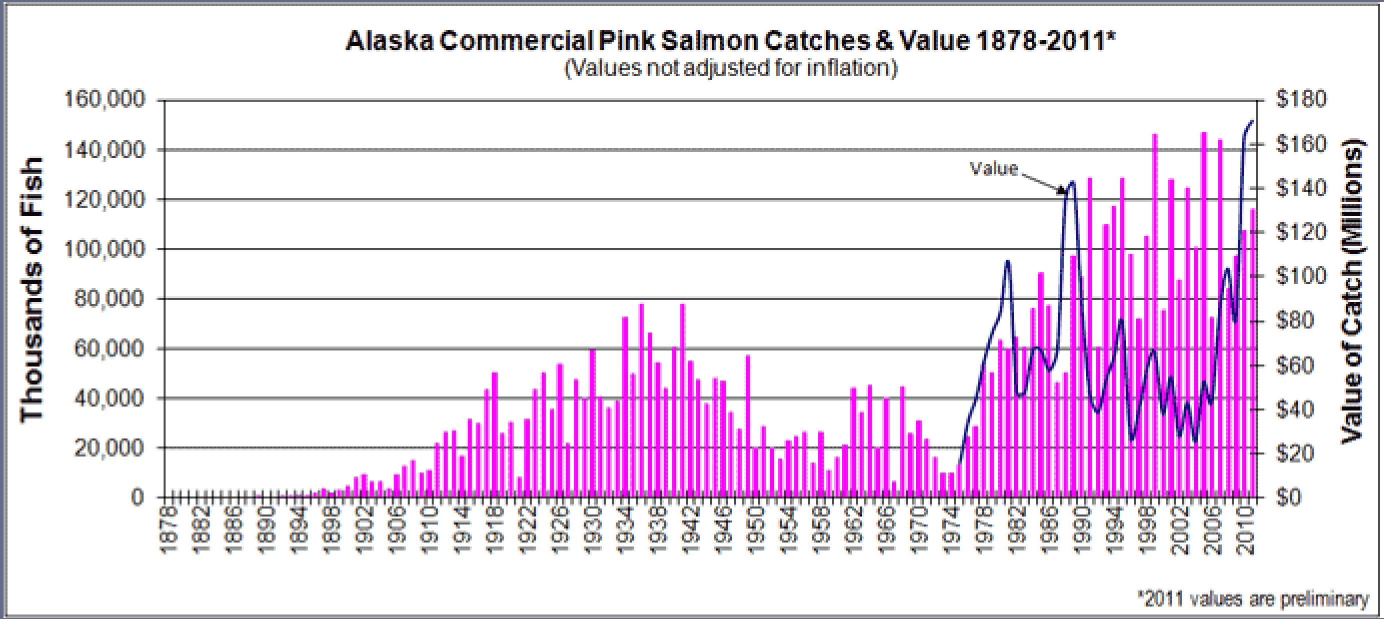
ASSESSING INTERACTIONS OF WILD & HATCHERY PINK AND CHUM SALMON

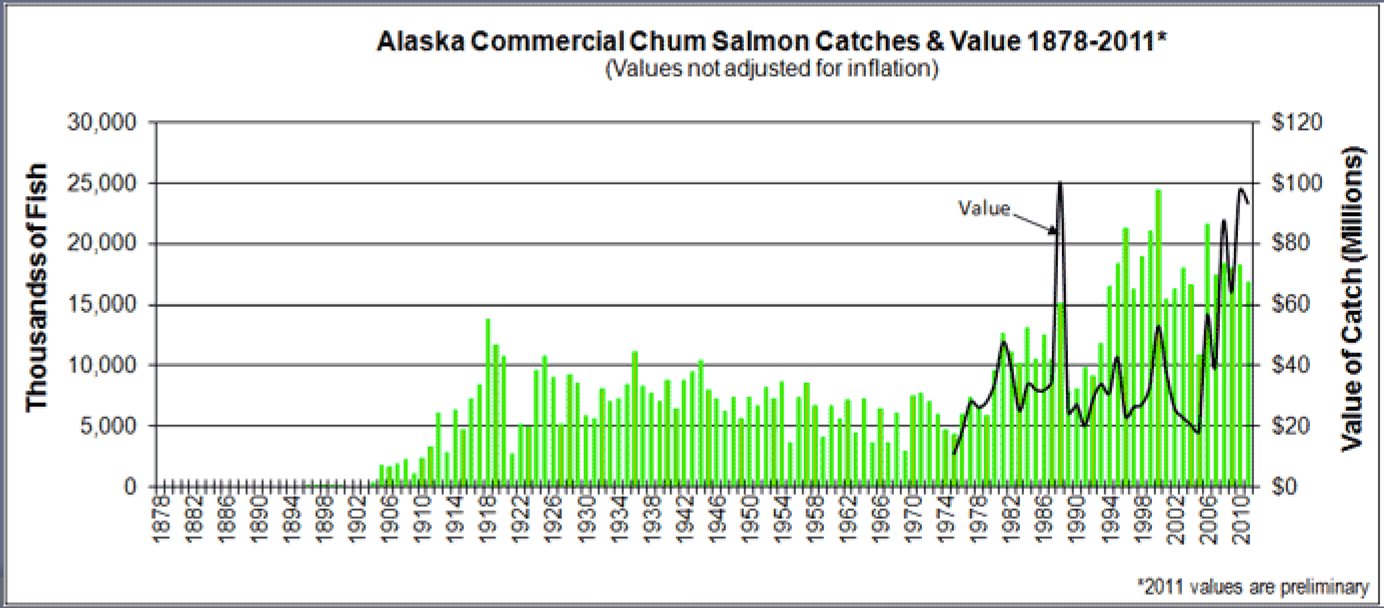
RESEARCH PROPOSAL

Steve Reifenstuhl General Manager, NSRAA
John Burke Ph.D. General Manager, SSRAA
Dave Bernard Ph.D. former ADF&G, Sport Fisheries consultant
John H. Clark Ph.D. ADF&G, Commercial Fisheries
Jeff Hard Ph.D. NOAA, Seattle
Ron Josephson ADF&G PNP Section Chief
Bill Smoker Ph.D. retired UAF professor
Bill Templin ADF&G, Genetics Lab
Alex Wertheimer retired NOAA research biologist

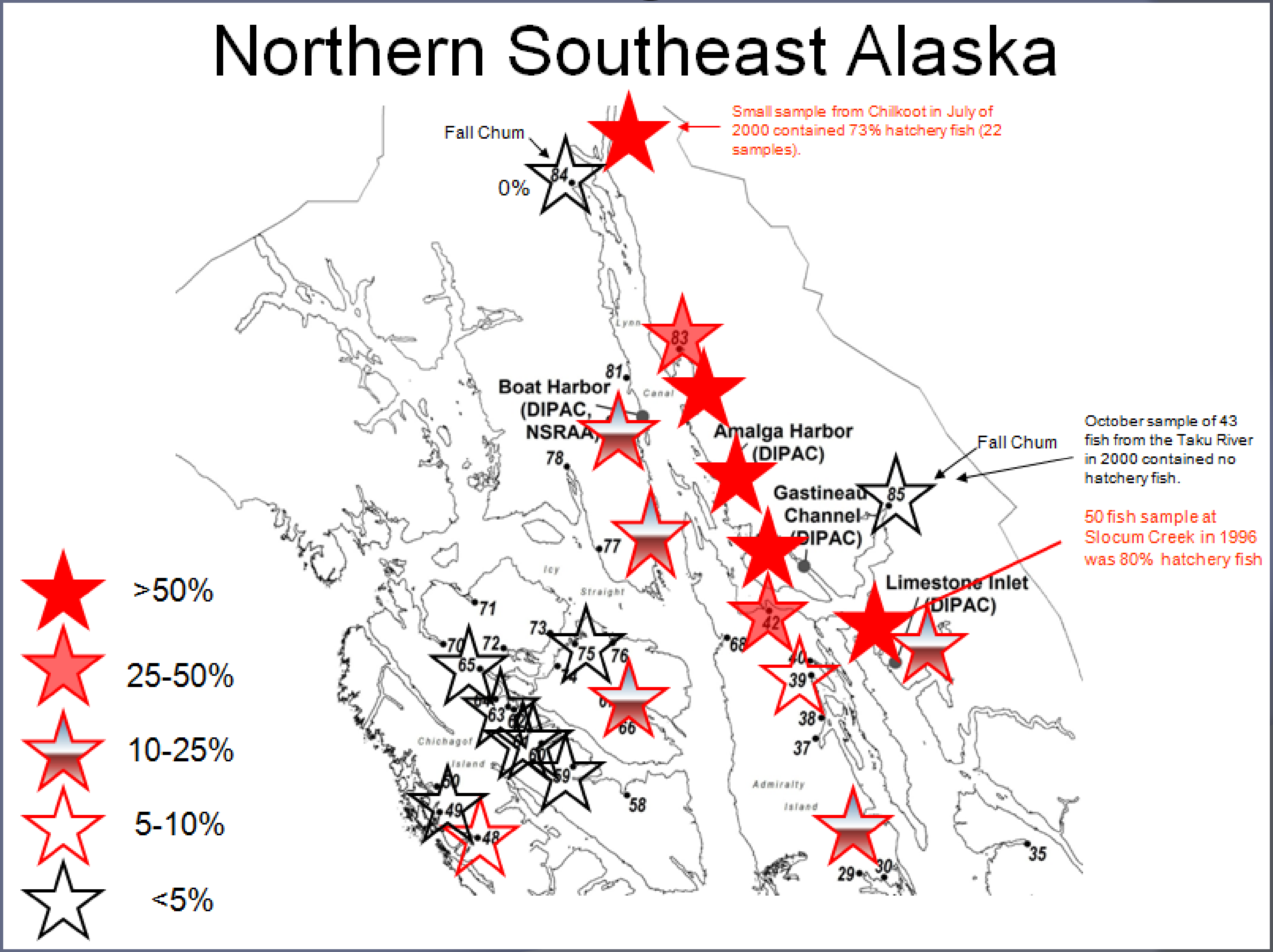
The Issue

Success….


Alaska Commercial Pink Salmon Catches & Value 1878-2011*
(Values not adjusted for inflation)
Thousands of Fish
Value of Catch (Millions)
Value
160,000
140,000
120,000
100,000
80,000
60,000
40,000
20,000
0
$180
$160
$140
$120
$100
$80
$60
$40
$20
$0
1878 1882 1886 1890 1894 1898 1902 1906 1910 1914 1918 1922 1926 1930 1934 1938 1942 1946 1950 1954 1958 1962 1966 1970 1974 1978 1982 1986 1990 1994 1998 2002 2006 2010
*2011 values are preliminary


Alaska Commercial Chum Salmon Catches & Value 1878-2011*
(Values not adjusted for inflation)
Thousands of Fish
Value of Catch (Millions)
Value
30,000
25,000
20,000
15,000
10,000
5,000
0
$120
$100
$80
$60
$40
$20
$0
1878 1882 1886 1890 1894 1898 1902 1906 1910 1914 1918 1922 1926 1930 1934 1938 1942 1946 1950 1954 1958 1962 1966 1970 1974 1978 1982 1986 1990 1994 1998 2002 2006 2010
*2011 values are preliminary

Chum Salmon Straying



Concerns to.... Questions

Is interbreeding negatively affecting fitness/productivity?

Is annual escapement of wildstocks biased by strays?

Do density interactions diminish productivity?

Components of Study

I. Genetic Stock Structure of Pinks & Chum Salmon

II. Extent of Annual Variability of Straying

III. Impact of Strays on Fitness (productivity) of Wild Salmon

Concentrate Research on Chum in Southeast and Pinks in PWS

I. Genetic Stock Structure of Pinks & Chum Salmon

Meta-populations

Allozyme mtDNA from 1990's

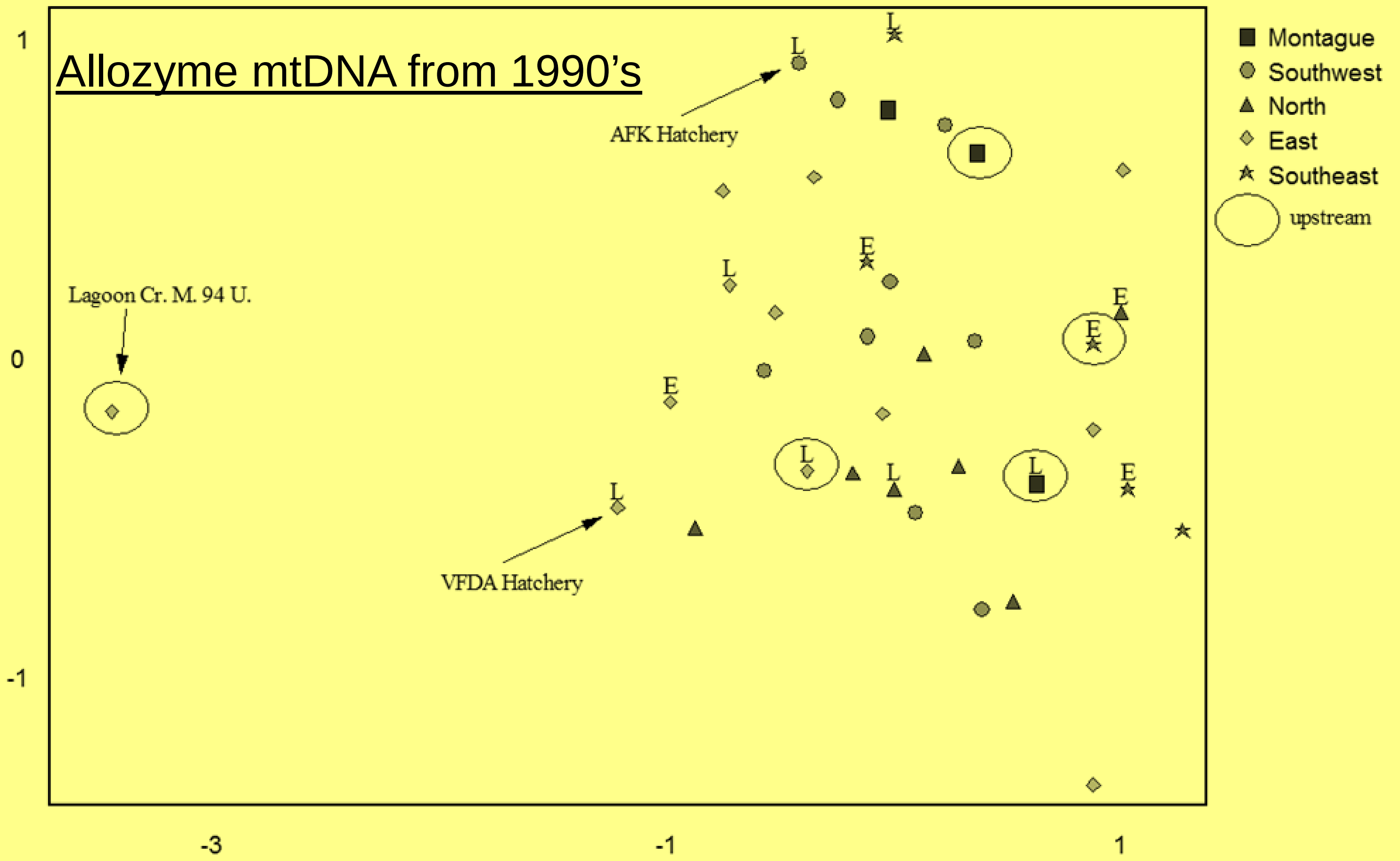


Figure 12. Multidimensional scaling analysis using mtDNA data of all even-year 1990s collections, after appropriate pooling within streams, from Prince William Sound, Alaska. Lagoon Creek., upstream, middle timing, 1994 is an outlier. No separation of early (E) and late (L) timing collections is apparent. No dispersal pattern of upstream collections and no separation by region are evident.

Comparing Odd and Even Year Pinks

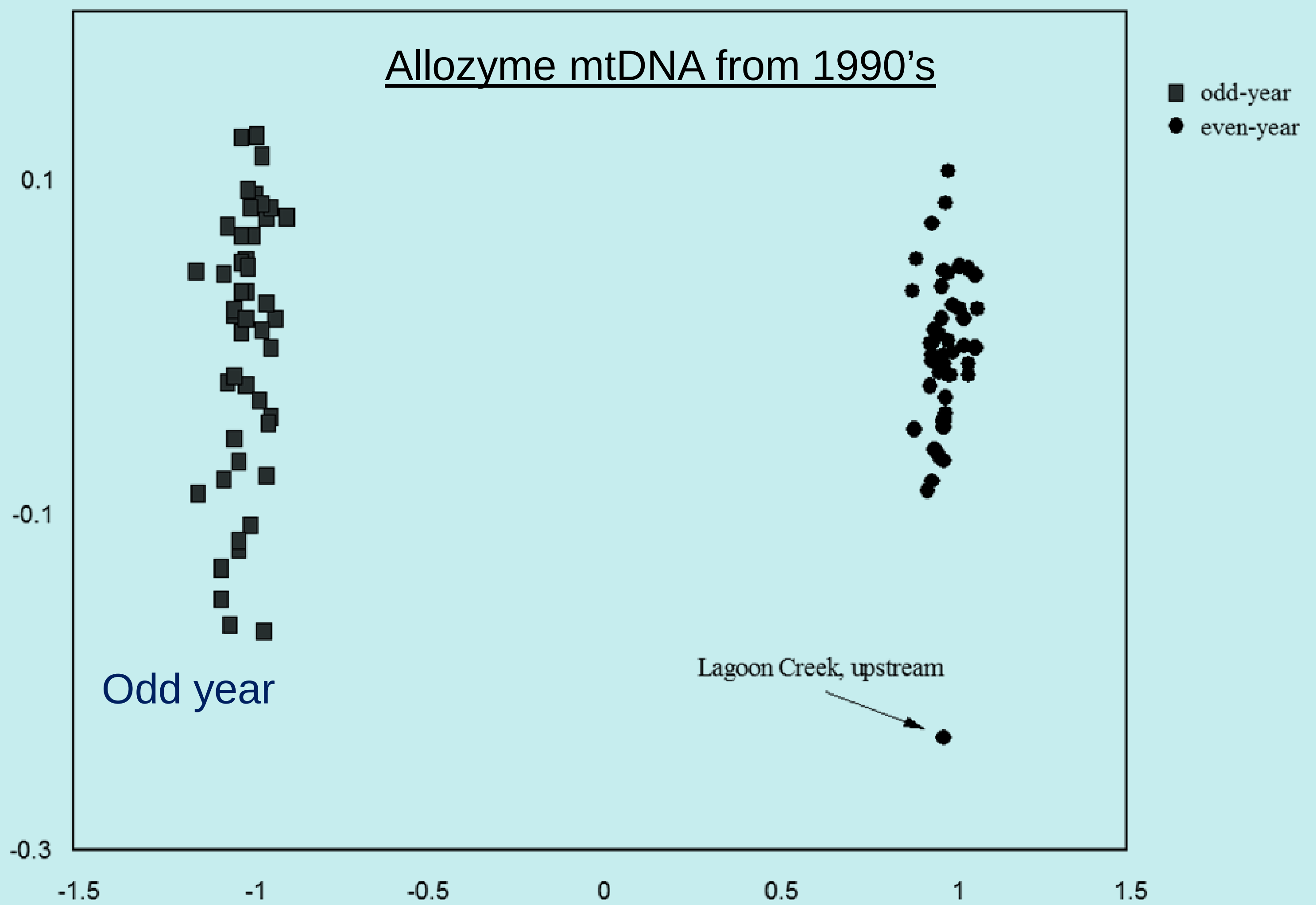


Figure 15. Multidimensional scaling analysis using allozyme data of all 1990s collections, after appropriate pooling within streams, from Prince William Sound, Alaska. Even- and odd-year pink salmon cluster with more variability within the odd-year fish than the even-year fish with the exception of the even-year upstream collection from Lagoon Creek.

I. Genetic Stock Structure of Pinks & Chum Salmon

- New Genetic Technique
- Advances in molecular technology provide large amounts of sequence information
- Single Nucleotide Polymorphism – SNP
- Thousands of SNP as genetic markers
- Digital capability – A, C, G, T

I. Genetic Stock Structure of Pinks & Chum Salmon

Establish genetic markers & information critical to fitness study

SNP analyses will enable description of population stock structure & provide for historical comparisons

I. Genetic Stock Structure of Pinks & Chum Salmon

ADF&G Genetics Lab will develop set of genetic markers that provide:

greater than 99% correct identification of individual salmon to one or two potential parents in the previous generation

Identification of biologically meaningful genetic differences among and within spawning aggregates

I. Genetic Stock Structure of Pinks & Chum Salmon

Collect tissue samples from 100 individuals from each of 20 spawning aggregates for both odd and even years and we will include:

Geographic distribution & temporal run timing.

Sample locations will include streams from previous studies or where scale sampling has occurred in past

Locations will be chosen in consideration of fitness portion of the study ….

I. Genetic Stock Structure of Pinks & Chum Salmon

Need to Genotype individual pink salmon at chosen genetic markers:

10,000 archival scales (1991 – 1997)

4,000 individual contemporary samples

Analyze genetic data for

Utility in parentage-based analyses for fitness element of study

and to compare

Contemporary and historical changes in population structure

II. Extent of Annual Variability of Straying

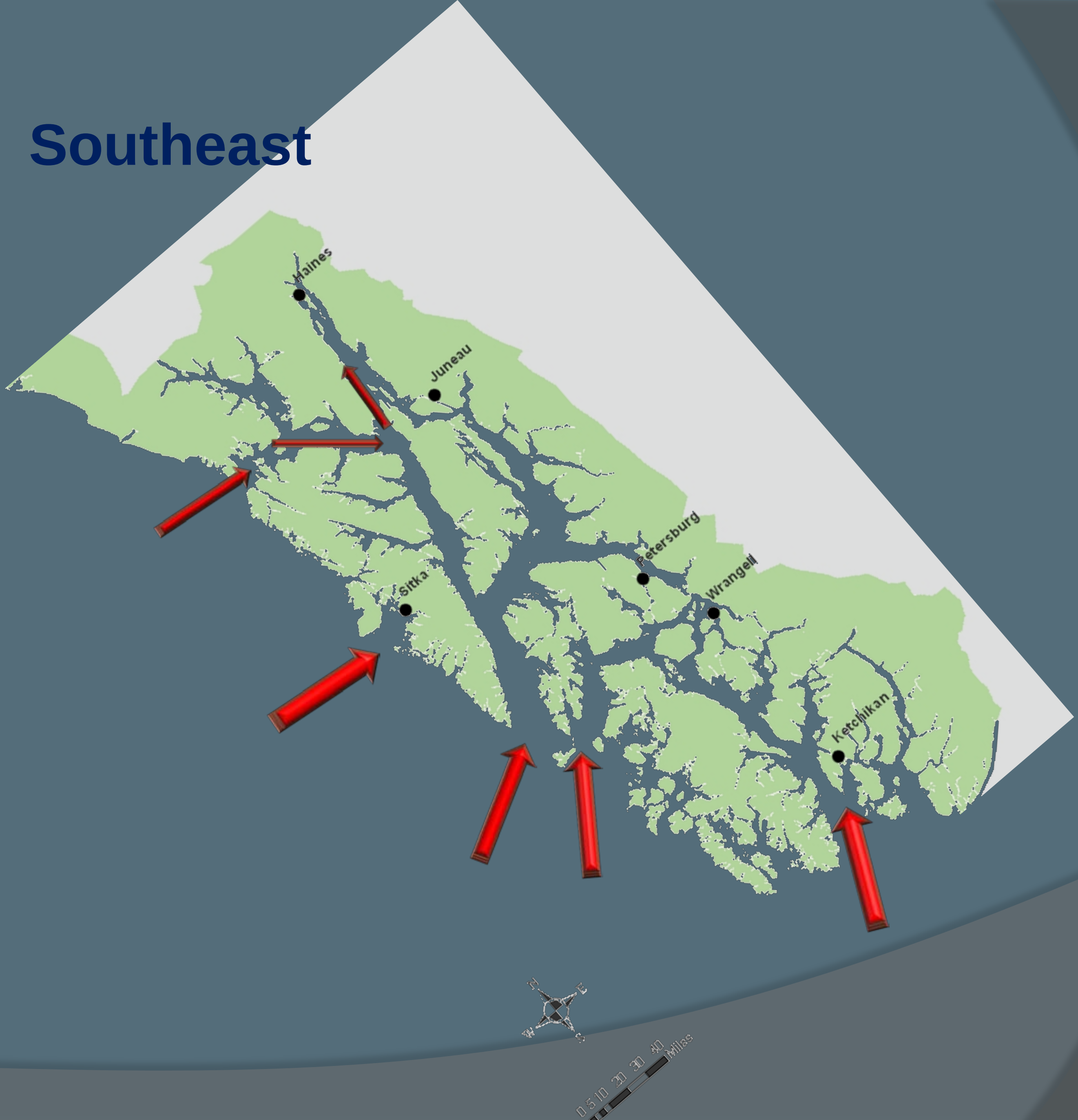
1. Ocean sampling in PWS
2. Stream sampling in Southeast & PWS

II. Extent of Annual Variability of Straying

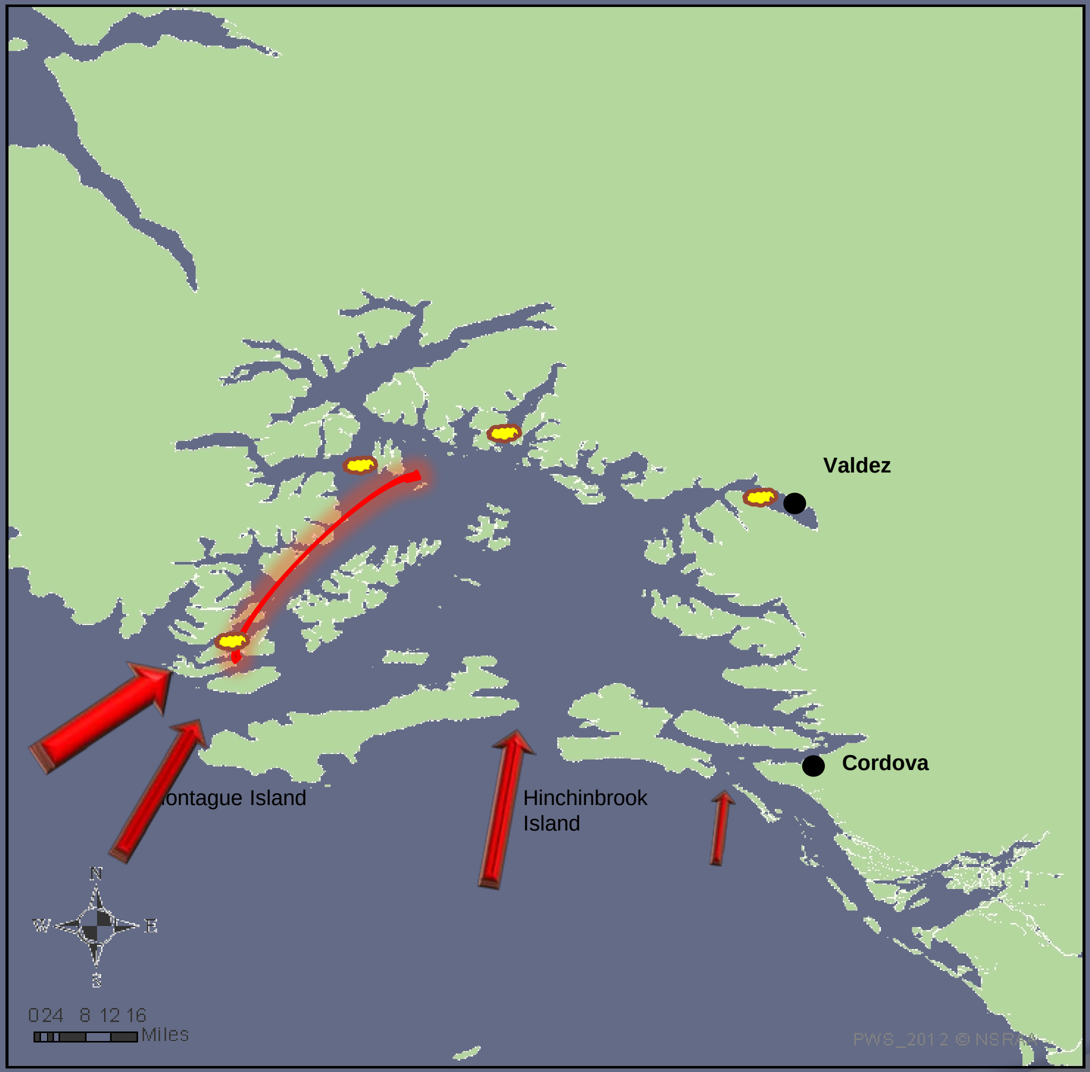
Estimate the following for PWS pinks and Southeast chum:

- Number of wild salmon spawning in streams
- Number of hatchery salmon spawning in the wild (hatchery strays)
- Production of hatchery salmon (including strays)
- Production of wild salmon (excluding hatchery strays)

Southeast



Prince William Sound



II. Extent of Annual Variability of Straying

Ocean Sampling – PWS only

Seine or drift gillnet sampling near Montague Strait & Hinchinbrook

Transects with 6 km or 2 km intervals

June to August 30 stratified sampling to establish hatchery/wild fractio

II. Extent of Annual Variability of Straying

Field Sampling to include:

40 to 60 streams selected from current aerial index of streams

Mix of small to large streams

Streams sampled @ early, middle, & late through run timing

To estimate hatchery fraction, up to 384 fish sampled per stream

Southeast will have 32 of the 81 index streams sampled

II. Extent of Annual Variability of Straying

$$\theta = \frac{R_W}{R_W + R_H} = \frac{R_W}{C_H + S_H + R_W}$$

Fraction of Wild Fish in Total Run

$$\lambda = \frac{S_H}{R_W - C_W + S_H}$$

Fraction of Hatchery Fish in Spawning Pop.

$$R_W = \frac{aC_H - abC_W}{1 - ab}$$

$$S_H = b(R_W - C_W)$$

$$\hat{R}_W = \frac{\hat{a}C_H - \hat{a}\hat{b}\hat{C}_W}{1 - \hat{a}\hat{b}}$$

$$\hat{S}_H = \hat{b}(\hat{R}_W - \hat{C}_W)$$

$$\hat{S}_W = \hat{R}_W - \hat{C}_W$$

III. Impact on Fitness (productivity) of Hatchery Strays in Wild Populations

To measure fitness:

Need to track individual salmon survival & reproduction

average contribution to next generation by type i.e. hatchery x wild vs wild x wild for ♀ and ♂

III. Impact on Fitness (productivity) of Hatchery Strays in Wild Populations

in PWS six streams, population of 3,000 pink;

3 streams with <20% stray rate and, 3 with ~50% stray rate

in Southeast four streams, population of 3,000 chum;

2 streams with <20% stray rate and, 2 with ~50% stray rate

III. Impact on Fitness (productivity) of Hatchery Strays in Wild Populations

Each of streams chosen - 500 adult post spawners sampled for otoliths and tissue for genetic determination

Following spring 2,500 alevins taken from 250 redds

Analyses of these can determine:

1. Their mother was one of 500 sampled previous year
2. Their father was one of 500 sampled previous year
3. Neither parent was sampled previously

III. Impact on Fitness (productivity) of Hatchery Strays in Wild Populations

These streams will be sampled in this manner for two complete generations:

Six years sampling for Pinks

Eleven years sampling for Chum

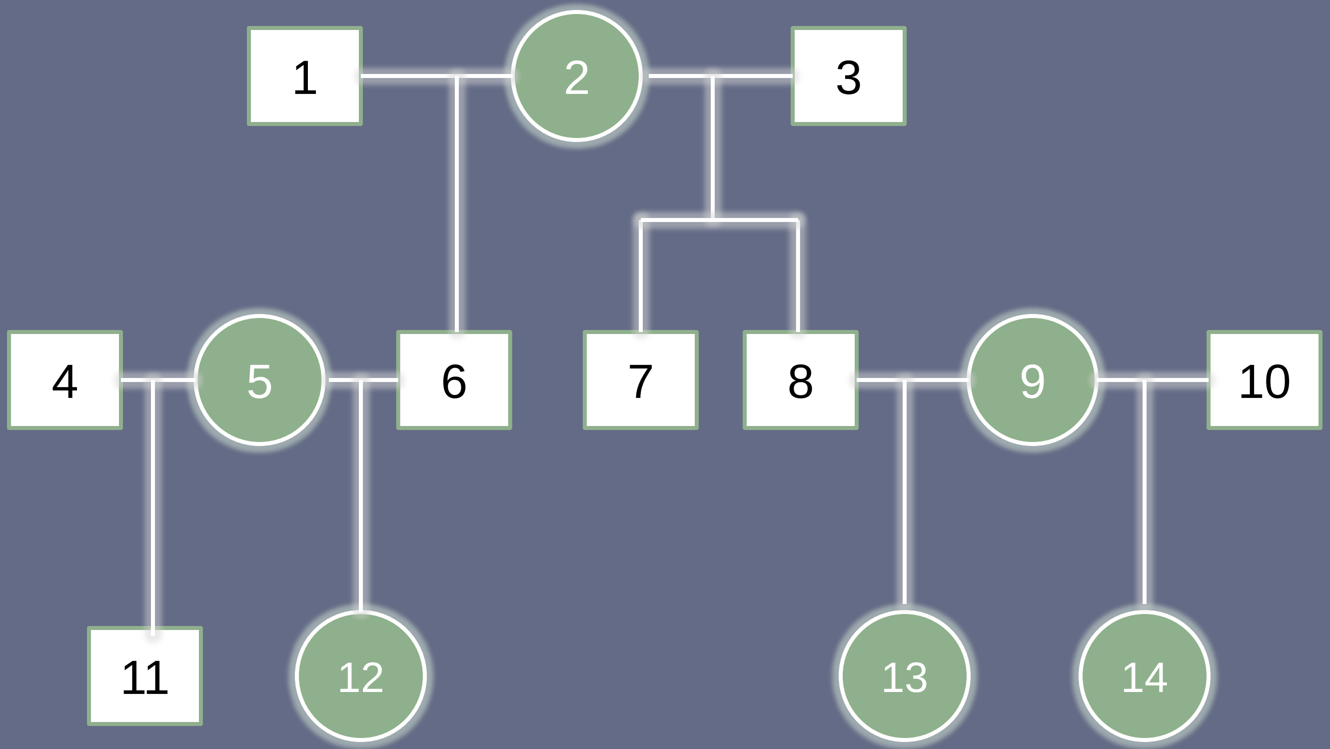
Generational sample design by year

Species	Sampling year 2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Chum (BY 1)	F_0	F_1		F_1	F_1	F_1/F_2	F_1/F_2	F_2	F_2	F_2	
Chum (BY 2)		F_0	F_1		F_1	F_1/F_2	F_1/F_2	F_2	F_2	F_2	F_2
Pink (odd yr, BYs 1 & 3)	F_0	F_1	F_1	F_2	F_2						
Pink (even yr, BYs 2 & 4)		F_0	F_1	F_1	F_2	F_2					

adults sampled annually ~ 500

juveniles sampled annually ~ 2500

Pedigree Reconstruction



Est. Costs: $1.5 mllion/yr.

Requests for Proposals to Third Party Bidders

Annual Review by Science Panel

Immediate Use of Data for Escapement & Stock Structure

ADF&G has been Heavily Invested in the Process


Thank You

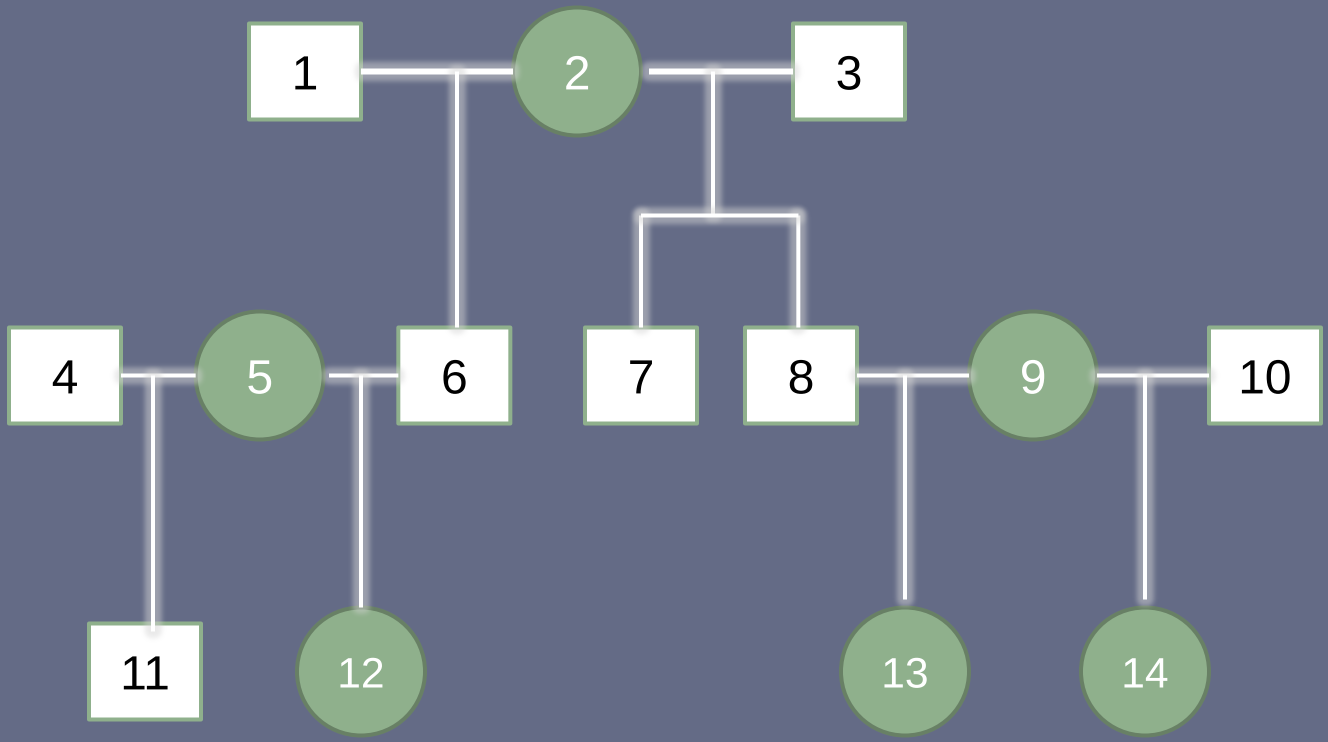
Table 1. Sampling design to evaluate relative reproductive success of hatchery and wild chum and pink salmon in a single stream (where both species are present). Orange cells indicate sampling of adults only, blue cells indicate sampling of juveniles only, and green cells indicate sampling of both life stages (hatched cells indicate no sampling). F_0, initial generation; F_1, 1st-generation progeny; F_2, 2nd-generation progeny. BY is brood year (cohort).

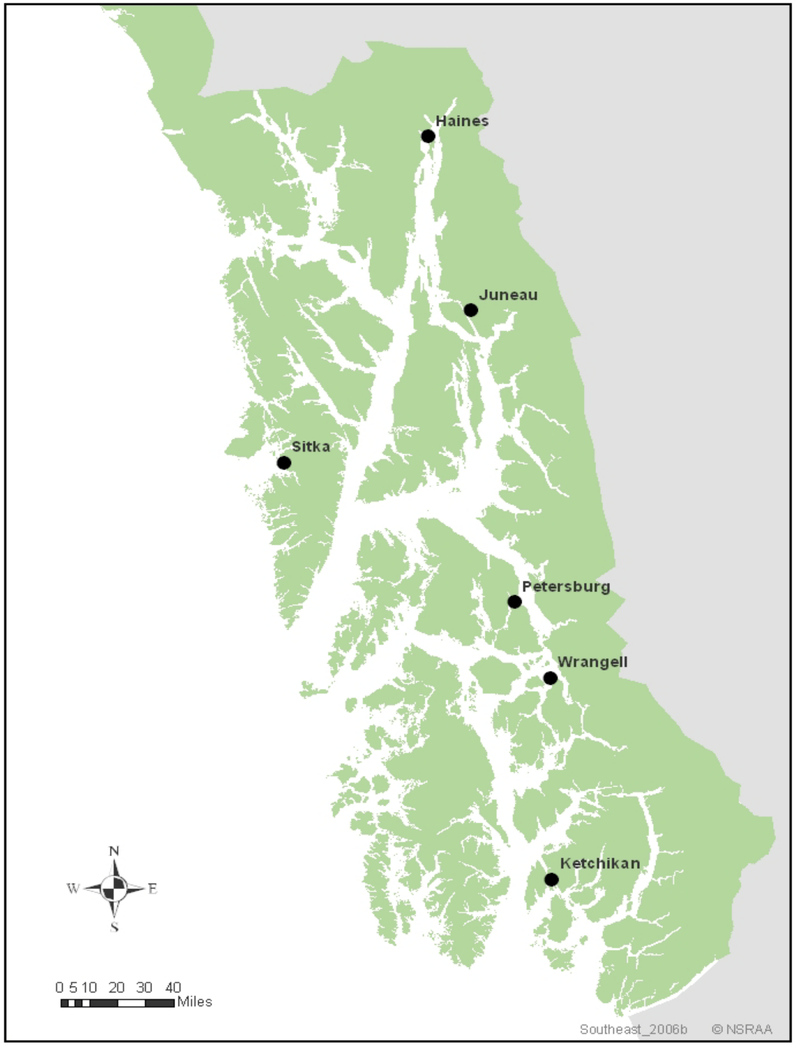
	Sampling year										
Species	**2013**	**2014**	**2015**	**2016**	**2017**	**2018**	**2019**	**2020**	**2021**	**2022**	**2023**
Chum (BY 1)	F_0	F_1		F_1	F_1	F_1/F_2	F_1/F_2	F_2	F_2	F_2	
Chum (BY 2)		F_0	F_1		F_1	F_1/F_2	F_1/F_2	F_2	F_2	F_2	F_2
Pink (odd yr, BYs 1 & 3)	F_0	F_1	F_1	F_2	F_2						
Pink (even yr, BYs 2 & 4)		F_0	F_1	F_1	F_2	F_2					

adults sampled annually ~ 500

juveniles sampled annually ~ 2500

Pedigree Reconstruction




Haines
Juneau
Sitka
Petersburg
Wrangell
Ketchikan
N
W
E
S
0 5 10 20 30 40
Miles
Southeast_2006b
© NSRAA