

# Population Structure of Pink Salmon in Prince William Sound

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Anchorage, Alaska  
December 12, 2014



# Outline

- Purpose
- Current knowledge
- Study design
- Progress
- Future work

# Purpose

- **What is the genetic stock structure of pink and chum salmon in each region?**
- **What is the extent and annual variability in straying of hatchery pink salmon in Prince William Sound (PWS) and chum salmon in PWS and Southeast Alaska (SEAK)?**
- **What is the impact on fitness (productivity) of wild pink and chum salmon stocks due to straying of hatchery pink and chum salmon?**

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# Genetic Stock Structure (Population Structure)

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  - **Natural selection**
  - **Genetic drift**
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# Genetic Stock Structure (Population Structure)

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  - **Natural selection**
  - **Genetic drift**
  - **Mutation**
  - **Migration**
- **Quantified by allele frequency variation  
(gene frequencies)**

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# Current Knowledge

## Genetic Characterization of Prince William Sound Pink Salmon Populations

Report  
to  
Alaska Department of Fish and Game  
Feb. 15, 1977  
by  
Jim Seeb  
and  
Lisa Wishard

## INFORMATIONAL LEAFLET NO. 181

SEPARATION OF SOME PINK SALMON (*Oncorhynchus gorbuscha* Walbaum)  
SUB-POPULATIONS IN PRINCE WILLIAM SOUND, ALASKA BY LENGTH-WEIGHT  
RELATIONSHIPS AND HORIZONTAL STARCH GEL ELECTROPHORESIS

By  
Richard B. Nickerson

*Ecology of Freshwater Fish 1999: 8: 122-140*  
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ECOLOGY OF  
FRESHWATER FISH  
ISSN 0906-6691

## Allozyme and mitochondrial DNA variation describe ecologically important genetic structure of even-year pink salmon inhabiting Prince William Sound, Alaska

Seeb JE, Habicht C, Templin WD, Seeb LW, Shaklee JB, Utter FM. Allozyme and mitochondrial DNA variation describe ecologically important genetic structure of even-year pink salmon inhabiting Prince William Sound, Alaska. *Ecology of Freshwater Fish 1999: 8: 122-140*. © Munksgaard, 1999

**Abstract** – Allozyme and mitochondrial DNA (mtDNA) data were obtained from pink salmon throughout Prince William Sound, Alaska, from two hatchery, five upstream, and 20 tidal locations distributed among five management regions collected during 1994. Screening for allozymes included 66 loci for 92 to 100 fish per sample. Thirty-four loci had variant allele frequencies >0.01 in one or more collections and were used for population analyses. Eight haplotypes were detected after screening 40 fish per collection for variation at the NDS/ND6 region of mtDNA using six restriction enzymes. Significant and apparently stable differences detected by both data sets permit rejecting a null hypothesis of panmixia and support managing native populations in Prince William Sound at the regional level. Distinctions between upstream and tidal collections were detected within Lagoon Creek (allozymes) and Koppen Creek (mtDNA). Significant regional heterogeneity was detected within upstream (allozymes and mtDNA) and tidal (allozymes) collections; however, upstream collections were more divergent from each other than were tidal collections. The absence of distinction of Armin F. Koernig Hatchery from almost all regions was consistent with multiple origins of this stock. Conversely, Solomon Gulch Hatchery in the East Region was distinct from all regions but East, consistent with a more restricted origin and influence.

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W. D. Templin<sup>1</sup>, L. W. Seeb<sup>1</sup>,  
J. B. Shaklee<sup>2</sup>, F. M. Utter<sup>3</sup>**

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Key words: allozyme; mtDNA; genetics; pink salmon

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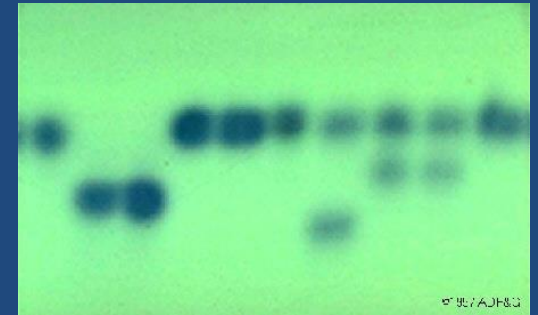
Accepted for publication April 9, 1999

Un resumen en español se incluye detrás del texto principal de este artículo.

# Current Knowledge

- **Allozymes**

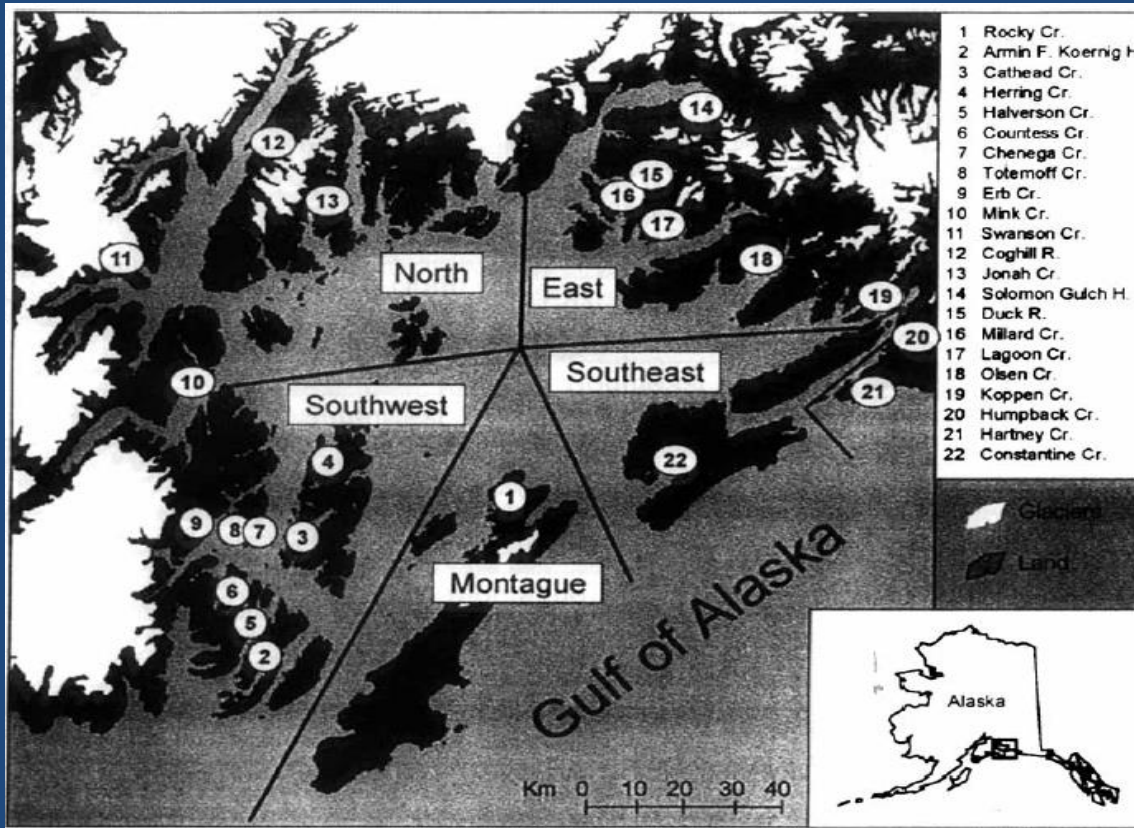
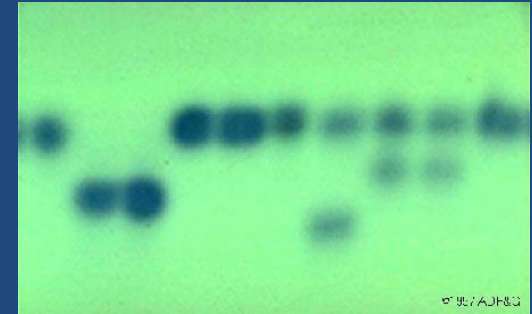
Variant forms of an enzyme



# Current Knowledge

- Allozymes

Variant forms of an enzyme



Found:

Intertidal-upstream  
East-West  
Hatchery-hatchery

# Outline

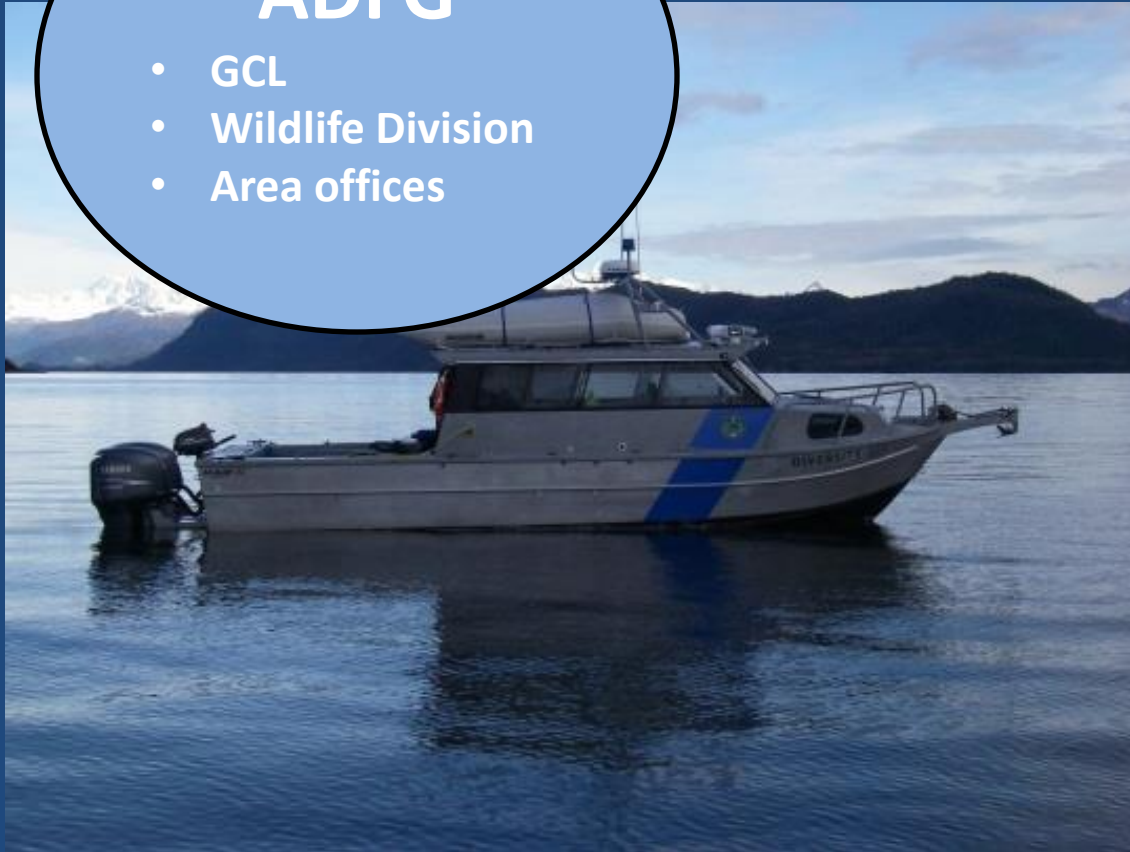
- Purpose
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# Field sampling

## ADFG

- GCL
- Wildlife Division
- Area offices



## Hatcheries

- PWSAC
- VFDA
- KRAA



## PWSSC



# Genetic Markers Used in This Study

- **Microsatellite DNA**

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- Microsatellite DNA

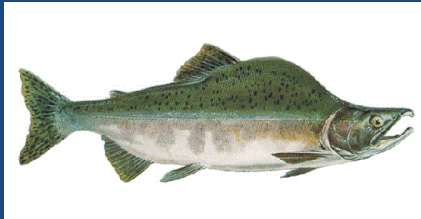
CAAGGCGTGTGTGTGTGTGTGTCTTATCA

7 repeats

CAAGGCGTGTGTGTGTGTGTGTGTGTCTTATCA

9 repeats

# Laboratory Work



Sample



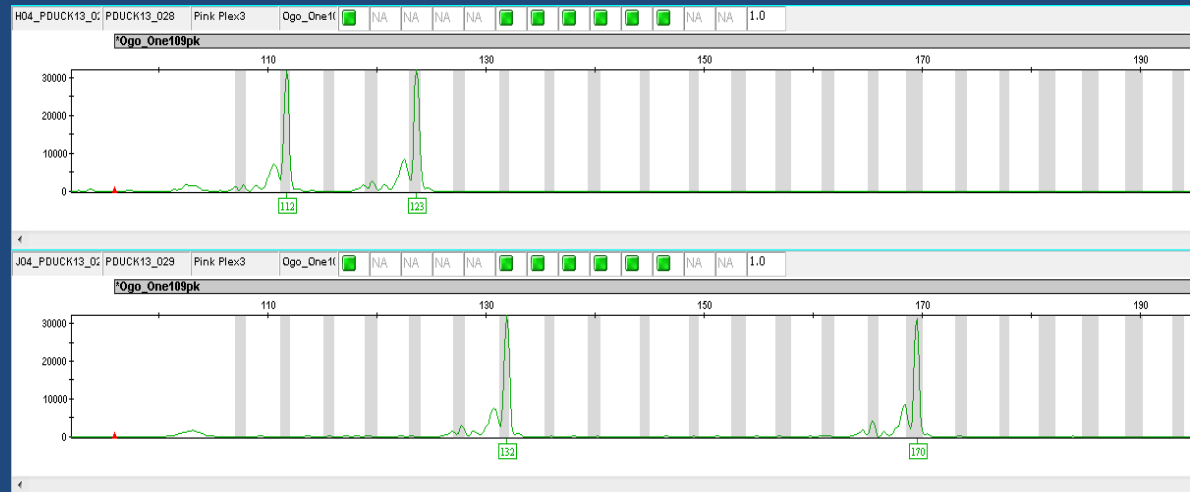
Extract DNA



PCR



Genotype





# Data Analysis

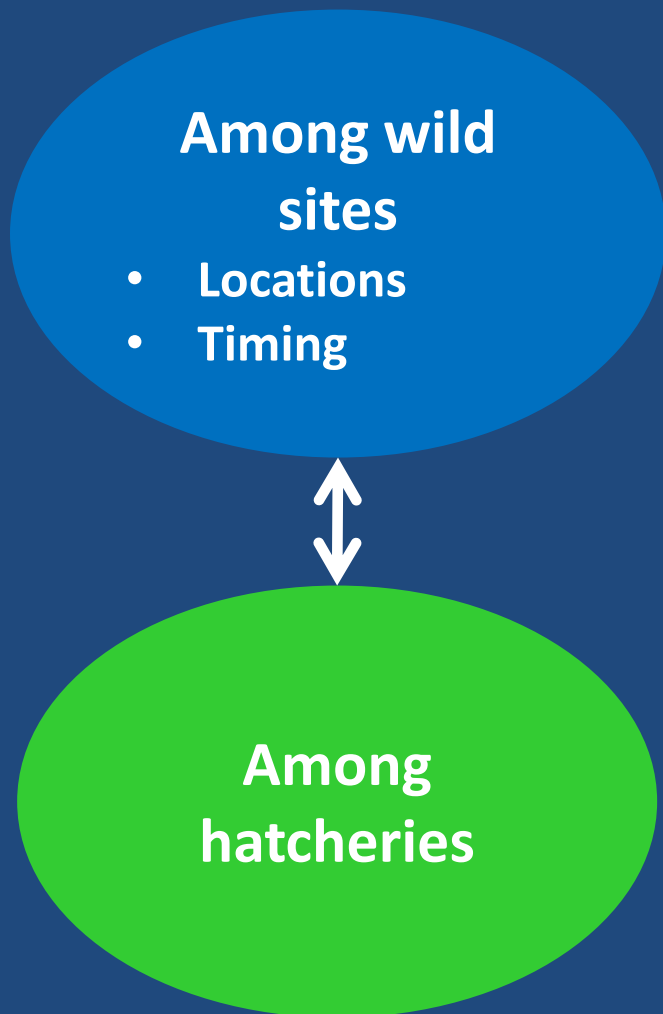
## Contemporary

### Among wild sites

- Locations
- Timing

# Data Analysis

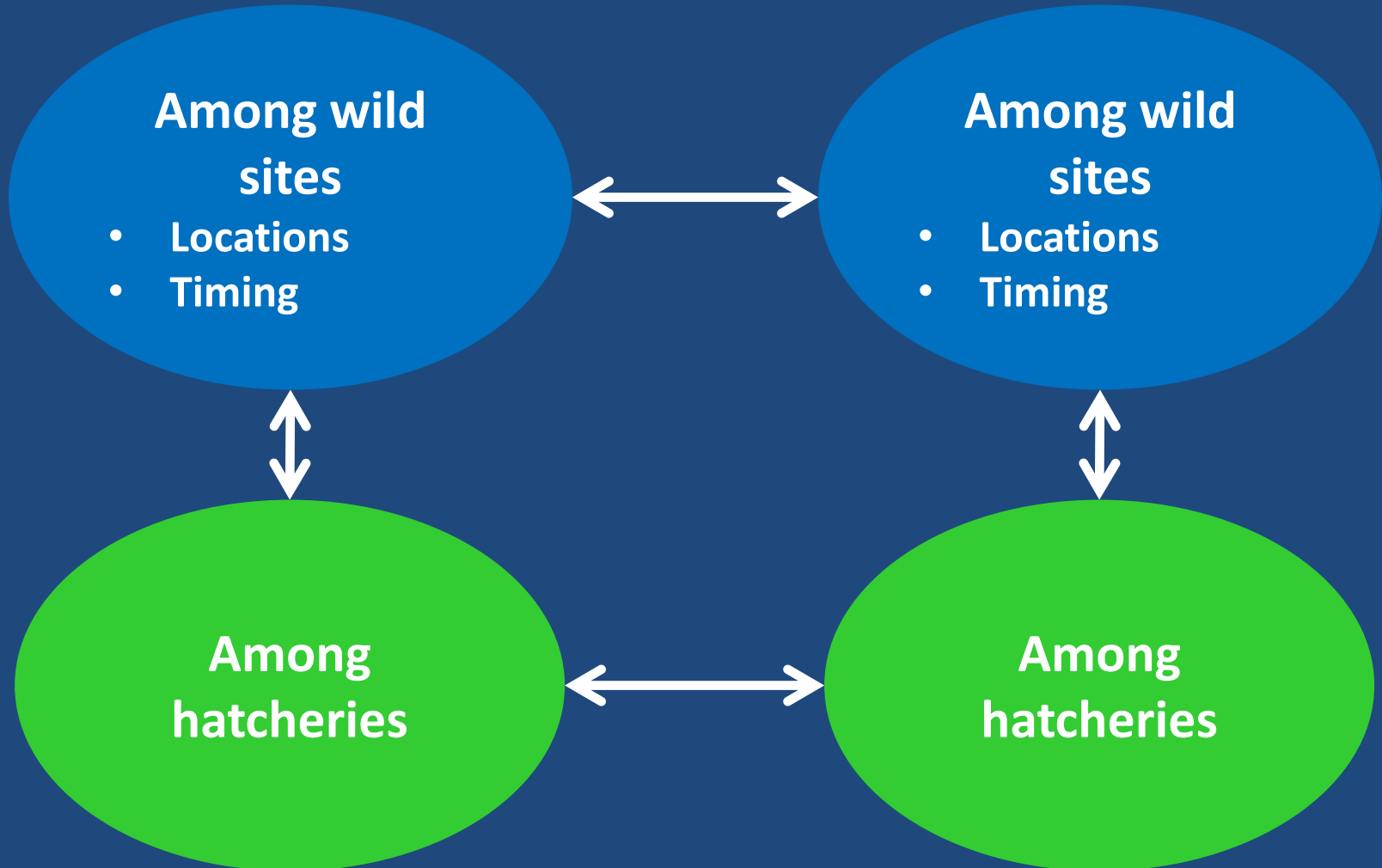
Contemporary



# Data Analysis

Contemporary

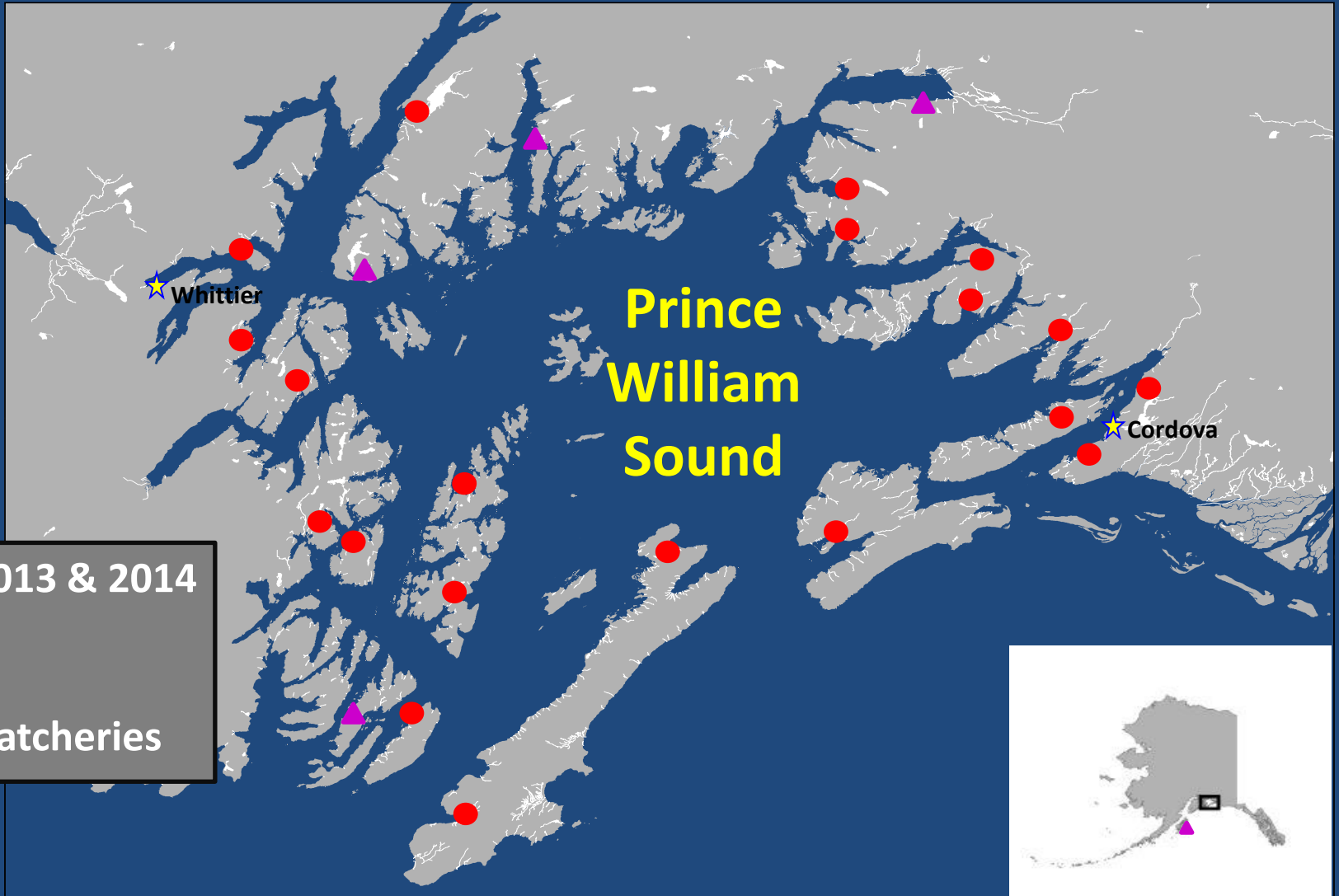
Historical



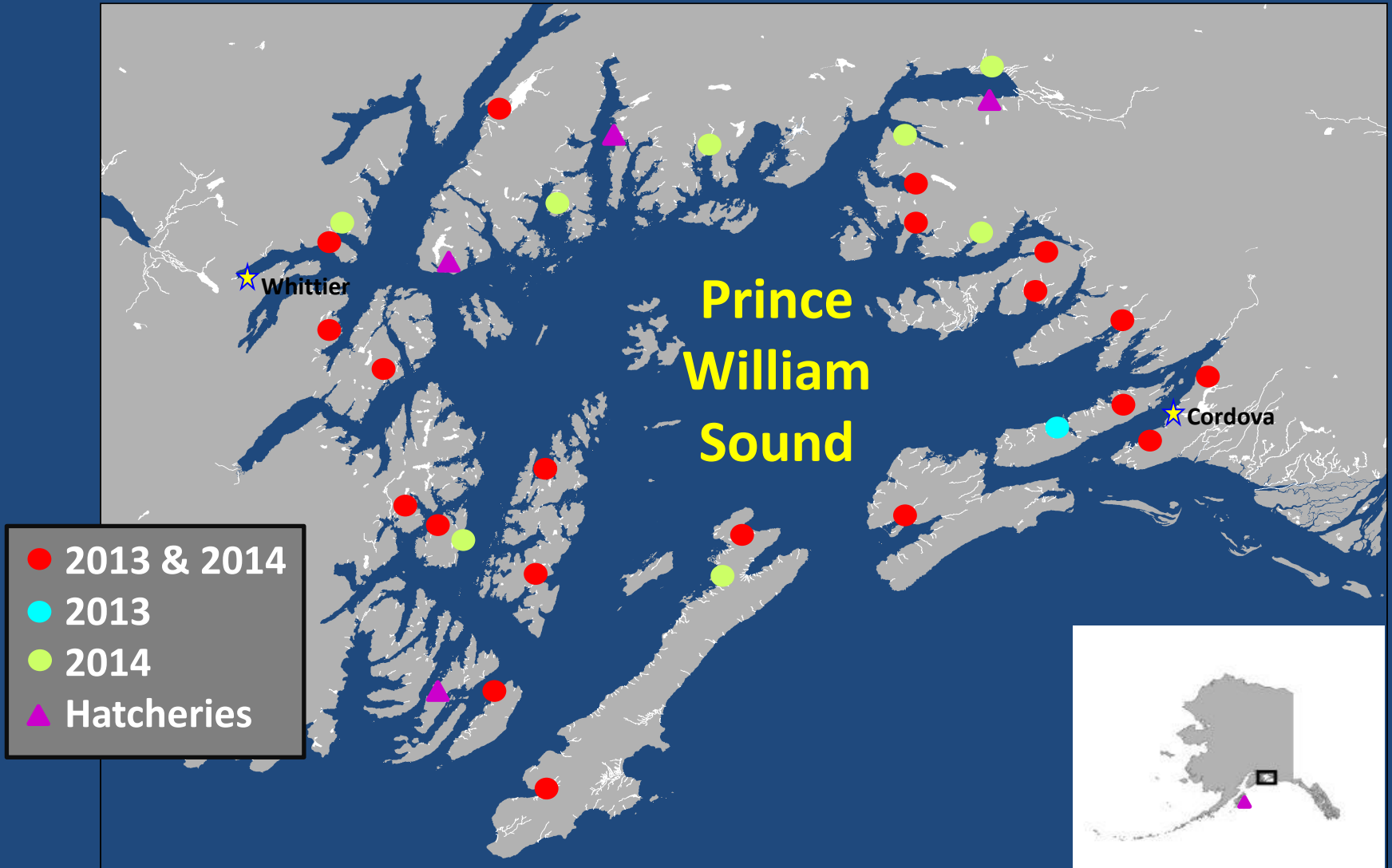
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# 2013 and 2014 Paired Collections



# 2013 and 2014 All Collections



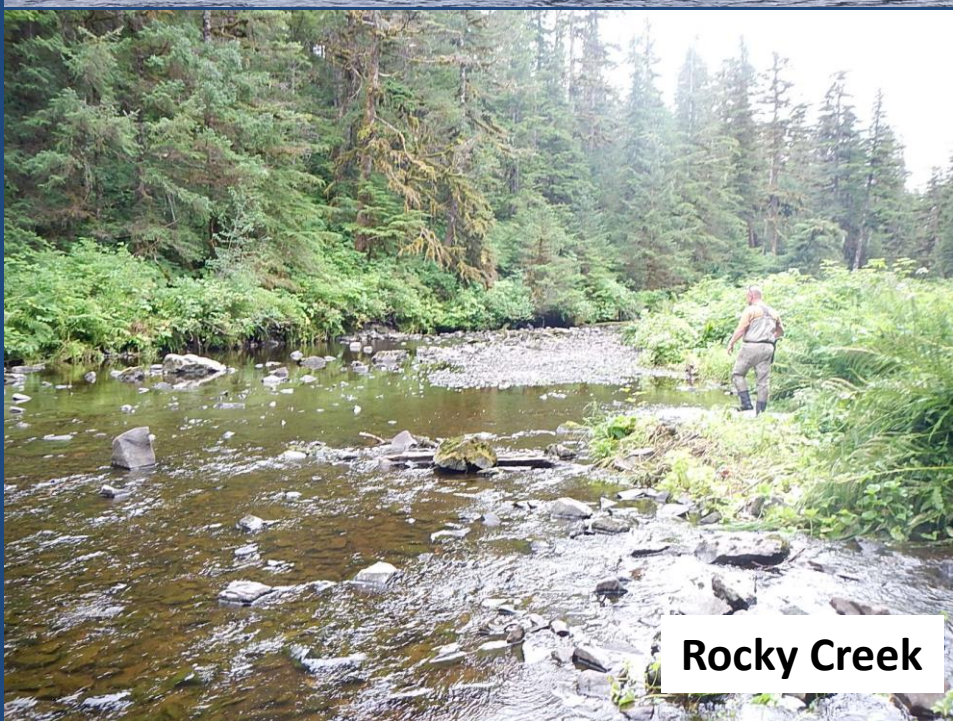




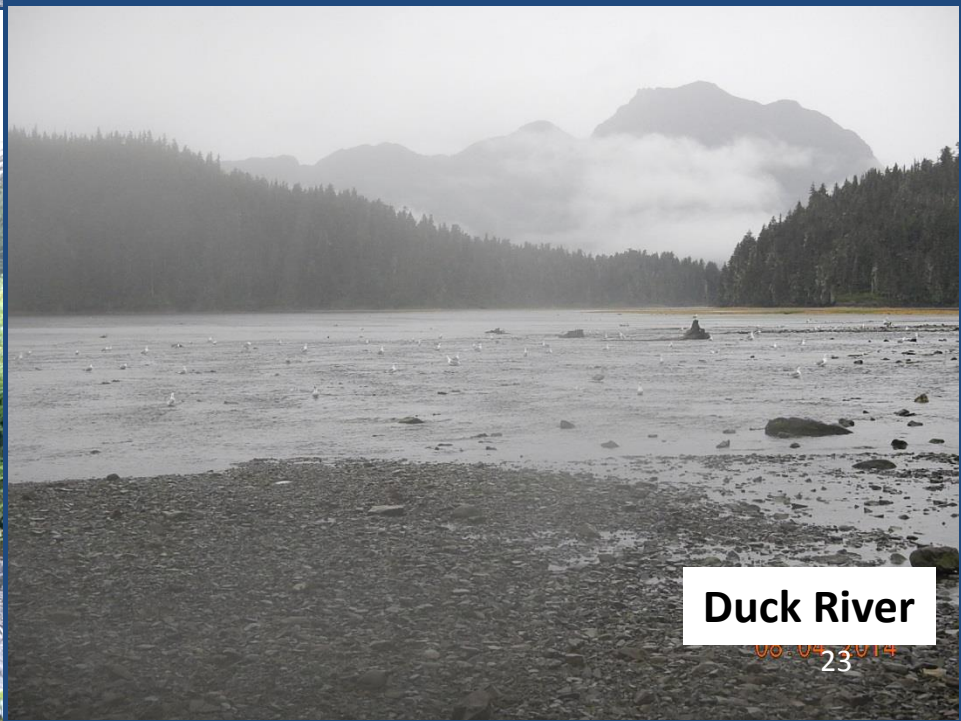
**Swanson Creek**



**McCleod Creek**



**Rocky Creek**



**Duck River**



# Number of Samples

**2013 (~3200)**

- Hatchery fish
- Natural fish

**2014 (~6500)**

- Hatchery fish
- Natural fish
  - Early run
  - Late run



# Laboratory Work (Complete)

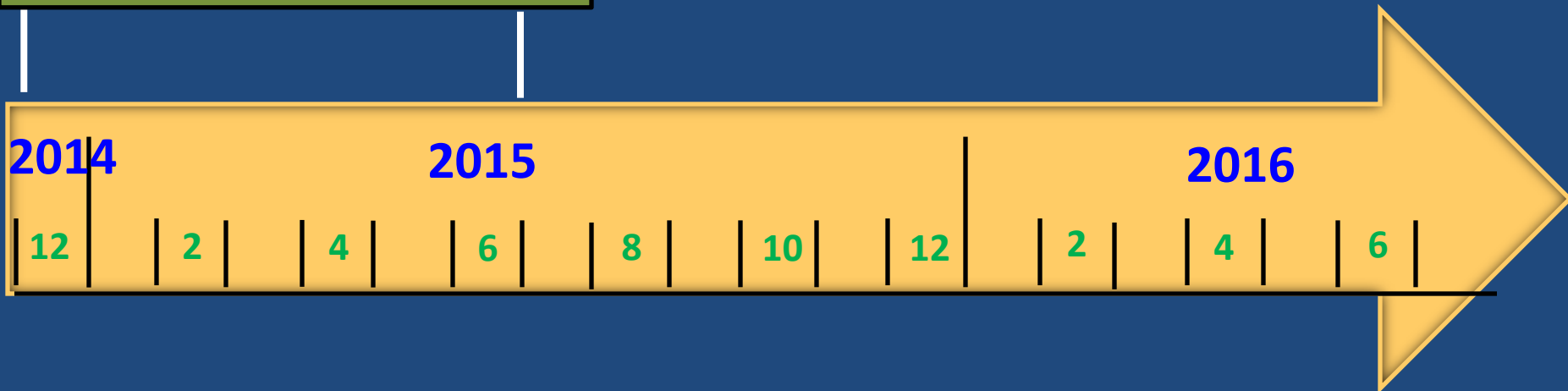
- **Primer optimization**
  - 16 microsatellite primers (Beacham et al. 2012)
- **Genotyping**
  - First pass for samples collected in 2013
  - Samples collected in 1990's

# Outline

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# Timeline

- Second pass genotyping 2013
- Preliminary data analysis
- Technical document for 2013



# Timeline

- Second pass genotyping 2013
- Preliminary data analysis
- Technical document for 2013

**2014**

**2015**

**2016**

12

2

4

6

8

10

12

2

4

6

- Genotyping 2014 samples
- Preliminary data analysis
- Technical document for 2014

# Timeline

- Second pass genotyping 2013
- Preliminary data analysis
- Technical document for 2013

- Contemporary-historical analysis of both odd and even-year data
- Advanced data analysis

**2014**

**2015**

**2016**

12

2

4

6

8

10

12

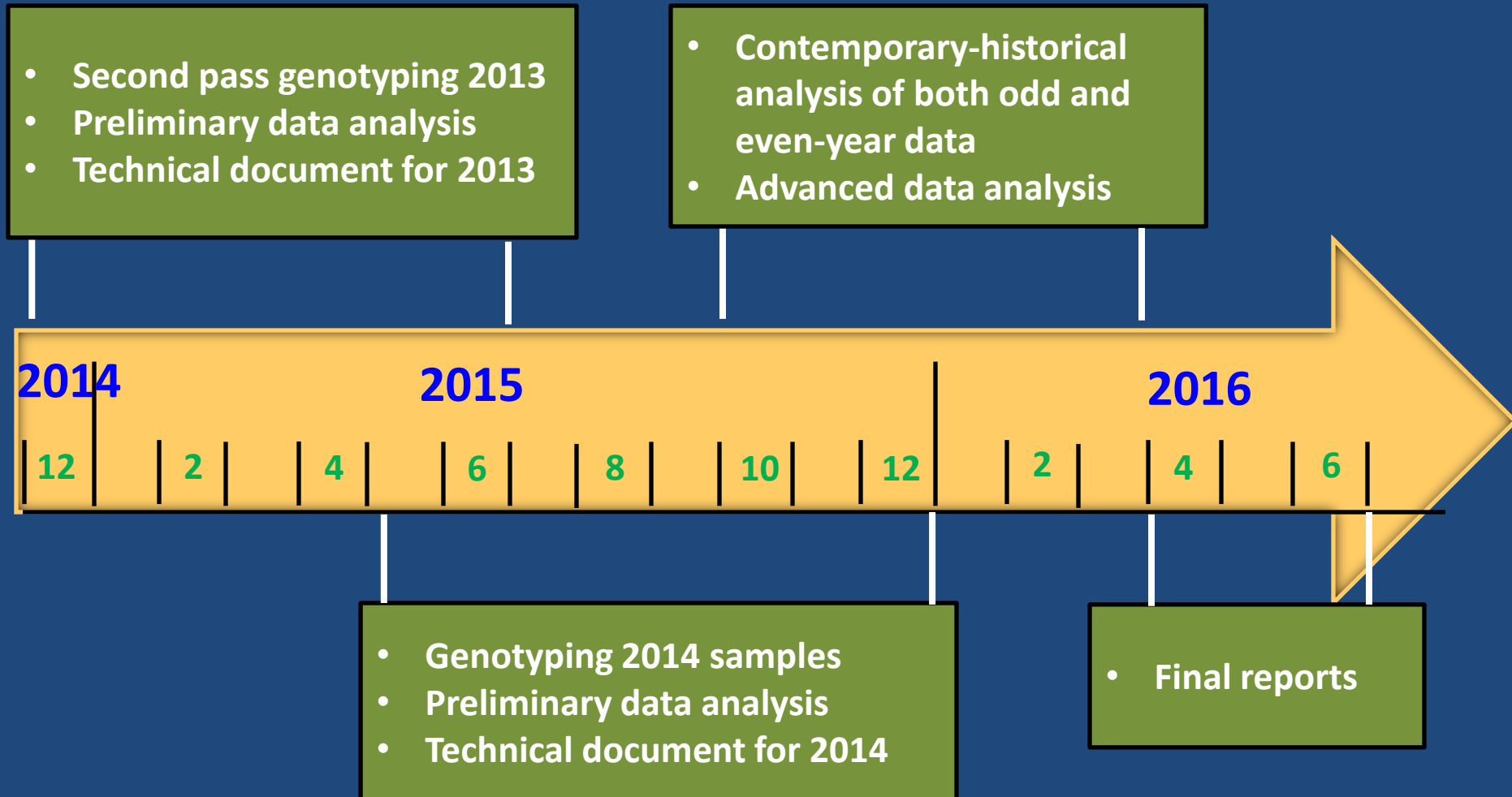
2

4

6

- Genotyping 2014 samples
- Preliminary data analysis
- Technical document for 2014

# Timeline



# Acknowledgements

- **Hatcheries**
  - PWSAC, VFDA, KRAA
- **University of Alaska Fairbanks – Juneau Center**
- **Prince William Sound Science Center**
- **Canadian Department of Fisheries and Oceans**
  - Pacific Biological Station
- **ADFG**
  - Division of Wildlife Conservation
  - Division of Sport Fish
  - Commercial Fisheries Division

# Acknowledgements

## Hatcheries

David Reggiani/ **his staff**; Jason Woodhull; Mike Wells/ **his staff**; Rob Unger; Tina Fairbanks/ **her staff**; Trent Dodson

## UAF

Bill Smoker; Milo Adkison; Megan McPhee

## PWSSC

Katrina Hoffman; Eric Knudsen/his staff; Kristen Gorman; Davis Randall

## DFO

Terry Beacham; Brenda McIntosh; Colin Wallace

## ADFG

Andy Barclay; Ashley Fitzsimmons; Ben Histan; Bruce Whelan; Chase Jalbert; Christina Cupp; Drew Hamilton; Eric Lardizabal; Eric Volk; Erica Chenoweth; Hans Thompson; Heather Hoyt; Heather Liller; Jim Jasper; Judy Berger; Katie Froning; Kyle Shedd; Laural Junge; Nick Decovich; Paul Kuriscak; Zac Grauvogel; Zach Pechacek

Heath Kimball; Bert Lewis; Jan Conitz; Katie Sechrist; Paul Salomone; Xinxian Zhang

Angelina Kelly; Darren Roberts; Elena Fernandez; Ellen Americus; Jane Allen-Schmid; Cindy Stimson; Jim Orourke; Jimmy Osga; Martin Schuster; Megan Urton; Rich Brenner; Steve Moffitt; Thomas Sheridan;

Dion Oxman; Lorna Wilson; Megan Lovejoy; Timothy Frawley

Lorraine Vercess; Mark Stopha; Ronald Josephson; Samuel Rabung

David Tessler; Howard Golden; Michael Harrington

Dan Bosch; Jiaqi Huang; Jay Baumer

Celia Rozen



# Questions?



08.02.2014

