
2008	233,677	4.5E+08	204,400	271,500	0.144	200,132	5.4E+08	161,865	238,660	0.192	0.283	0.86
2009	139,168	1.2E+08	123,160	158,340	0.057	108,295	5.2E+08	74,442	148,864	0.344	0.218	0.78
2010	151,774	1.3E+08	135,260	171,580	0.120	118,263	2.8E+08	91,472	146,738	0.234	0.096	0.78
2011	290,801	6.2E+08	253,500	334,400	0.139	114,652	2.8E+08	86,790	142,026	0.241	0.000	0.39
2012	109,981	1.1E+08	95,290	129,080	0.154	69,704	3.0E+08	45,763	101,692	0.401	0.046	0.63
Mean					0.135					0.263		0.74

Note: Mark–recapture estimates of sockeye salmon abundance based upon radiotelemetry studies in 2006–2007 (Yanusz 2007, 2011a) are included for comparison. *Z*-test statistics indicate tests for differences between genetic mark–recapture and adjusted-sonar abundance estimates. The ratio of the mark–recapture and the adjusted-sonar estimates is indicated for comparison.

Table 11.–Total Susitna sockeye salmon run sizes estimated using genetic estimates of Susitna sockeye salmon commercial harvests, 2006–2012, and estimated Susitna sockeye salmon drift-gillnet harvests and drift gillnet harvest rates, 2006–2012.

	Inriver abundance estimates								
Year	Yentna	Susitna	Total	Commercial harvest[a]	Sport harvest[b]	Total run	Drift gillnet harvest[a]	Drift gillnet[c]	Drift gillnet harvest rate
2006	311,197 [d]	107,000 [d]	418,197	43,888	2,308	464,393	37,306	10,296	0.08
2007	239,849 [d]	87,883 [d]	327,732	238,952	4,921	571,605	183,403	36,840	0.32
2008	233,677 [e]	70,772 [d]	304,449	135,751	4,689	444,889	97,233	24,144	0.22
2009	139,168 [e]	79,873 [f]	219,041	102,661	9,783	331,485	84,675	28,344	0.26
2010	151,744 [e]	38,716 [f]	190,460	114,083	3,873	308,416	93,568	31,884	0.30
2011	290,801 [e]	23,646 [f]	314,447	216,669	6,395	537,511	182,343	37,356	0.34
2011	114,652 [g]	23,646 [f]	138,298	216,669	6,395	361,362	182,343	37,356	0.50
2012	109,981 [e]	31,823 [f]	141,804	179,221	5,203	326,228	170,360	45,828	0.52

Note: Susitna sockeye salmon run sizes and drift-gillnet harvest rates in 2011 were calculated using genetic mark–recapture and adjusted-sonar estimates of sockeye salmon abundance passing the Yentna sonar site for comparison.

[a] Barclay et al. 2010a, 2010b, 2013, 2014.

[b] Alaska Sport Fishing Survey database. Available from: http://www.adfg.alaska.gov/sf/sportfishingsurvey/.

[c] Shields 2007a, 2007b, 2009, 2010a, 2010b; Shields and Dupuis 2012, 2013.

[d] Yanusz et al. 2011a, 2011b.

[e] Genetic mark–recapture estimate of sockeye salmon passage at the Yentna sonar site.

[f] Larson Lake sockeye salmon weir count expanded using Susitna mainstem mark–recapture estimates (Yanusz et al. 2011a, 2011b).

[g] Adjusted-sonar estimate of sockeye salmon passage at the Yentna sonar site.

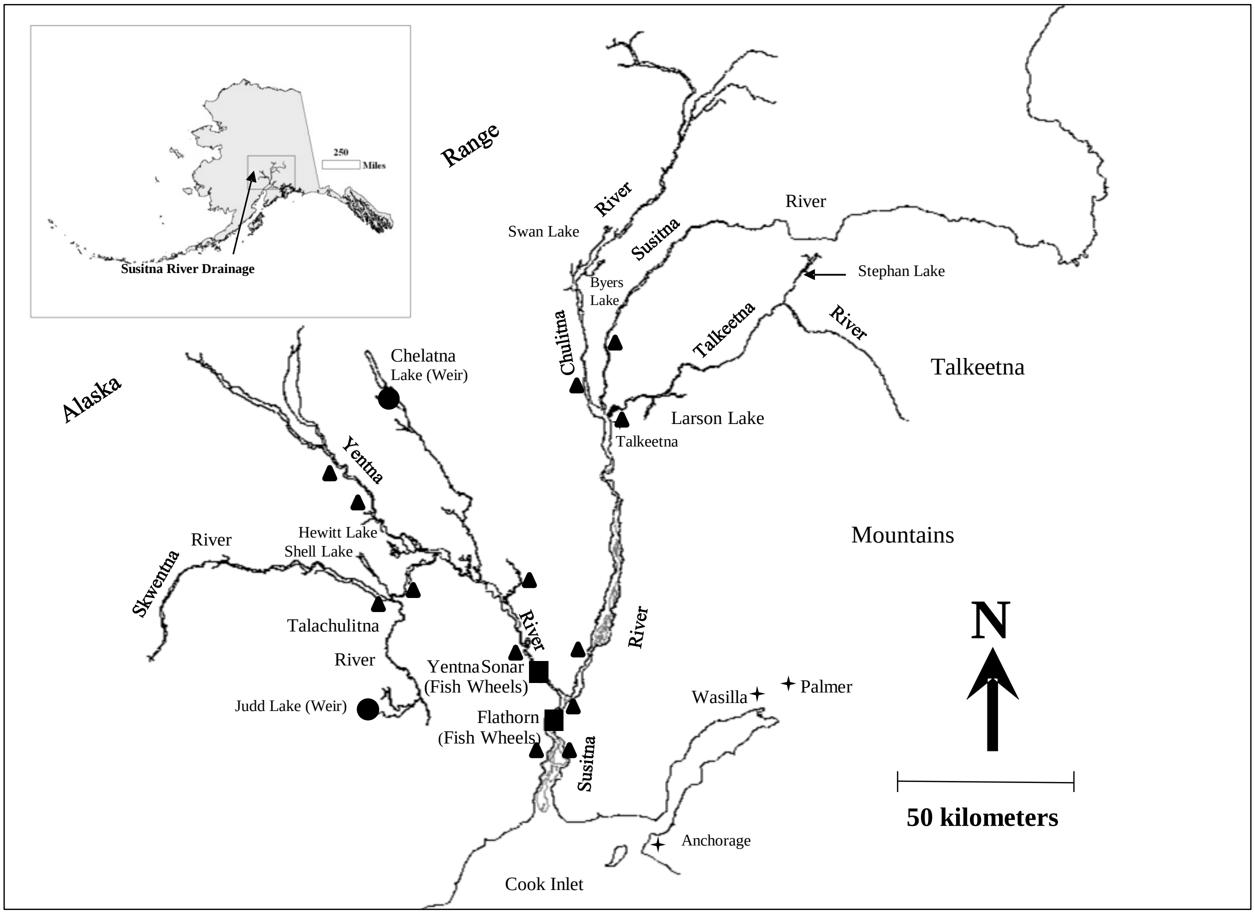


Figure 1.–Locations of Flathorn tagging site (solid square), the sonar site on the lower Yentna River (solid square), Judd and Chelatna lake weirs (solid circles), and radiotelemetry fixed receivers (solid triangles) in the Susitna River drainage.

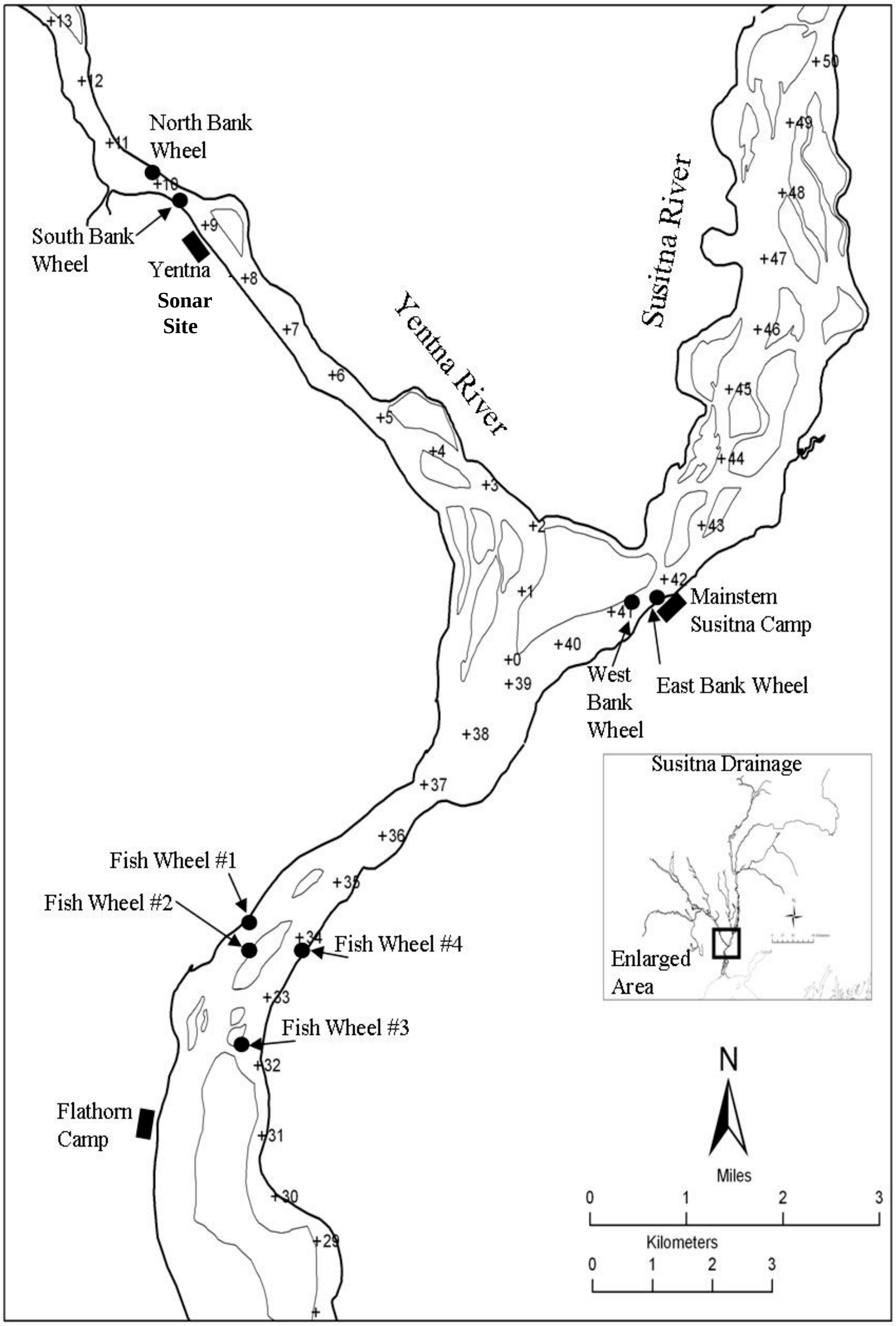


Figure 2.–Locations of 4 fish wheels operated at the Flathorn tagging site and 2 fish wheels located at the sonar site on the lower Yentna River. The locations of 2 other fish wheels operated by Sport Fish Division to recapture tagged chum and coho salmon on the mainstem Susitna River are also shown. River kilometers are indicated next to plus signs.

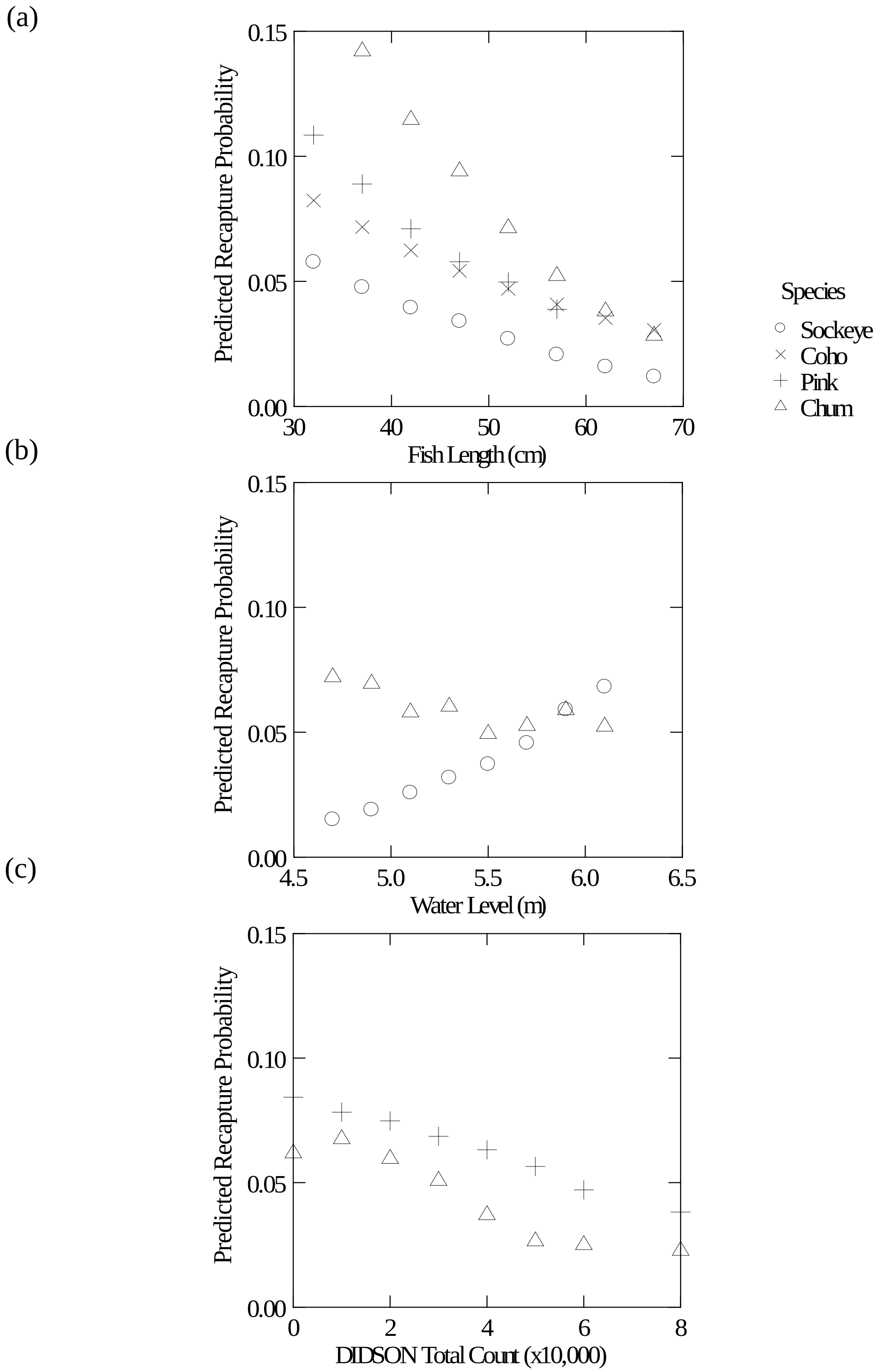


Figure 3.–Tag–recapture probabilities predicted by logistic-regression models for sockeye, coho, pink, and chum salmon in relation to (a) fish length, (b) water level, and (c) DIDSON total fish counts.

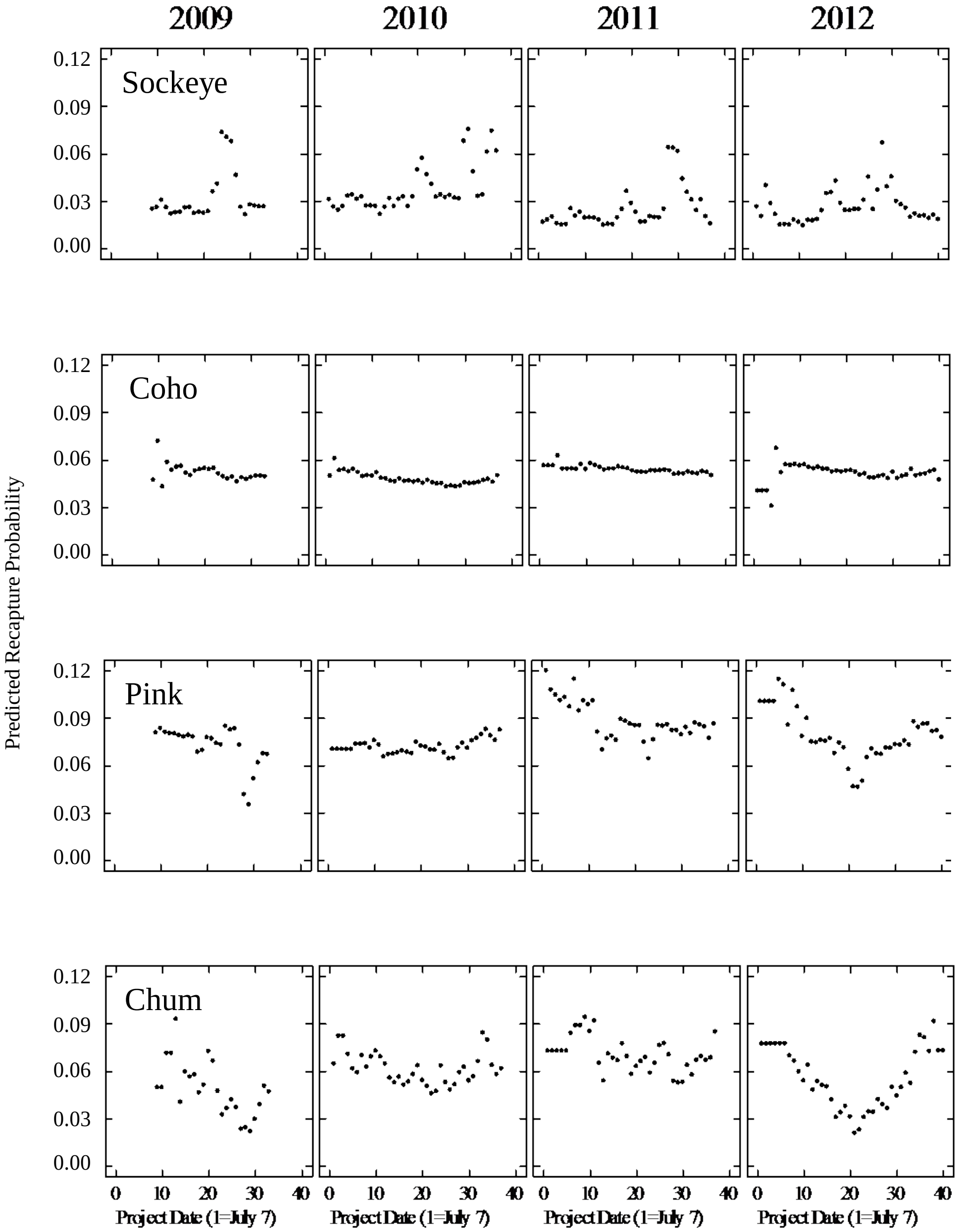


Figure 4.–Tag–recapture probabilities predicted by logistic-regression models for sockeye, coho, pink, and chum salmon in relation to date in 2009–2012.

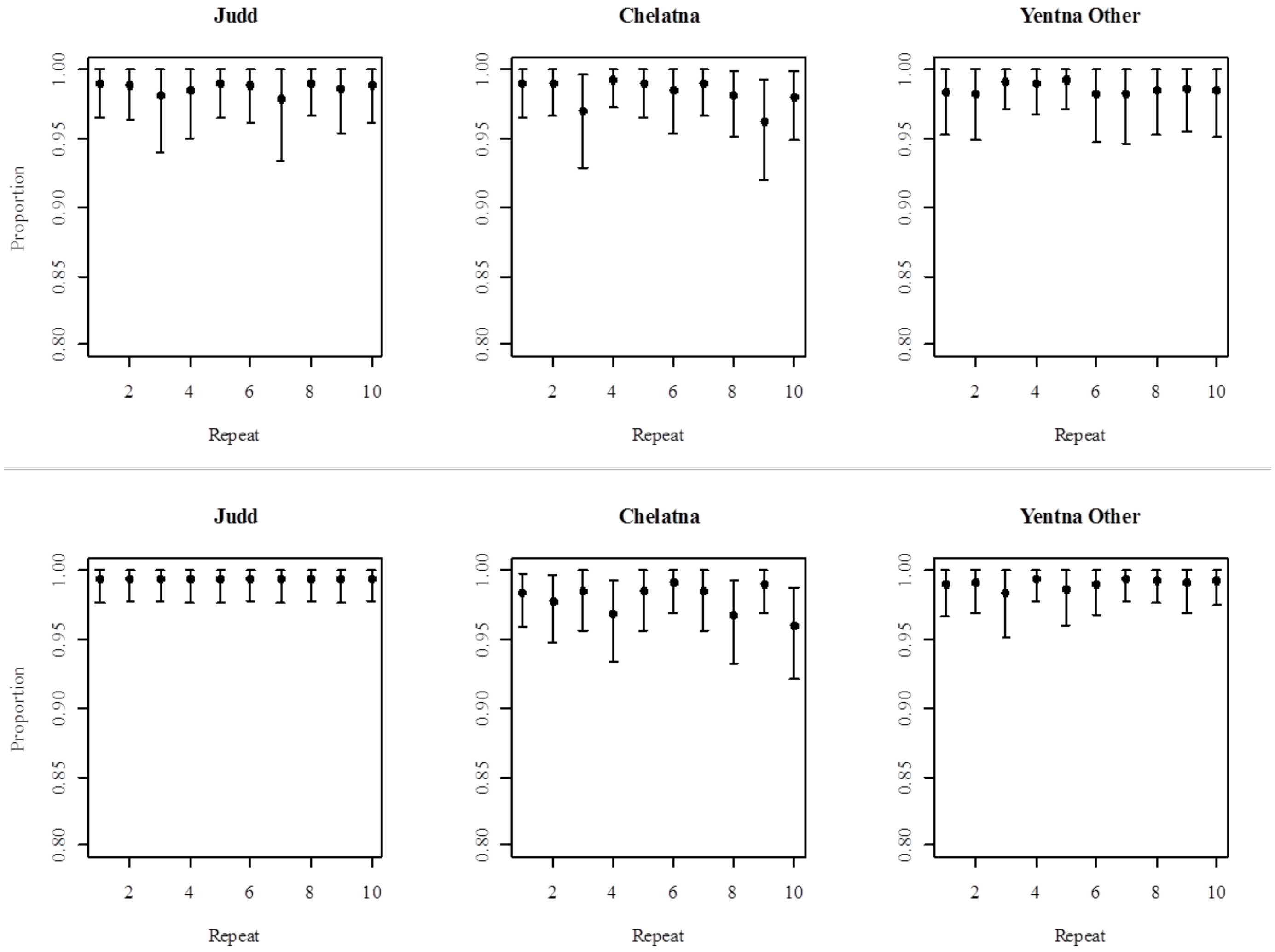


Figure 5.–Stock composition estimates and 90% credibility intervals from baseline evaluation tests (proof tests) for the (a) 45 SNP set and (b) 96 SNP set.

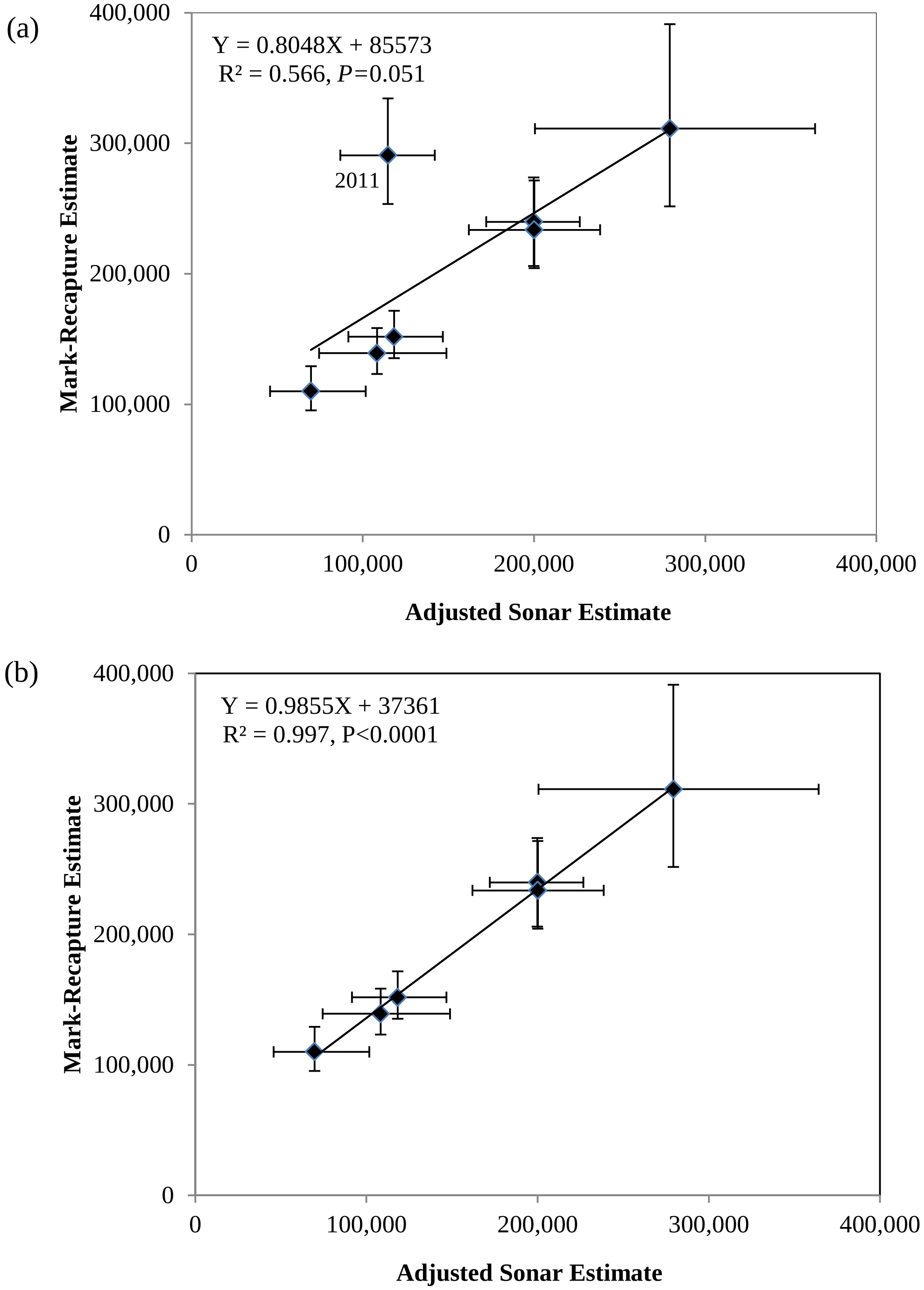


Figure 6.–Relationship between genetic mark–recapture and sonar estimates of sockeye salmon abundance adjusted for fish wheel selectivity at the Yentna sonar site, 2006–2012 (a). Relationship between genetic mark–recapture and sonar estimates of sockeye salmon abundance adjusted for fish wheel selectivity with 2011 data omitted (b).

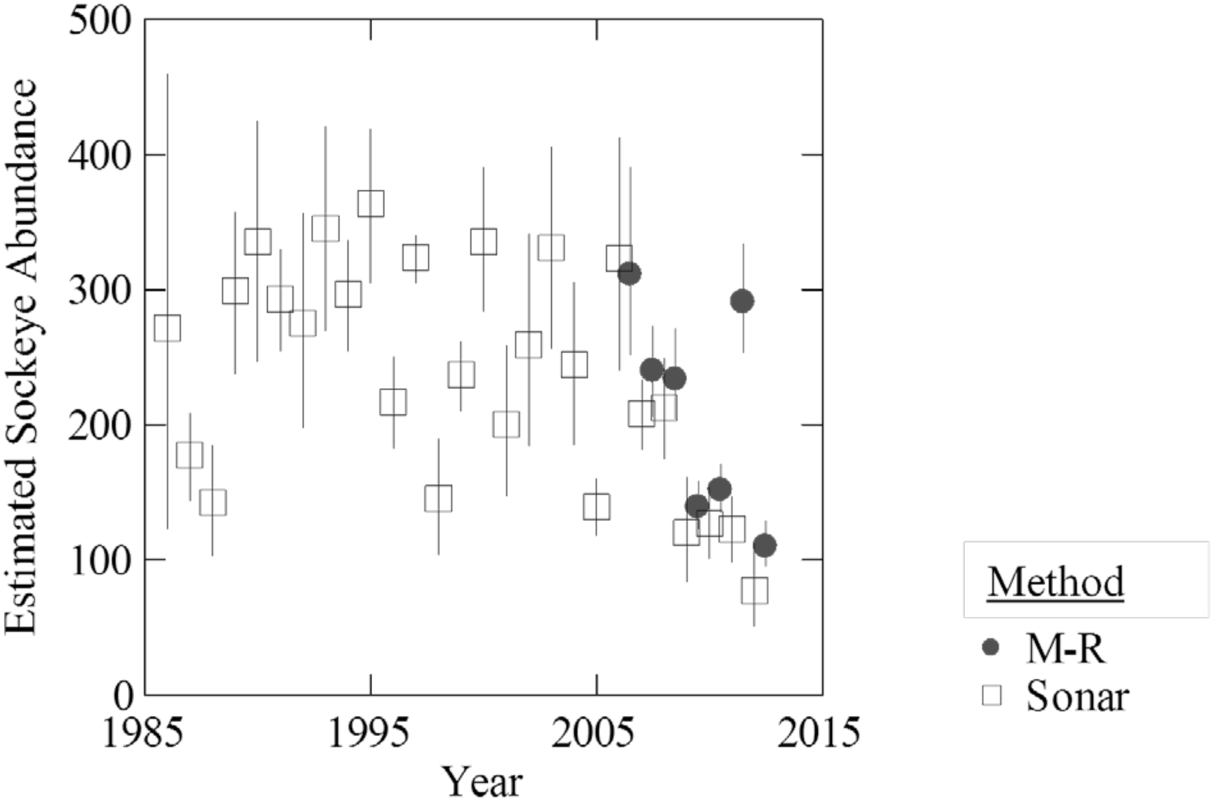


Figure 7.–Historic time series (1986–2012) of sonar estimates of sockeye salmon abundances adjusted for fish wheel selectivity (open squares) and genetic mark–recapture estimates of sockeye salmon abundance (solid circles) at the Yentna sonar site.

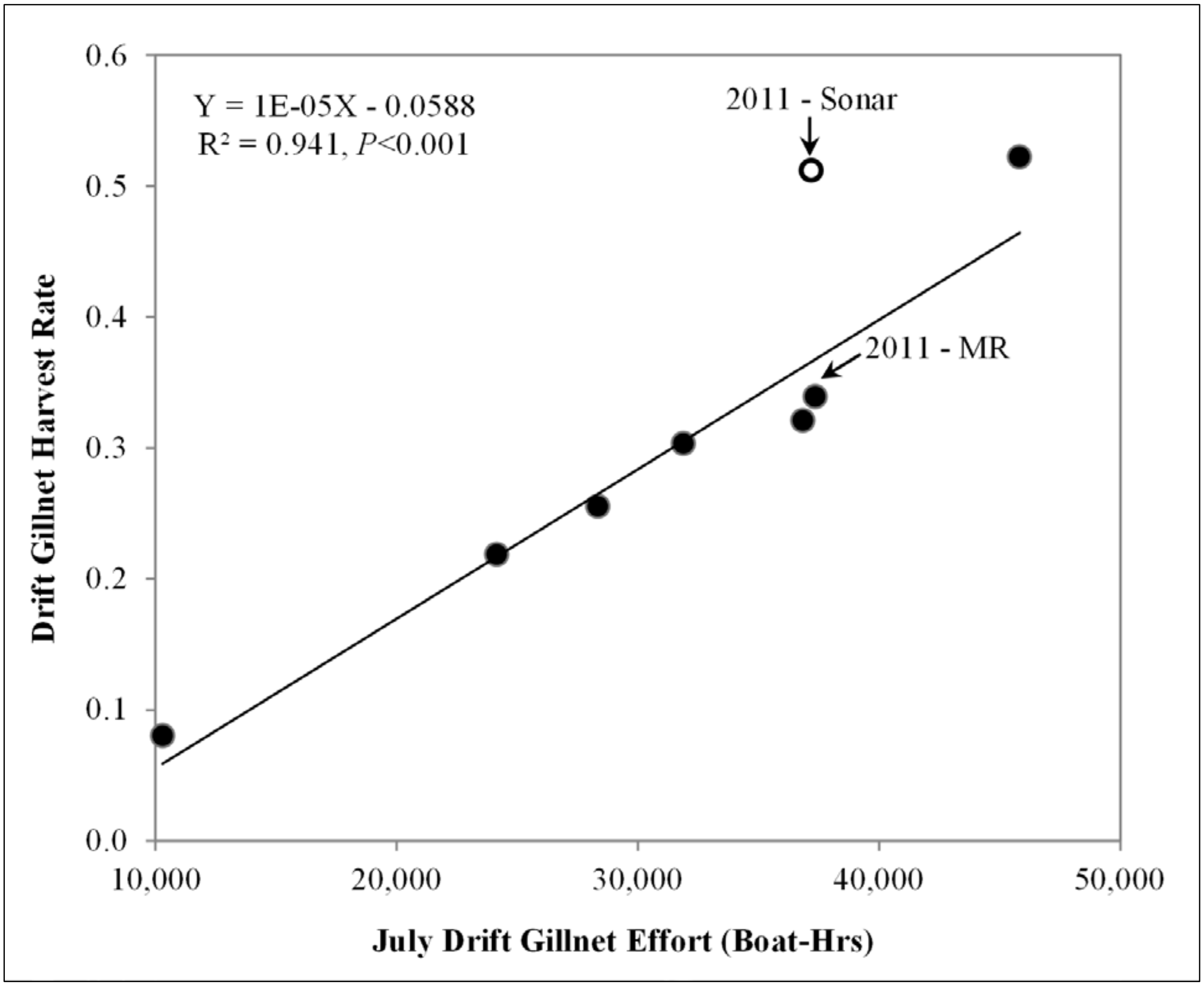
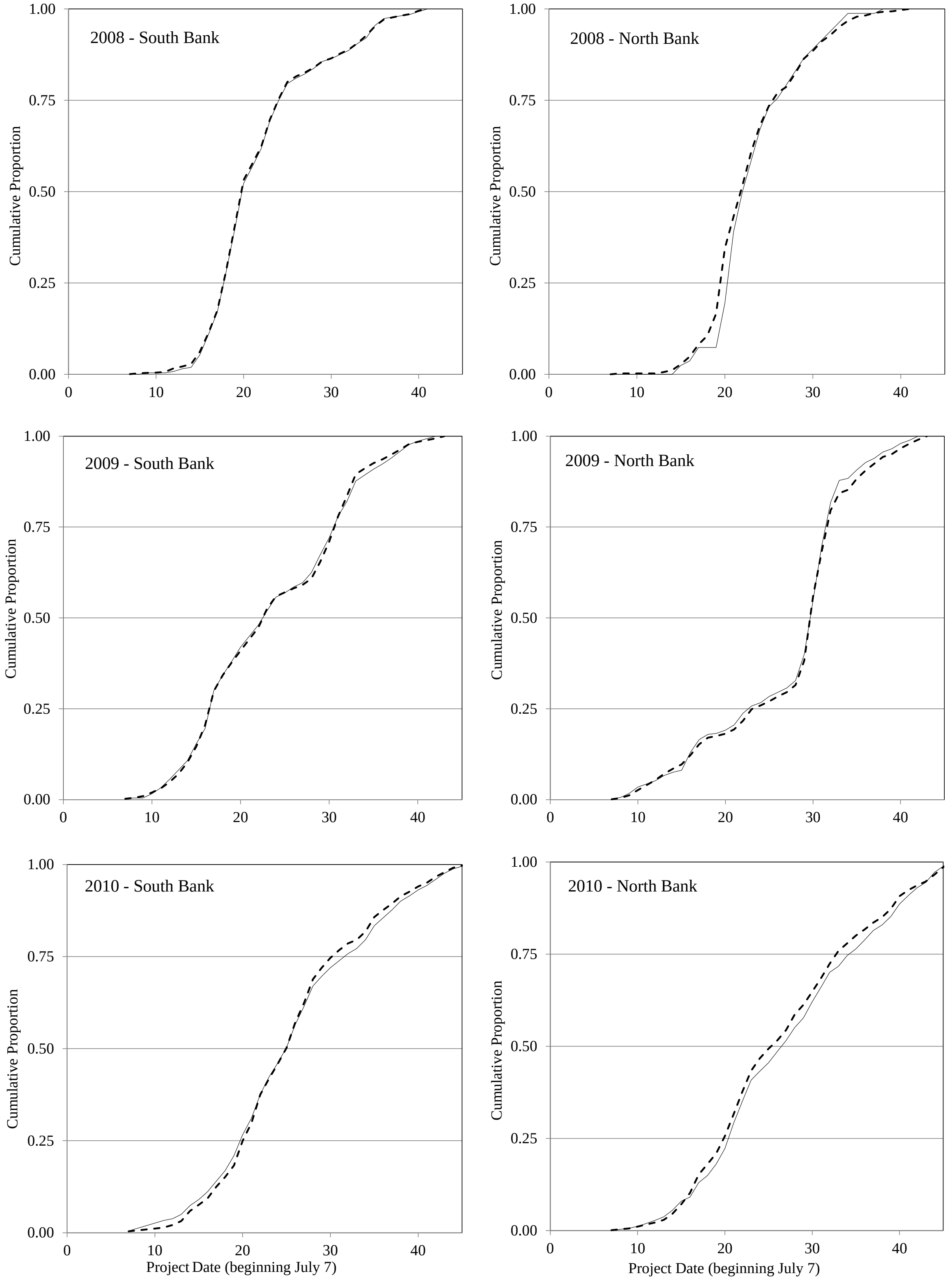


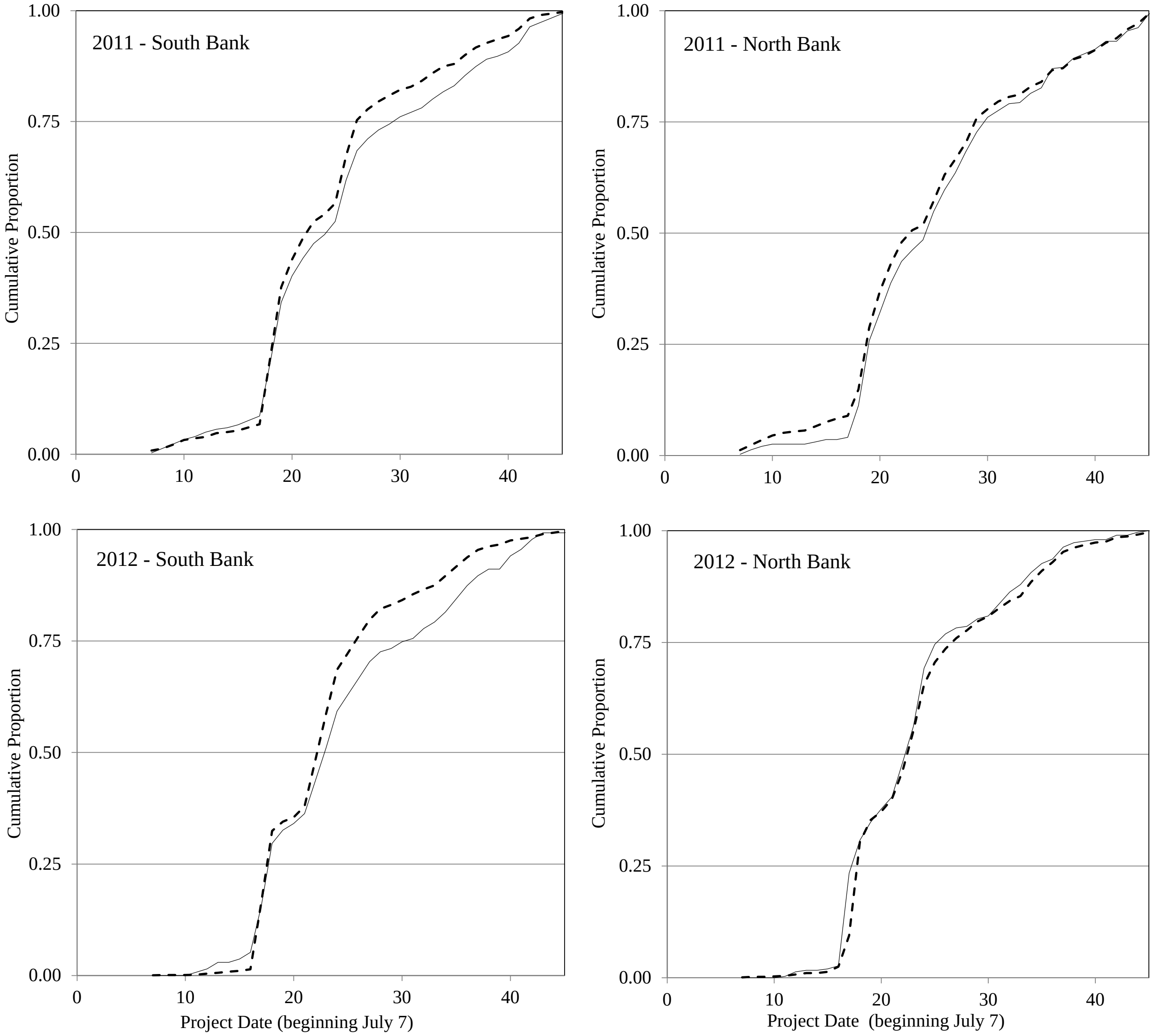
Figure 8.–Relationship between drift-gillnet effort (boat-hours) in July and the drift-gillnet harvest rate for Susitna sockeye salmon, 2006–2012.

Note: The 2011 drift-gillnet harvest rate was calculated using the genetic mark–recapture (solid circle) and adjusted-sonar estimate (open circle) of sockeye salmon abundance passing the Yentna sonar site for comparison. The regression analysis did not include the harvest rate calculated using the adjusted-sonar estimate of sockeye salmon abundance in 2011.

APPENDIX A

Appendix A1.–Comparison of the cumulative proportion of the number of genetic samples (solid line) collected each day and the cumulative proportion of daily catch per hour (dashed line) in fish wheels at the Yentna sonar site, 2008–2012.




2011 - South Bank
2011 - North Bank
2012 - South Bank
2012 - North Bank
Cumulative Proportion
1.00
0.75
0.50
0.25
0.00
0
10
20
30
40
Project Date (beginning July 7)

Appendix A2.–Single nucleotide polymorphism markers (total: 102) used for this project with reduced sets for each analysis.

	45 SNP set[a]		96 SNP set[b]			
Marker	Original	Reduced	Original	Reduced	Linked Markers[c]	Invariant
One_ACBP-79	X	X	X	X		
One_agt-132			X	X		
One_aldB-152			X	X		
One_ALDOB-135	X					
One_apoe-83			X	X		
One_c3-98			X	X		
One_CD9-269			X	X		
One_cetn1-167			X	X		
One_CFP1			X	X		
One_cin-177			X	X		
One_CO1	X	X	X	X	1	
One_ctgf-301	X	X	X	X		
One_Cytb_17	X	X	X	X	1	
One_Cytb_26	X	X	X	X	1	
One_E2-65	X	X	X	X		
One_gdh-212			X	X		
One_GHII-2165	X	X	X	X		
One_ghsR-66			X	X		
One_GPDH-201	X	X	X	X	2	
One_GPDH2-187	X	X	X		2	
One_GPH-414	X	X	X	X		
One_HGFA-49	X	X	X	X		
One_HpaI-71	X	X	X	X		
One_HpaI-99	X	X	X	X		
One_hsc71-220	X	X	X	X		
One_Hsp47			X	X		
One_IL8r-362	X	X	X	X		
One_ins-107	X					
One_KCT1-453			X	X		
One_KPNA-422	X	X	X	X		
One_LEI-87	X	X	X	X		
One_lpp1-44			X	X		
One_MARCKS-241	X					
One_metA-253			X	X		

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Appendix A2.–Page 2 of 3.

	45 SNP set[a]		96 SNP set[b]			
Marker	Original	Reduced	Original	Reduced	Linked Markers[c]	Invariant
One_MHC2_190	X	X	X	X	3	
One_MHC2_251	X	X	X	X	3	
One_Mkpro-129			X	X		
One_ODC1-196			X	X		
One_Ots208-234			X	X		
One_Ots213-181	X	X	X	X		
One_p53-534	X	X	X	X		
One_pax7-248			X	X		
One_PIP			X	X		
One_Prl2	X	X	X	X		
One_rab1a-76			X	X		
One_RAG1-103	X	X	X	X		
One_RAG3-93	X	X	X	X		
One_redd1-414			X	X		
One_RFC2-102	X	X	X	X		
One_RFC2-285	X	X	X	X		
One_RH2op-395	X					
One_rpo2j-261			X	X		
One_sast-211			X	X		
One_serpin-75	X					
One_spf30-207			X	X		
One_srp09-127			X	X		
One_ssrd-135			X	X		
One_STC-410	X	X	X	X		
One_STR07	X	X	X	X		
One_SUMO1-6			X	X		
One_sys1-230			X	X		
One_taf12-248			X			X
One_Tf_ex11-750	X	X	X	X		
One_Tf_in3-182	X	X	X	X		
One_tshB-92			X	X		
One_txnip-401			X			X
One_U1003-75			X	X		
One_U1004-183			X	X		
One_U1009-91			X	X		
One_U1010-81			X	X		

-continued-

Appendix A2.–Page 3 of 3.

	45 SNP set[a]		96 SNP set[b]			
Marker	Original	Reduced	Original	Reduced	Linked Markers[c]	Invariant
One_U1012-68			X	X		
One_U1013-108			X	X		
One_U1014-74			X	X		
One_U1016-115			X	X		
One_U1024-197			X	X		
One_U1101			X	X		
One_U1103			X	X		
One_U1105			X	X		
One_U1201-492			X	X		
One_U1202-1052			X	X		
One_U1203-175			X	X		
One_U1204-53			X	X		
One_U1205-57			X	X		
One_U1206-108			X	X		
One_U1208-67			X	X		
One_U1209-111			X	X		
One_U1210-173			X	X		
One_U1212-106			X	X		
One_U1214-107			X	X		
One_U1216-230			X	X		
One_U301-92	X	X	X	X		
One_U401-224	X	X	X	X		
One_U404-229	X	X	X	X		
One_U502-167	X	X	X	X		
One_U503-170	X	X	X	X		
One_U504-141	X	X	X	X		
One_U508-533	X					
One_vamp5-255			X	X		
One_vatf-214			X	X		
One_VIM-569	X	X	X	X		
One_ZNF-61	X	X	X	X		
One_Zp3b-49	X	X	X	X		

[a] Used in the analysis of the 2009 mixtures.

[b] Used in the analysis of the 2008 and 2010–2012 mixtures.

[c] 1) These SNPs were combined into haplotypes and treated together as a single mtDNA locus, One_CO1_Cytb17-26; 2) One_GPDH2-187 is linked with One_GPDH-201 and dropped from the 96 SNP set; 3) These SNPs were combined into haplotypes and treated together as a single locus, One_MHC2_190-251. See linkage disequilibrium methods and results in Barclay and Habicht (2012).