

# Contemporary Population Structure of Pink Salmon from Prince William Sound, Alaska

Wei Cheng<sup>1,2</sup>, Christopher Habicht<sup>1</sup>, William D. Templin<sup>1</sup>,  
Zachary D. Grauvogel<sup>1</sup>, and Anthony J. Gharrett<sup>2</sup>

<sup>1</sup>Alaska Department of Fish and Game Gene Conservation Laboratory

<sup>2</sup>University of Alaska Fairbanks  
College of Fisheries and Ocean Sciences

Alaska Hatchery Research Program Informational Meeting  
March 6, 2020

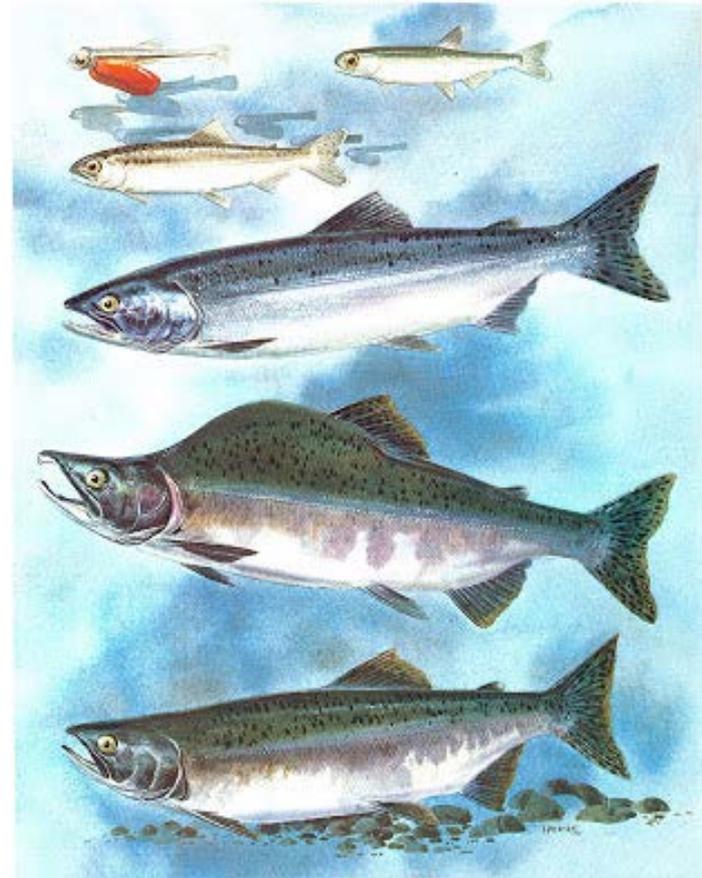


# Alaska Hatchery Research Program

- 1) What is the genetic structure of **pink** and chum in **PWS** and SEAK?
- 2) What is the extent and annual variability of straying?
- 3) What is the impact on fitness (productivity) of natural pink and chum stocks due to straying hatchery pink and chum salmon?

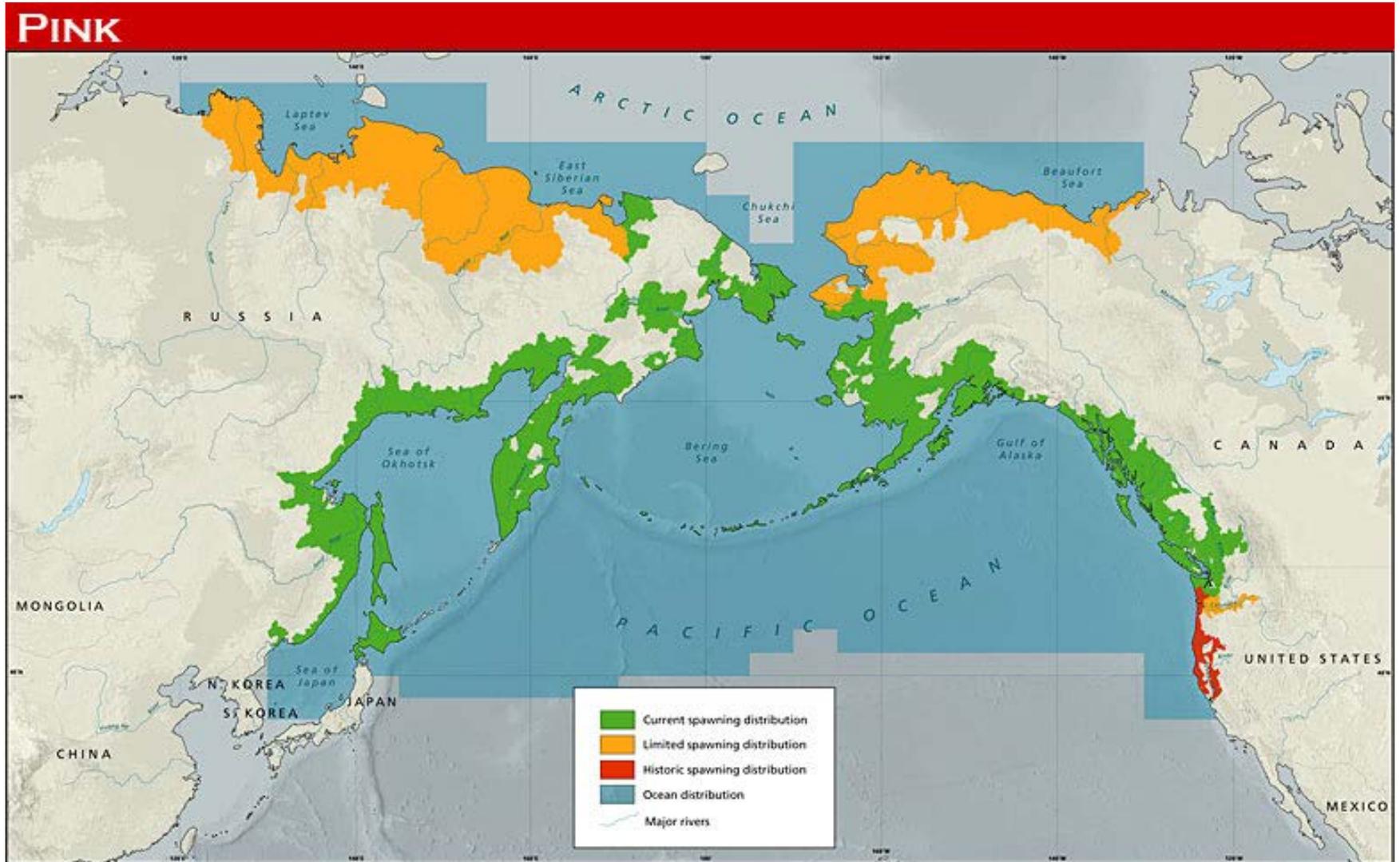
# Life History of Pink Salmon

- **Two-year life cycle**
  - Odd year
  - Even year
- **Limited freshwater life history**



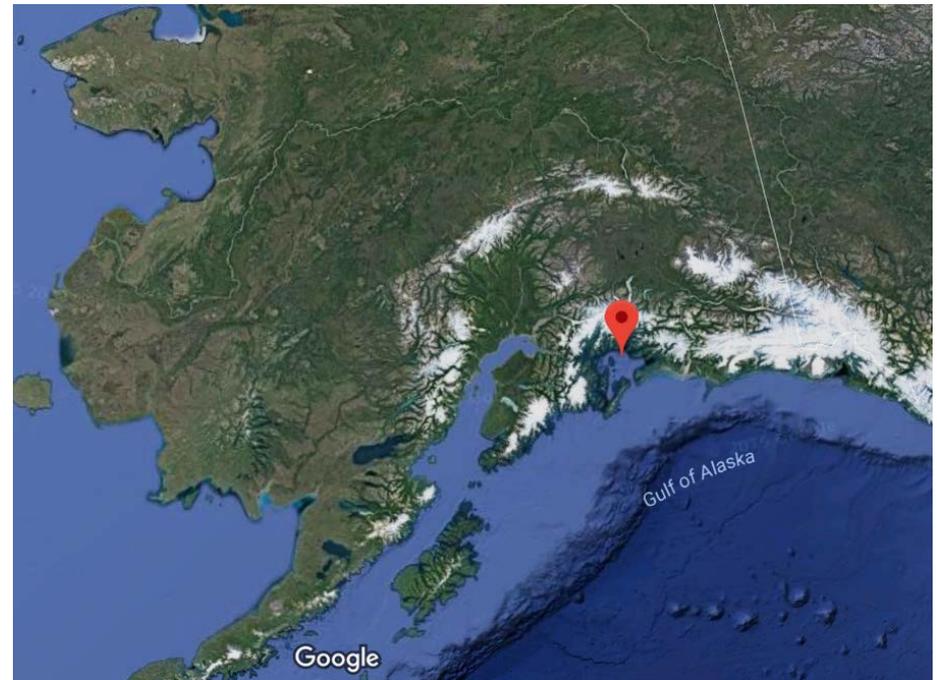
<https://www.n-sea.org/pink-salmon>

# Distribution of Pink Salmon



# PWS Pink Salmon

- **Number of streams in Prince William Sound (PWS)**
  - Over 800 streams
- **Variation in run timing across streams**



# Previous Studies: Pink Salmon in PWS

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.

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

<sup>1</sup>Alaska Department of Fish & Game, Commercial Fisheries Division, Anchorage, Alaska. <sup>2</sup>Washington Department of Fish & Wildlife, Olympia. <sup>3</sup>School of Fisheries, University of Washington, Seattle, Washington, USA

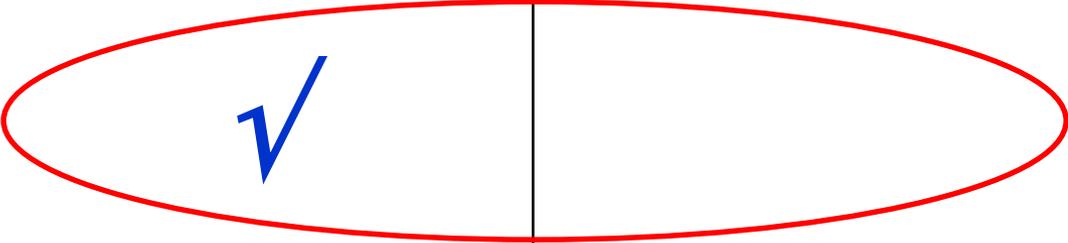
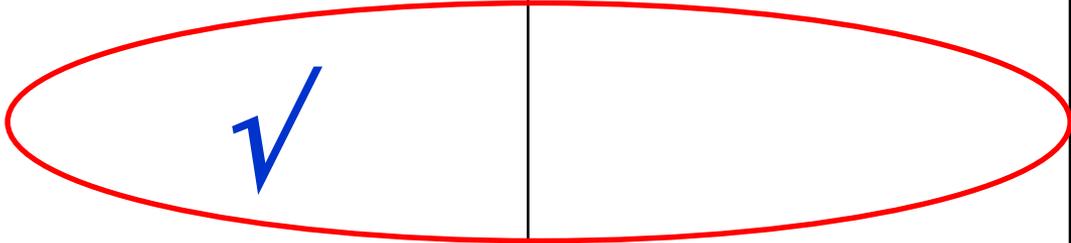
Key words: allozyme; mtDNA; genetics; pink salmon

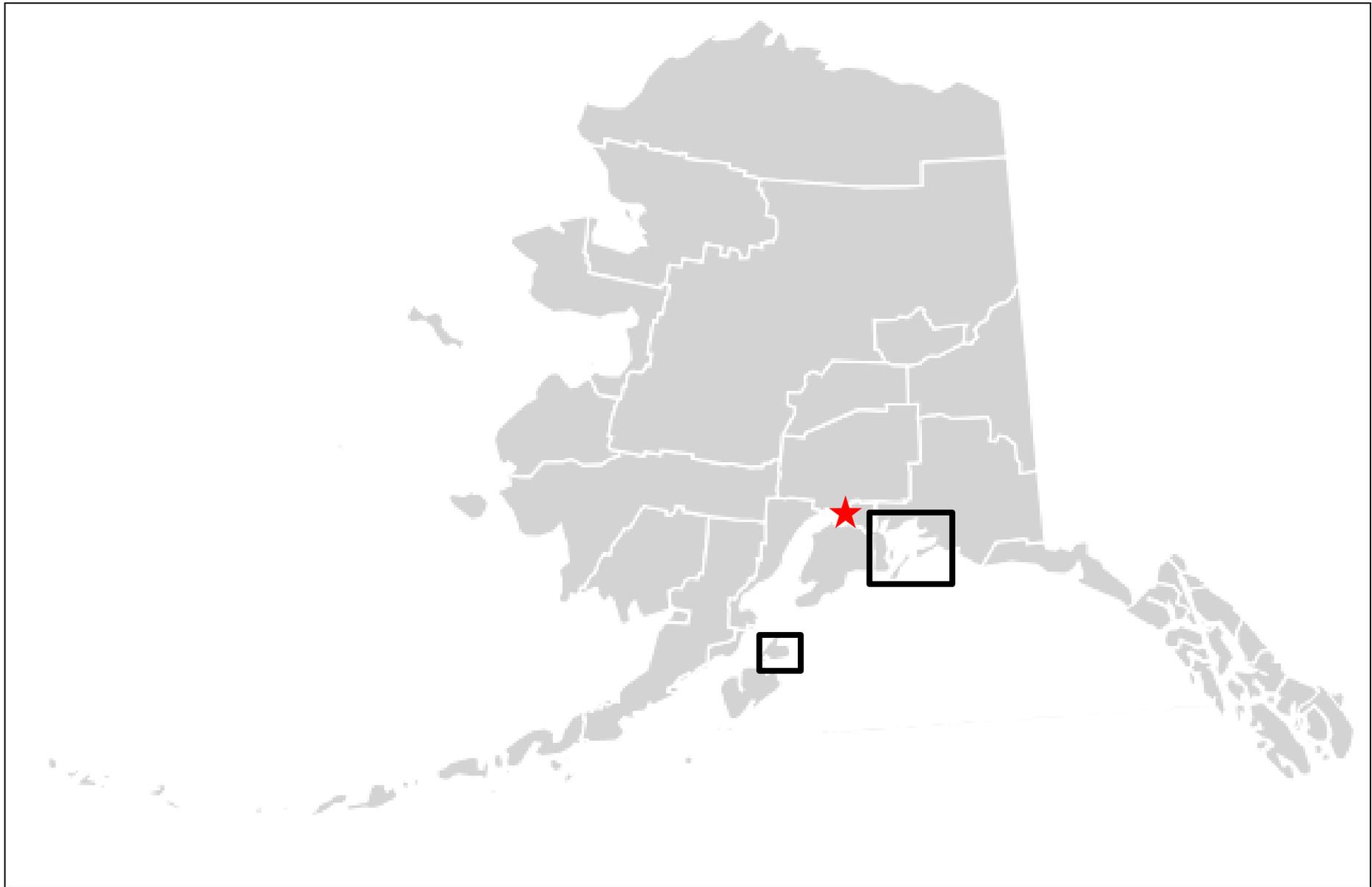
J. E. Seeb, Alaska Department of Fish & Game, Commercial Fisheries Division, Anchorage, AK 99518, USA

Accepted for publication April 9, 1999

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

# Study Design

	<b>Contemporary</b>	<b>Historical</b>
<b>Natural</b>		
<b>Hatchery</b>		



# Swanson Creek



07.28.2014

# McCleod Creek



07.31.2014

# Rocky Creek



08.01.2014

# Duck River



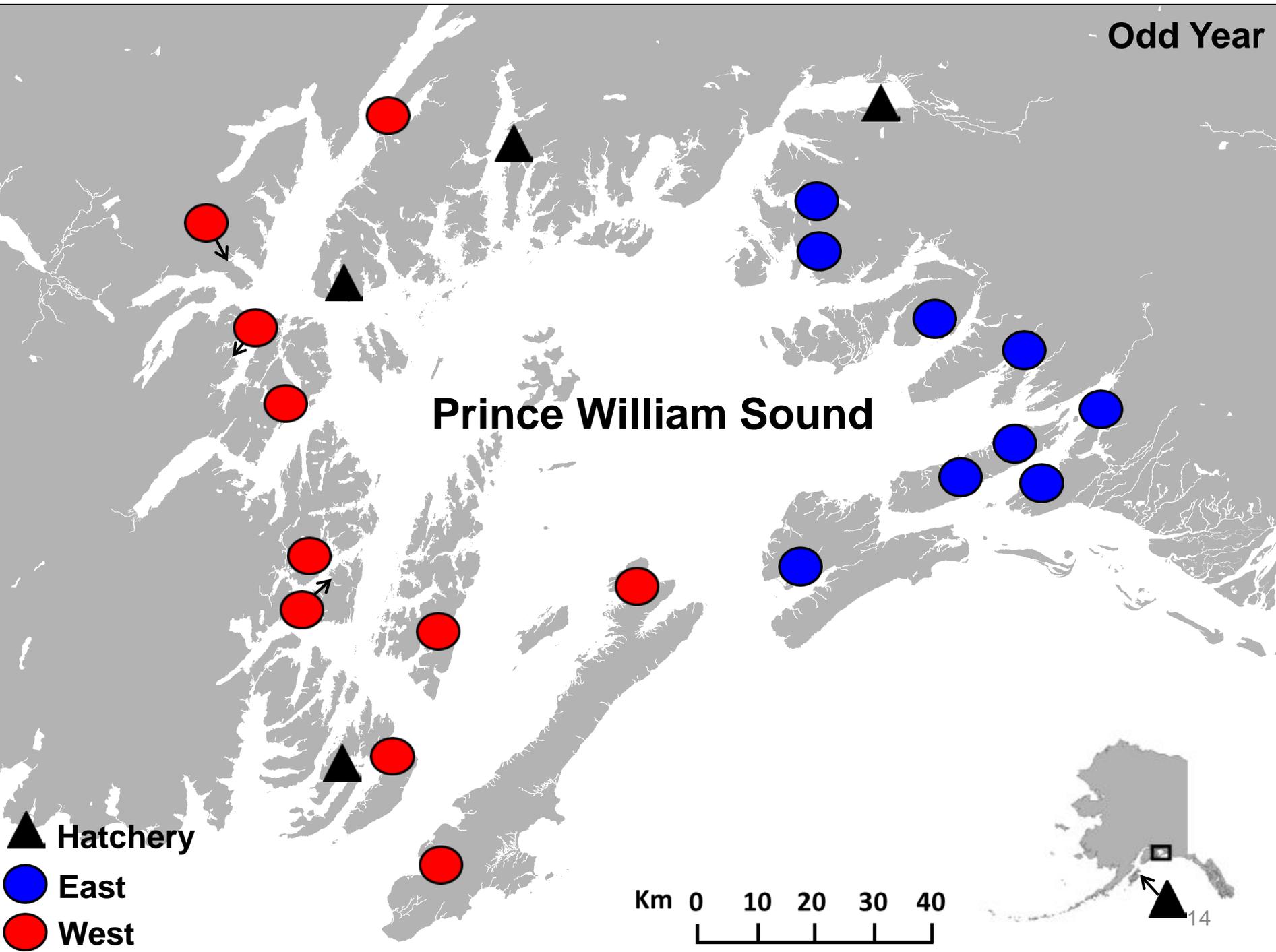
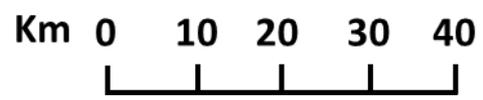
08.04.2014

# Study Design

	<b>Contemporary</b>	<b>Historical</b>
<b>Natural</b>	✓	
<b>Hatchery</b>	✓	

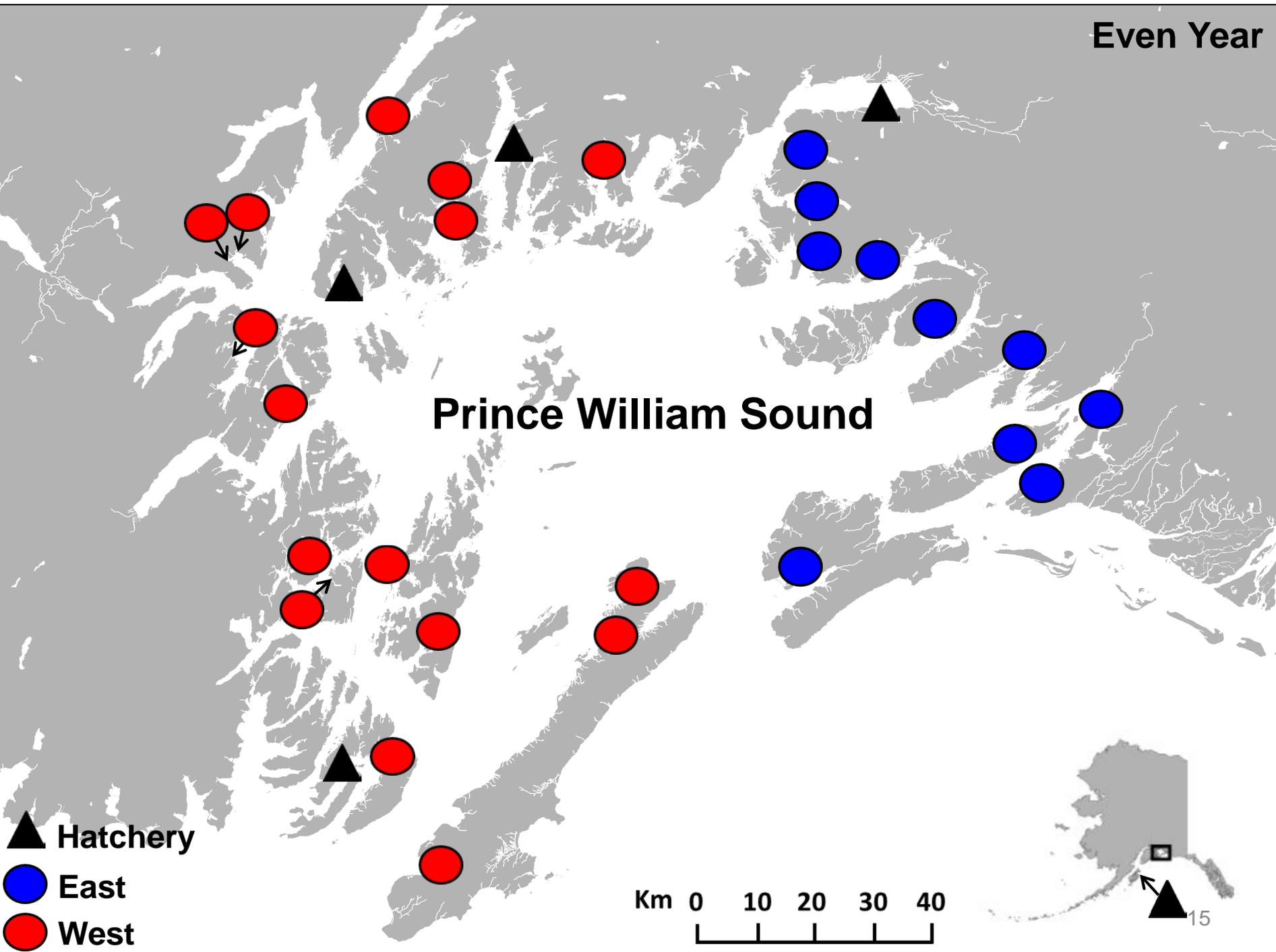
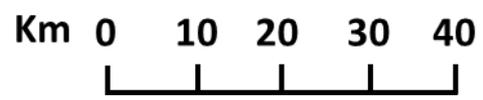
Prince William Sound

- ▲ Hatchery
- East
- West



Prince William Sound

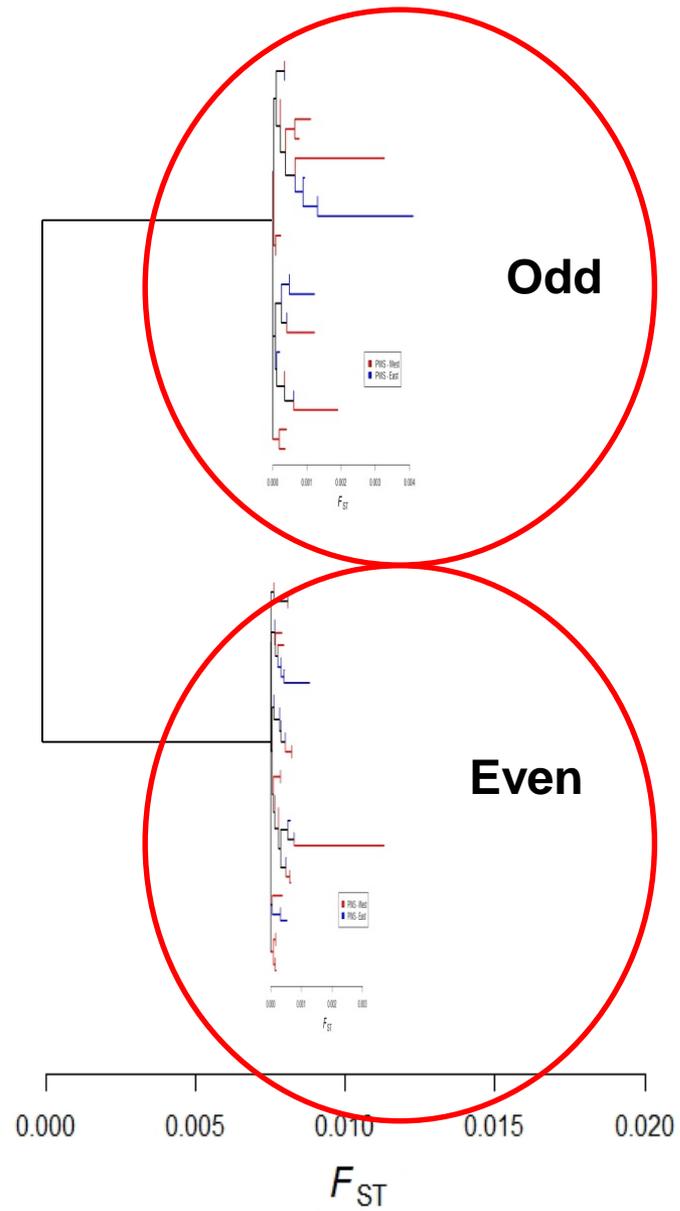
- ▲ Hatchery
- East
- West



# Population Structure Analyses

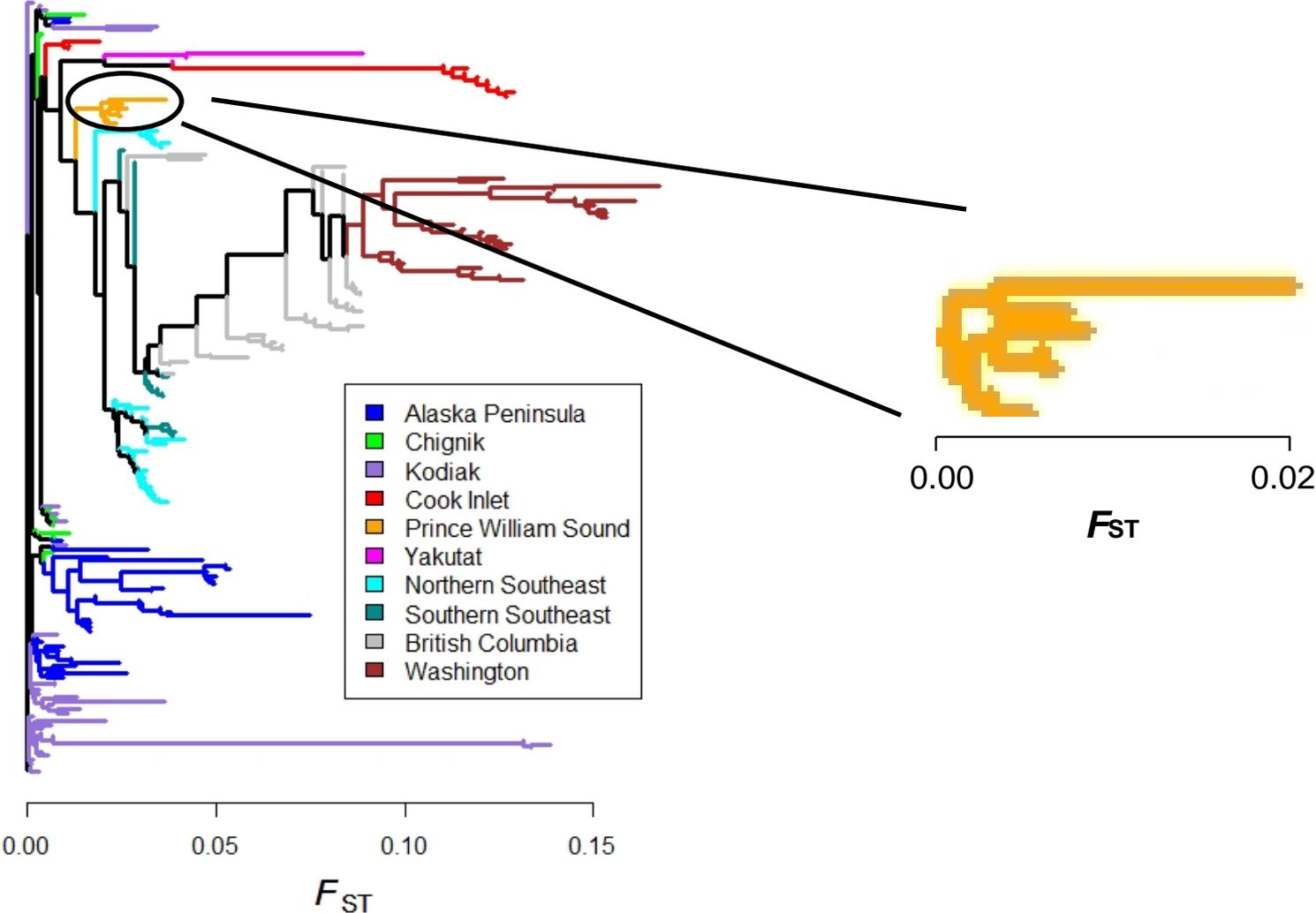
- **Calculate genetic differences among collections**
- **Test for significance of these differences**
- **Visualize the relationships among collections**

# PWS Pink Salmon

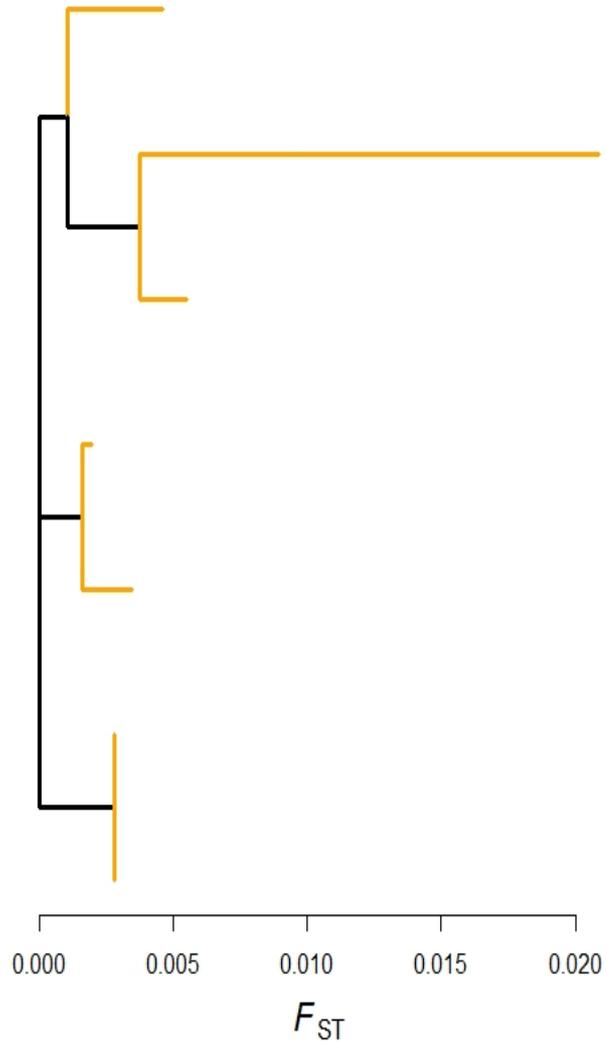


# Pacific Rim Chum Salmon

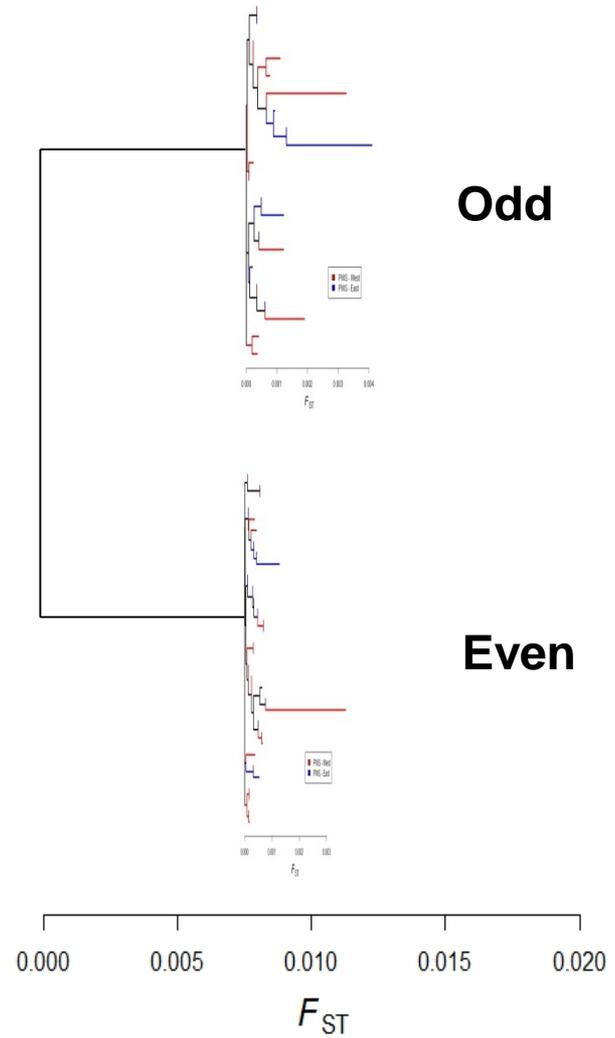
# PWS Chum Salmon



# PWS Chum Salmon



# PWS Pink Salmon



Title: Population Genetic Structure of Odd-Year Pink Salmon from Prince William Sound Based on a Single Year (2013) Version: 1.0

Authors: W. Cheng, C. Habicht, W. D. Templin, Z. D. Grauvogel, S. D. Moffitt, R. E. Bremner, R. P. Josephson, and A. J. Gharrett  
Date: May 13, 2016

### Abstract

Pink salmon (*Oncorhynchus gorbuscha*) are commercially and ecologically important. In Prince William Sound (PWS), Alaska, pink salmon are the most abundant salmon harvested and generating the highest total value. An understanding of their population genetic structure is useful for conservation and management, especially given the magnitude of the hatchery program in the sound. We analyzed the population genetic structure of pink salmon from four hatcheries and 19 natural spawning areas in PWS and one hatchery in Kodiak Management Area (KMA) by genotyping 16 microsatellite loci for nearly 3000 pink salmon sampled in 2013. Across all populations in PWS, the number of alleles observed per locus ranged from 11 (*Ob7e*) to 87 (*Ok10l*), and the total for all loci was 726. The fixation index ( $F_{ST}$ ), a measure of population differentiation, was 0.002 over all loci and the  $F_{ST}$  of individual loci ranged from 0.001 to 0.003. Significant difference was detected among those populations from PWS, which means that pink salmon in PWS are not from a single large homogeneous population. The KMA collection was the most divergent. Within PWS, Solomon Gulch Hatchery in the northeastern PWS was distinct from all other collections and suggested that it had not received many migrants from other PWS areas. Early-run fish from Snug Harbor Creek were distinct from other samples.

Key words: Pink salmon, odd-year, Prince William Sound, population genetic structure, microsatellite.

## Population structure of odd-broodline Asian pink salmon and its contrast to the even-broodline structure

S. L. HAWKINS\*, N. V. VARNAVSKAYA†, E. A. MATZAK‡, V. V. EFREMOV¶, C. M. GUTHRIE III\*, R. L. WILMOT\*, H. MAYAMA§, F. YAMAZAKI|| AND A. J. GHARRETT#\*\*\*

\*National Marine Fisheries Service, Atke Bay Laboratory, 11305 Glacier Hwy, Juneau, AK 99801-8626, U.S.A., †Kamchatka Scientific Research Institute of Fisheries and Oceanography, KamchatNIRO, Petropavlovsk-Kamchatsky 683602, Kamchatka, Russia, ‡Pacific Research Fisheries Centre (TINRO-CENTRE), 4 Shevchenko Alley, Vladivostok 690600, Russia, ¶Russian Academy of Sciences, Far East Branch, Institute of Marine Biology, Vladivostok 690041, Russia, §National Salmon Resources Center, Nakanoshima, Sapporo 062-0922, Japan, ||Hokkaido University, Laboratory of Genetics and Embryology, Faculty of Fisheries, Hakodate 041, Japan and #Division of Fisheries, University of Alaska Fairbanks, 11120 Glacier Hwy, Juneau, AK 99801, U.S.A.

(Received 6 June 2001, Accepted 28 November 2001)

Most of the variation (99%) of Asian odd-broodline pink salmon *Oncorhynchus gorbuscha*, based on data at 32 variable (46 total) allozyme loci from 35 populations, occurred within populations. The remaining interpopulation variation was attributable to: (1) differences between northern (the northern Sea of Okhotsk, eastern Kamchatka Peninsula and western Kamchatka Peninsula) and southern (Hokkaido Island, Kuril Islands and Sakhalin Island) populations; (2) differences between the southern areas; (3) low variation among populations within some areas. The pattern contrasted strongly with that observed for Asian even-broodline populations, which had a strong structure, possibly related to geographic and oceanographic influences. Isolation-by-distance analyses of each of the two broodlines showed a stronger relationship ( $\times 4.8$ ) among even- than odd-broodline populations. Allele frequency differences between even- and odd-broodlines reflected the reproductive isolation of the broodlines. However, there were no fixed frequency differences which, considered with the differing population structures, suggests that migration-drift equilibrium has not yet obtained in one or both broodlines. The structural differences also suggest it is likely that the even- and odd-broodlines are of different ages and that one is derived from the other. Allozyme data do not provide a genealogical basis for identifying the ancestral lineage.

Key words: *Oncorhynchus gorbuscha*; pink salmon; population structure; allozyme; isolation by distance.

## Genetic Interpretation of Broad-Scale Microsatellite Polymorphism in Odd-Year Pink Salmon

JEFFREY B. OLSEN\*<sup>1</sup> AND LISA W. SEEB

Alaska Department of Fish and Game, Genetics Program  
333 Raspberry Road, Anchorage, Alaska 99518, USA

PAUL BENTZEN

Marine Molecular Biotechnology Laboratory, University of Washington  
3707 Brooklyn Avenue Northeast, Seattle, Washington 98105-6715, USA

JAMES E. SEEB

Alaska Department of Fish and Game, Genetics Program

**Abstract.**—We examined genetic variation at five microsatellite loci in 12 odd-year populations and one even-year population of pink salmon *Oncorhynchus gorbuscha* from six geographic regions of North America. The degree of polymorphism varied widely among loci. The total number of alleles in the odd-year samples varied from 4 (*Oneμ3*) to 53 (*Sta5*). A probability test revealed significant heterogeneity in allele frequencies among all odd-year samples and among pooled odd-year samples from six regions. We compared estimates of a standard index of population structure ( $\theta$ ) based on variance in allele frequency with a new index suggested for microsatellites ( $\rho_{ST}$ ) based on variance in allele size. Our results suggest  $\theta$  is a better estimator of intralineage (odd-year  $\times$  odd-year) population structure, whereas  $\rho_{ST}$  is best suited for estimating interlineage (odd-year  $\times$  even-year) population structure. The difference in performance of  $\theta$  and  $\rho_{ST}$  for estimating intralineage and interlineage population structure suggests high migration rates and possibly recent low divergence times are dominant influences on genetic population structure in odd-year pink salmon. We showed statistical support for genetic isolation by distance and geographically correlated allele frequency clines, suggesting broad-scale gene flow is best described by a linear stepping-stone model. An analysis of molecular variation showed weak but significant regional structuring under two different population grouping schemes. Our results suggest broad-scale population aggregations of odd-year pink salmon are temporally stable but that differentiation is weak, presumably due to migration.

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

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J. B. Shaklee<sup>2</sup>, F. M. Utter<sup>3</sup>

<sup>1</sup>Alaska Department of Fish & Game, Commercial Fisheries Division, Anchorage, Alaska. <sup>2</sup>Washington Department of Fish & Wildlife, Olympia. <sup>3</sup>School of Fisheries, University of Washington, Seattle, Washington, USA

Key words: allozyme; mtDNA; genetics; pink salmon

J. E. Seeb, Alaska Department of Fish & Game, Commercial Fisheries Division, Anchorage, AK 99518, USA

Accepted for publication April 9, 1999

**Abstract**—Population structure of pink salmon (*Oncorhynchus gorbuscha*) from British Columbia and Washington was examined with a survey of microsatellite variation to describe the distribution of genetic variation. Variation at 16 microsatellite loci was surveyed for approximately 46,500 pink salmon sampled from 146 locations in the odd-year broodline and from 116 locations in the even-year broodline. An index of genetic differentiation,  $F_{ST}$ , over all populations and loci in the odd-year broodline was 0.005, with individual locus values ranging from 0.002 to 0.025. Population differentiation was less in the even-year broodline, with a  $F_{ST}$  value of 0.002 over all loci, and with individual locus values ranging from 0.001 to 0.005. Greater genetic diversity was observed in the odd-year broodline. Differentiation in pink salmon allele frequencies between broodlines was approximately 5.5 times greater than regional differentiation within

## Population structure of pink salmon (*Oncorhynchus gorbuscha*) in British Columbia and Washington, determined with microsatellites

Terry D. Beacham (contact author)<sup>1</sup>

Brenda McIntosh<sup>1</sup>

Cathy MacConnachie<sup>1</sup>

Brian Spilsted<sup>2</sup>

Bruce A. White<sup>3</sup>

E-mail address for contact author: Terry.Beacham@dfg-mpo.gc.ca

<sup>1</sup> Fisheries and Oceans Canada

Pacific Biological Station  
3190 Hammond Bay Road  
Nanaimo, B. C., Canada V9T 6N7

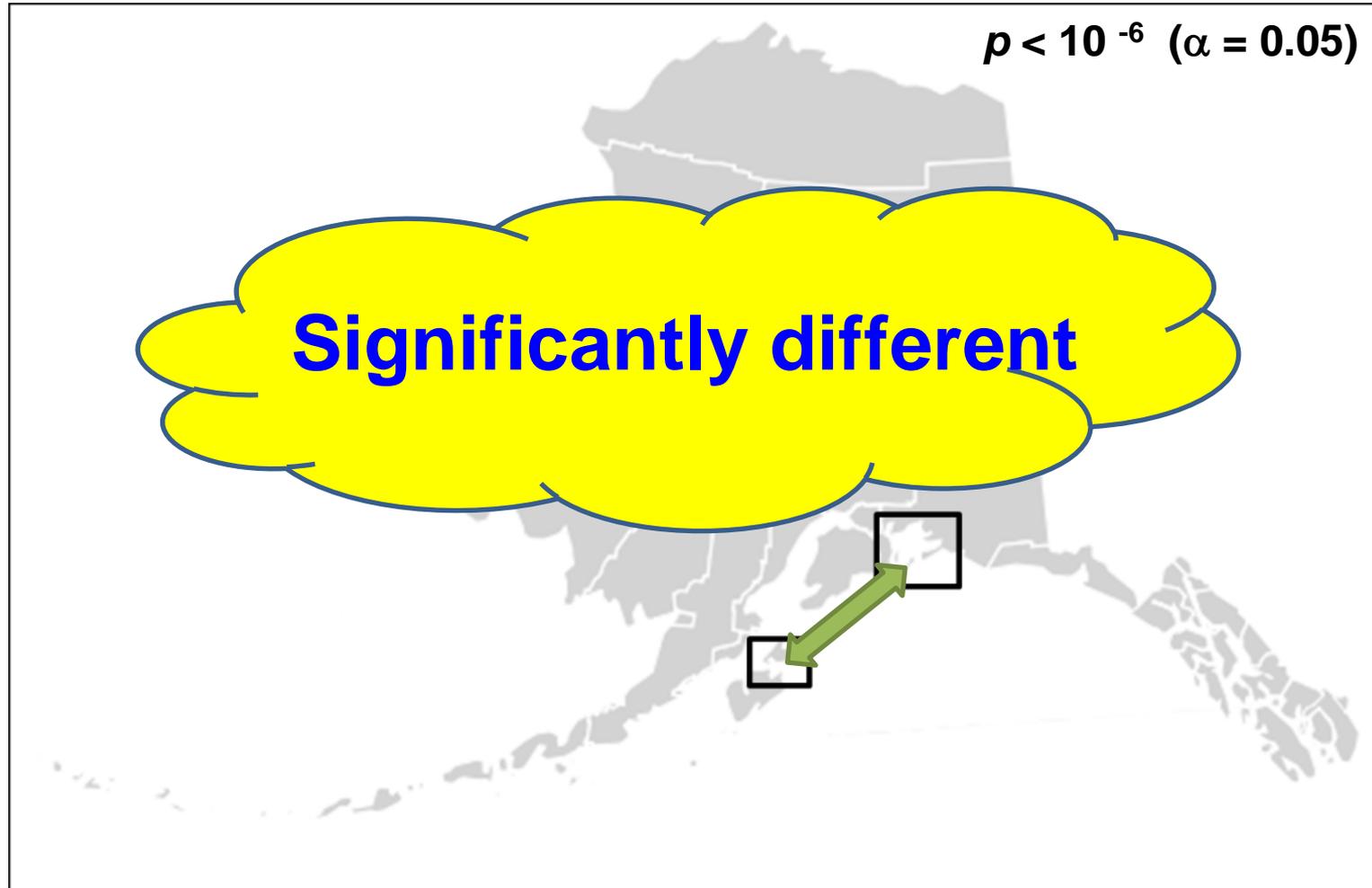
<sup>2</sup> Fisheries and Oceans Canada  
417-2nd Avenue West  
Prince Rupert, B. C. Canada V8J 1G8

<sup>3</sup> Pacific Salmon Commission  
600-1155 Robson Street  
Vancouver, B. C., Canada V6E 1B5

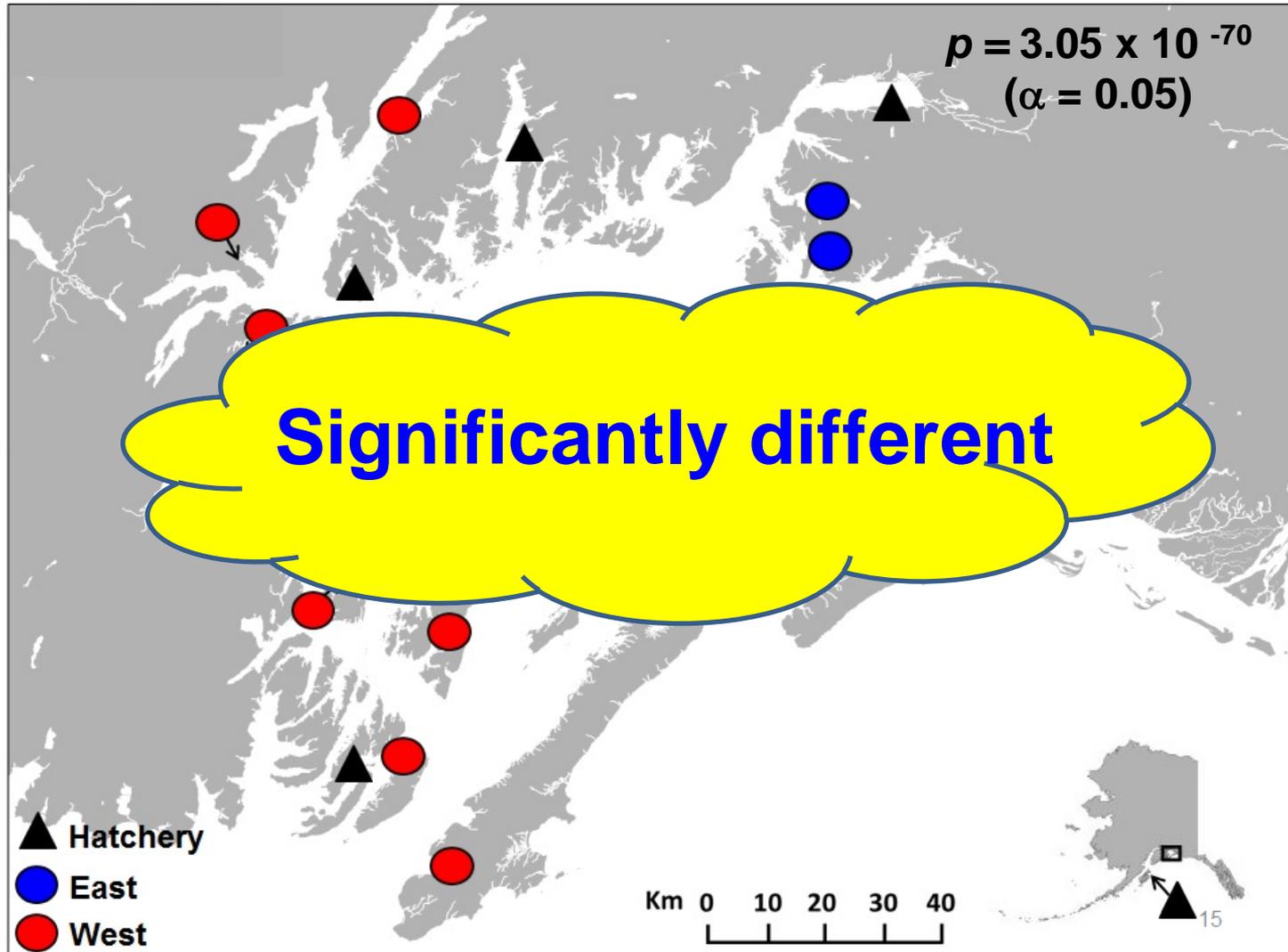
# Population Structure Analyses

- Calculate genetic differences among collections
- **Test for significance of these differences**

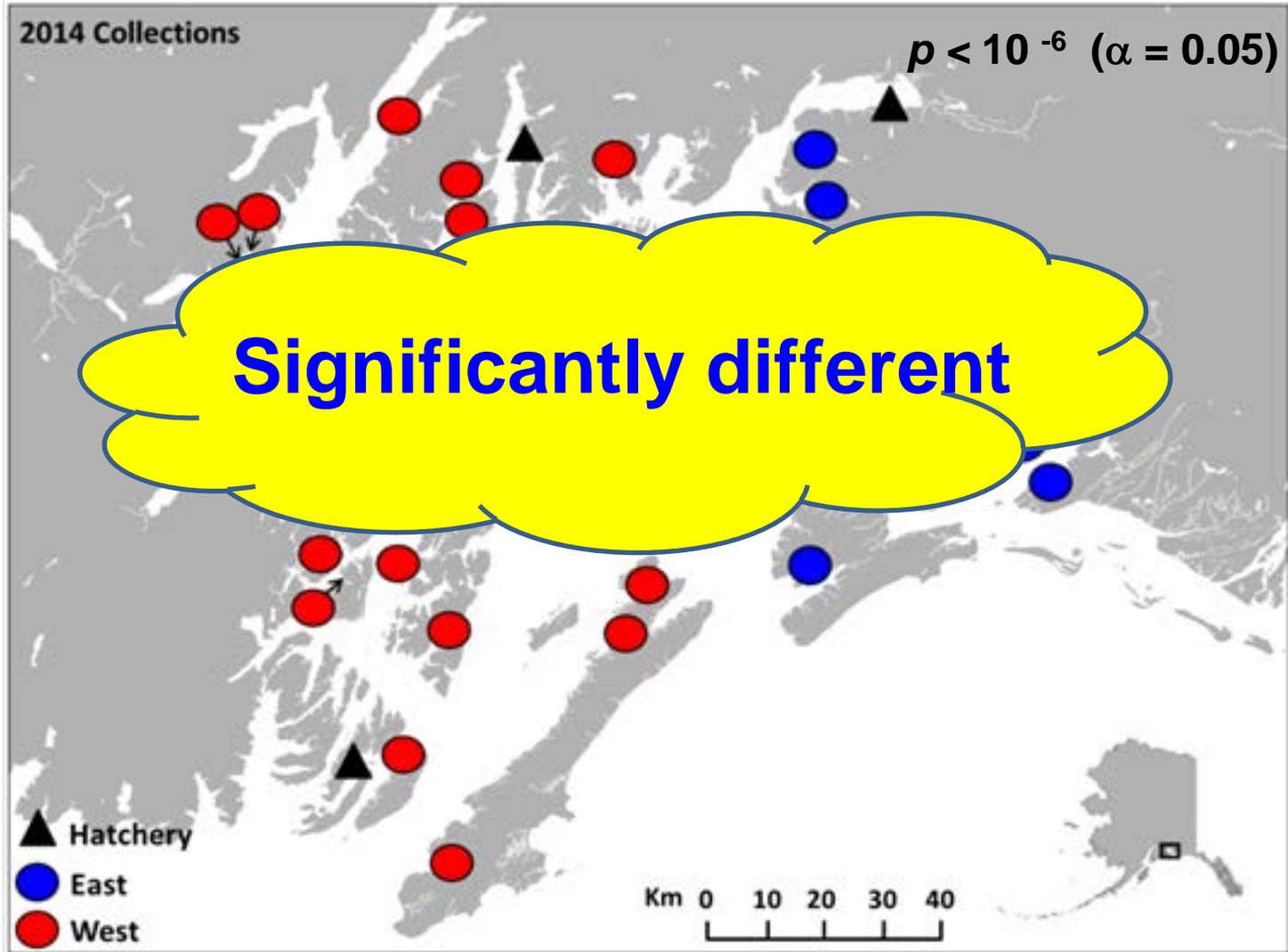
# Testing for Difference: Kodiak vs. Prince William Sound



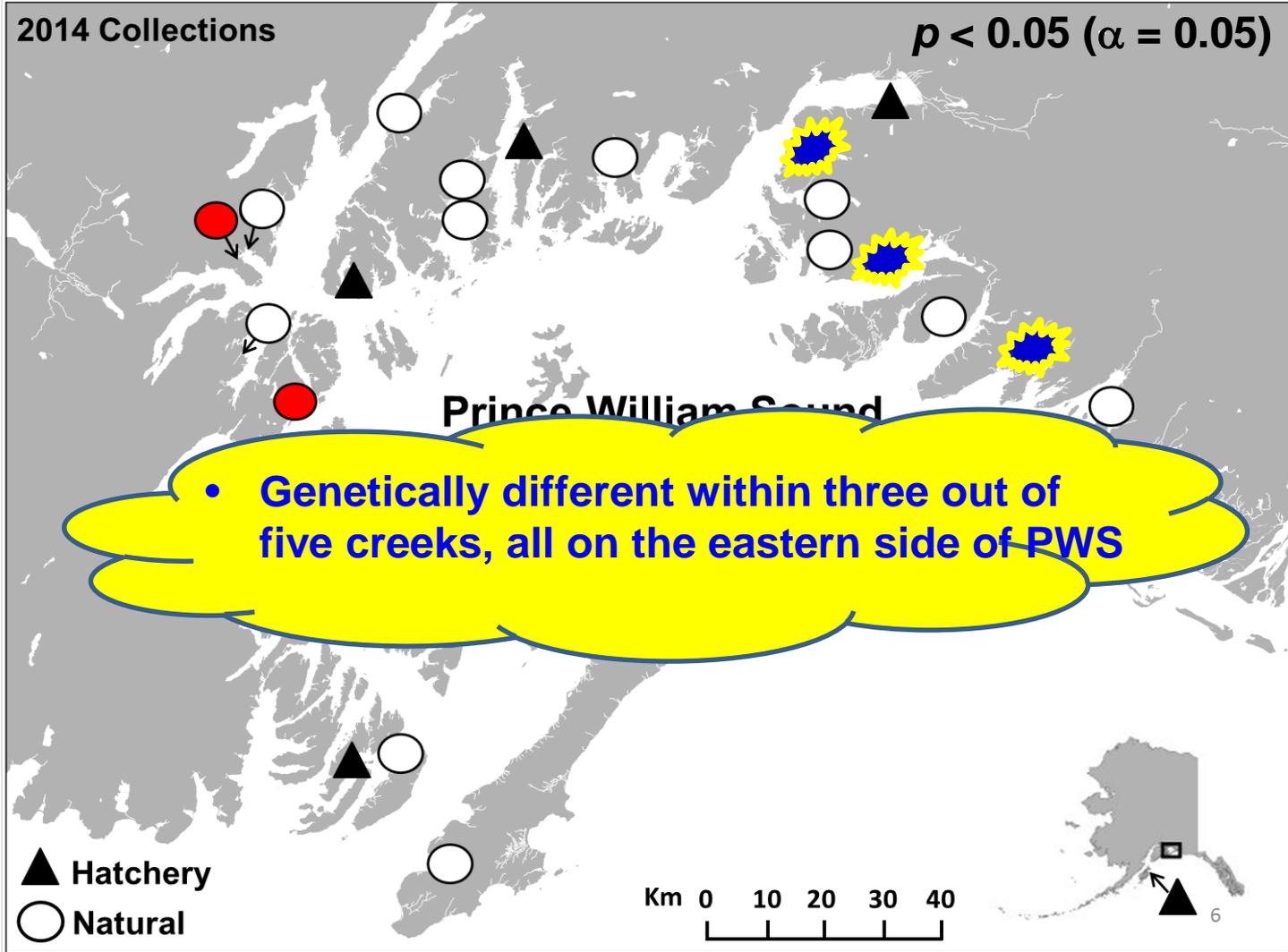
# Testing for Differences: among Prince William Sound



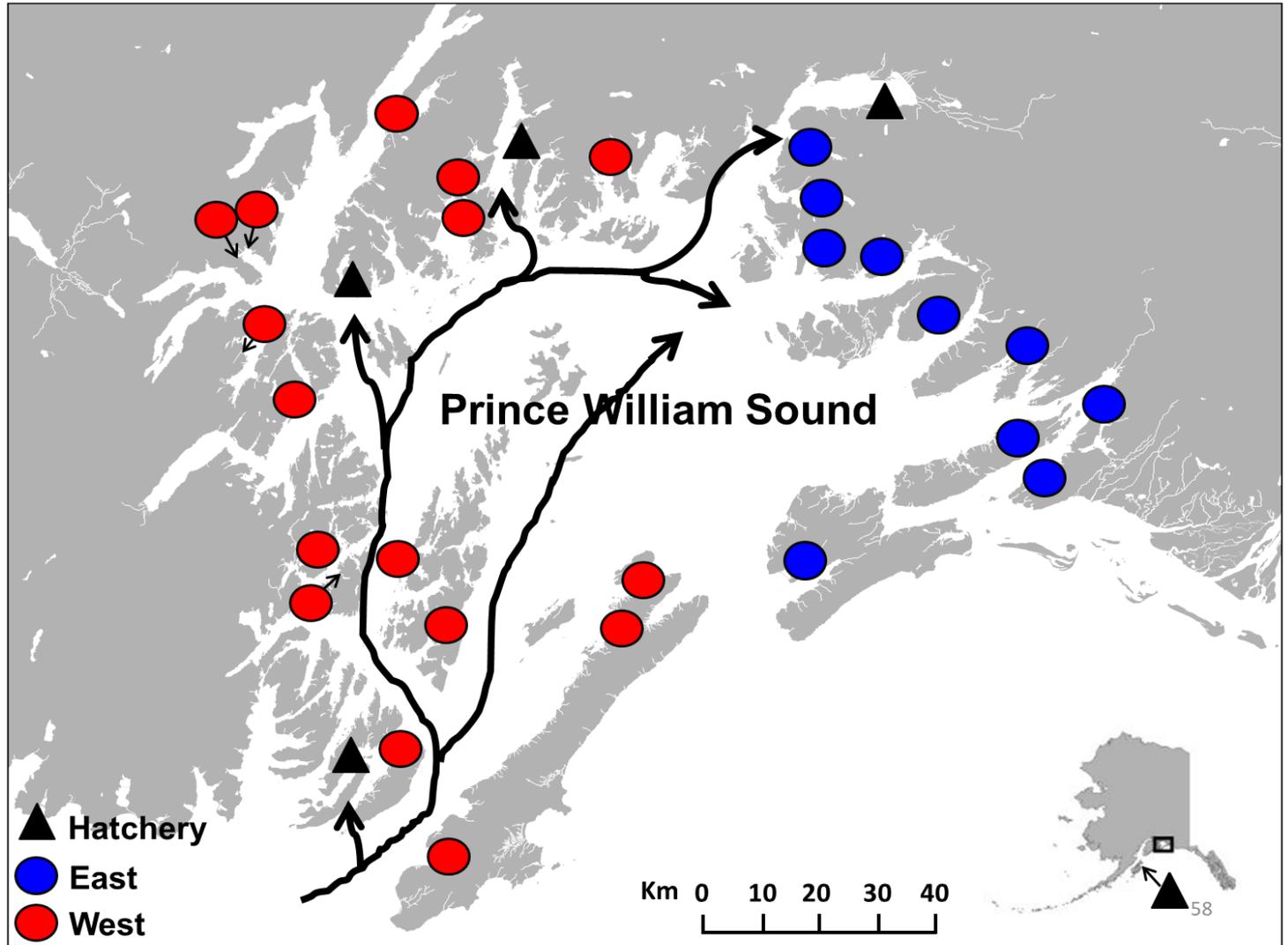
# Testing for Differences: among Prince William Sound



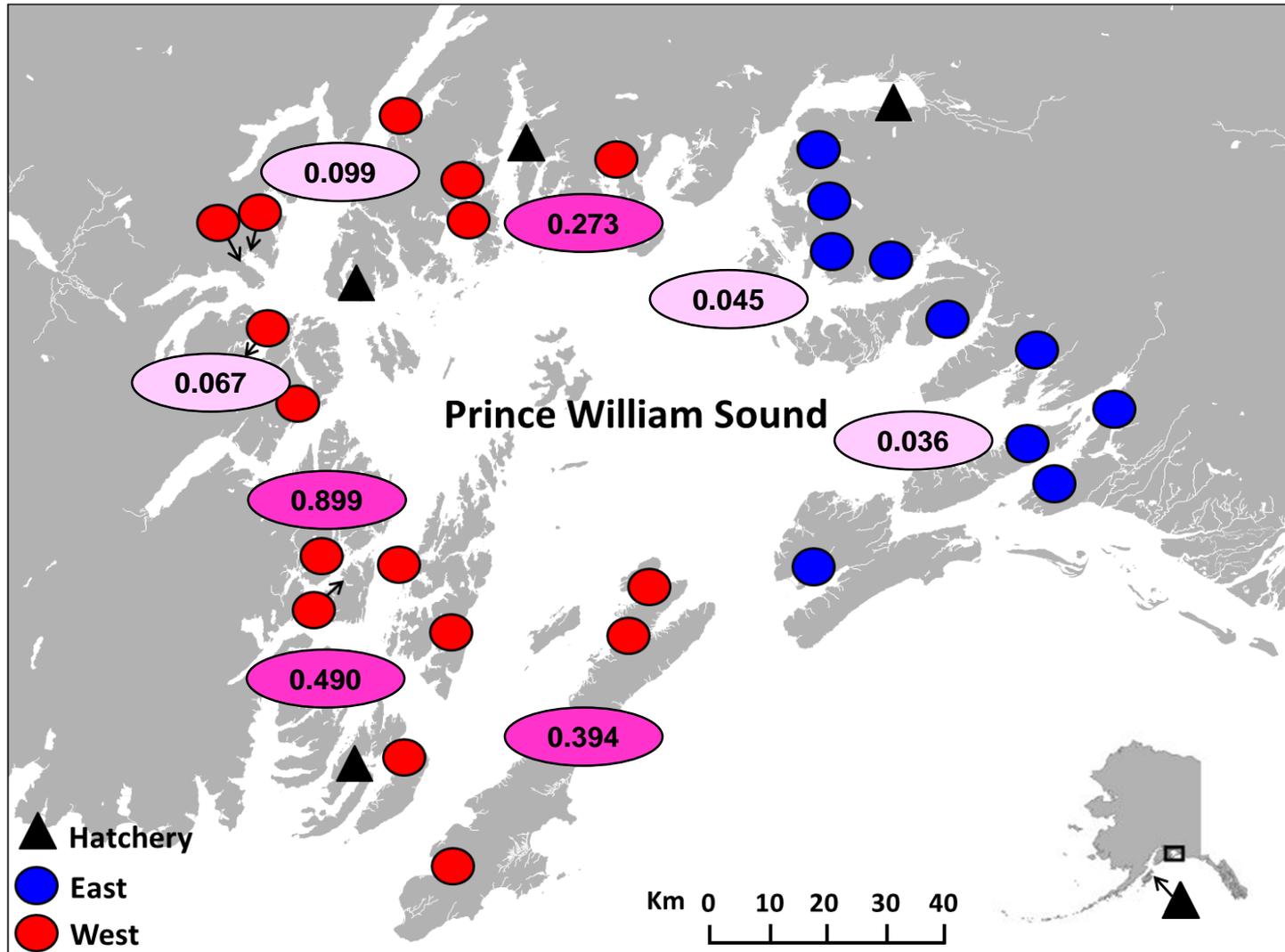
# Testing for Differences: Between Early and Late Collections



# Assumed Migration Pathway



# Estimated Hatchery Pink Salmon Fraction within Prince William Sound Streams



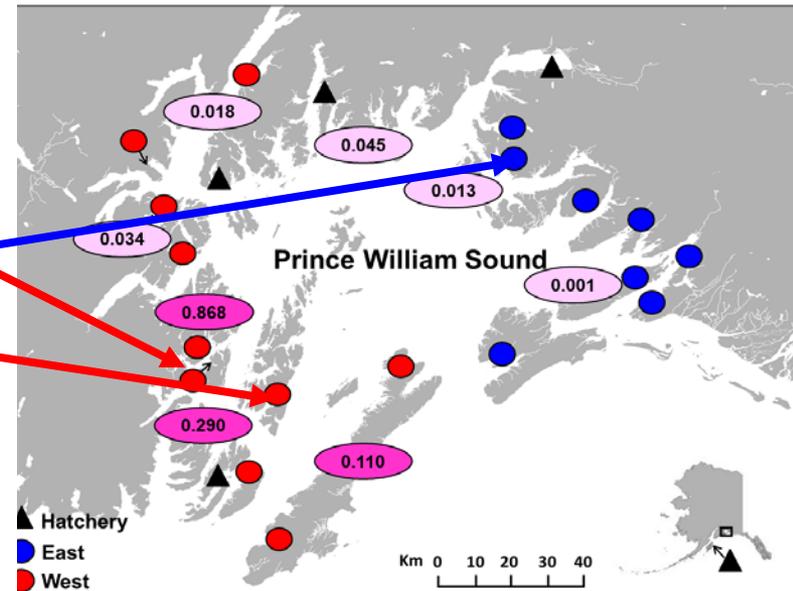
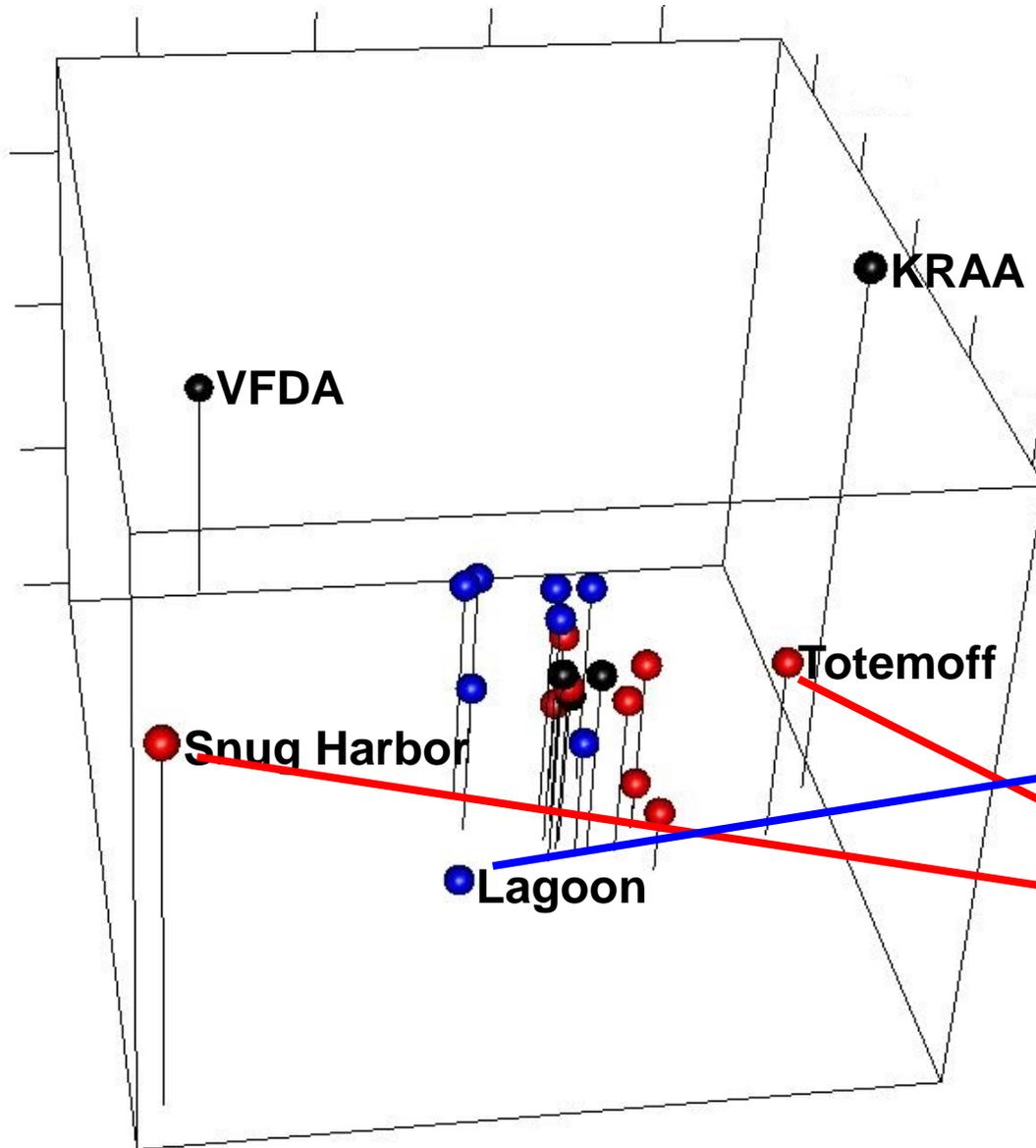
Data from Knudsen *et al.* 2015

# Population Structure Analyses

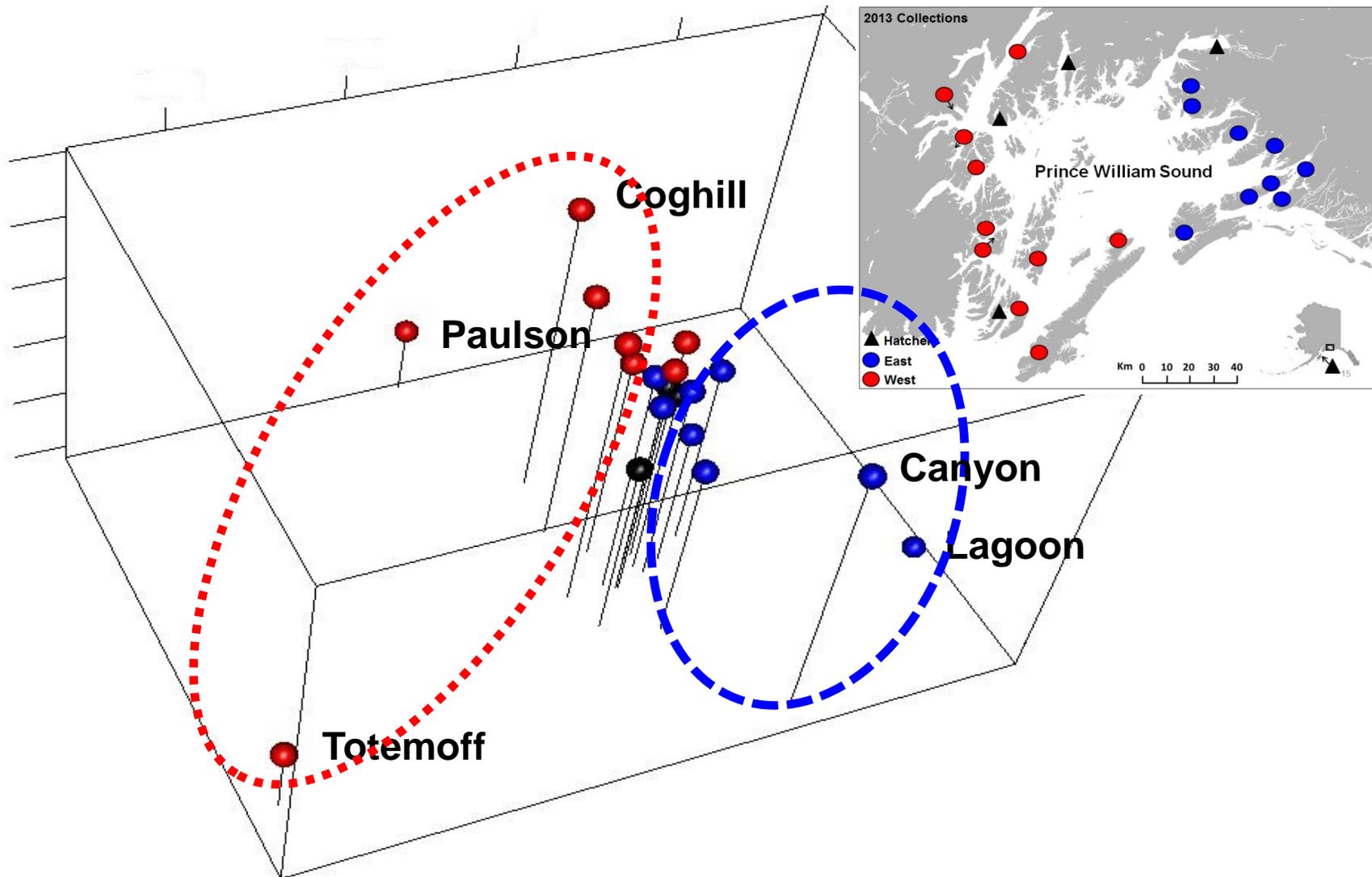
- Calculate genetic differences among collections
- Test for significance of these differences
- **Visualize the relationships among collections**

# Visualizing the Relationships among Collections

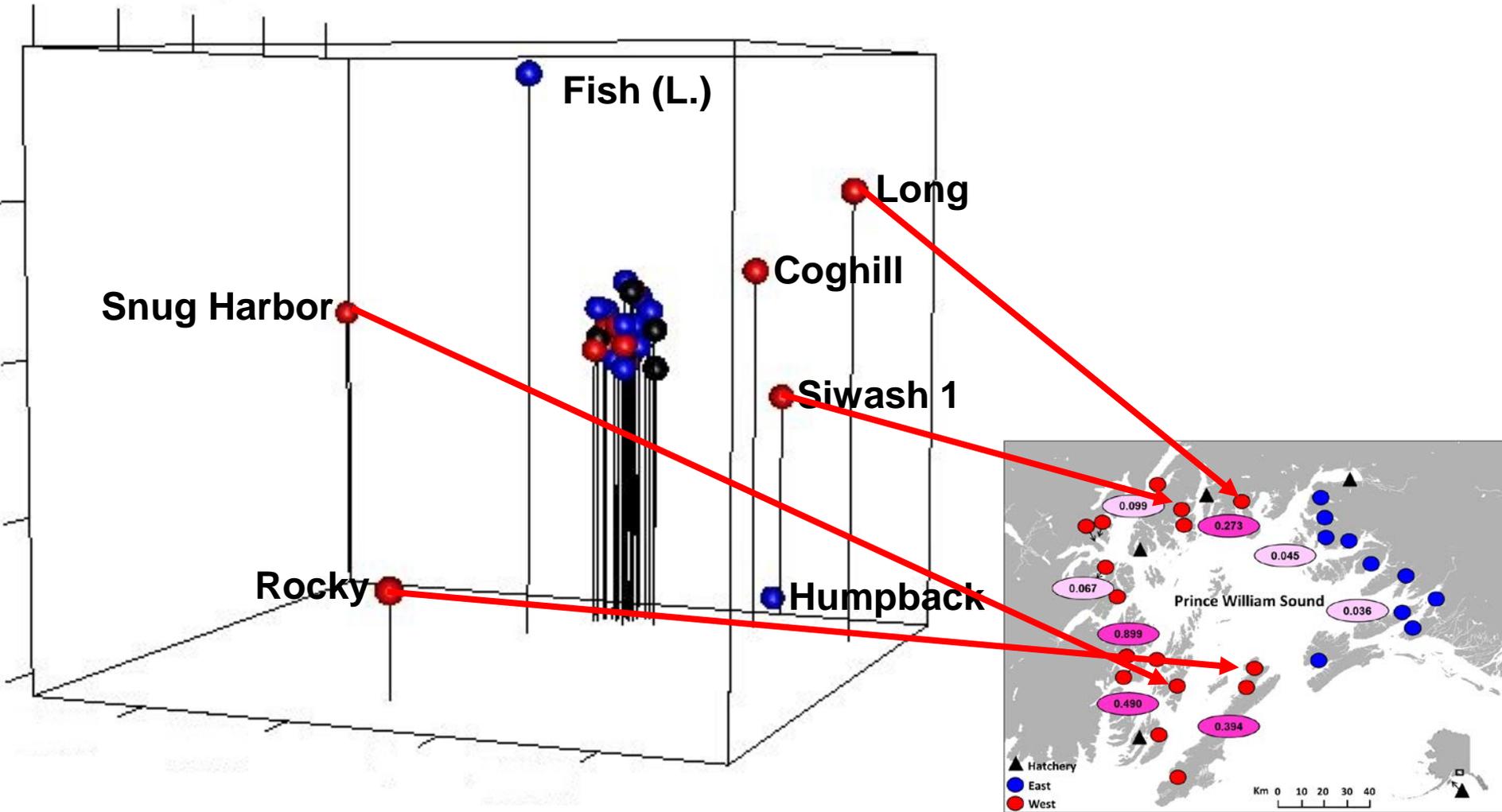
Odd Year



# Visualizing the Relationships among Collections – Zooming in



# Visualizing the Relationships among Collections



# Summary to date

- **Genetic variation among pink salmon populations in PWS is very small**
  - ✓ **Odd year – small**
  - ✓ **Even year – even smaller**
  
- **Kodiak vs. Prince William Sound (PWS)**
  - ✓ **Significantly different in both lineages**

# Summary to date

- **Genetic difference within PWS**
  - ✓ **Significantly different in both lineages**
  
- **Within lineage patterns**
  - ✓ **Odd year:**
    - ✓ **East vs. West**
    - ✓ **Early vs. Late?**
  - ✓ **Even year:**
    - ✓ **Early vs. Late (eastern side only)**

# Future Work

- **Historical samples**
  - ✓ **1991 – 1997**
  - ✓ **No otolith information**
  
- **Investigate the mechanisms driving the structure**

# Acknowledgements

- **Hatcheries**
  - **PWSAC, VFDA, KRAA**
- **Prince William Sound Science Center**
- **Fisheries and Oceans Canada**
  - **Pacific Biological Station**
- **Alaska Department of Fish and Game**
- **Alaska Hatchery Research Program Science Panel**
- **University of Alaska Fairbanks – Juneau Center**