

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

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Alaska Hatchery Research Program Informational Meeting
March 9, 2022



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?

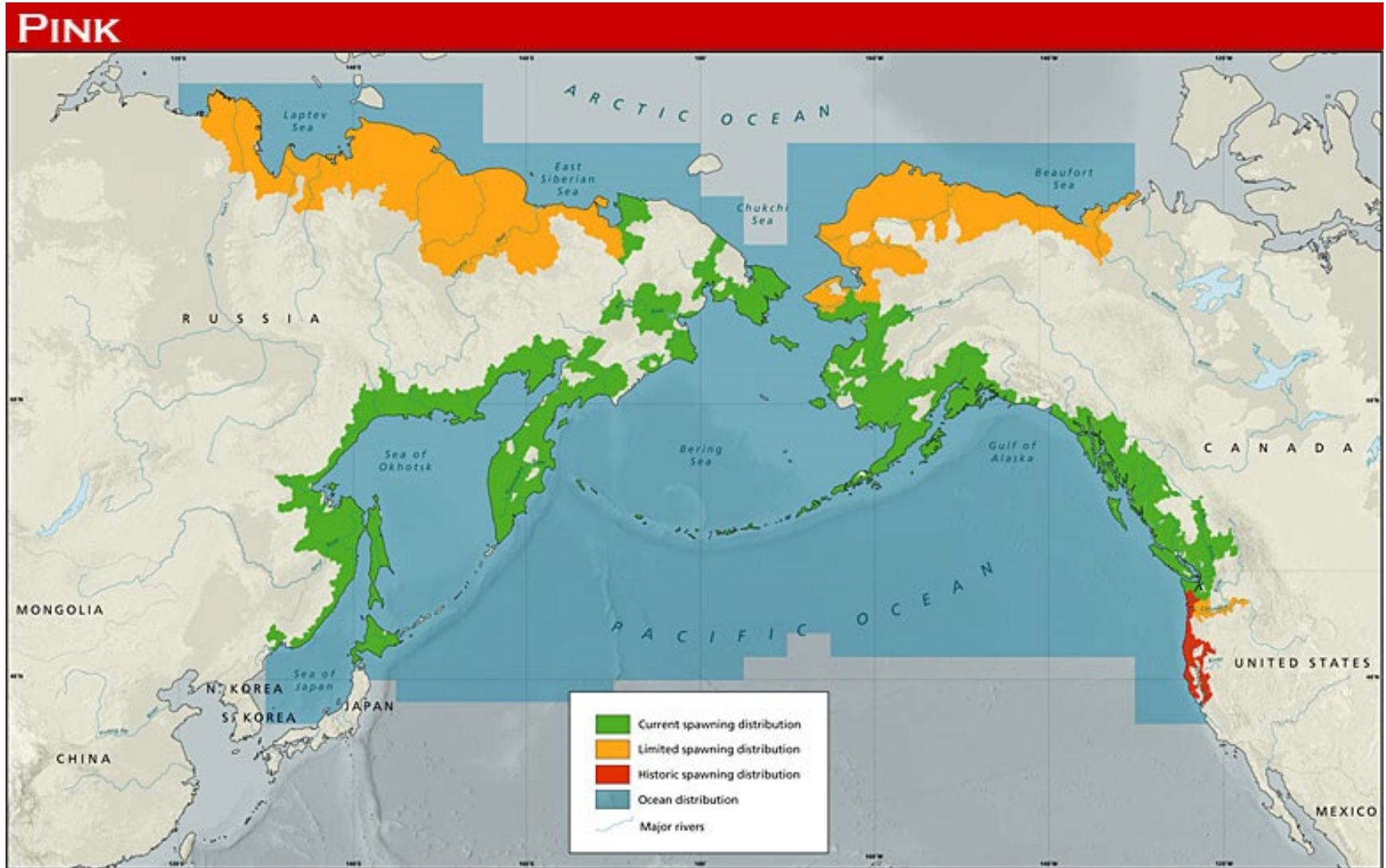
Life History of Pink Salmon

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



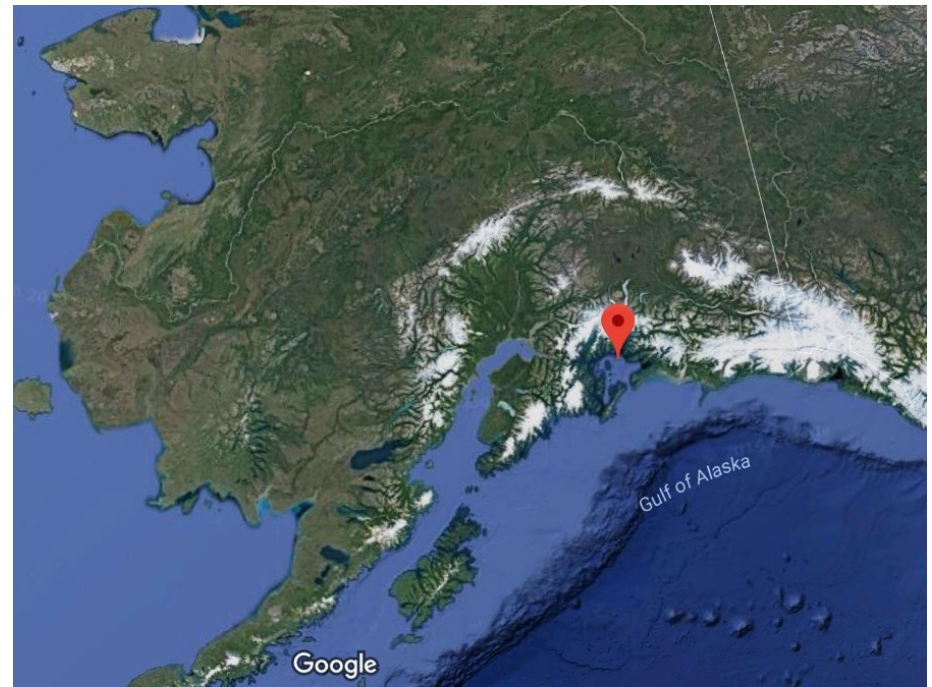
<https://www.n-sea.org/pink-salmon>

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.

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Key words: allozyme; mtDNA; genetics; pink salmon

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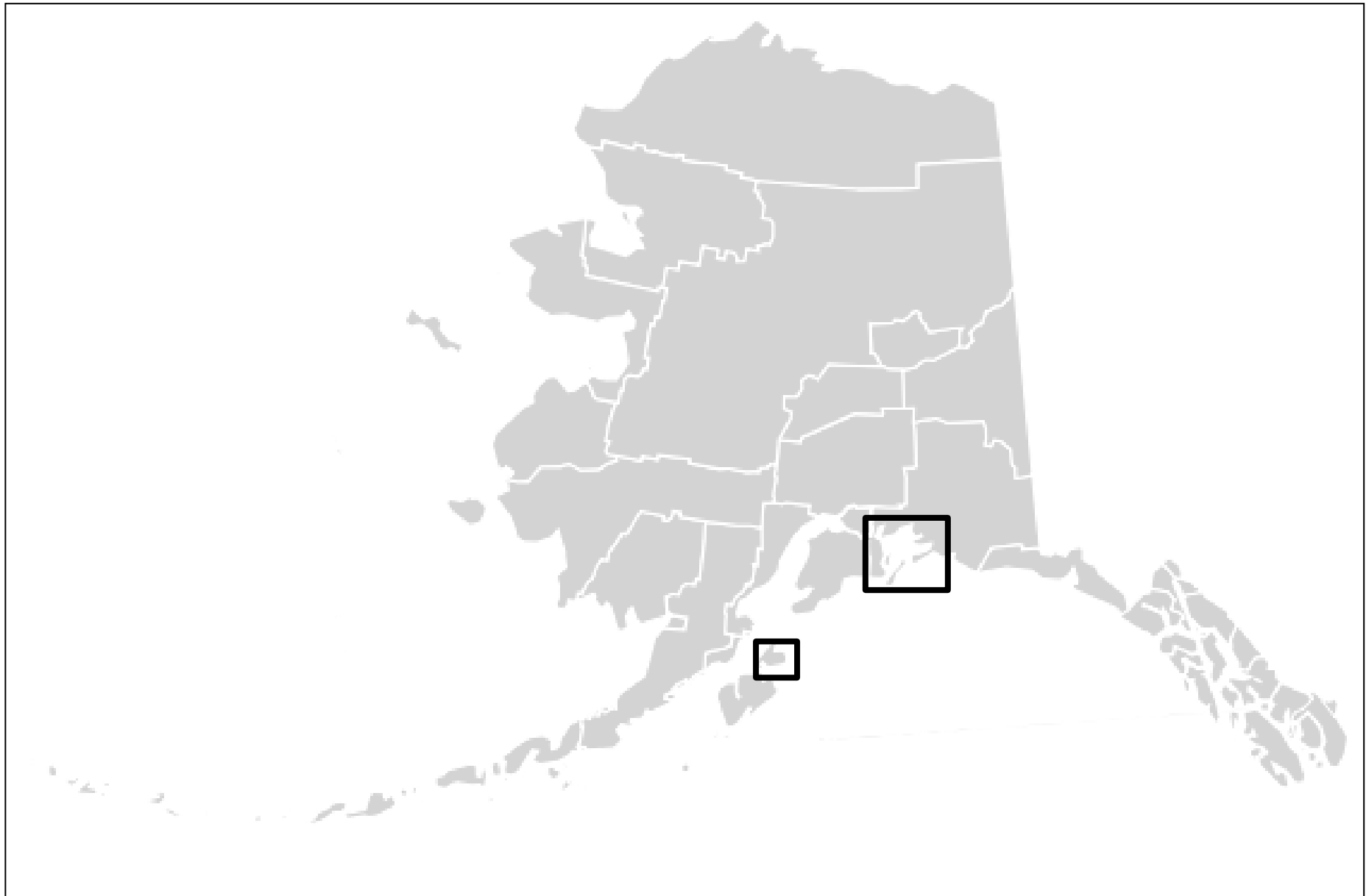
Accepted for publication April 9, 1999

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

Study Design

| | Contemporary | Historical |
|----------|--------------|------------|
| Natural | ✓ | ✓ |
| Hatchery | ✓ | ✓ |

The table is a 2x2 grid. The columns are labeled 'Contemporary' and 'Historical'. The rows are labeled 'Natural' and 'Hatchery'. In the 'Natural' row, there is a blue checkmark under 'Contemporary' and a red checkmark under 'Historical'. In the 'Hatchery' row, there is a blue checkmark under 'Contemporary' and a red checkmark under 'Historical'. A red oval encircles the checkmarks in the 'Natural' row, and another red oval encircles the checkmarks in the 'Hatchery' row.



Swanson Creek



07.28.2014

McCleod Creek



07.31.2014

Rocky Creek



08.01.2014

Duck River



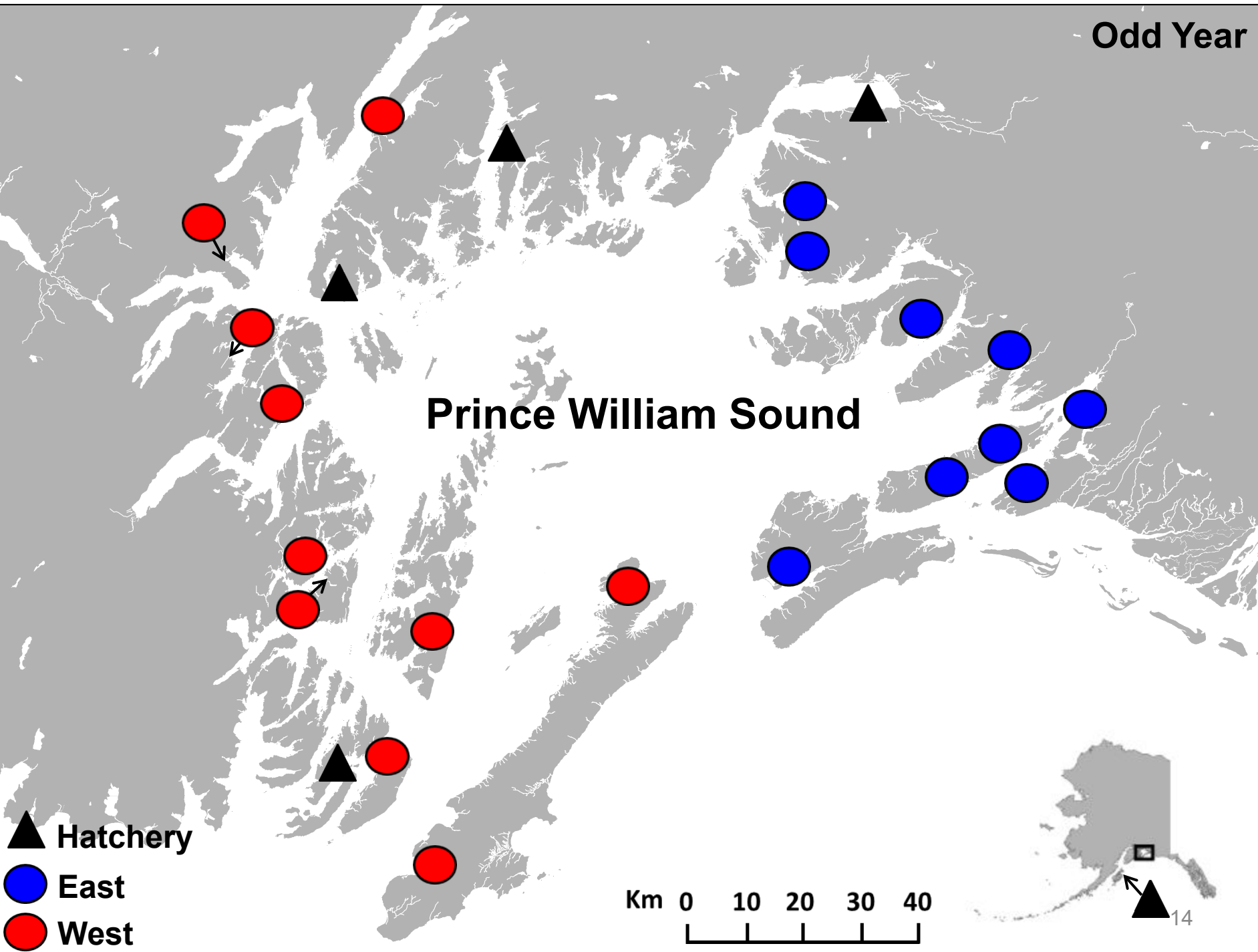
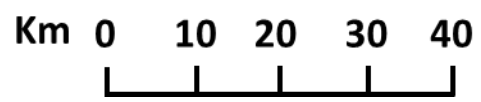
08.04.2014

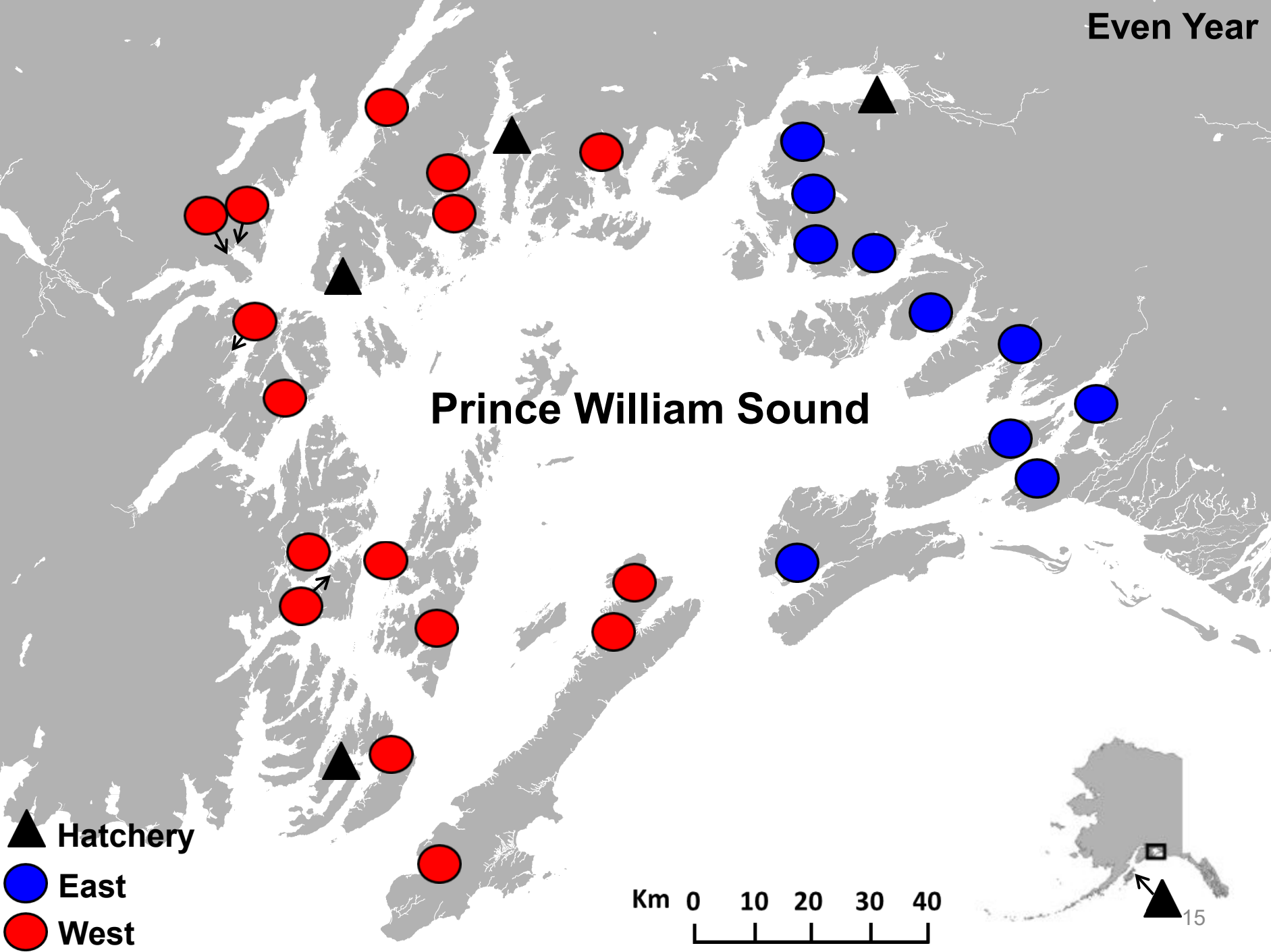
Study Design

| | Contemporary | Historical |
|-----------------|---------------------|-------------------|
| Natural | ✓ | |
| Hatchery | ✓ | |

Prince William Sound

- ▲ Hatchery
- East
- West

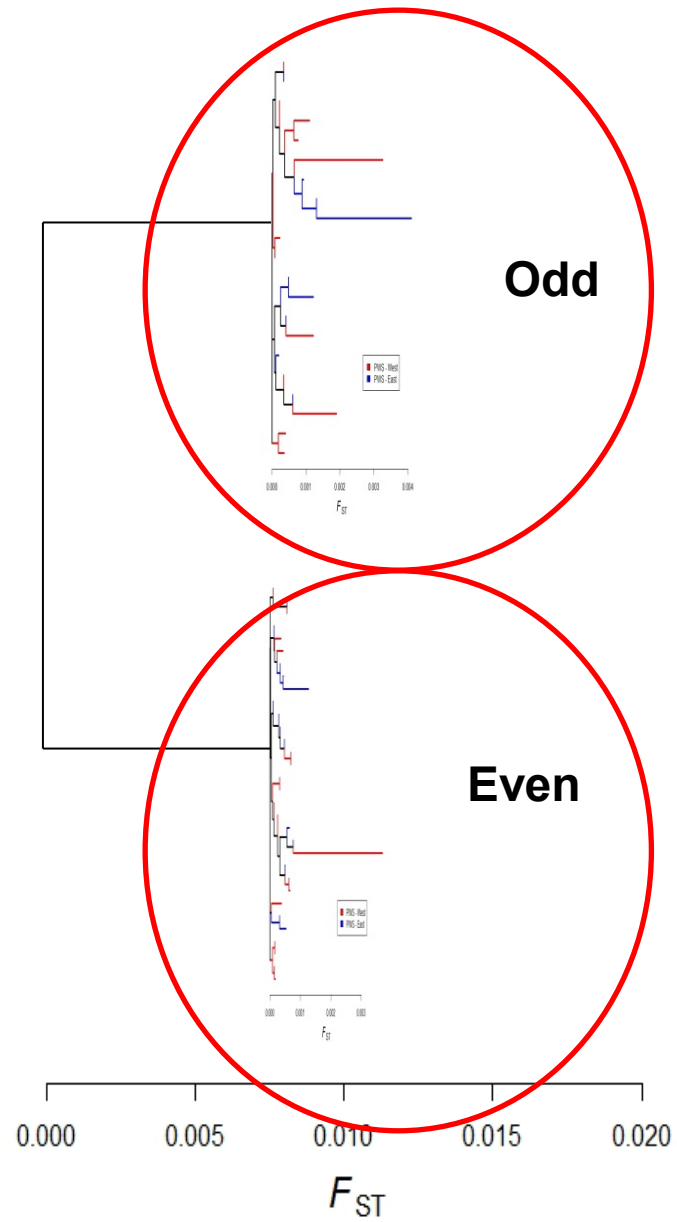




Population Structure Analyses

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

PWS Pink Salmon



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 (*O67e*) to 87 (*Oki101*), 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

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(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

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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 (*Oney3*) to 53 (*Sta85*). 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 (θ) based on variance in allele frequency with a new index suggested for microsatellites (ρ_{ST}) based on variance in allele size. Our results suggest θ is a better estimator of intralineage (odd-year \times odd-year) population structure, whereas ρ_{ST} is best suited for estimating interlineage (odd-year \times even-year) population structure. The difference in performance of θ and ρ_{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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Key words: allozyme; mtDNA; genetics; pink salmon

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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

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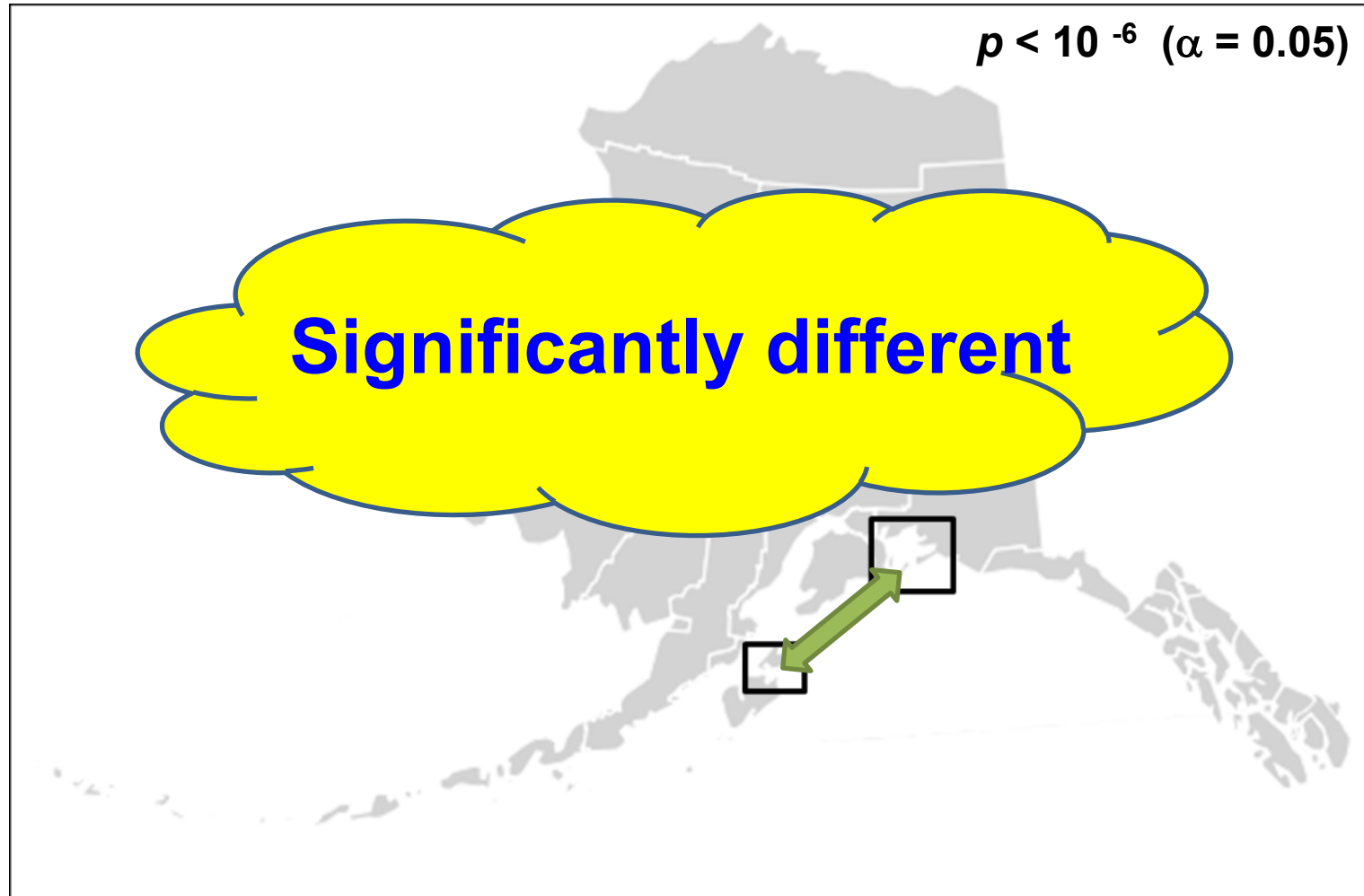
³ Pacific Salmon Commission

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Vancouver, B. C., Canada V6E 1B5

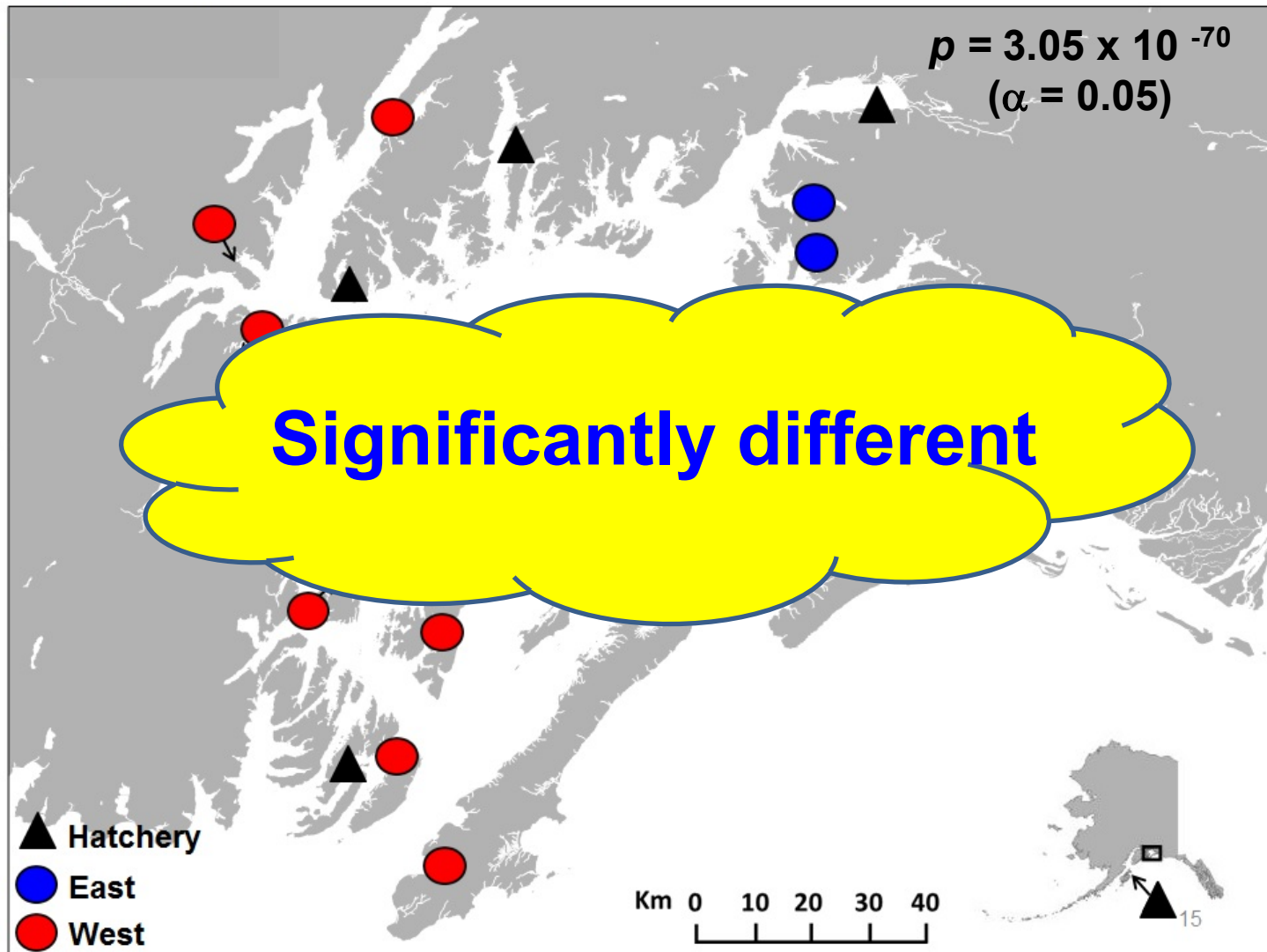
Population Structure Analyses

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

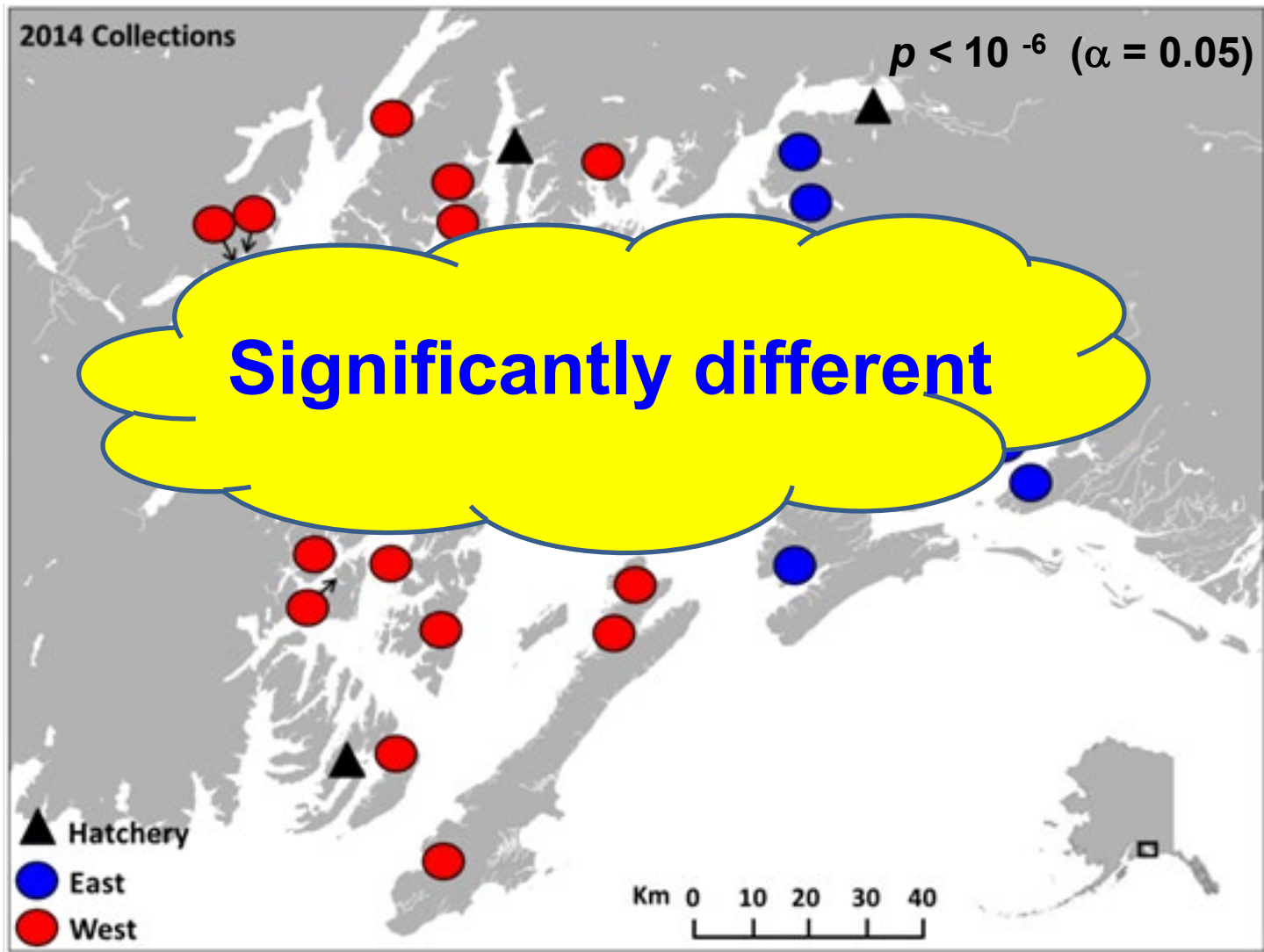
Testing for Difference: Kodiak vs. Prince William Sound



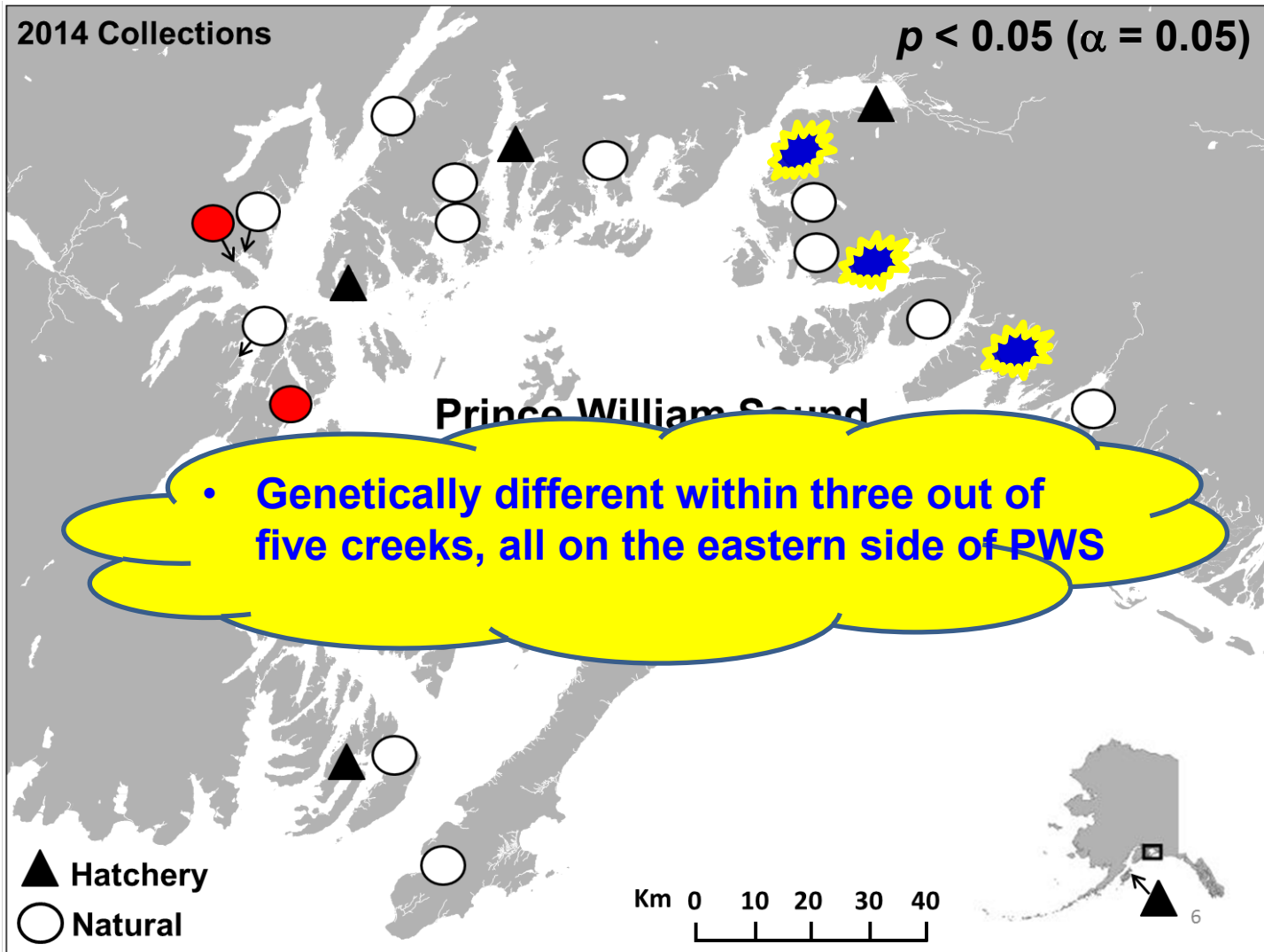
Testing for Differences: among Prince William Sound



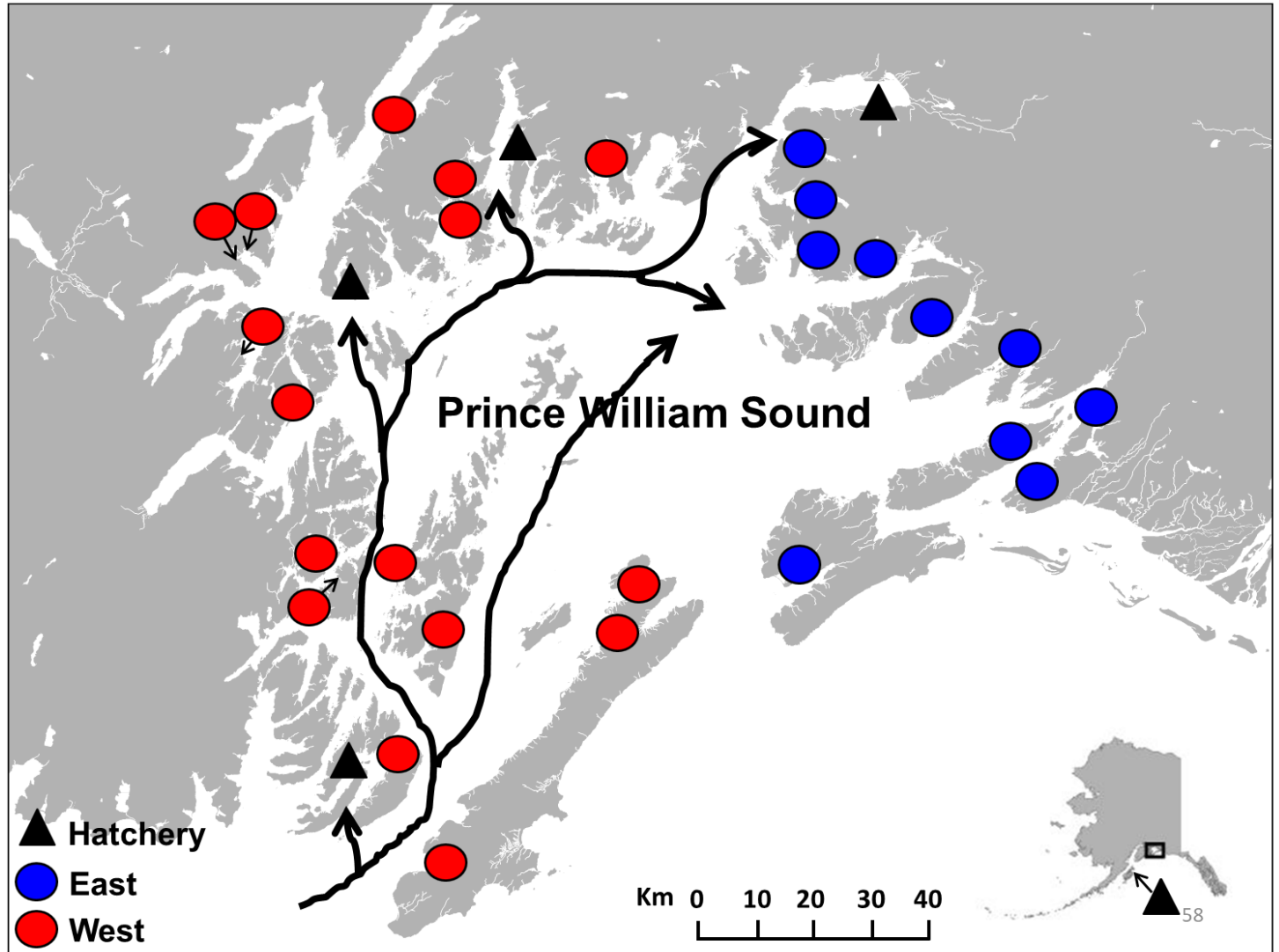
Testing for Differences: among Prince William Sound



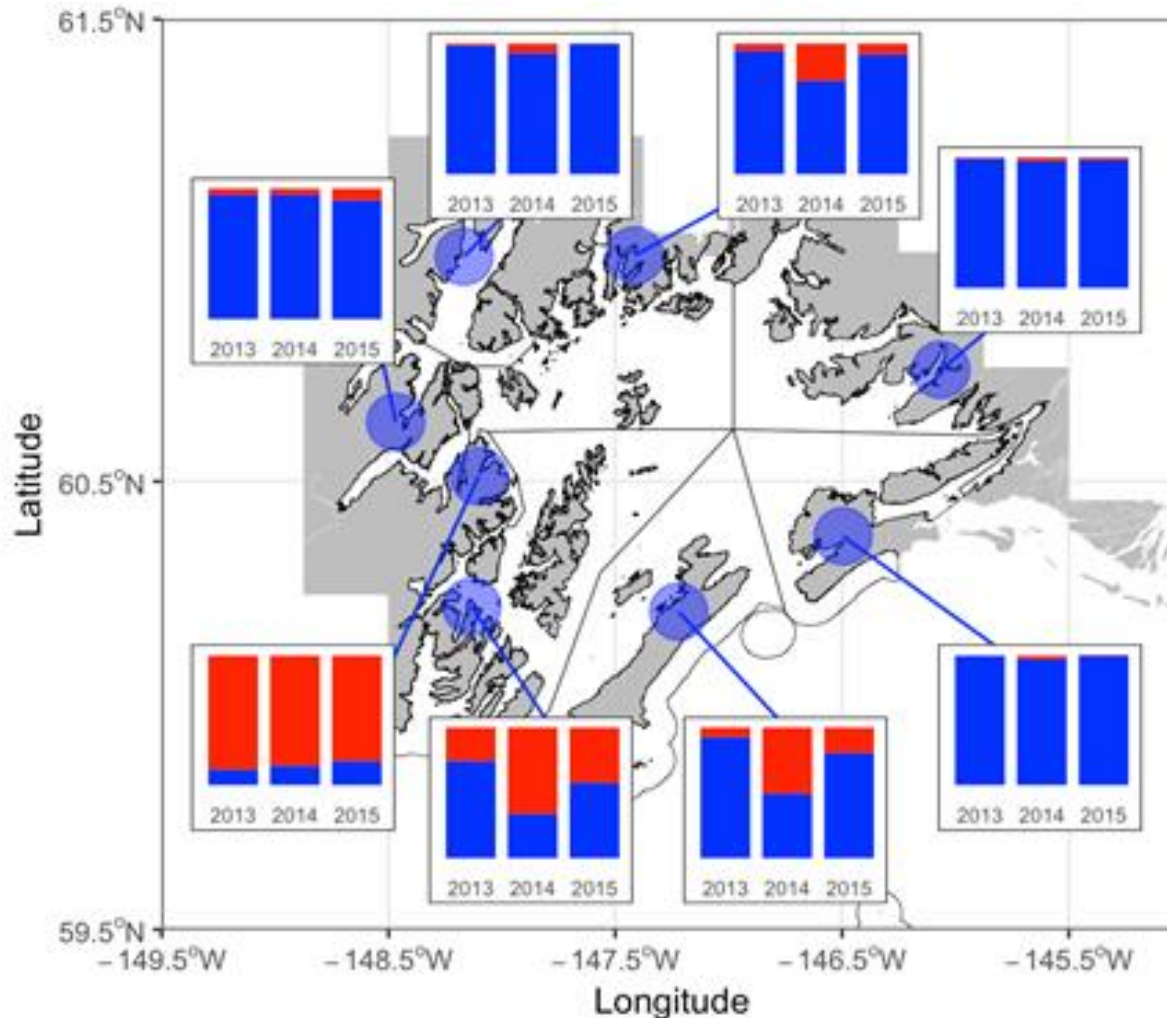
Testing for Differences: Between Early and Late Collections



Assumed Migration Pathway



Estimated Hatchery Pink Salmon Fraction within Prince William Sound Streams

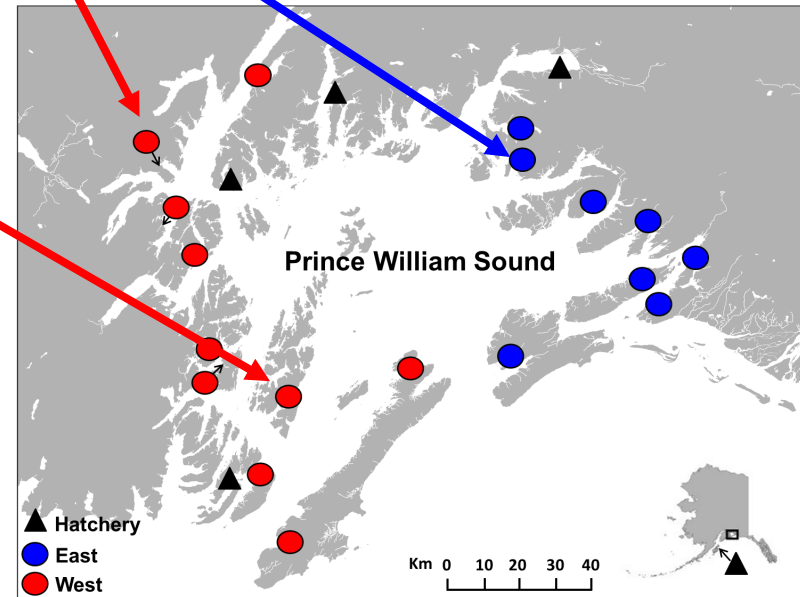
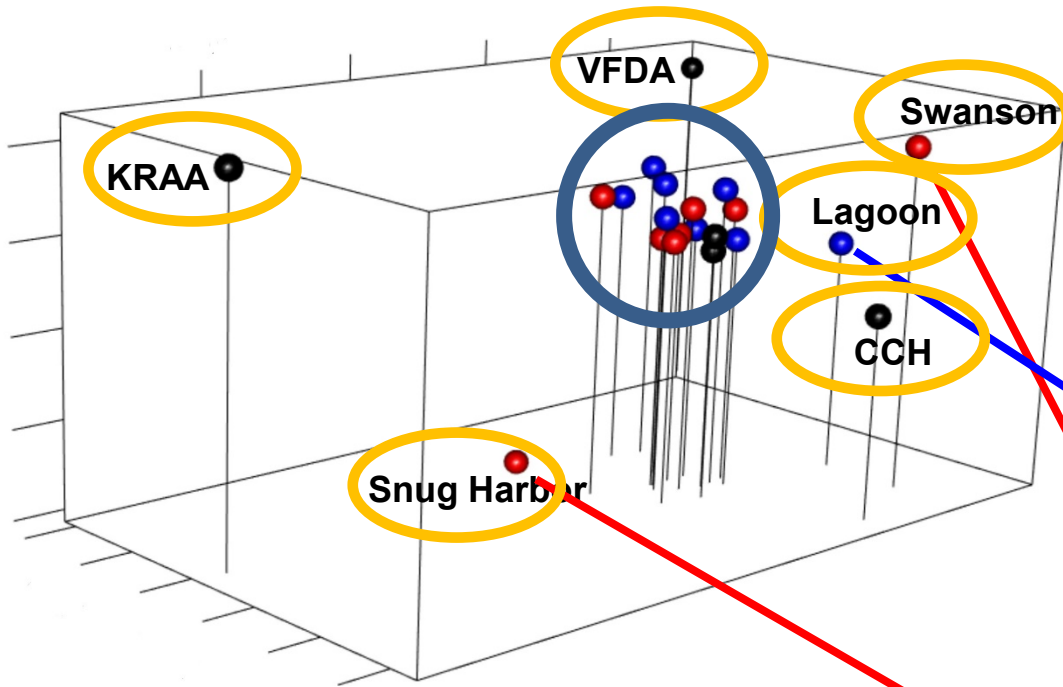


Population Structure Analyses

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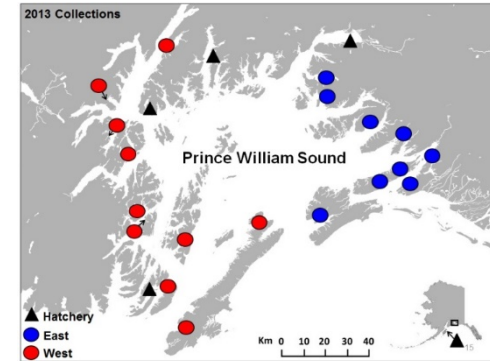
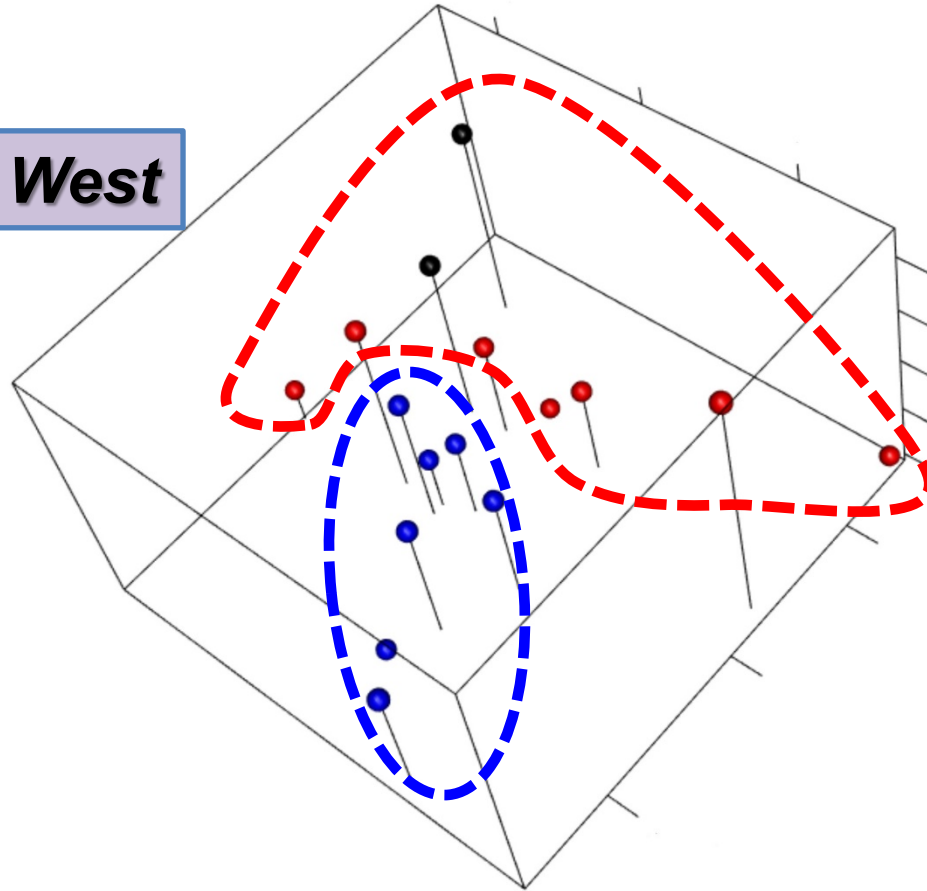
Visualizing the Relationships among Collections

Odd Year

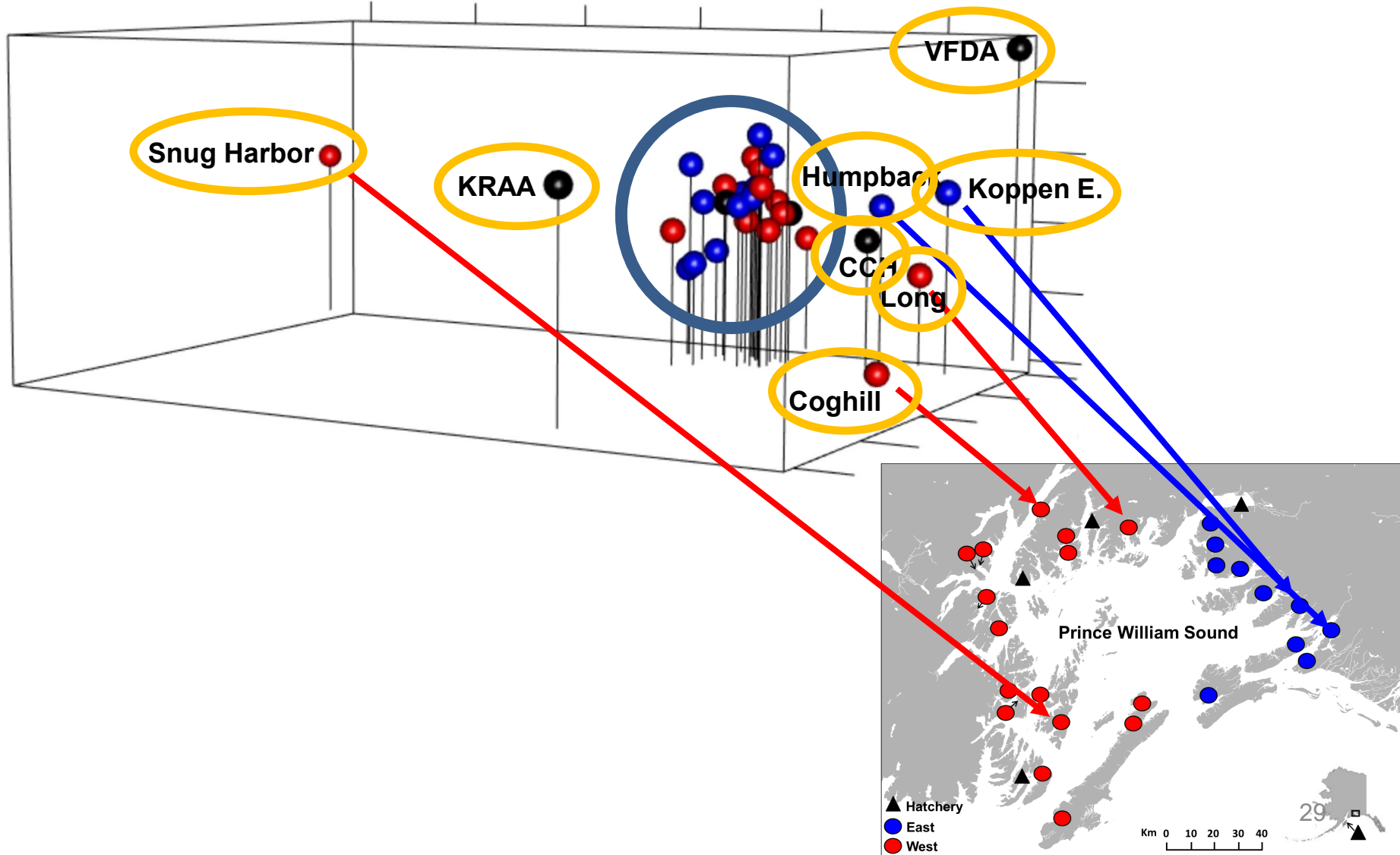


Visualizing Relationships Among Collections – Zooming In

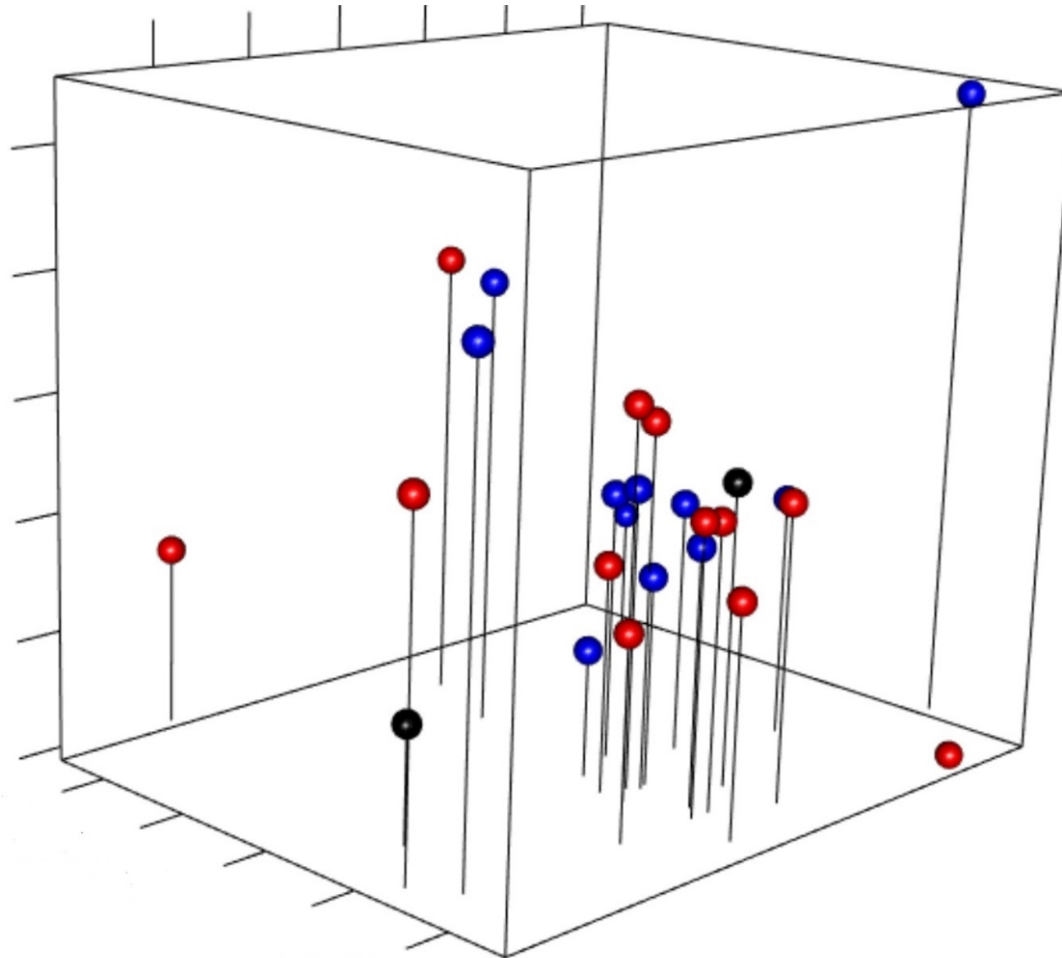
East vs. West



Visualizing the Relationships among Collections



Visualizing the Relationships among Collections



Summary to date

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

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