Fishery Data Series No. 24-09

Mainstem Susitna River Chinook Salmon Abundance, 2021

by

Nick DeCovich

Andrew Barclay

Stephen Dotomain

and

Adam Reimer

July 2024

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

Symbols and Abbreviations

The following symbols and abbreviations, and others approved for the Système International d'Unités (SI), are used without definition in the following reports by the Divisions of Sport Fish and of Commercial Fisheries: Fishery Manuscripts, Fishery Data Series Reports, Fishery Management Reports, and Special Publications. All others, including deviations from definitions listed below, are noted in the text at first mention, as well as in the titles or footnotes of tables, and in figure or figure captions.

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

FISHERY DATA SERIES NO. 24-09

MAINSTEM SUSITNA RIVER CHINOOK SALMON ABUNDANCE, 2021

by
Nick DeCovich
Alaska Department of Fish and Game, Division of Sport Fish, Palmer

Andrew Barclay
Alaska Department of Fish and Game, Division of Commercial Fisheries, Anchorage

Stephen Dotomain
Alaska Department of Fish and Game, Division of Sport Fish, Palmer

and

Adam Reimer
Alaska Department of Fish and Game, Division of Sport Fish, Research and Technical Services, Anchorage

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

July 2024

This investigation was financed by Susitna Salmon Research and Enhancement Initiative (SSREI) and the Pacific Coastal Salmon Recovery Fund (PCSRF).

ADF&G Fishery Data Series was established in 1987 for the publication of Division of Sport Fish technically oriented results for a single project or group of closely related projects, and in 2004 became a joint divisional series with the Division of Commercial Fisheries. Fishery Data Series reports are intended for fishery and other technical professionals and are available through the Alaska State Library and on the Internet: http://www.adfg.alaska.gov/sf/publications/. This publication has undergone editorial and peer review.

Nick DeCovich,
Alaska Department of Fish and Game, Division of Sport Fish,
1801 S. Margaret Dr., Palmer, AK 99645-6736, USA

Andrew W. Barclay,
Alaska Department of Fish and Game, Division of Commercial Fisheries,
333 Raspberry Rd., Anchorage, AK 99518-1565, USA

Stephen Dotomain,
Alaska Department of Fish and Game, Division of Sport Fish,
1801 S. Margaret Dr., Palmer, AK 99645-6736, USA

and

Adam Reimer,
Alaska Department of Fish and Game, Division of Sport Fish, Research and Technical Services
333 Raspberry Rd., Anchorage, AK 99518-1565, USA

This document should be cited as follows:
DeCovich, N., A. W. Barclay, S. Dotomain, and A. Reimer. 2024. Mainstem Susitna River Chinook salmon abundance, 2021. Alaska Department of Fish and Game, Fishery Data Series No. 24-09, Anchorage.

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF APPENDICES

ABSTRACT

Adult Chinook salmon abundance and distribution were estimated for the mainstem Susitna River drainage above river mile (RM) 34 in 2021 for the ninth consecutive year. Abundances were produced using mark–recapture techniques to deploy tags on fish caught via fish wheel and gillnet at a site in the lower river (RM 34) and recover tags using a passive integrated transponder (PIT) tag detection system at the Deshka River (RM 7) weir site. Spawning distribution was assessed with radiotelemetry. Fish were radiotagged at the lower river (RM 34) site and tracked along their spawning migration with an array of fixed-antenna tracking stations. Upstream movement of each tag was categorized into 1 of 5 stocks (spawning groups): Chulitna River, Susitna River (RM 102.4–153.4), Deshka River, Eastside Susitna River, or Talkeetna River. The estimated mainstem Susitna River abundance at RM 34 (and 95% CI) of Chinook salmon ≥500 mm mid eye to tail fork (METF) length was 62,438 (95% CI = 50,049–76,487). The estimated Chinook salmon spawning group abundances were 13,500 (SE = 4,126) for the Eastside Susitna River, 21,094 (SE = 4,126) for the Deshka River, 6,750 (SE = 2,354) for the Talkeetna River, 5,906 (SE = 2,207) for Susitna RM 102.4–153.4, and 15,188 (SE = 3,524) for the Chulitna River.

Keywords Chinook salmon, *Oncorhynchus tshawytscha*, Susitna River, abundance, mark–recapture, radiotelemetry

INTRODUCTION

In response to downturns in productivity and abundance of Chinook salmon (*Oncorhynchus tshawytscha*) stocks across Alaska and the social and economic hardships that followed, in 2013 the Alaska Department of Fish and Game (ADF&G) selected the Susitna River as 1 of 12 critical indicator stocks to address knowledge gaps with studies of productivity, abundance, and other essential information needed to understand the root causes of these widespread declines (ADF&G Chinook Salmon Research Team 2013). Since that time, the Susitna River Chinook salmon abundance and distribution project has addressed knowledge gaps in productivity and abundance with various studies on both the mainstem Susitna River and the Yentna River.

In 2021, ADF&G estimated the inriver abundance and spawner distribution for Chinook salmon in the mainstem Susitna River. These data, presented in this report, complement and supplement similar data collected in 2013–2017 for the Yentna River and 2012–2020 for the mainstem Susitna River (Yanusz et al. 2018; DeCovich and Campbell 2022). The data generated by this and previous studies will be used in a comprehensive Bayesian run-reconstruction model from which spawner–recruit relationships will be estimated (see Reimer and DeCovich 2020). Model results will help advise the Alaska Board of Fisheries regulatory process and be useful for land-use planning and permitting.

In addition to abundance and distribution estimates, this project investigated the stock composition of the sport harvest of Deshka River Chinook salmon. The model described above incorporates the Deshka River Chinook salmon sport harvest to derive the inriver run (escapement at the weir combined with harvest below the weir). The harvest data are provided by the ADF&G Statewide Harvest Survey, which uses a mail-in survey of anglers who buy a State of Alaska fishing license to estimate the number of fish harvested in a given waterbody by species, in this case, Deshka River Chinook salmon. Anecdotal evidence, namely adipose finclipped fish caught near the mouth of the Deshka River, indicates that reported harvests may include some non-Deshka River Chinook salmon. The adipose finclipped fish were likely hatchery releases bound for Deception Creek, a tributary of Willow Creek approximately 14 river miles (RM) upstream of the mouth of the Deshka River. If true, it is plausible that other stocks could be present in the Deshka River fishery, and adjustments to the reported harvest may be necessary. The presence of non-Deshka River fish in this fishery seemed plausible, and we designed a study using genetic stock identification to detect these fish.

OBJECTIVES

PRIMARY OBJECTIVES

1) Estimate the abundance of Chinook salmon ≥500 mm mid eye to tail fork (METF) length in the mainstem Susitna River upstream of the mouth of the Yentna River at RM 34[1] using mark–recapture tagging methods such that the estimate is within 25% of the true value 90% of the time.
2) If the sport fishery is opened to harvest, estimate the proportion of the non-Deshka River fish in the sport harvest from each of 2 sections of the Deshka River downstream of the weir such that the estimated proportions are within 10% of the true values 90% of the time.[2]
3) Estimate the distribution of Chinook salmon ≥500 mm mid eye to tail fork (METF) length over 5 management areas in the mainstem Susitna River upstream of the mouth of the Yentna River at RM 34 such that the estimate is within 15% of the true value 95% of the time.

SECONDARY OBJECTIVES

This study also collected tissue samples and scales during the marking event for later genetic stock identification analysis and age determination (Campbell et al. 2022). The analyses of these sampling efforts are ongoing and therefore not reported here.

METHODS

Chinook salmon inriver abundance and distribution were assessed for the mainstem Susitna River (Figure 1) using mark–recapture and telemetry techniques. The proportions of mainstem Chinook salmon ≥500 mm METF length returning to 4 management groups defined in Reimer and DeCovich (2020) were also estimated.

Study Design

A 2-event, capture–recapture abundance assessment was used to estimate the inriver abundance of Chinook salmon ≥500 mm METF length in the mainstem Susitna River during 2021. Two fish wheels and several gillnets were used at RM 34 (river kilometer [RKM] 55; Figures 1 and 2) to capture Chinook salmon for marking with a dart tag fitted with a passive integrated transponder (PIT tag). These PIT tags were the primary mark, and an upper caudal fin hole punch was used as a secondary mark. A subset of captured Chinook salmon was also radiotagged to determine spawning distribution and to estimate dropouts and drainage switching. We define dropouts as fish that were not detected upstream of the tagging site and did not switch drainages, and drainage switching as a fish tagged at the mainstem tagging site that actually traveled to and presumably spawned in the Yentna River drainage.

This study was restricted to fish ≥500 mm METF length due to radiotagging constraints. The esophageal radio tags (see description and explanation below) measured approximately 50 mm × 20 mm and were therefore not appropriate for implanting in smaller fish. By keeping the length criterion consistent for both radio and PIT tags, information from both study components is

[1] Defined by Alaska Energy Authority, Watana Hydroelectric Studies.

[2] "Within d% of the true value A% of the time" implies $P\left(p - \frac{d}{100} \leq \hat{p} \leq p + d/100\right) = A/100$ where p denotes the population age proportion.

comparable. Additionally, a similar mark–recapture study conducted in 2013 and 2014 (LGL and ADF&G 2014) used radio tags as the primary tag, so the tagging of fish ≥500 mm METF has been maintained in subsequent years to make results comparable among years.

Fish were examined for marks at a weir on the Deshka River at RM 7 (RKM 11; the Deshka River mouth is at Susitna RM 38.8 [RKM 54.4]). PIT tags were detected using swim-through PIT-tag antennas at the Deshka River weir. The Deshka River weir provided very large sample sizes for recapture events. The use of PIT tags allowed for automated sampling of all tagged fish at the Deshka River weir, which maximized sample size while avoiding the labor and run disruptions necessary when hand sampling at a weir.

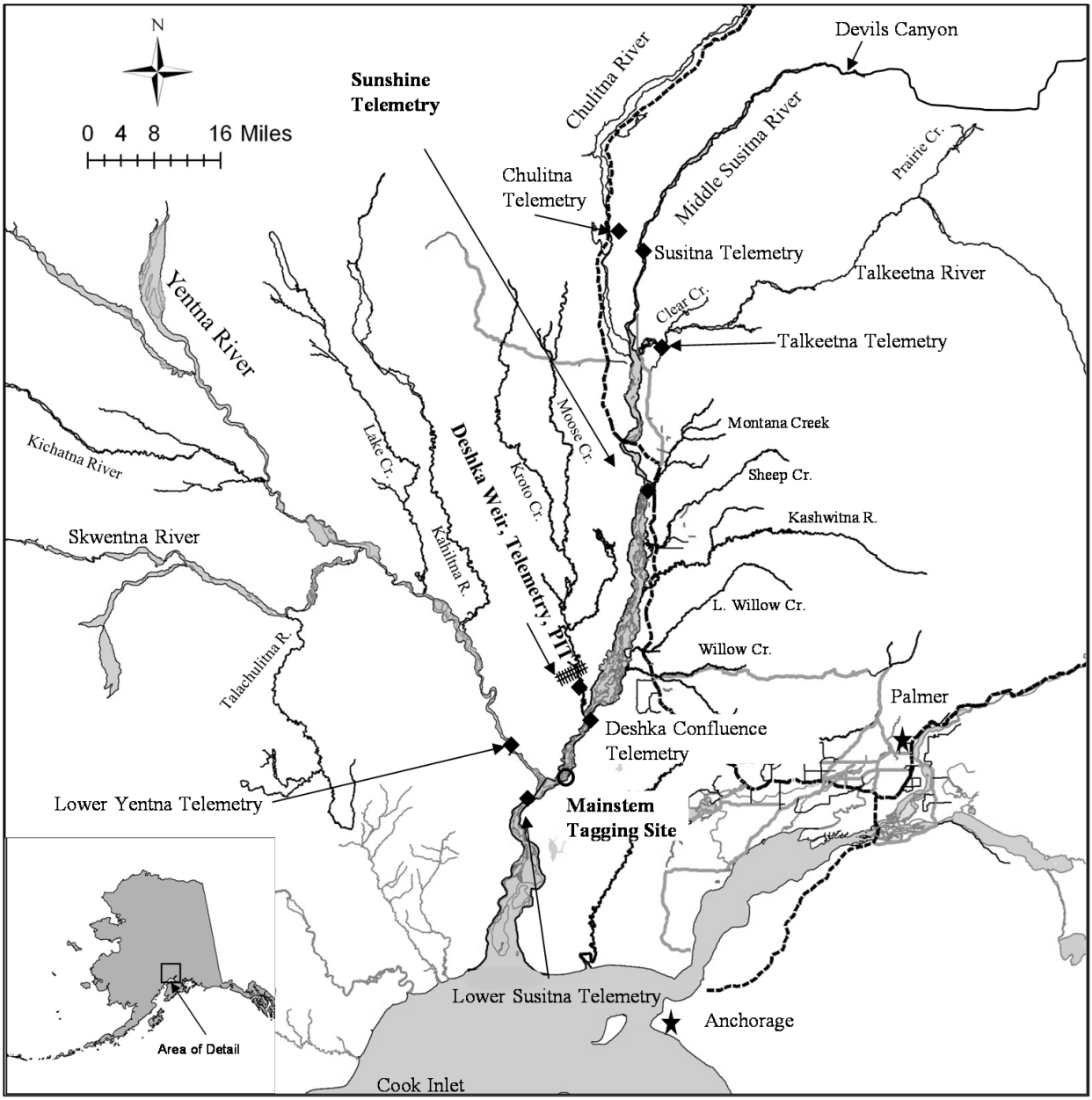

Figure 1.–Locations of fish wheels (open circle), fixed telemetry stations (diamonds), and Deshka weir site in the Susitna River drainage, Alaska.

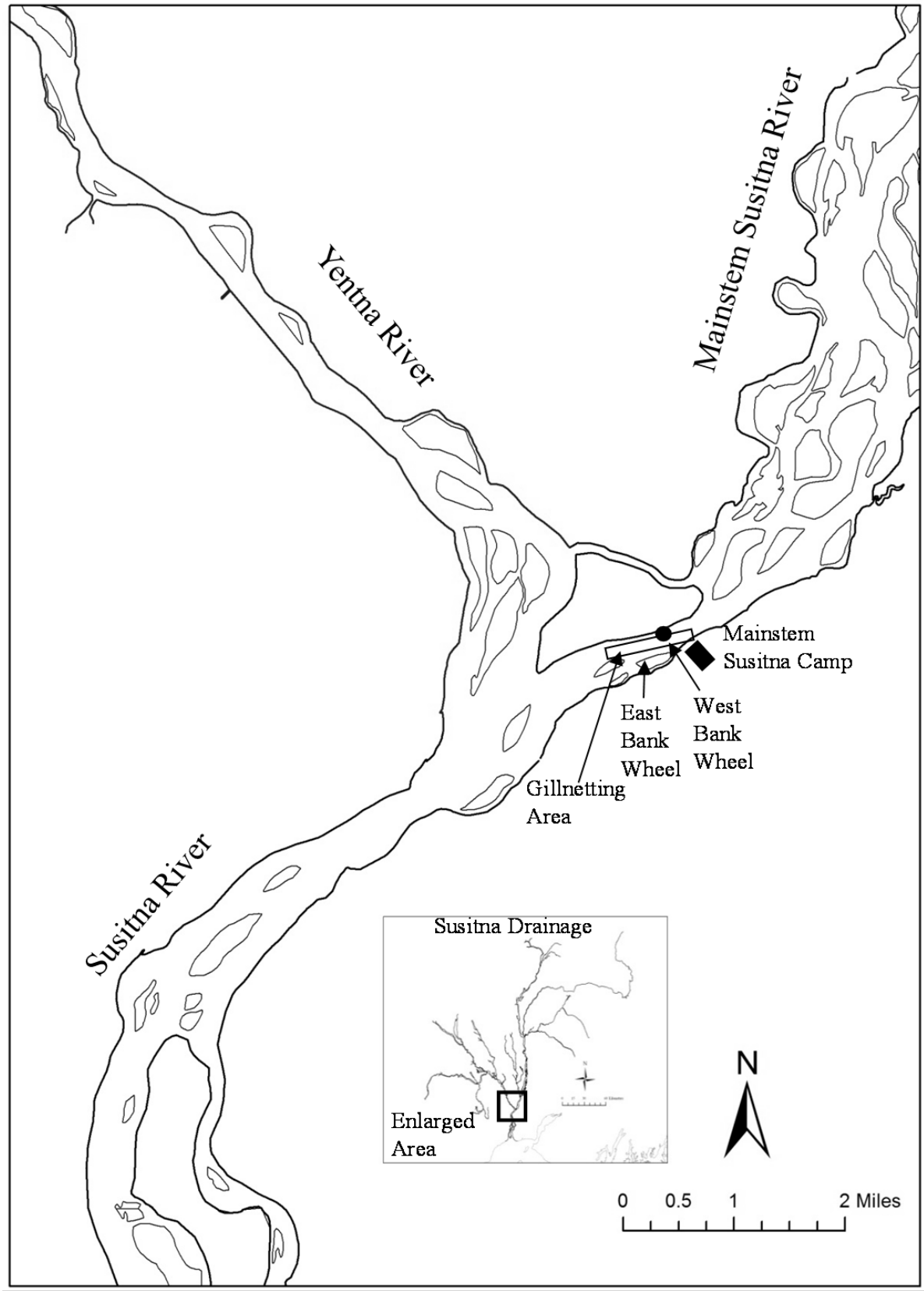

Figure 2.–Locations of fish wheels and gillnetting area at the RM 34 tagging site.

In 2021, there was harvest allowed in the sport fishery beginning on June 18, the approximate midpoint of the run. Genetic tissue samples were collected from fish harvested in 2 river sections: (1) the confluence of the Deshka River and the mainstem Susitna River to an island approximately three-quarters of a mile from the confluence, and (2) from the island to the weir (Figure 3). Subsamples of tissues from sport harvested Chinook salmon per river section were analyzed genetically to estimate the Deshka and non-Deshka components of the harvest from both sections. This project component addressed the second primary objective.

Figure 3.–Sampling locations (Sections 1 and 2) for genetic analysis of Chinook salmon harvested in the Deshka River sport fishery, 2021.

Fixed tracking stations were used to monitor radio tags on major tributaries, below the tagging site (to detect dropouts), and at the Deshka River weir. The purpose of this component was to partition the abundance estimate among the stock groups of mainstem Susitna River Chinook salmon, addressing the third of our primary objectives.

ABUNDANCE ESTIMATION

Marking

Chinook salmon were tagged with PIT and radio tags at the mainstem Susitna River marking site (Figure 2). Two fish wheels, 1 anchored to each bank, and gillnets were used to capture fish. Each of the fish wheels was operated during 2 tagging periods (05:00–13:00, 14:00–22:00) to complete a 6-hour morning shift and a 6-hour afternoon shift for a total effort of 12 h/day. Details on fish wheel construction are described in the operational plan for this project (Campbell et al. 2022). Gillnets were operated during the tagging period in two 3.75-hour shifts each day. All gillnets had a stretch mesh size of 5.5 inches (14 cm) but were of 2 net sizes: 10–12 ft (3.0–3.7 m) deep and 15–17 ft (4.6–5.2 m) deep. Drift locations, duration, and net depth were adjusted to fish the most productive locations and depths or to avoid net snags. One crew of 2 technicians made as many drifts as possible during a 7.5-hour split shift. To reduce bias due to possible but unknown differences in the run timing of any individual stock, start times were rotated daily until a cycle was completed each week. The desired gillnet capture technique was to entangle fish by the snout to avoid injuries that gilling may cause. The net was watched continuously and when sinking corks were observed, the net was pulled in immediately. Fish species other than Chinook salmon caught in fish wheels and gillnets were tallied and released; tally categories included coho salmon (*O. kisutch*), chum salmon (*O. keta*), pink salmon (*O. gorbuscha*), sockeye salmon (*O. nerka*), whitefish (*Coregonus* spp.), and "other."

PIT tags

During the marking event, all Chinook salmon captured in fish wheels or gillnets were measured for METF length. Healthy fish (no fresh injuries or bleeding) ≥500 mm METF length were placed in a water-filled tote and tagged below the base of the dorsal fin with an orange PIT tag (passive integrated transponder embedded dart tag, Model PDAT-PIT [HPT-12] from Hallprint, Australia) anchored in the dorsal pterygiophores (bones) on the fish's left side. This was the primary mark. A single hole was punched into the upper caudal fin as the secondary mark to assess tag loss. For fish caught in fish wheels, only those that had been in the fish wheel live box for less than 1 hour were tagged. Fish were selected quickly to reduce handling time. Each PIT tag was associated with a unique dart-tag number and unique PIT code.

Radio Tags

One hundred of the PIT-tagged (and with a caudal fin hole punch) Chinook salmon (evenly distributed from among the 2 fish wheels and the gillnets) were also radiotagged at the mainstem tagging site. Radio tags were deployed systematically in proportion to the historical average run timing of Chinook salmon ≥500 mm METF length (the planned deployment schedule can be found in Campbell et al. [2022]). To avoid selection bias by the crew, the first available healthy fish caught during a shift was always radiotagged. After the scheduled number of radio tags had been deployed for a particular fish wheel or gillnet shift, the fishing and PIT-tagging resumed for the remainder of the shift. If the scheduled number of radio tags could not be deployed at a given fish wheel due to low catch during that shift, the leftover tags were deployed during the next shift.

Radio tags were inserted through the esophagus and into the upper stomach using a 0.38-inch (0.97 cm; inside diameter) by 18-inch (46 cm) long plastic PEX (cross-linked polyethylene) tubing. The antenna of the radio transmitter was threaded through one end of the tube and pinched

by hand at the other end of the tube such that the radio transmitter was held tightly against the tube before insertion.

A fixed radiotracking station located at the mouth (confluence) of the Deshka River (Susitna RM 38.8) was used as the gateway station to define when a radiotagged fish had entered the abundance assessment area or had dropped out (Table 1, Figure 1). The product of the number of all tags applied and proportion of radiotagged fish that entered the assessment area were used to estimate valid tags in the mark–recapture abundance assessment.

Table 1.–Locations of fixed radiotracking stations, 2021

Drainage	Site name	Latitude	Longitude
Susitna	Deshka confluence (RM 38.8)	61.69127	−150.30632
	Deshka weir	61.78585	−150.34572
	Talkeetna (Clear Creek)	62.36500	−150.01800
	Chulitna (Princess Lodge)	62.55397	−150.23167
	Middle Susitna	62.45601	−150.12609

Genetics

The distal 0.5 inches (1.3 cm) of the left axillary process clipped from each PIT-tagged fish, and from every 5th fish captured under 500 mm METF, was placed in a uniquely numbered (radio-tag number) vial and preserved in ethyl alcohol following methods described in (Campbell et al. 2022). These samples were archived for possible future genetics studies. All genetics samples and relevant collection data were shipped to the ADF&G Division of Commercial Fisheries Gene Conservation Lab in Anchorage at the end of the season. All genetics sample processing, data storage, and data analysis were the responsibility of the ADF&G Gene Conservation Lab.

Scales

For every fish sampled for genetic tissue, 4 scales were taken from the left side of the body at a point on a diagonal line from the posterior insertion of the dorsal fin to the anterior insertion of the anal fin and 2 rows above the lateral line (Welander 1940; Scarnecchia 1979). If the preferred scales could not be obtained, another scale was taken from as close to the preferred scale as possible, always from the first or second row above the lateral line, to capture the early life history portion of the age. If no scales were available in the preferred area on the left side of the fish, scales were collected from the preferred area on the right side of the fish. All scale collections were prepped for age determination by imprinting onto acetate cards using an acetate scale press then labeled and stored at the Palmer ADF&G office.

Recapture

The recapture event for the mainstem Susitna mark–recapture abundance assessment consisted of a PIT-tag reader at the Deshka River weir (RM 7). The floating resistance-board weir and its operation at RM 7 of the Deshka River is described in detail in Lescanec (2022).

A double-antenna, Biomark PIT detection system was installed immediately upstream of the fish cage at the Deshka River weir. Construction and operation details are provided in Campbell et al. (2022). PIT-tag readers, deployed upstream of the weir traps, recorded PIT-tagged fish as they swam past the antennas. Two tests were run each day to verify proper operation of the PIT-tag detection array. The first test involved waving a PIT tag attached to a 2 m wooden dowel through all areas of each antenna's supposed field of detection. If "dead spots" were encountered, the

antenna was reconfigured. The second test consisted of checking recorded PIT-tag detections at the times tags were visually detected by the weir crew.

A trap incorporated into the weir allowed capture of a subsample of passing fish for measurement of age (scales), sex, and length (Lescanec 2022). METF lengths from this sampling allowed for testing of capture bias with respect to length (see *Data Analysis* section). This sampling also allowed inspection of fish for secondary marks to assess tag loss. Other species were tallied as they were passed through the weir, although these data are not presented here.

SPAWNING DISTRIBUTION

Movements of radiotagged Chinook salmon were monitored from time of release using 5 tracking stations placed on important migratory corridors, including the mouth of the Deshka River, to monitor entry of tags into the mark–recapture abundance assessment (Table 1, Figure 1). Each tracking station consisted of 2 Yagi antennas (Cushcraft), a receiver-logger (ATSTM Model R4500C), and a self-contained 12-volt power system. Radiotagged fish within reception range were detected and identified by the stations. The receiver recorded the date and time a fish was present at the site, the signal strength of the transmitter, and the relative position of the fish (i.e., upriver or downriver from the station). This information was summarized and recorded at 10-minute intervals and used to determine when the fish moved past the site. Sites were visited throughout the field season to check the voltage levels for the station components and whether the reference transmitter at the site was being properly recorded.

All raw telemetry data and tagging data from radiotagged fish were analyzed postseason to assign a spawning location for every transmitter (Appendix A1). Each transmitter was then included into 1 of 5 spawning groups: Chulitna River, Susitna River (RM 102.4–153.4), Deshka River, Eastside Susitna River, or Talkeetna River, where spawning was defined as occurring in the 2017 mainstem Susitna River distribution (DeCovich et al. 2020).

PROPORTION OF NON-DESHKA CHINOOK SALMON IN THE DESHKA RIVER SPORT FISHERY

Tissue sampling

An ADF&G biologist was present at the Deshka River landing boat launch from 18 to 24 June 2021, the first week the Deshka River sport fishery was open to the retention of Chinook salmon. Most boat anglers fishing the Deshka River launch their boats from the Deshka Landing so this provides maximum opportunity for interaction with anglers. Most returning anglers are off the river by noon, and catch rates are generally greater in the morning. Therefore, the landing was monitored from roughly 8:00 AM until noon. Catch rates dropped dramatically after June 24 and staff sampling efforts were concluded on this day. Anglers in each returning boat were approached to determine if they had harvested Chinook salmon from the Deshka River. If so, anglers were asked permission to collect a tissue sample from each harvested fish. Each tissue sample was stored according to whether the fish was harvested in Section 1 (the Deshka River mouth to an island three-quarters of a mile upstream) or from Section 2 (the island to Deshka River weir; Figure 3). A map of the area was provided to each angler to help them accurately identify where their harvest occurred. In addition to ADF&G staff, 2 local fishing guides collected samples. Each guide was supplied with two 250 ml bottles filled with ethanol: one labeled “mouth to island” and the other labeled “between island and weir.”

The genetic tissue samples collected throughout the season were subsampled postseason to form a mixture sample of Chinook salmon for genetic mixed stock analysis (MSA) for each section of river.

Assaying Genotypes

Tissue samples were genotyped and genomic DNA was extracted from tissue samples using NucleoSpin 96 Tissue Kits by Macherey-Nagel (Düren, Germany). DNA was screened for the 83 variant single nucleotide polymorphism (SNP) markers using Fluidigm 96.96 Integrated Fluidic Circuits (A. Barclay and C. Habicht, ADF&G Division of Commercial Fisheries, unpublished methods). The Integrated Fluidic Circuits were read on a Biomark or EP1 System (Fluidigm) after amplification and scored using Fluidigm SNP Genotyping Analysis software. Genotypes were imported and archived in the Gene Conservation Laboratory Oracle database, LOKI.

Laboratory Failure Rates and Quality Control

Overall failure rate was calculated by dividing the number of failed single-locus genotypes by the number of assayed single-locus genotypes. An individual genotype will be considered a failure when a locus for a fish cannot be satisfactorily genotyped.

Quality control (QC) measures were used to identify laboratory errors and to determine the reproducibility of genotypes. In this process, 8 of every 96 fish (1 row per 96-well plate) were reanalyzed for all markers by staff not involved with the original analysis. Laboratory errors found during the QC process were corrected, and genotypes were corrected in the database. Inconsistencies not attributable to laboratory error were recorded, but original genotype scores were retained in the database.

Reporting Groups

Three reporting groups that perform adequately for MSA within the Susitna River drainage were chosen for this study:

1) *Yentna* (Yentna River populations)
2) *Mainstem Susitna* (Susitna River mainstem populations excluding Alexander Creek and Deshka River)
3) *Deshka* (Deshka River population)

Genetic Baseline

To estimate the proportion of *Yentna*, *mainstem Susitna*, and *Deshka* reporting groups in the fish wheel mixture, a baseline was used containing the 30 populations from the Susitna and Yentna Rivers and 83 variant SNPs (A. Barclay and C. Habicht, ADF&G Division of Commercial Fisheries, unpublished methods).

DATA ANALYSIS

Abundance

Estimation

A 2-sample mark–recapture model was used to estimate the number of Chinook salmon passing the first-event sampling site. The appropriate abundance estimator depended on the results of tests of model assumptions presented below. If stratification by size was not required, a modification of

Chapman's (1951) version of Petersen's abundance estimator for closed populations (Seber 1982) was used. A size-stratified estimator was used otherwise (Seber 1982). Abundance using the Chapman model was estimated as follows:

$$\hat{N} = \frac{(\hat{M}_U + 1)(\hat{C} + 1)}{(R + 1)} - 1 \quad (1)$$

where

$\widehat{M}_U$ = the estimated number of marked Chinook salmon moving upstream of the Susitna River mainstem tagging site,

$\widehat{C}$ = the estimated number of Chinook salmon ≥500 mm METF that are inspected for marks at the second event sampling site, and

R = number of marked Chinook salmon recaptured during second event sampling.

For Chinook salmon, $\widehat{M}_U$ was estimated as follows:

$$\hat{M}_U = \hat{p}_{UP} M \quad (2)$$

where M is the total number of marked Chinook salmon, and

$$\hat{p}_{UP} = \frac{r_{up}}{r} \quad (3)$$

where r is the number of radio tags applied and r_{up} is the number of r that entered the mark–recapture abundance assessment.

$\widehat{C}$ was calculated as follows:

$$\widehat{C} = C_T \hat{p}_{500+} \quad (4)$$

where

C_T = total number of Chinook salmon counted past second event sampling site (weir) and

$\hat{p}_{500+}$ = estimated proportion of Chinook salmon at the weir site that were ≥500 mm METF length.

The proportion $\hat{p}_{500+}$ was calculated from length composition data:

$$\hat{p}_{500+} = \frac{n_{500+}}{n} \quad (5)$$

where

n = total number of Chinook salmon sampled at the weir, and

n_{500+} = those fish out of n that were greater than or equal to 500 mm METF.

If stratification by size was required (see *Mark–Recapture Assumptions* section), the data were fully stratified and estimates for each size stratum were generated using Equations 1–5. Stratum

estimates of abundance and variance (see Equations 1 and 6) were summed over size strata for estimates pertinent to the entire population.

An estimate of the variance for $\widehat{N}$ within a size stratum was obtained through simulation. The estimated number of marks continuing upstream was simulated as a binomial variable ($\widehat{M}_U^* \sim \text{bin}[M, \hat{p}_{UP}]$) and the number of recaptures R was modeled as a binomial variable ($R^* \sim \text{bin}[\widehat{C}, \widehat{M}_U/\widehat{N}]$). The number of Chinook salmon greater than or equal to 500 mm METF length at the recapture location was modeled as a binomial variable bin(C_T,$\hat{p}_{500+}$), with simulated values $\widehat{C}^*$ calculated using Equation 4. A large number of simulated values for R^*, $\widehat{M}_U^*$, and $\widehat{C}^*$ were generated, and simulated samples of the abundance estimate $\widehat{N}^*$ were calculated using Equation 1.

A minimum of 1,000,000 simulations (B) were drawn. The approximate variance of $\widehat{N}$ was calculated as follows:

$$\text{var}(\hat{N}) = \frac{\sum_{b=1}^{B} (\hat{N}_b^* - \hat{\bar{N}}^*)^2}{B-1} \tag{6}$$

where $\widehat{\bar{N}}^*$ is the average of the $\widehat{N}_b^*$. Confidence intervals were calculated from the B simulations using the percentile method.

Mark–Recapture Assumptions

Ideally, Chinook salmon abundance is estimated with a Petersen-type estimator. For Petersen estimates of abundance to be unbiased, certain assumptions must be met (Seber 1982). These assumptions, expressed in the circumstances of this study, along with their respective design considerations and test procedures are described below.

Assumption I: The population is closed to births, deaths, immigration, and emigration.

Taking into consideration the life history of Chinook salmon, there should be no recruitment (births, immigration) between sampling events. First event sampling (marking) began prior to any significant passage of fish past the tagging site and continued through the run until passage dropped to near zero. With respect to emigration, some fish marked at the mainstem Susitna River marking site leave the system and migrate to the Yentna River drainage. Also, some marked fish fail to enter the assessment due to handling stress. Losses of fish due to either reason were estimated from a sample of marked fish that were also radiotagged; marked fish were adjusted accordingly ($\widehat{M}_U$ in Equations 1 and 2).

Assumption II: There is no trap-induced behavior.

There is no explicit test for this assumption because the behavior of unhandled fish cannot be observed. We attempted to meet this assumption by minimizing holding and handling time of all captured fish. Any obviously stressed or injured fish was not tagged. Examples of injuries were fresh seal bites that penetrate the muscle, capture injuries such as torn opercula, large skin wounds, broken snouts, or being dropped in the boat while tagging.

Assumption III: Tagged fish will not lose their marks between sampling events and all marks are recognizable.

Although there was no fish wheel sampling in the recapture portion of the assessment and limited age-sex-length sampling at the Deshka weir to assess this assumption, we assumed tag loss to have a negligible effect on the abundance estimate. Little evidence of tag loss in similar assessments on the mainstem Susitna and Yentna Rivers has been found (Cleary et al. 2016a, 2016b).

Assumption IV: At least 1 of the following 3 conditions was met:

1) Marked fish mixed completely with unmarked fish between marking and recovery events.
2) All Chinook salmon had the same probability of being captured in the second event.
3) All Chinook salmon had the same probability of being caught in the first event.

With respect to Condition 1, it is impossible that marked and unmarked fish mixed completely. Marking fish wheels and gillnets operated continuously during the run, so marked fish from the early part of the run never had the opportunity to mix with unmarked fish from the latter part of the run by the time they were sampled in the second event.

With respect to Condition 2, although a substantial portion of the population (Deshka River stock) was exposed to second event sampling, there was no chance that probability of capture was uniform across all Chinook salmon because non-Deshka River stocks were not recaptured.

With respect to Condition 3, consistent use of fish wheels and gillnets at the marking event made uniform sampling possible, although uniform sampling was not guaranteed. Fluctuations in water levels can affect the efficiency of fish wheels, resulting in variation in probability of capture over time. Also, fish wheel capture probability may vary between banks due to differences in channel morphology and water flow (Yanusz et al. 2007), and gillnets and fish wheels may differ in fishing efficiency and effort, resulting in uneven probability of capture between bank-oriented populations. Finally, probability of capture may be affected by fish size.

Like the previous Susitna River mark–recapture studies during 2018–2020 (DeCovich and Campbell 2022), contingency table analyses (Appendices B1–B3) were used to address Condition 3 with respect to fish size and ascertain whether the Petersen-type model could be used or whether a more complicated Darroch-type model was needed. Size-based tests of differential probability of capture were possible using length data from marked fish from the first event and captured and recaptured fish from the second event at the Deshka weir. If different probabilities of capture by size were indicated, data were fully stratified into size groups where probability of capture was homogeneous within groups, and abundance estimates were calculated for each size group and summed.

Like the 2018–2020 studies, the spatial diagnostic "Equal Proportions" test (Consistency Test II, Appendix C1) could not be conducted for the 2021 study because there is only a single recapture event (Deshka weir). In addition, temporal "Equal Proportions" tests are considered unreliable due to the documented effects of tagging on sulking behavior of Chinook salmon (Bernard et al. 1999). Both the limited recapture and potential for sulking also mean a significant "Complete Mixing" test (Consistency Test III, Appendix C1) is of informational value only and negates the possibility of using a Darroch-type model in the current studies. However, an insignificant "Complete Mixing" test could still be used to support the Petersen model. Under this condition, the final abundance estimate would be calculated using a Petersen model, possibly stratified by size. Its

validity depends on the partially untestable assumption that the probability of capture in the first event was even or nonsignificant in "Complete Mixing" spatial and temporal tests.

It is noted that all 6 ADF&G mark–recapture estimates of Chinook salmon abundance at RM 34 of the Susitna River from 2015 through 2020 were analyzed as simple Petersen estimates within 2 size strata (DeCovich et al. 2020; DeCovich and Campbell 2022; Decovich and Campbell, Fishery Biologists, ADF&G, Palmer, unpublished analysis). The spatial test of probability of capture was only significant in 1 of 6 instances in these estimates. In the significant case, the "Complete Mixing Test" (Arnason et al. 1996) allowed the Petersen estimate to be used. Given our ability to continue testing and correcting for size-related probability of capture effects and our historical success at using the Petersen estimate, we believe that the Petersen model, stratified by size if needed, yields unbiased results for these studies.

Genetic Analysis of Deshka River Sport Harvest

The proportion of Deshka and non-Deshka River Chinook salmon harvested in the 2 river sections defined herein was estimated using the R package *rubias* (Pella and Masuda 2001). The *rubias* package is a Bayesian approach to the conditional genetic stock identification model based upon computationally efficient C code implemented in R (Moran and Anderson 2019). It uses cross-validation and simulation to quantify and correct for biases in reporting group estimates. The mixture samples were analyzed with a single Markov Chain Monte Carlo chain (MCMC), with 25,000 iterations and the first 5,000 iterations discarded to remove the influence of starting values. The prior parameters for each reporting group were defined to be equal and sum to 1 (i.e., a flat prior). Within each reporting group (Deshka River, Susitna River, and Yentna River), the population prior parameters were divided equally among the populations. To correct for bias in the MCMC reporting group estimates, an additional parametric boot-strapping step was performed by simulating 100 mixtures with similar stock composition as the MCMC estimates. The degree of bias observed in the simulated mixture analyses was then used to correct the MCMC estimates. Stock proportion estimates and the 90% credibility intervals for each proof test mixture were calculated by taking the mean and 5% and 95% quantiles of the posterior distribution from the single chain output.

RESULTS

MAINSTEM SUSITNA RIVER ABUNDANCE IN 2021

RM 34 Tagging in 2021

A total of 1,602 Chinook salmon were captured at the Susitna River RM 34 tagging site from May 20 through June 26, 2021; 901 were caught in the west-bank fish wheel, 489 in the east-bank fish wheel, and 206 in drift gillnets (Table 2, Figure 4). Of the 1,602 Chinook salmon caught, the crew were able to tag 495 fish $\geq$500 mm with a PIT tag: 217 from the west-bank fish wheel, 168 from the east-bank fish wheel, and 110 from the drift gillnets. Tagging rates may have been down slightly from previous years because 169 fish were eligible for tagging but had the tag voided from the assessment over a crew error. Tags that were ultimately voided were deployed in the first week of June by fish wheel crews and in the second week of June by the gillnet crew. Voided tags were detected at the weir but could not be individually identified at the time of release, which made them unusable for assumption testing or in a size-stratified estimate.

Additionally, 99 PIT–tagged Chinook salmon ≥500 mm METF received esophageal radio tags (Table 2). A total of 16 radio tags were associated with fish with voided dart tags. Radio telemetry final fates were still determined for these fish, but they could not be associated with a capture method.

The west-bank and east-bank fish wheels operated for at least 12 hours each day 97% of the time (Figure 5). The average daily soak time when operating gillnets was 3.5 hours. The greatest catch rates of fish ≥500 mm occurred in early to mid-June. The west-bank fish wheel reached a peak catch rate of 1.5 fish per hour on 2 days: May 28 and June 8. The east-bank fish wheel exceeded 1 fish per hour on 3 days between June 6 and June 10. Gillnet catch rates exceeded 4 fish per hour on 2 days: June 11 and 15. The cumulative catch of fish ≥500 mm reached 50% on June 5, June 9, and June 11 for the west-bank fish wheel, the east-bank fish wheel, and the gillnets, respectively.

Radio telemetry was used to estimate the number of PIT–tagged Chinook salmon with "valid" tags that could be used for the mark–recapture estimate (that is, the estimated number of PIT tags entering the mark–recapture assessment). Of the 99 radio tags applied at RM 34, 25 dropped out or switched to the Yentna River drainage. It was estimated that 0.64 of 32 tags applied at the west-bank fish wheel, 0.96 of 35 tags applied at the east-bank fish wheel, and 0.54 of 31 tags applied from gillnets maintained upstream migration from RM 34 (did not succumb to handling stress and did not switch to the Yentna River drainage). These proportions were applied to the respective numbers of PIT-tagged Chinook salmon at RM 34 resulting in an estimated 359 tagged Chinook salmon that entered the mainstem Susitna River mark–recapture assessment area ($\widehat{M}_U$ in Equation 2).

Table 2.–Mainstem Susitna River catch and tagging summary at RM 34, 2021.

	Chinook salmon				Other salmon					
Gear type	Total captured	PIT-tagged	Not tagged[a]	Radio-tagged[b]	Coho	Chum	Pink	Sockeye	Whitefish	Other
West fish wheel	901	217	690	32	0	0	2	23	10	29
East fish wheel	489	168	321	35	0	0	1	11	3	3
Gillnet	206	110	96	31	0	0	0	0	0	0
Grand total	1,602	495	1107	99	0	0	3	24	13	32

[a] Not tagged indicates fish that were injured, escaped, <500 mm, recaptured, or had their tag voided.

[b] There was 1 tag release for which the capture gear was not recorded.

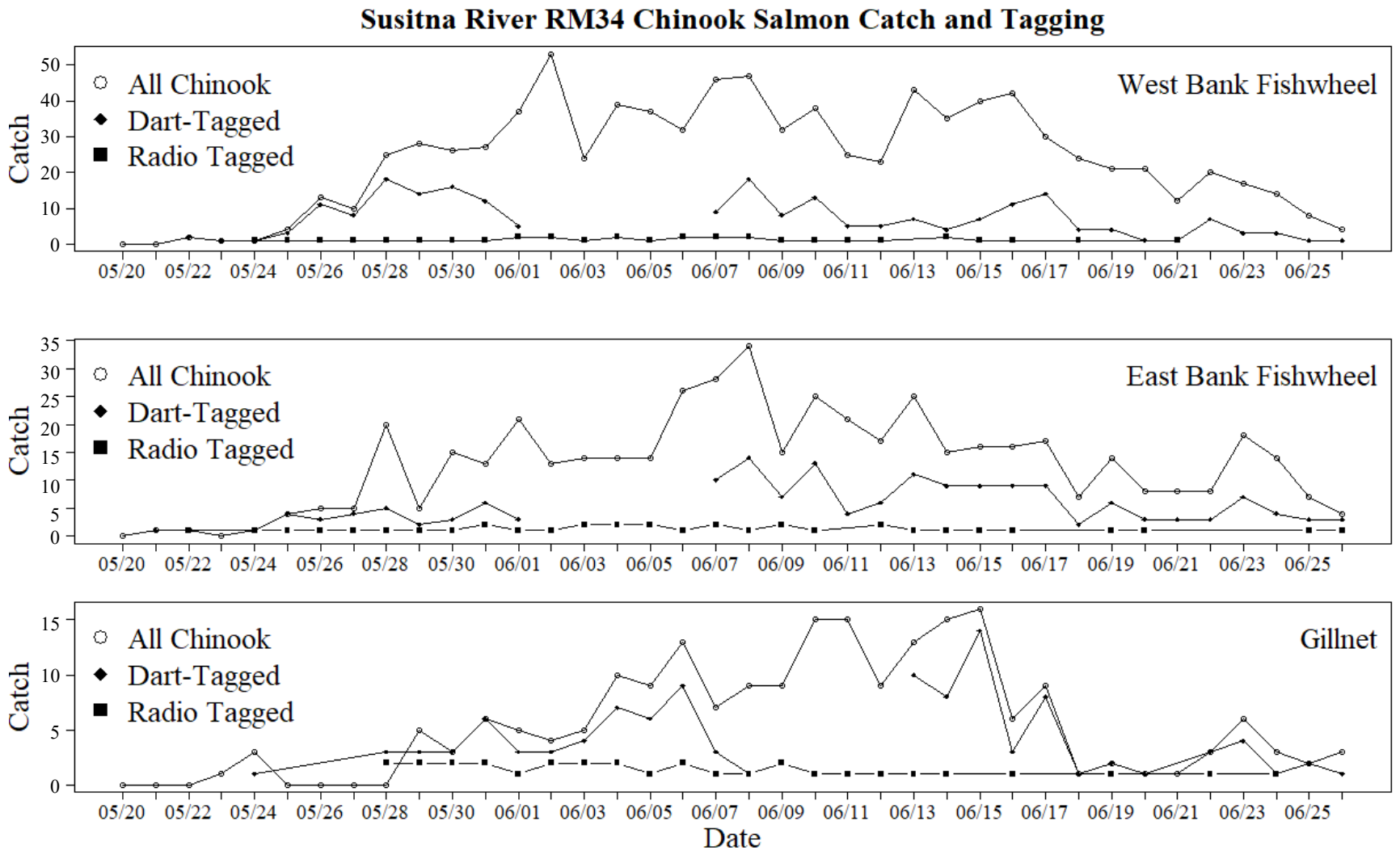

Figure 4.–Catch (all lengths) and tagging of Chinook salmon at the RM 34 mainstem Susitna River tagging operation for the west-bank fish wheel (top), east-bank fish wheel (middle), and gillnets (bottom), 2021.

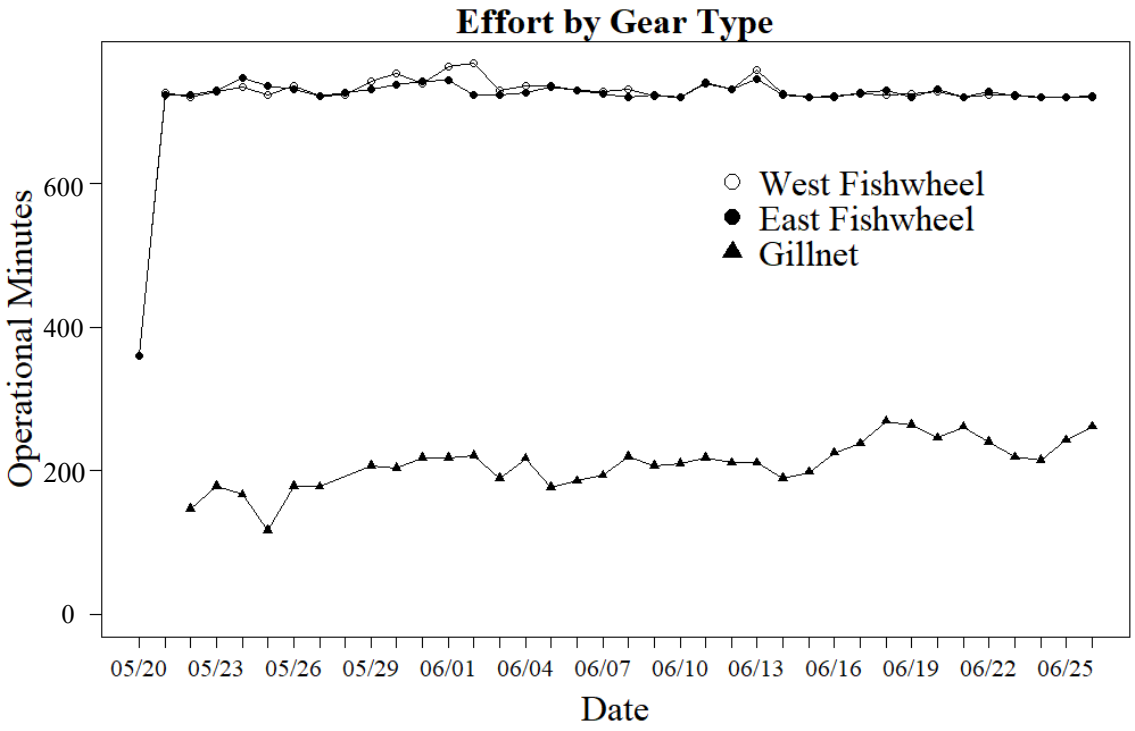

Figure 5.–Effort by gear for the mainstem Susitna River tagging operation at RM 34, 2021.

Deshka River Tag Recovery in 2021

The total Chinook salmon passage at the Deshka River weir from May 20 through August 12, 2021, was 18,647 fish of all sizes (D. Lescanec and S. Dotomain, ADF&G, Division of Sport Fish, Palmer, unpublished data). A total of 105 PIT-tagged fish were detected passing the weir.

Multiple daily tests of the PIT detection system were performed by passing a PIT tag through each antenna of the PIT reader, showing whether the detector apparatus was functioning without major problems. Field staff recorded the time tagged fished were observed moving through the array and checked to confirm a detection by the system at that time. All tests indicated the system operated properly throughout the season.

To estimate the number of Chinook salmon ≥500 mm METF passing through the Deshka weir, size data collected from the Deshka River age-sex-length sampling program (Lescanec 2022) were used. There was no significant difference in the proportion of Chinook salmon ≥500 mm METF among 3 temporal strata (Fisher exact test; $P = 1$), and sampling approximated overall abundance. Therefore, applying the pooled proportion of fish ≥500 mm METF (0.984) to the 18,674 Chinook salmon that passed the Deshka River weir gave an estimated 18,371 fish ≥500 mm METF length.

Estimated Chinook Salmon Abundance at RM 34 in 2021

Size selectivity tests (Kolmogorov-Smirnov [KS] Tests 1 and 2 in Appendix B1) were conducted to test for equal probability of capture (Assumption IV listed in *Mark–Recapture Assumptions* in *Methods*) and to determine whether stratification of the abundance estimate was required. KS Test 1 was used to determine whether probability of capture at the Deshka weir recovery event was affected by fish size in the tagging event. The Deshka weir test was significant (type 1 error rate of 0.05; Figure 6; $D = 0.279$, $P < 0.001$), suggesting size selectivity at the tagging event (RM 34). KS Test 2, used to determine whether the probability of capture during the second event was

affected by size, was not significant (Figure 7; D = 0.134, P = 0.073), suggesting the second event was not size selective. Because the test for size selectivity during the second event was not significant, a pooled abundance estimate was used.

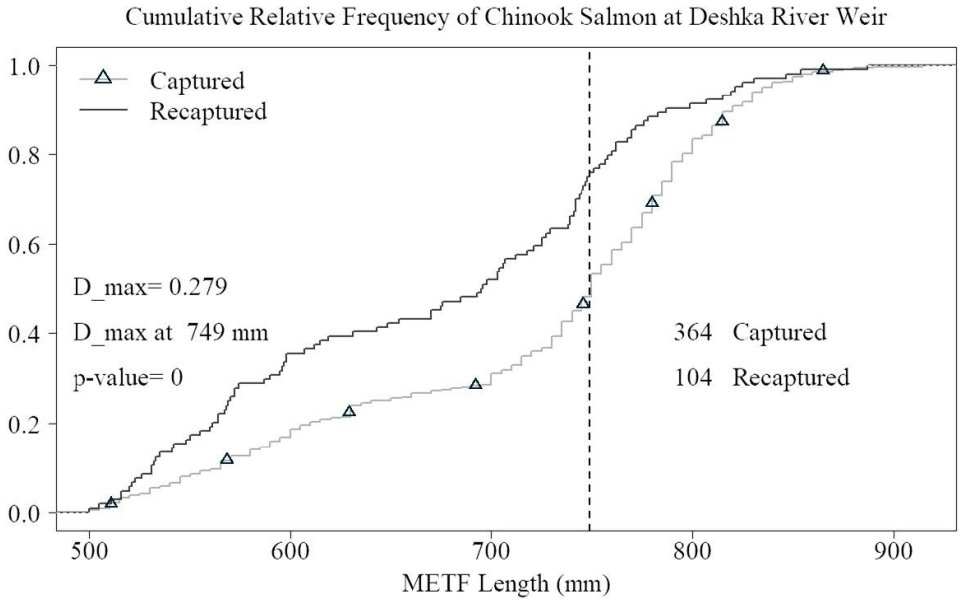

Figure 6.–Cumulative relative frequency of all Chinook salmon ≥500 mm METF captured at the Deshka River weir (lower line) and tagged fish that were recaptured at the Deshka River weir (upper line), 2021.

Note: Vertical dashed line indicates D-max.

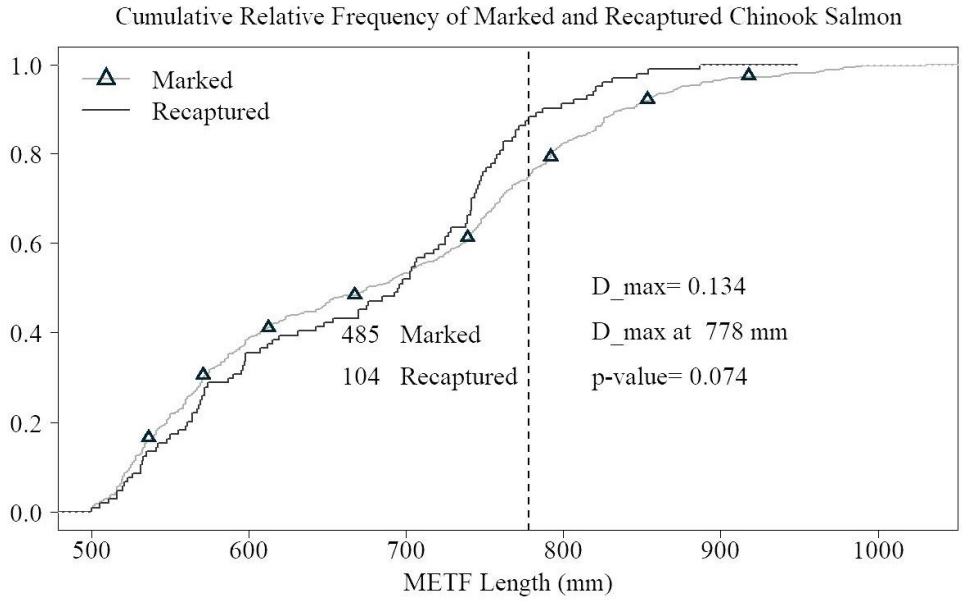

Figure 7.–Cumulative relative frequency of Chinook salmon ≥500 mm METF tagged at Susitna RM 34 (lower line) and recaptured at the Deshka River weir (upper line), 2021.

Note: Vertical dashed line indicates D-max.

Consistency Test III ("Complete Mixing" in Appendix C1) was also conducted. Tests I and II were not carried out for reasons stated earlier. The temporal Consistency Test III was not significant ($\chi^2 = 1.41$, df = 3, $P = 0.70$), whereas the spatial Consistency Test III was significant ($\chi^2 = 41.3$, df = 2, $P < 0.001$). We therefore had to rely on the historical insignificance of Test II (Appendix C1) to satisfy the consistency requirements of the pooled Peterson estimator.

The estimated abundance of all Chinook salmon ≥500 mm METF passing the RM 34 tagging site in 2021 was 62,438 (simulated SE = 6,863; 95% simulated confidence interval: 50,049–76,487). We also produced 2 alternative estimates to determine the magnitude of bias introduced by some of the analysis decisions we made. For one alternative estimate, we used a size-stratified estimator (with a 750 mm stratification point), which resulted in an estimate that was 13% higher than the pooled Peterson estimate. For a second alternative estimate, we included the voided tags in the estimate. The abundance estimate using voided tags was 4% smaller than the pooled Peterson estimate.

PROPORTION OF NON-DESHKA CHINOOK SALMON IN THE DESHKA RIVER SPORT FISHERY

The sport fishery for Chinook salmon was opened by ADF&G emergency order on June 18. Tissue samples were collected from 107 fish, 57 from the mouth of the Deshka River and 50 from the upper section of the river. The laboratory quality control analysis did not find any samples with missing data or duplicate genotypes. The overall failure rate for both area strata combined was about 1.2%.

For the mouth area stratum, *Deshka* was the predominant stock, accounting for 63.4% of the mixture sample, followed by the *mainstem Susitna* stock at 32.6%, and *Yentna* stock at 4.1%. *Deshka* fish made up almost all of the upper area stratum (91.6%), *mainstem Susitna* made up 7.2%, and *Yentna* fish were present at 1.2% (Table 3, Figure 8).

Table 3.–Stock composition (%) estimates for Chinook salmon harvested in the Deshka River sport fishery, 2021.

					90% CRI (%)	
Stratum	n[a]	Reporting group	Mean (%)	SD (%)	5%	95%
Mouth	57					
		Mainstem Susitna	32.6	7.1	21.6	44.6
		Deshka	63.4	7.0	52.0	74.8
		Yentna	4.1	3.9	0.0	11.4
Upper	50					
		Mainstem Susitna	7.2	4.7	1.1	15.8
		Deshka	91.6	5.0	81.8	98.2
		Yentna	1.2	2.1	0.0	5.0

Note: Estimates include mean, standard deviation (SD), and 90% credibility interval (CRI).

[a] n = successfully analyzed sample size.

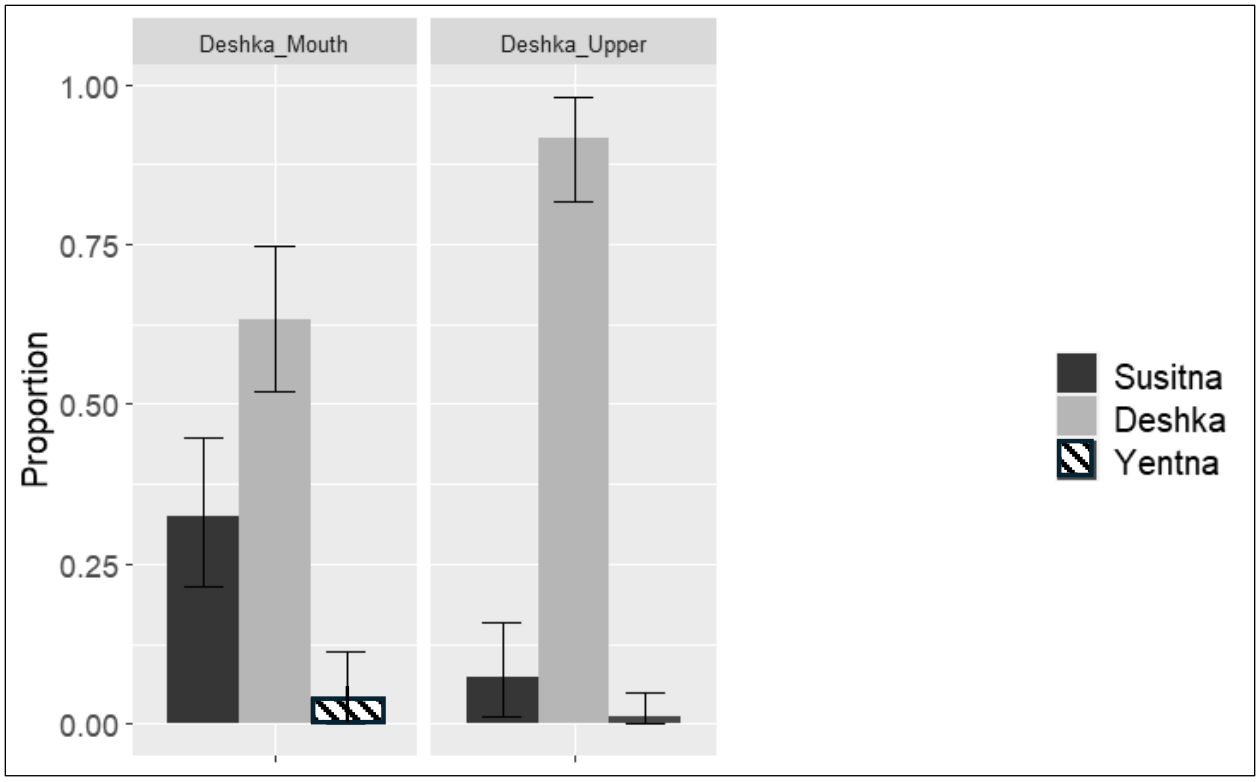

Figure 8.–Proportion of Susitna, Deshka, and Yentna River Chinook salmon harvested by the Deshka River sport fishery in the mouth and upper river sections, 2021.

MAINSTEM SUSITNA RIVER DISTRIBUTION IN 2021

Individual drainage estimates were assembled into 5 spawning groups with each group representing an ADF&G management area. Of the 99 radio tags applied at RM 34 of the Susitna River, 81 were assigned a final spawning group (Table 4). Radiotagged Chinook salmon were widely distributed throughout the mainstem Susitna River drainage in 2021. The number of detected radio tags in each spawning group ranged from 7 (Susitna RM 102–153.4 group) to 25 (Deshka River group). The Deshka River group contributed 21,094 fish ≥500 mm (SE = 4,126) to the drainage abundance, and the Eastside Susitna River group accounted for 13,500 fish ≥500 mm (SE = 3,328; Table 4).

Table 4.–Tag assignments, proportion of abundance (P), estimated abundance (N), and associated standard error (SE) for all fish ≥500 mm in the mainstem Susitna River, 2021.

Group	Tags assigned	P	N	SE (N)
Deshka River	25	0.338	21,094	4,126
Eastside Susitna River	16	0.216	13,500	3,328
Talkeetna River	8	0.108	6,750	2,354
Susitna RM 102.4–153.4	7	0.095	5,906	2,207
Chulitna River	18	0.243	15,188	3,524
Grand total	81	1	62,438	6.863

The test of uniform probability of radiotagging by size (KS Test 1 in Appendix B1) was not significant ($D = 0.163$, $P = 0.62$), although the test had low power with only 18 of 25 radio tags in fish with known length assigned to the Deshka River. Some evidence of size selectivity was apparent because the estimated proportion of Chinook salmon ≥500 mm and <750 mm (stratification point for abundance estimate) was 0.37, whereas the proportion of radiotagged fish ≥500 mm and <750 mm was higher at 0.53.

There was also evidence of selectivity by gear type for spawning groups migrating past the RM 34 site of the mainstem Susitna River. A contingency table test of independence found that tag distribution among the 5 spawning groups was significantly different between tagging gear (west fish wheel, east fish wheel, and gillnet; $P = 0.002$; Table 5). Different spawning distribution estimates by gear type are thought to be associated with bank orientation has been seen in previous iterations of this study.

Table 5.–Number and proportion of radiotagged Chinook salmon assigned to spawning groups in the mainstem Susitna River by RM 34 capture gear, 2021.

	Number				Proportion		
Susitna River spawning group	West-bank fish wheel	East-bank fish wheel	Gillnets	Total	West-bank fish wheel	East-bank fish wheel	Gillnets
Chulitna River	4	12	2	18	0.191	0.363	0.105
Susitna RM 102.4–153.4	1	3	3	7	0.048	0.091	0.158
Deshka River	12	9	4	25	0.571	0.273	0.211
Eastside Susitna River	0	6	6	12	0	0.182	0.474
Talkeetna River	4	3	1	8	0.19	0.091	0.052
Total	21	33	16	70	1	1	1

Note: Some radio tags could not be associated with a capture method due to a crew error.

To investigate the effect of ignoring size stratification, we applied spawning distribution estimates for each size group to our size stratified estimate of abundance. Size stratified estimates of abundance were 10%, 34%, and 41% larger for the Deshka, Susitna RM 102.4–153.4, and Chulitna spawning groups, respectively, and 4% and 17% lower for the Eastside and Talkeetna spawning groups, respectively.

COMPARISON TO PAST YEARS

ADF&G has estimated mainstem Susitna River Chinook salmon abundance at RM 34 from 2013 through 2021 (Table 6), and spawning distribution has been estimated every year from 2012 to 2020, except 2018. The estimated abundance for 2021 (62,438) was close to the historical average (2013–2020).

On average from 2013 to 2020, the Eastside Susitna River group accounted for the largest proportion of the mainstem Susitna River abundance (31%; Table 7). The Deshka River spawning group ranged from 16% to 41% of the mainstem Susitna River Chinook salmon abundance during that time but contributed slightly less than the Eastside Susitna River group on average (25%; Table 7). In 2021, the Deshka River group represented a larger proportion of the total spawning abundance than the historical average whereas both the Eastside and Talkeetna spawning groups represented a smaller proportion of the historical average.

Table 6.–Estimated abundance and 95% CI of Chinook salmon ≥500 mm at the mainstem–Yentna River confluence (RM 34 tagging site) for the mainstem Susitna River, 2013–2021.

Return year	Abundance	95% CI
2013	89,463	77,720–114,954
2014	68,225	53,473–94,240
2015	88,580	77,500–101,100
2016	65,826	58,358–74,201
2017	45,503	38,526–53,610
2018	30,605	23,262–40,396
2019	57,850	43,132–76,408
2020	62,346	46,245–87,888
Average 2013–2020	63,550	
2021	62,438	50,049–76,487

Source: LGL and ADF&G (2014); LGL and ADF&G (2015); DeCovich et al. 2020; N. DeCovich ADF&G, Division of Sport Fish, Palmer, unpublished data.

Table 7.–Abundance (*N*) of Chinook salmon ≥500 mm and spawning distributions (percentage by spawning group) estimated at the mainstem Susitna River RM 34 tagging site, 2013–2020.

		Tributary group					
Year	Estimate	Deshka River	Eastside Susitna River	Talkeetna River	Susitna RM 102.4–153.4 [a]	Chulitna River	Total
2013	N	18,469	19,299	24,408	7,680	19,607	89,463
	%	21%	22%	27%	9%	22%	100%
2014	N	14,024	17,171	14,024	6,609	16,397	68,225
	%	21%	25%	21%	10%	24%	100%
2015	N	25,454	33,090	13,236	6,109	10,691	88,580
	%	29%	37%	15%	7%	12%	100%
2016	N	26,922	22,676	6,779	2,226	7,223	65,826
	%	41%	34%	10%	3%	11%	100%
2017	N	13,610	16,104	7,044	2,432	6,313	45,503
	%	30%	35%	15%	5%	14%	100%
2018				no estimates			
2019	N	9,425	14,121	7,400	4,027	22,877	57,850
	%	16%	24%	13%	7%	40%	100%
2020	N	11,341	21,933	8,975	1,617	18,480	62,346
	%	18%	35%	14%	3%	30%	100%
Average 2013–2020	%	25%	31%	16%	6%	22%	100%
2021	N	21,094	13,500	6,750	5,906	15,188	62,438
	%	34%	22%	11%	9%	24%	100%

Source: LGL and ADF&G 2014; LGL and ADF&G 2015; N. DeCovich, ADF&G SF, Palmer, unpublished data.

Note: Rounding of some values means percentages do not always equal 100%.

[a] Chulitna River confluence to Devils Canyon.

DISCUSSION

Examination of radiotag spawning destination assignments reveals a clear pattern where Deshka River bound Chinook salmon dominate fish wheel catches on the western bank of the Susitna River. This bank orientation complicates the study of spawning distribution. Ideally, radio tags are applied proportionally, both temporally and spatially, to all stocks migrating past the tagging point. However, radio tags are expensive and only a certain quantity can be purchased preseason to distribute in proportion to catch rates, making proportional sampling difficult should a strong run materialize (depleting tag reserves). To ensure complete spatial coverage with available tags, we applied fixed numbers of tags at each of the fish wheel and gillnet sites, which exposed us to potential problems if some stocks exhibited bank orientation, especially when combined with differences in run timing. Unbiased tagging rates also assume gillnets are sampling at the same rate as fish wheels, which is very unlikely. Selectivity of stocks by gear type was detected statistically not only in this 2021 study, but also during the 2015–2017 studies, when substantially larger sample sizes were available (e.g., DeCovich et al. 2020). Furthermore, we have often seen that stocks spawning higher in the drainage tend to migrate earlier than those spawning lower in the drainage (LGL and ADF&G 2015; DeCovich et al. 2020).

To examine impacts of potential gear selectivity on the estimation of abundance, we compared the Deshka River weir count (≥500 mm) to the mark–recapture estimate of Deshka River abundance. The weir count and mark–recapture estimate will deviate if radio tags were not deployed in proportion to the actual abundance of the Deshka River stock passing upstream of the tagging site (RM 34). The Deshka River weir count was 18,371 Chinook salmon ≥500 mm (D. Lescanec, ADF&G, Division of Sport Fish, Palmer, unpublished data). For comparison, the estimated abundance of Deshka River Chinook salmon (calculated from the proportions of radiotagged fish assigned to the Deshka River applied to the mark–recapture estimated abundances for the mainstem Susitna River and corrected for harvest below the weir) was 21,094 (SE = 4,126) fish ≥500 mm (Table 7), suggesting stock specific abundance estimates were not badly biased by our radiotag deployment method. Similar findings were made in 2015–2017 for this same comparison when radiotag sample sizes were much higher. Furthermore, after the 2017 study, stock-specific estimates of abundance were not calculated using gear-specific abundance estimates to weight gear-specific distribution estimates because they were similar to the pooled estimate (DeCovich et al. 2020).

Despite potential selectivity bias, we elected to generate our 2021 stock composition estimate without size stratification and using all radiotagged fish. We included radiotagged fish associated with the voided pit tags because their removal had a negligible effect on the stock composition estimate. Lack of a size-stratified estimate differs from most previous years' stratified estimates. Because most estimates were stratified by size historically, and because of the marginal insignificance of the KS Test 2 for equal probability of capture by size during the second event in 2021, we conducted a size-stratified estimate of abundance to compare to the pooled estimate of 2021 abundance. Stock-specific stratified estimates were within 10% for the Deshka and Eastside spawning groups, which supported the most active fisheries in the Susitna River drainage. It is noted the use of a size-stratified estimate would have pulled the estimate of spawning abundance for the Deshka River stock farther away from the weir count.

Due to fiscal reasons, the abundance assessment described in this study only used the Deshka weir as a recovery site. In previous years, various other recovery sites have been used, including a weir

at Montana Creek and a fish wheel site at Sunshine (RM 83). These additional recovery sites allowed us to conduct more diagnostic testing of the mark–recapture assumptions (see *Methods*), and gave us access to other Darroch-type models should assumptions appear violated. By using only the Deshka weir as a recovery site, we had to rely on the results from these more extensive studies to assume the Petersen model of abundance estimation was appropriate. It is acknowledged that this situation is not ideal, and the 2021 estimates must be given this caveat. Furthermore, the 2021 estimates suffered from implementation issues because some pit tags had to be voided from the assessment. This meant we failed to deploy pit tags through time with methods identical to the more robust assessments. This concern is somewhat mitigated because naïve use of the voided tags (without assumption testing) did not meaningfully change the abundance estimate.

The genetic estimates reported here are the first look at the stock composition of the Susitna River sport fishery harvest. As suspected, the harvest near the mouth of the Deskha River contained Chinook salmon from the *mainstem Susitna* and *Yentna* reporting groups, and harvests farther up the Deshka River contained more *Deshka* Chinook salmon. Harvest estimates from the Statewide Harvest Survey consider both of these spatial strata as Deshka River origin fish. This generalization may be fine in some contexts but presents a problem for run reconstructions because we estimate the inriver run from the weir count plus the harvest below the weir. This approach produces an overestimate of the inriver run because some of the harvested fish would have migrated out of the mouth area to spawn elsewhere. Because of this, we have only reported the harvest stock compositions for 2021 here and have not extrapolated the number of Deshka River Chinook salmon harvested. However, the 2021 study successfully estimated stock proportions, and such an approach in future years when run sizes are large enough to allow harvest could enable more accurate estimates of run size and escapements alike.

ACKNOWLEDGEMENTS

This study was funded by the State of Alaska through the State Wildlife Grant program. Mainstem Susitna River camp RM 34 was operated by the following Fish and Wildlife Technicians: Caleb Owen, Sadie Oswald, Nathan Beroff, Krista Mahan, Mathew Lewis, and Jordan Houk.

REFERENCES CITED

ADF&G Chinook Salmon Research Team. 2013. Chinook salmon stock assessment and research plan, 2013. Alaska Department of Fish and Game, Special Publication No. 13-01, Anchorage. http://www.adfg.alaska.gov/FedAidPDFs/SP13-01.pdf.

Arnason, A. N., C. W. Kirby, C. J. Schwarz, and J. R. Irvine. 1996. Computer analysis of data from stratified mark–recovery experiments for estimation of salmon escapements and other populations. Canadian Technical Report of Fisheries and Aquatic Sciences No. 2106.

Bernard, D. R., J. J. Hasbrouck, and S. J. Fleischman. 1999. Handling-induced delay and downstream movement of adult Chinook salmon in rivers. Fisheries Research 44:37–46.

Campbell, J., N. A. DeCovich, A. Reimer, and A. W. Barclay. 2022. Operational Plan: Susitna River Chinook salmon inriver abundance, 2021. Alaska Department of Fish and Game, Division of Sport Fish, Regional Operational Plan No. ROP.SF.2A.2022.16, Anchorage. http://www.adfg.alaska.gov/FedAidPDFs/ROP.SF.2A.2022.16.pdf.

Chapman, D. G. 1951. Some properties of the hypergeometric distribution with applications to zoological censuses. University of California Publications in Statistics 1:131–160.

Cleary, P. M., R. J. Yanusz, J. W. Erickson, D. J. Reed, R. A. Neustel, J. P. Bullock, and N. J. Szarzi. 2016a. Abundance and spawning distribution of Susitna River chum *Oncorhynchus keta* and coho *O. kisutch* salmon, 2012. Alaska Department of Fish and Game, Fishery Data Series No. 16-52, Anchorage. http://www.adfg.alaska.gov/FedAidPDFs/FDS16-52.pdf.

Cleary, P. M., R. J. Yanusz, J. W. Erickson, D. J. Reed, R. A. Neustel, and N. J. Szarzi. 2016b. Abundance and spawning distribution of Susitna River chum *Oncorhynchus keta* and coho *O. kisutch* salmon, 2011. Alaska Department of Fish and Game, Fishery Data Series No. 16-35, Anchorage. http://www.adfg.alaska.gov/FedAidPDFs/FDS16-35.pdf.

Darroch, J. N. 1961. The two-sample capture-recapture census when tagging and sampling are stratified. Biometrika 48:241–260.

DeCovich, N., and J. Campbell. 2022. Susitna River Chinook salmon abundance and distribution, 2018–2020. Alaska Department of Fish and Game, Fishery Data Series No. 22-22, Anchorage. http://www.adfg.alaska.gov/FedAidPDFs/FDS22-22.pdf.

DeCovich, N., J. Campbell, and D. Evans. 2020. Susitna River Chinook salmon abundance and distribution, 2017. Alaska Department of Fish and Game, Fishery Data Series No. 20-04, Anchorage. http://www.adfg.alaska.gov/FedAidPDFs/FDS20-04.pdf.

Lescanec, D. 2022. Operational Plan: Deshka River weir, 2021–2025. Alaska Department of Fish and Game, Division of Sport Fish, Regional Operational Plan No. ROP.SF.2A.2022.10, Anchorage. http://www.adfg.alaska.gov/FedAidPDFs/ROP.SF.2A.2022.10.pdf.

LGL and ADF&G (LGL Research Associates, Inc. and Alaska Department of Fish and Game, Division of Sport Fish). 2014. Salmon escapement study, Study plan Section 9.7:Initial Study Report–Part A: Sections 1-6, 8-10 (SuWa223). Alaska Energy Authority, Susitna-Watana Hydroelectric Project, Anchorage.

LGL and ADF&G (LGL Research Associates, Inc. and Alaska Department of Fish and Game, Division of Sport Fish). 2015. Salmon Escapement Study, Study Plan Section 9.7, Study Completion Report. (SuWa289). Alaska Energy Authority, Susitna-Watana Hydroelectric Project, Anchorage.

Moran, B. M., and E. C. Anderson. 2019. Bayesian inference from the conditional genetic stock identification model. Canadian Journal of Fisheries and Aquatic Sciences 76(4):551–560.

Pella, J., and M. Masuda. 2001. Bayesian methods for analysis of stock mixtures from genetic characters. Fishery Bulletin 99:151–167.

Reimer, A. M., and N. A. DeCovich. 2020. Susitna River Chinook salmon run reconstruction and escapement goal analysis. Alaska Department of Fish and Game, Fishery Manuscript No. 20-01, Anchorage. http://www.adfg.alaska.gov/FedAidPDFs/FMS20-01.pdf.

REFERENCES CITED (Continued)

Scarnecchia, D. L. 1979. Variation of scale characteristics of coho salmon with sampling location on the body. Progressive Fish Culturist 41(3):132–135.

Schwarz, C. J., and C. G. Taylor. 1998. Use of stratified-Petersen estimator in fisheries management: estimating the number of pink salmon (*Oncorhynchus gorbuscha*) spawners in the Fraser River. Canadian Journel of Fisheries and Aquatic Sciences 55:281–296.

Seber, G. A. F. 1982. The estimation of animal abundance and related parameters. 2nd edition. Griffin and Company, Ltd. London.

Welander, A. D. 1940. A study of the development of the scale of Chinook salmon *Oncorhynchus tshawytscha*. Master's thesis. University of Washington, Seattle.

Yanusz, R., R. Merizon, D. Evans, M. Willette, T. Spencer, and S. Raborn. 2007. Inriver abundance and distribution of spawning Susitna River sockeye salmon *Oncorhynchus nerka*, 2006. Alaska Department of Fish and Game, Fishery Data Series No. 07-83, Anchorage. http://www.adfg.alaska.gov/FedAidpdfs/fds07-83.pdf.

Yanusz, R. J., P. M. Cleary, J. Campbell, G. Horner-Neufeld, D. Reed, and N. A. DeCovich. 2018. Abundance, distribution, and surveys of spawning Chinook salmon 2012–2014 and spawning coho salmon, 2013–2014 in the Susitna River. Alaska Department of Fish and Game, Fishery Data Series No. 18-16, Anchorage. http://www.adfg.alaska.gov/FedAidPDFs/FDS18-16.pdf.

APPENDIX A: RULES USED TO INCLUDE OR CENSOR FISH IN MARK–RECAPTURE OR SPAWNING DISTRIBUTION STUDIES

Appendix A1.–Rules used to censor or include radiotagged fish in the mark–recapture and spawning distribution studies for 2018–2020 aerial survey and stationary telemetry data.

Outcome	Mark–recapture study	Spawning distribution study	Spawning (final) location
Fish detected and failed to migrate past mark–recapture gateway (mainstem gateway:1 mile upstream of RM 35)	–	–	NA
Fish that display initial upstream movement, regardless later downstream movement, or display a single location.	X	X	Assigned to upstream-most location.
Fish that display a cluster of locations (locations within 20 miles of each other but not less than 2 miles of each other).	X	X	Assigned a known location in the middle of the cluster but if less than 2 miles assign upstream-most location.
Fish that display a cluster of locations with 1 "outlier."	X	X	Assigned a known location in the middle of the cluster unless the outlier is documented during a late season survey. In that case, the assigned location will be the upstream-most location.
Fish migrates up river *A* then has strong signal locations in river *B*.	X	X	Assigned to river *B*.
Fish caught by angler.	X	–	NA
Fish that have tagging data but are never detected by stationary or aerial telemetry.	X	–	NA
Fish that migrated past the gateway point for the mark–recapture study, but then came back down below the gateway within 48 hours and never migrated past the gateway again.	X	–	NA

Note: "X" indicates the fish was used in the study; an en dash indicates it was not; NA means not applicable.

APPENDIX B: DETECTION AND MITIGATION OF SELECTIVE SAMPLING DURING A 2-EVENT MARK–RECAPTURE EXPERIMENT

Size- and sex-selective sampling may cause bias in 2-event mark-recapture estimates of abundance and size and sex composition. Kolmogorov-Smirnov (KS) 2-sample tests are used to detect size-selective sampling, and contingency table analyses (chi-square tests of independence) are used to detect evidence of sex-selective sampling.

Results of the KS and chi-square tests will dictate whether the mark–recapture data needs to be stratified to obtain an unbiased estimate of abundance. The nature of the detected selectivity will also determine whether the first, second, or both event samples are used for estimating size and sex compositions.

DEFINITIONS

M = Lengths or sex of fish marked in the first event.

C = Lengths or sex of fish inspected for marks in the second event.

R = Lengths or sex of fish marked in the first event and recaptured in the second event.

SIZE-SELECTIVE SAMPLING: KS TESTS

Three KS tests are used to test for size-selective sampling:

Test 1	C vs. R	Used to detect size selectivity during the first sampling event. H_o: Length distributions of populations associated with C and R are equal.
Test 2	M vs. R	Used to detect size selectivity during the second sampling event. H_o: Length distributions of populations associated with M and R are equal.
Test 3	M vs. C	Used to corroborate the results of the first 2 tests. H_o: Length distributions of populations associated with M and C are equal.

SEX-SELECTIVE SAMPLING: CHI-SQUARE TESTS

Three contingency table analyses (chi-square tests on 2 × 2 tables) are used to test for sex-selective sampling.

Test 1	C vs. R	Used to detect sex selectivity during the first sampling event. H_o: Sex is independent of the C–R classification.
Test 2	M vs. R	Used to detect sex selectivity during the second sampling event. H_o: Sex is independent of the M–R classification.
Test 3	M vs. C	Used to corroborate the results of the first 2 tests. H_o: Sex is independent of the M–C classification.

Appendix B2 presents possible results of selectivity testing, their interpretation, and prescribed action.

Appendix B2.–Interpretation and actions based on size or sex selectivity testing.

Case	KS or chi-square test: M vs. R (2nd event test)	KS or chi-square test: C vs. R (1st event test)	KS or chi-square test: M vs. C (1st vs 2nd event)	Interpretation and action
I	Fail to reject H_o	Fail to reject H_o	Fail to reject H_o	**Interpretation**: No selectivity during either sampling event. **Action**: Abundance: Use a Petersen-type model without stratification. Composition: Use all data from both sampling events.
II	Reject H_o	Fail to reject H_o	Reject H_o	**Interpretation:** No selectivity during the first event but there is selectivity during the second event. **Action**: Abundance: Use a Petersen-type model without stratification. Composition: Use data from the first sampling event without stratification. Second event data only used if stratification of the abundance estimate is performed, with weighting according to Equations 1–3 in Appendix B3.
III	Fail to reject H_o	Reject H_o	Reject H_o	**Interpretation:** No selectivity during the second event but there is selectivity during the first event. **Action**: Abundance: Use a Petersen-type model without stratification. Composition: Use data from the 2nd sampling event without stratification. 1st event data may be incorporated into composition estimation only after stratification of the abundance estimate and appropriate weighting according to Equations 1–3 in Appendix B3.
IV	Reject H_o	Reject H_o	Either result	**Interpretation:** Selectivity during both first and second events. **Action**: Abundance: Use a stratified Petersen-type model with estimates calculated separately for each stratum. Sum stratum estimates for overall abundance. Composition: Combine stratum estimates according to Equations 1–3 in Appendix B3.
V	Fail to reject H_o	Fail to reject H_o	Reject H_o	**Interpretation:** The results of the 3 tests are inconsistent. **Action:** Need to determine which of Cases I–IV best fits the data. Inconsistency can arise from high power of the M vs. C test or low power of the tests involving R. Examine sample sizes (generally M or C samples <100 fish and R samples <30 are considered small), magnitude of the test statistics (D_{max}), and the *P*-values of the 3 tests to determine which of Cases I–IV best fits the data.

COMPOSITION ESTIMATION FOR SIZE OR SEX STRATIFIED ESTIMATES

An estimate of the proportion of the population in the *k*th size or sex category for stratified data with *I* strata is calculated as follows:

$$\hat{p}_k = \sum_{i=1}^{I} \frac{\hat{N}_i}{\hat{N}} \hat{p}_{ik} \tag{1}$$

with variance estimated as

$$var\left[\hat{p}_k\right] \approx \frac{1}{\hat{N}^2} \sum_{i=1}^{I} \left(\hat{N}_i^2 var\left[\hat{p}_{ik}\right] + \left(\hat{p}_{ik} - \hat{p}_k \right)^2 var\left[\hat{N}_i\right] \right) \tag{2}$$

where

$\hat{p}_{ik}$ = estimated proportion of fish belonging to category *k* in stratum *i*,

$\widehat{N}_i$ = estimated abundance in stratum *i,* and

$\widehat{N}$ = estimated total abundance where

$$\hat{N} = \sum_{i=1}^{I} \hat{N}_i \,. \tag{3}$$

APPENDIX C: TESTS OF CONSISTENCY FOR THE PETERSON ABUNDANCE ESTIMATOR

Appendix C1.–Test of temporal or spatial consistency for the Petersen abundance estimator (from Seber 1982: p. 438).

Three contingency table analyses are used to determine if the Petersen estimate can be used to estimate abundance (Seber 1982). If any of the null hypotheses are not rejected, then a Petersen estimator may be used. If all three of the null hypotheses are rejected, a temporally or spatially-stratified estimator (Darroch 1961) should be used to estimate abundance.

Seber (1982) describes 4 conditions that lead to an unbiased Petersen estimate, some of which can be tested directly:

1) Marked fish mix completely with unmarked fish between events.
2) Equal probability of capture in the first event and equal movement patterns of marked and unmarked fish.
3) Equal probability of capture in the second event.
4) The expected number of marked fish in recapture strata is proportional to the number of unmarked fish.

In the following tables, the terminology of Seber (1982) is followed, where a represents fish marked in the first event, n fish are captured in the second event, and m marked fish recaptured; $m_{\bullet j}$ and $m_{i\bullet}$ represent summation over the ith and jth indices, respectively.

I. Mixing Test

This tests the hypothesis (condition 1) that movement probabilities (θ_{ij}), describing the probability that a fish moves from marking stratum i to recapture stratum j, are independent of marking stratum: H_0: $\theta_{ij} = \theta_j$ for all i and j.

Area or time marking strata (i)	Area or time recapture strata (j)				Not recaptured
	1	2	…	t	$a_i - m_{i\bullet}$
1	m_{11}	m_{12}	…	m_{1t}	$a_1 - m_{1\bullet}$
2	m_{21}	m_{22}	…	m_{2t}	$a_2 - m_{2\bullet}$
…	…	…	…	…	…
s	m_{s1}	m_{s2}	…	m_{st}	$a_s - m_{s\bullet}$

II. Equal Proportions Test[1] (SPAS[2] terminology)

This tests the hypothesis (Condition 4) that the marked to unmarked ratio among recapture strata is constant: H_0: $\Sigma_i a_i\theta_{ij}/U_j = k$, where k is a constant, U_j is the number of unmarked fish in stratum j at the time of second event sampling, and a_i is the number of marked fish released in stratum i. Failure to reject H_0 means the Petersen estimator should be used only if the degree of closure among tagging strata is constant; i.e., $\Sigma_j\theta_{ij} = \lambda$ (Schwarz and Taylor 1998: p. 289). A special case of closure is when all recapture strata are sampled, such as in a fish wheel-to-fish wheel experiment, where $\Sigma_j\theta_{ij} = 1.0$, otherwise biological and experimental design information should be used to assess the degree of closure.

-continued-

[1] There is no 1:1 correspondence between Tests II and III and conditions 2–3 above. Note that equal probability of capture in the first event will lead to (expected) nonsignificant Test II results as will mixing, and that equal probability of capture in the second event and equal closure ($\Sigma j\theta ij = \lambda$) will also lead to (expected) non-significant Test III results.

[2] Stratified Population Analysis System (Arnason et al. 1996).

Equal proportions test, continued:

	Area or time recapture strata (j)			
Number	1	2	…	t
Recaptured ($m_{\cdot j}$)	$m_{\bullet 1}$	$m_{\bullet 2}$	…	$m_{\bullet t}$
Unmarked ($n_j - m_{\cdot j}$)	$n_1 - m_{\bullet 1}$	$n_2 - m_{\bullet 2}$	…	$n_t - m_{\bullet t}$

III. Complete Mixing Test (SPAS terminology)

Tests the hypothesis that the probability that resighting a released animal is independent of its stratum of origin: H_0: $\Sigma_j \theta_{ij} p_j = d$, where p_j is the probability of capturing a fish in recapture stratum j during the second event, and d is a constant.

	Area or time marking strata (i)			
	1	2	…	s
Recaptured (m_i)	$m_{1\bullet}$	$m_{2\bullet}$	…	$m_{s\bullet}$
Not recaptured ($a_i - m_{i\bullet}$)	$6 - m_{1\bullet}$	$7 - m_{2\bullet}$	…	$a_s - m_{s\bullet}$