

Population Structure of Pink Salmon from Prince William Sound, Alaska

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Alaska Hatchery Research Program Informational Meeting
March 7, 2019



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?

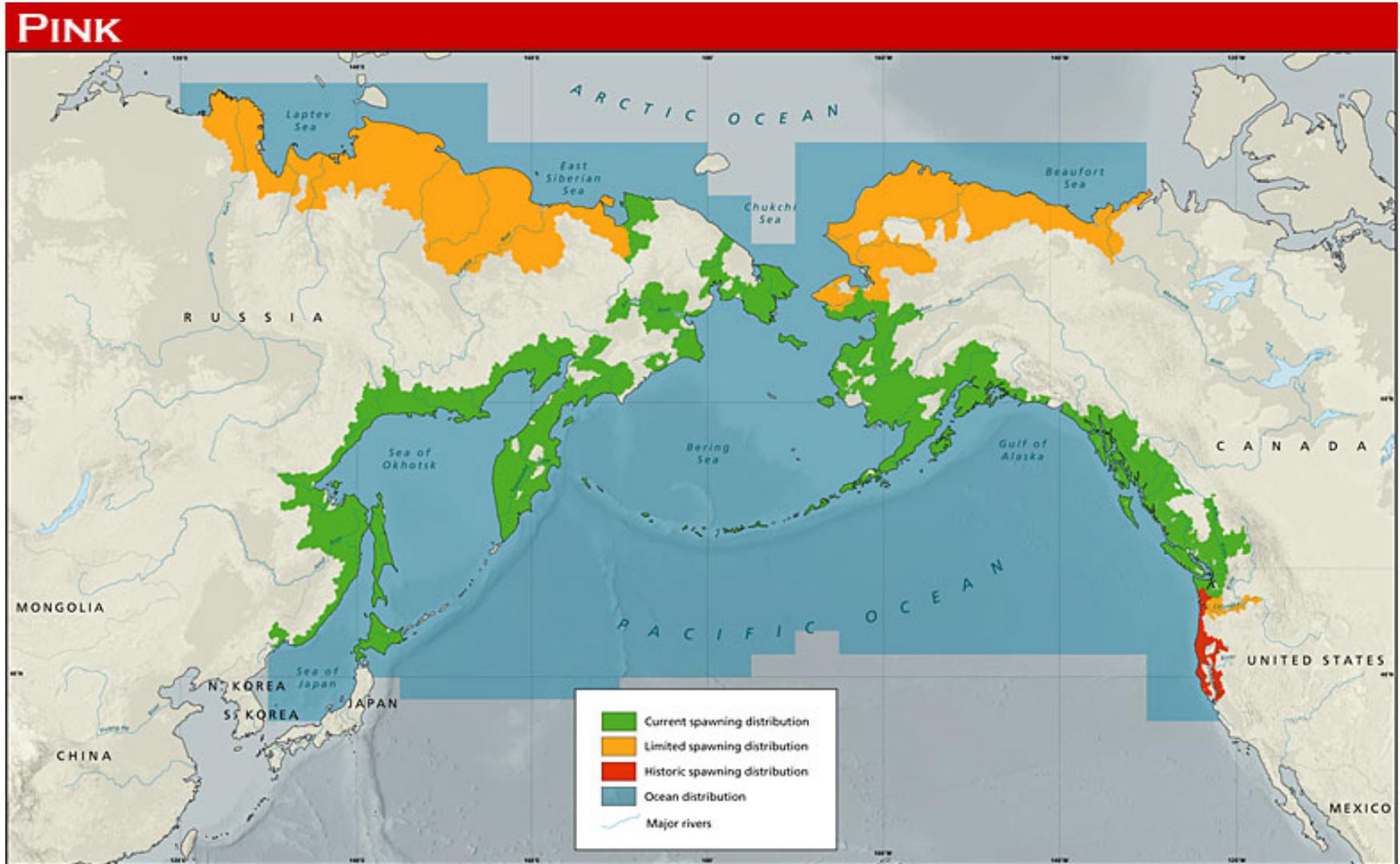
Life History of Pink Salmon

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



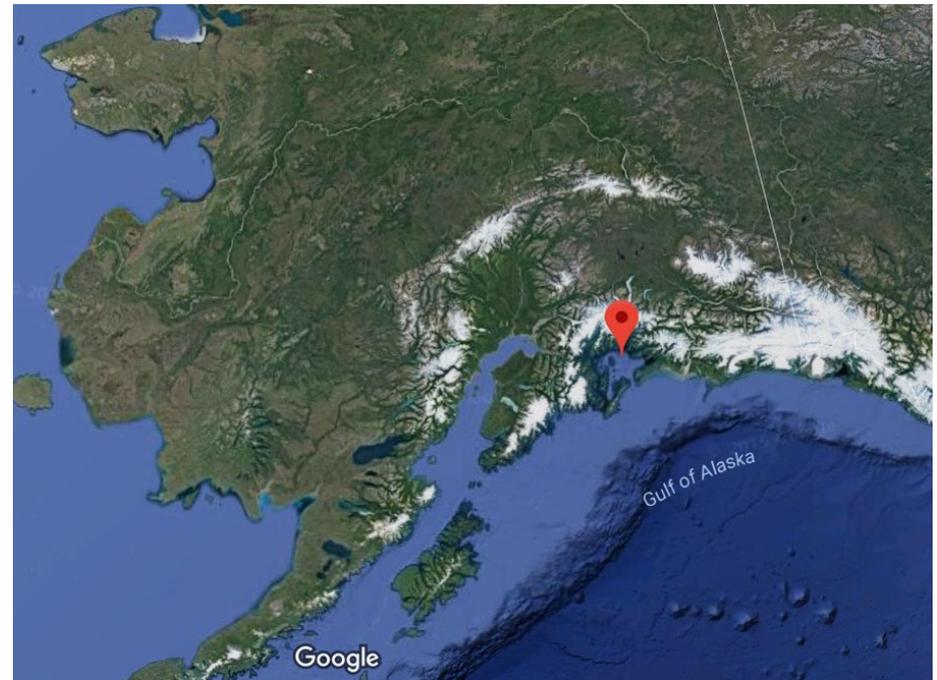
<https://www.n-sea.org/pink-salmon>

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

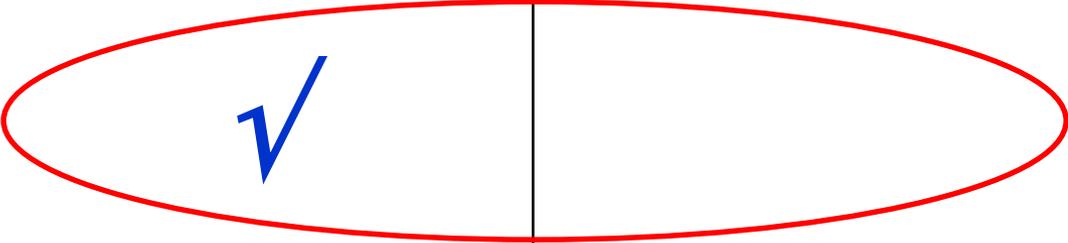
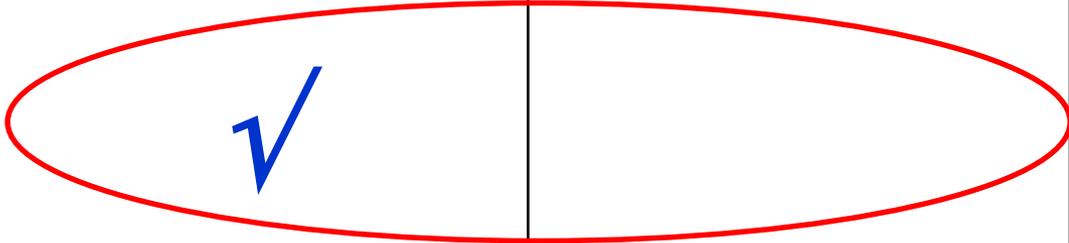
Key words: allozyme; mtDNA; genetics; pink salmon

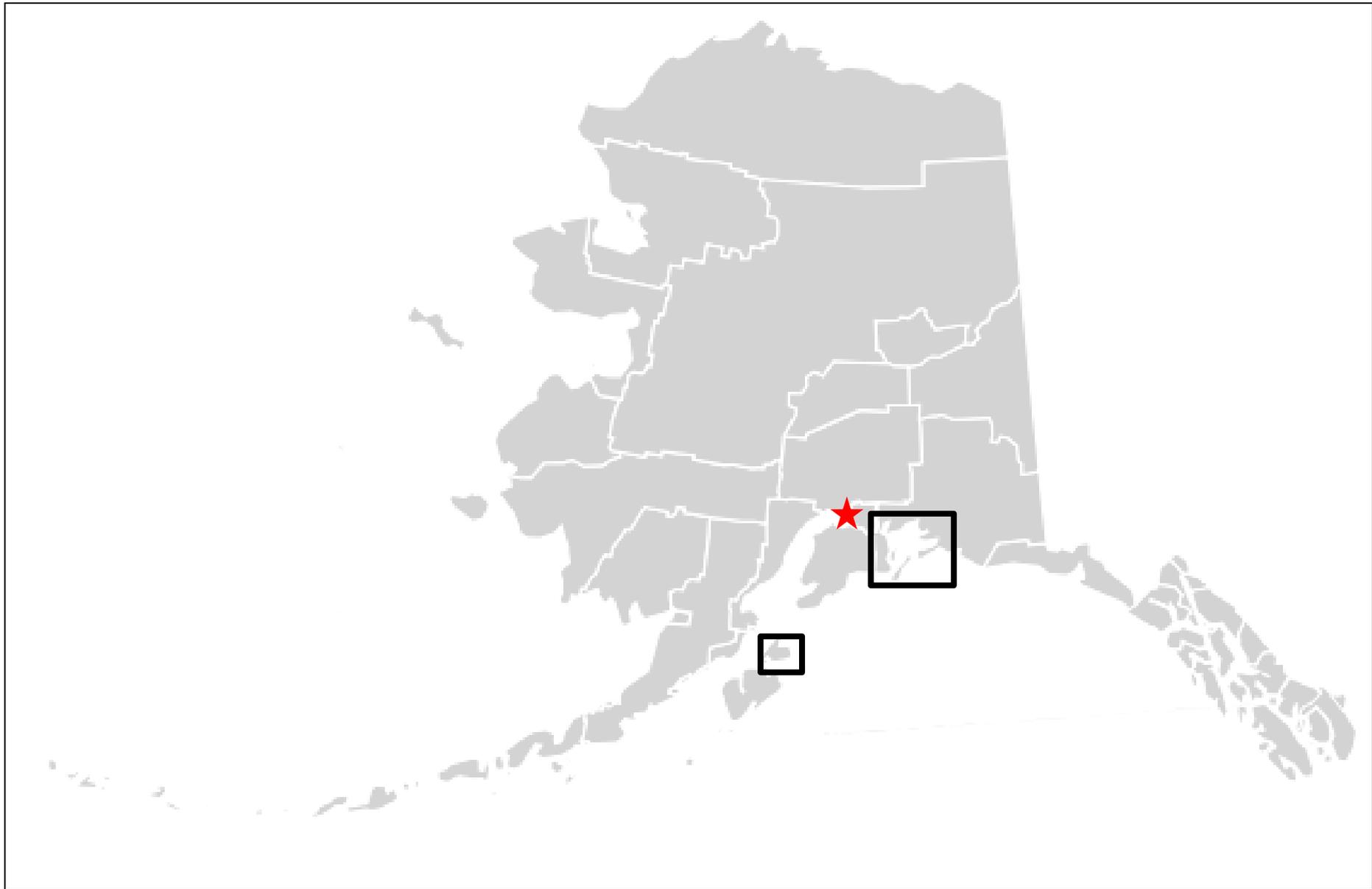
J. E. Seeb, Alaska Department of Fish & Game, Commercial Fisheries Division, Anchorage, AK 99518, USA

Accepted for publication April 9, 1999

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

Study Design

	Contemporary	Historical
Natural		
Hatchery		



Swanson Creek



07.28.2014

McCleod Creek



07.31.2014

Rocky Creek



08.01.2014

Duck River



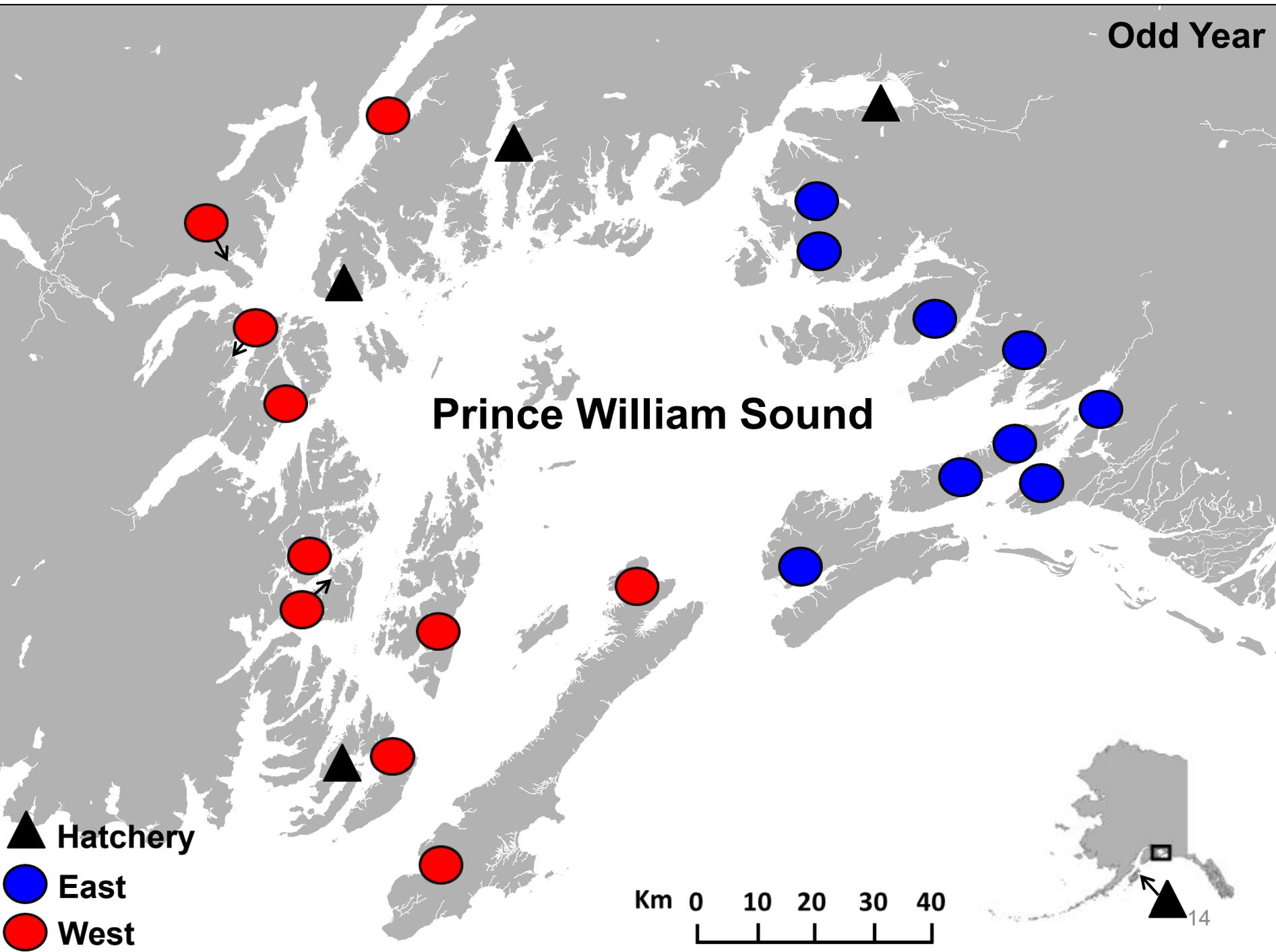
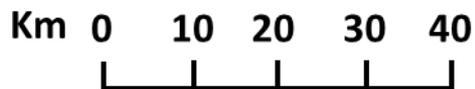
08.04.2014

Study Design

	Contemporary	Historical
Natural	✓	
Hatchery	✓	

Prince William Sound

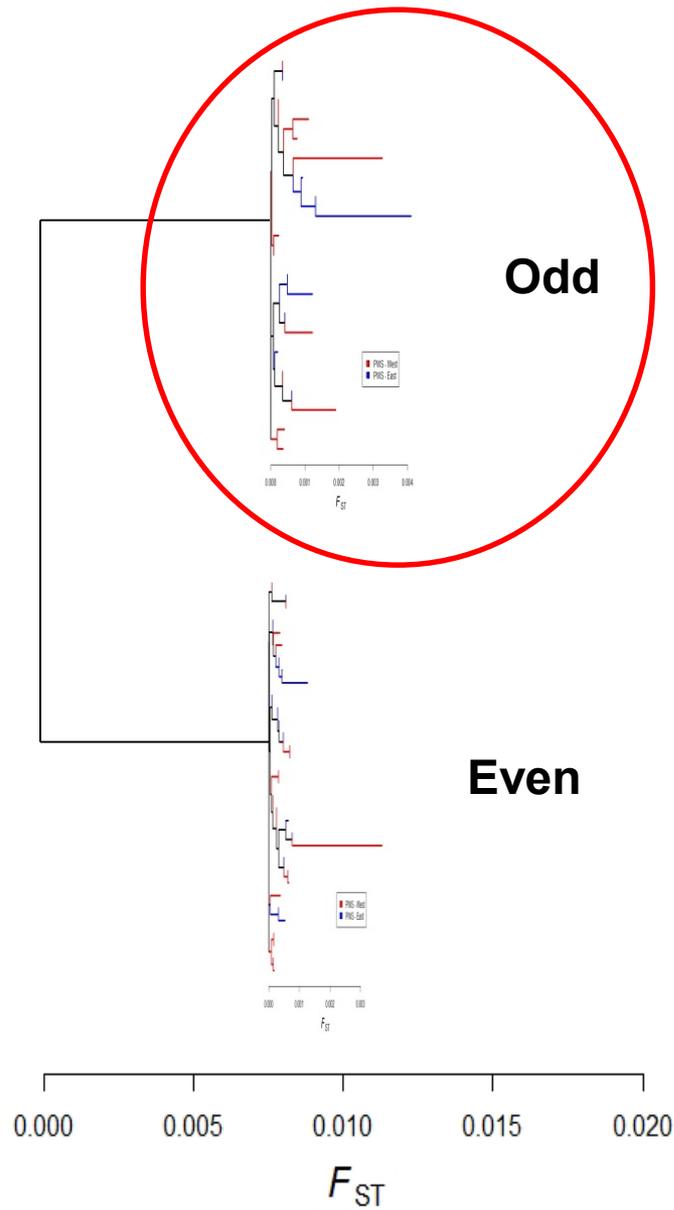
- ▲ Hatchery
- East
- West



Population Structure Analyses

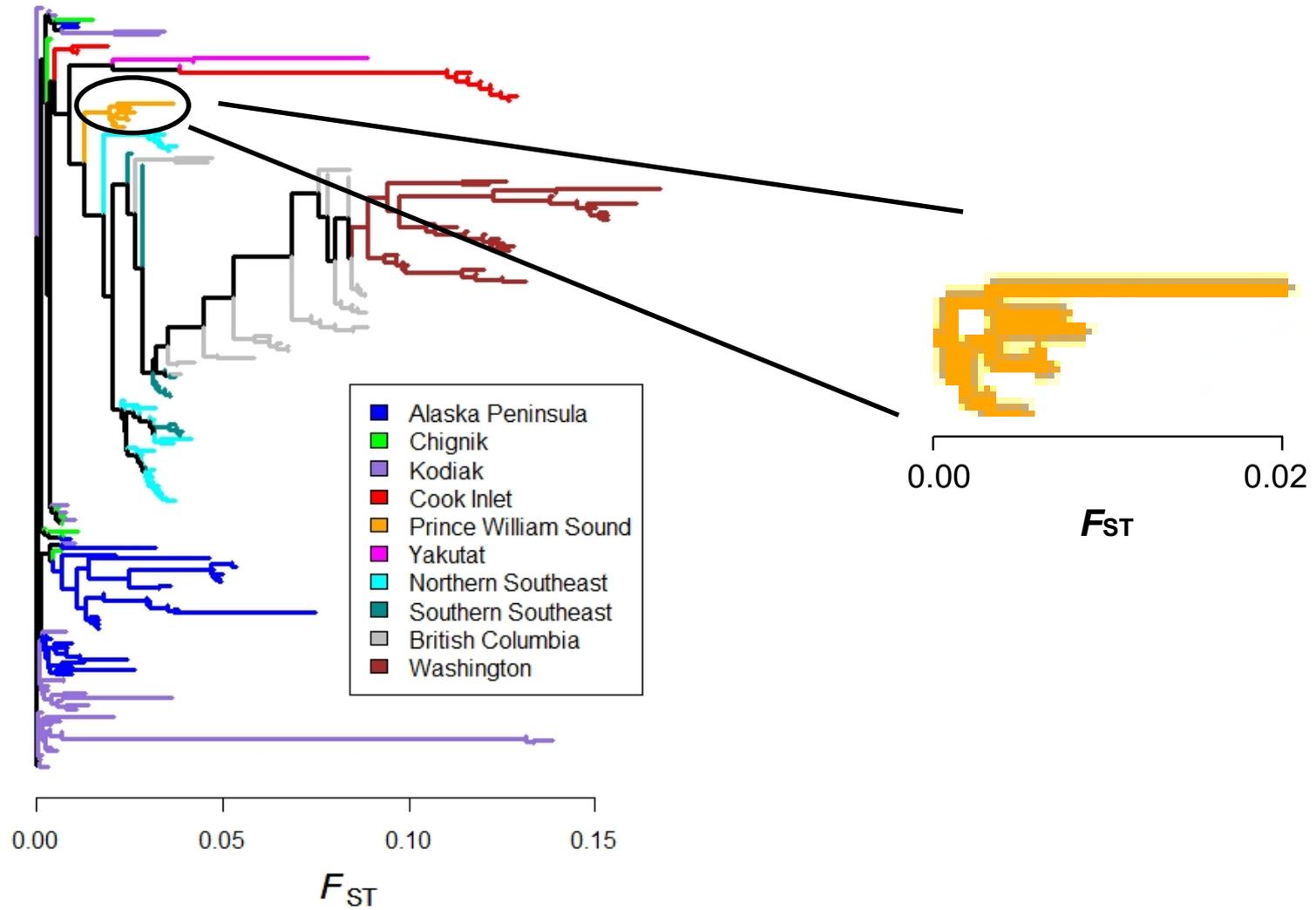
- **Calculate genetic differences among collections**
- **Test for significance of these differences**
- **Visualize the relationships among collections**

PWS Pink Salmon

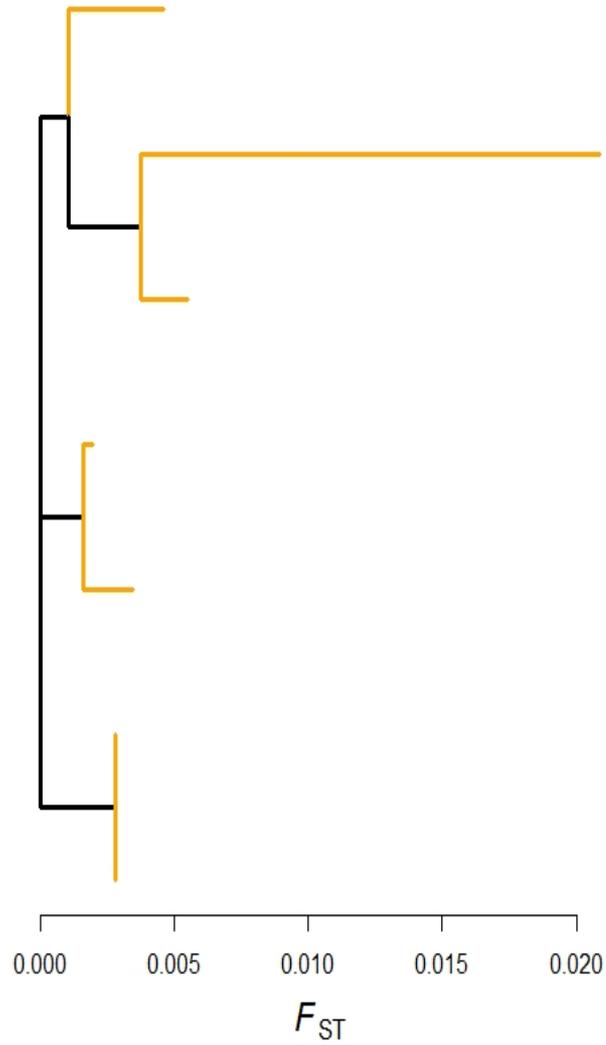


Pacific Rim Chum Salmon

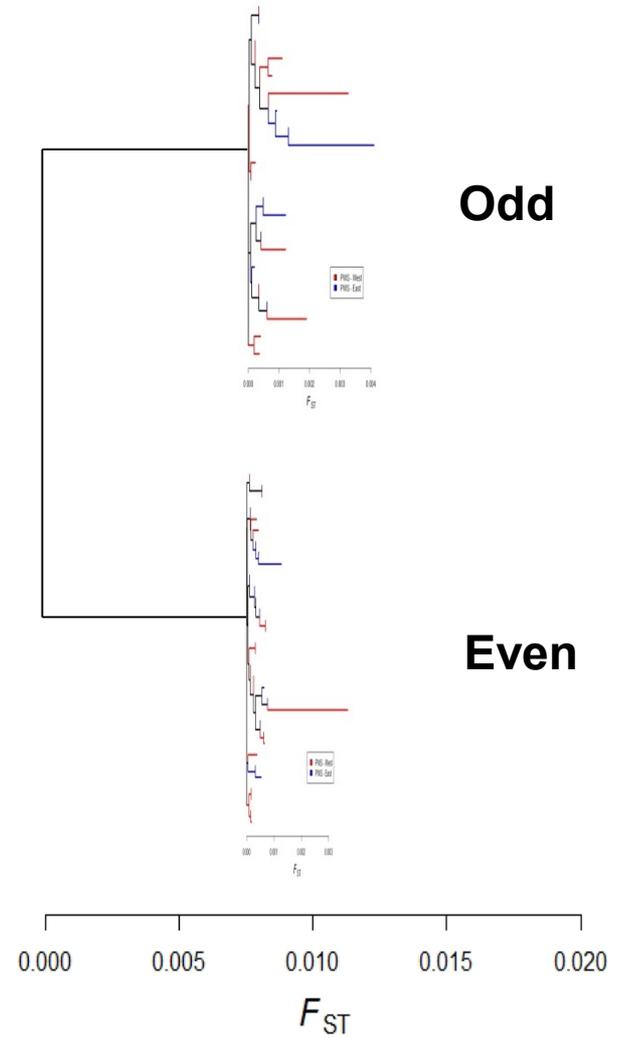
PWS Chum Salmon



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 (*Oki10l*), 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

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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 (*Onej3*) 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.

Electrophoretic Characterization of Odd-Year Pink Salmon (*Oncorhynchus gorbuscha*) Populations from the Pacific Coast of Russia, and Comparison with Selected North American Populations

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and Natalya V. Varnavskaya

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Shaklee, J.B., and N.V. Varnavskaya. 1994. Electrophoretic characterization of odd-year pink salmon (*Oncorhynchus gorbuscha*) populations from the Pacific Coast of Russia, and comparison with selected North American populations. *Can. J. Fish. Aquat. Sci.* 51(Suppl. 1): 158–171.

We collected and electrophoretically analyzed a total of 558 fish from eight locations along the Pacific Coast of Russia. We successfully screened 44 enzyme-coding loci: 14 loci were polymorphic at the 0.95 level in at least one collection, an additional eight were polymorphic at the 0.99 level but not at the 0.95 level, and the remaining 22 were either monomorphic or exhibited only very rare variation in these collections. Contingency χ^2 tests using the 23 most variable loci revealed significant heterogeneity among all eight collections ($p = 0.028$) but little or no significant heterogeneity among collections within areas (northeastern Kamchatka peninsula, $p = 0.180$; southwestern Kamchatka, $p = 0.533$; and mainland adjacent to the northwestern Sea of Okhotsk, $p = 0.071$). Multidimensional scaling and minimum spanning tree analyses using genetic distances among collections indicated that geographic proximity of spawning sites was not associated with genetic similarity. The eight odd-year pink salmon (*Oncorhynchus gorbuscha*) collections from Russia were compared with 16 collections from North America (southeastern Alaska, British Columbia, and Washington) using data for 33 loci. The Russian populations differed from the North American populations in their patterns of allelic variation at many loci. The amount of genetic differentiation among populations from different rivers in Russia was comparable to that seen within similar-sized areas in North America.

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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Cathy MacConnachie¹

Brian Spilsted²

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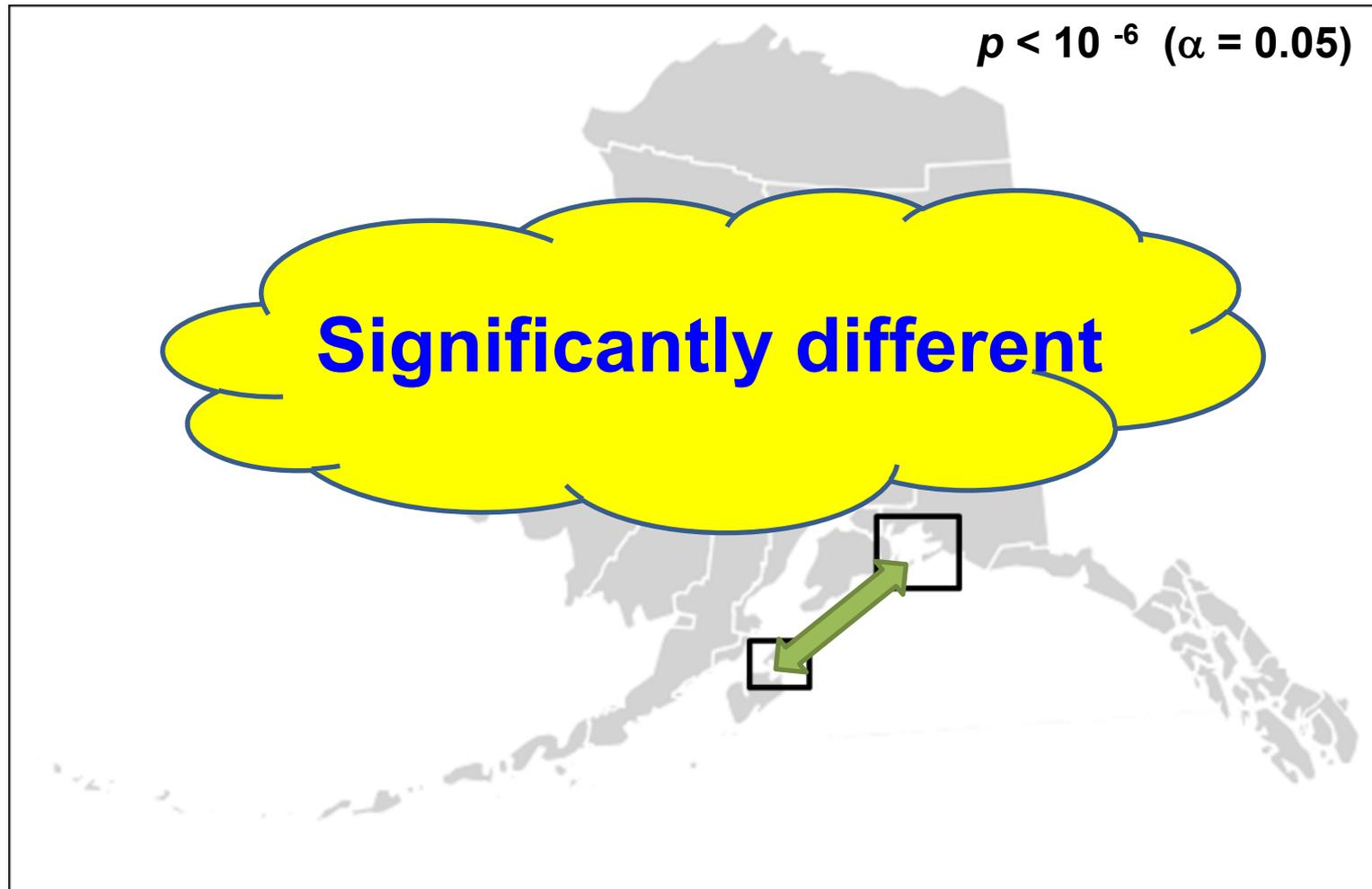
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³ Pacific Salmon Commission
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Vancouver, B. C., Canada V6E 1B5

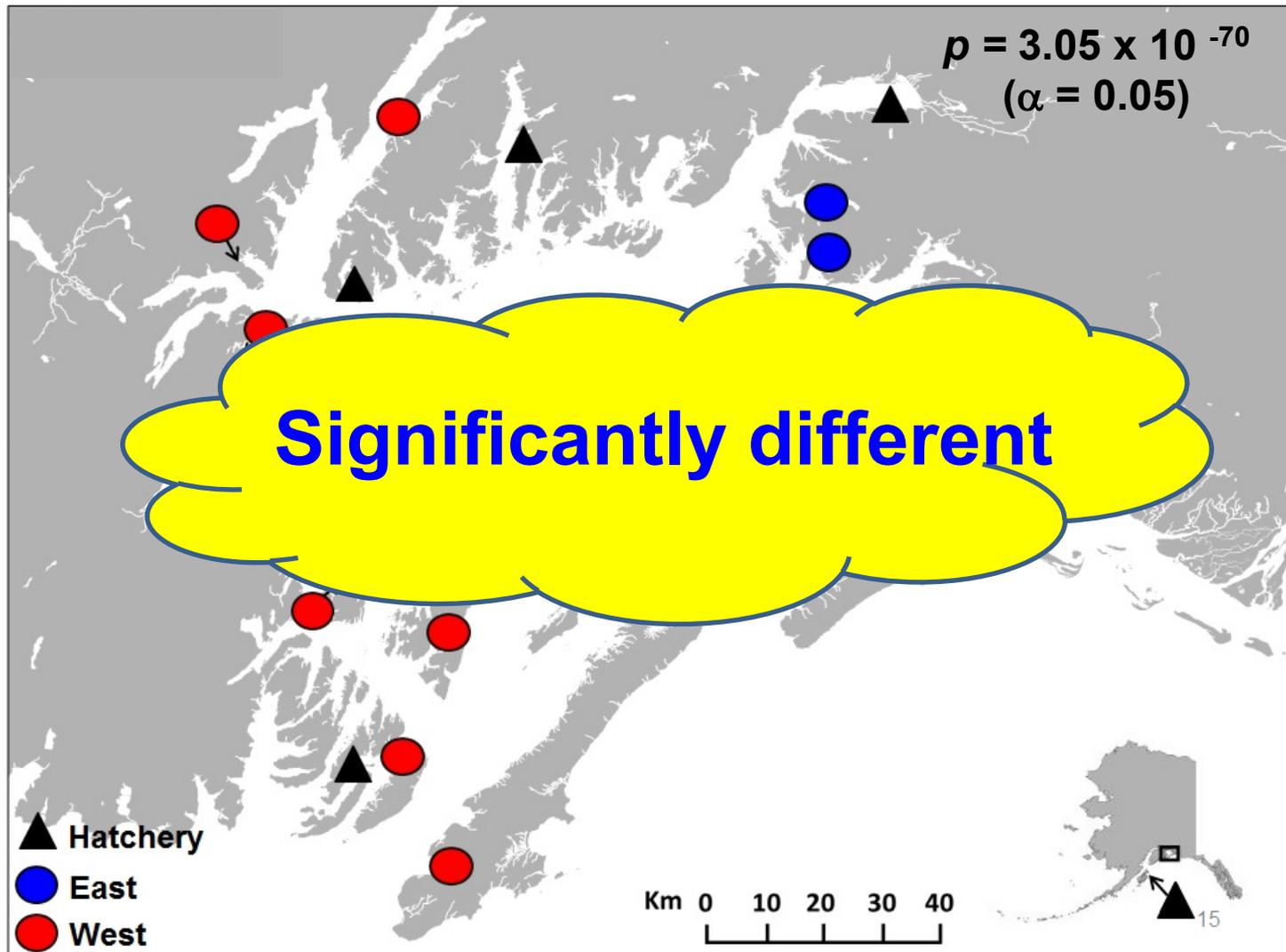
Population Structure Analyses

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

Testing for Difference: Kodiak vs. Prince William Sound



Testing for Differences: among Prince Willian Sound

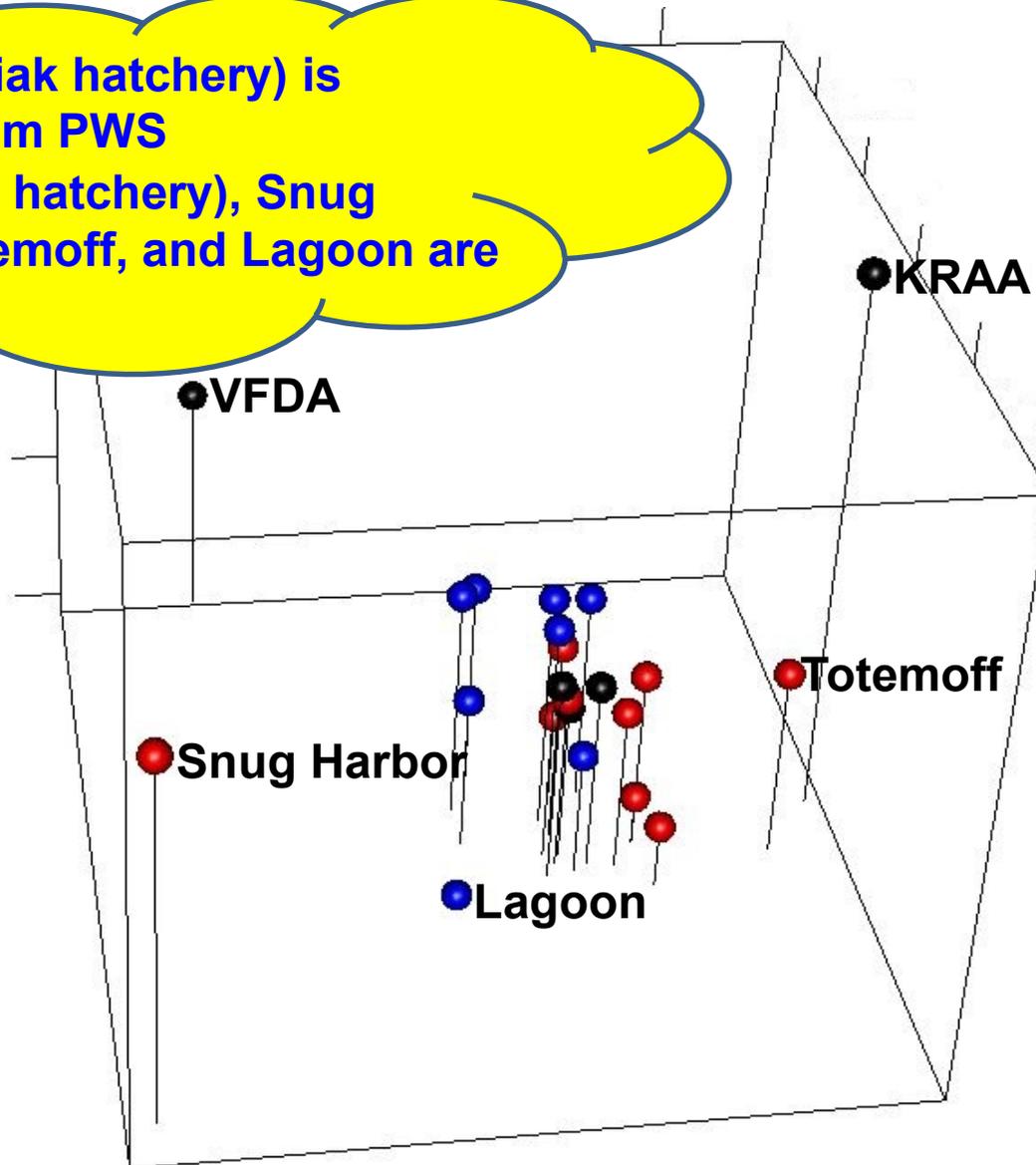


Population Structure Analyses

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

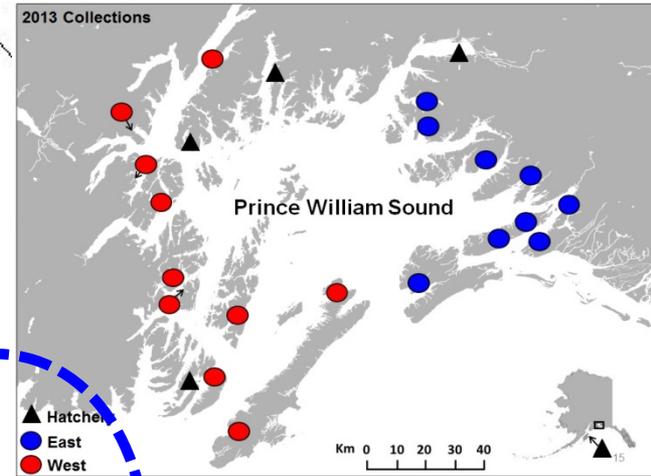
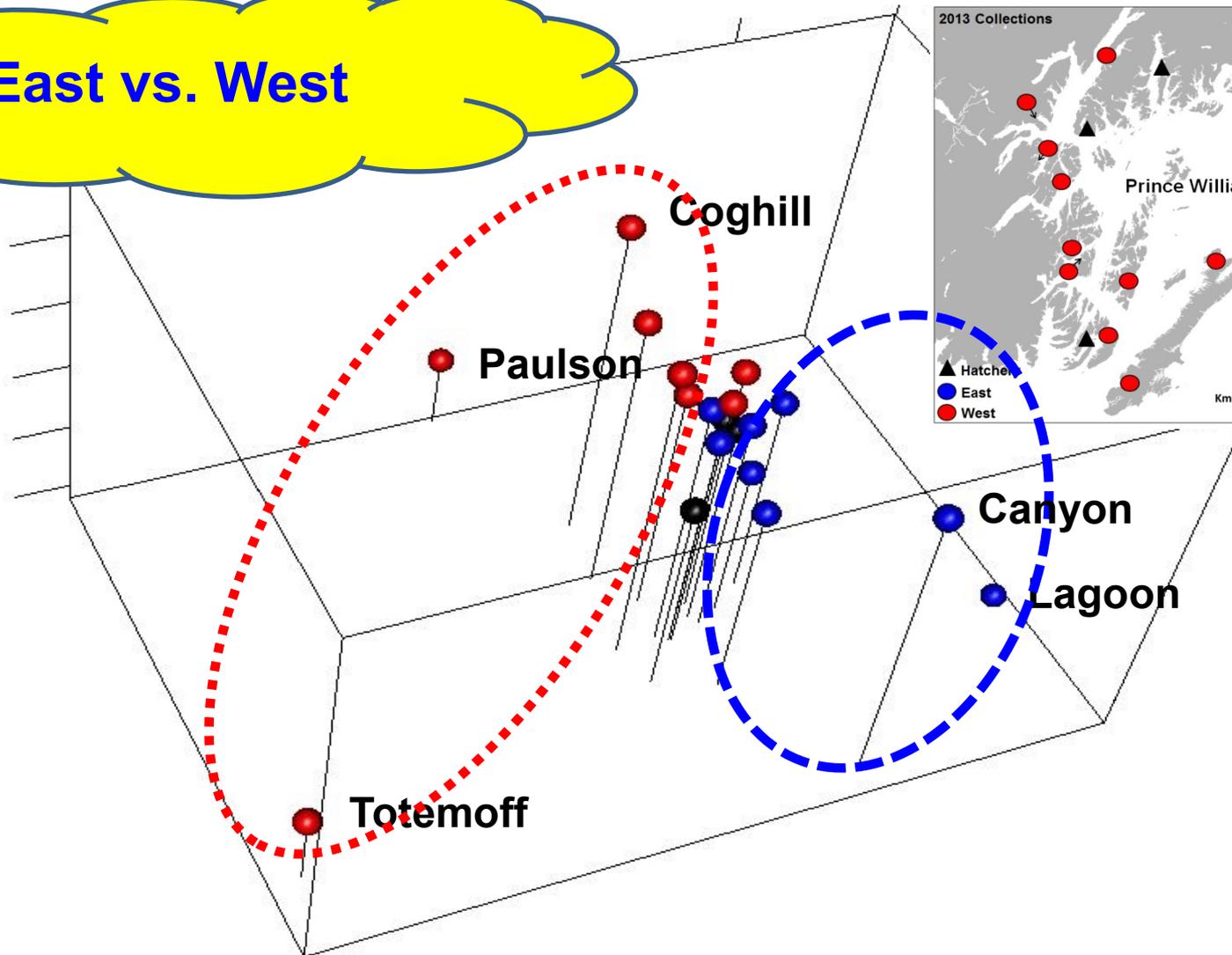
Visualizing the Relationships among Collections

- KRAA (Kodiak hatchery) is different from PWS
- VFDA (PWS hatchery), Snug Harbor, Totemoff, and Lagoon are outliers



Visualizing the Relationships among Collections – Zooming in

• East vs. West

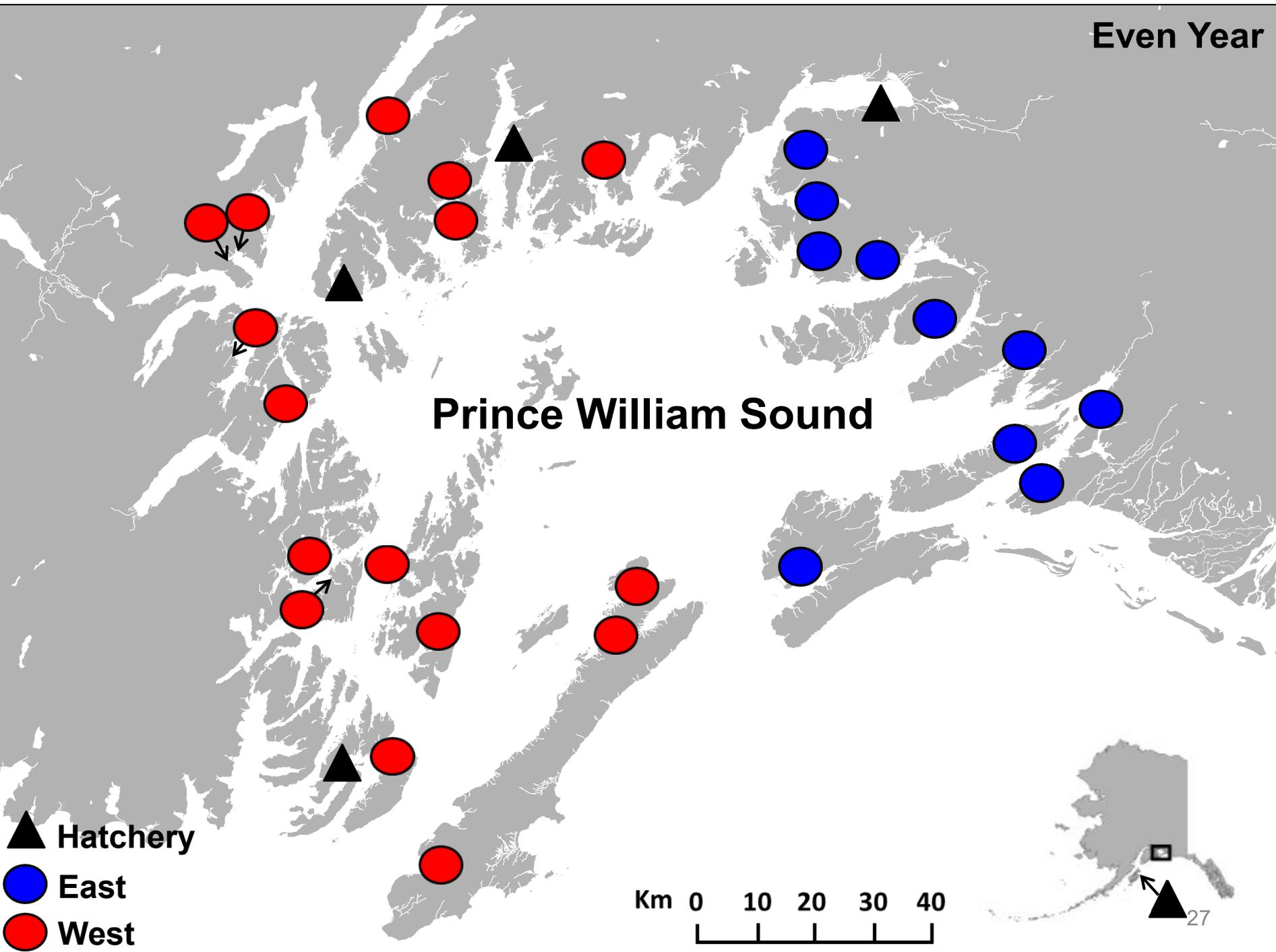
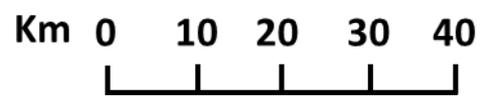


Study Design

	Contemporary	Historical
Natural	✓	
Hatchery	✓	

Prince William Sound

- ▲ Hatchery
- East
- West



PWS Pink Salmon



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

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

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Accepted for publication April 9, 1999

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

Terry D. Beacham (contact author)¹

Brenda McIntosh¹

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Title: Population Genetic Structure of Even-Year Pink Salmon from Prince William Sound Based on a Single Year (2014)

Authors: W. Cheng, C. Habicht, W. D. Templin, Z. D. Grauvogel, and A. J. Gharrett

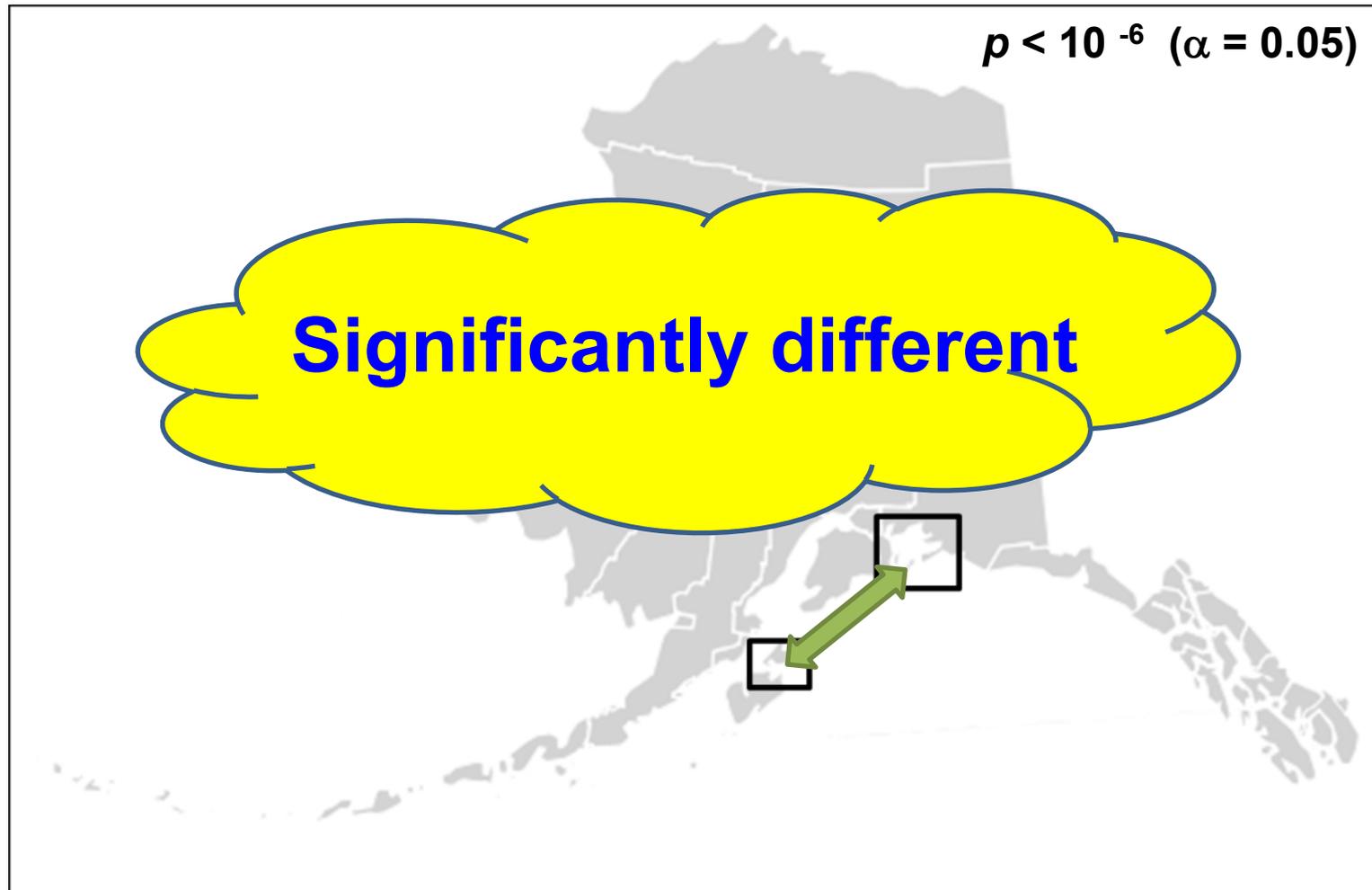
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Abstract

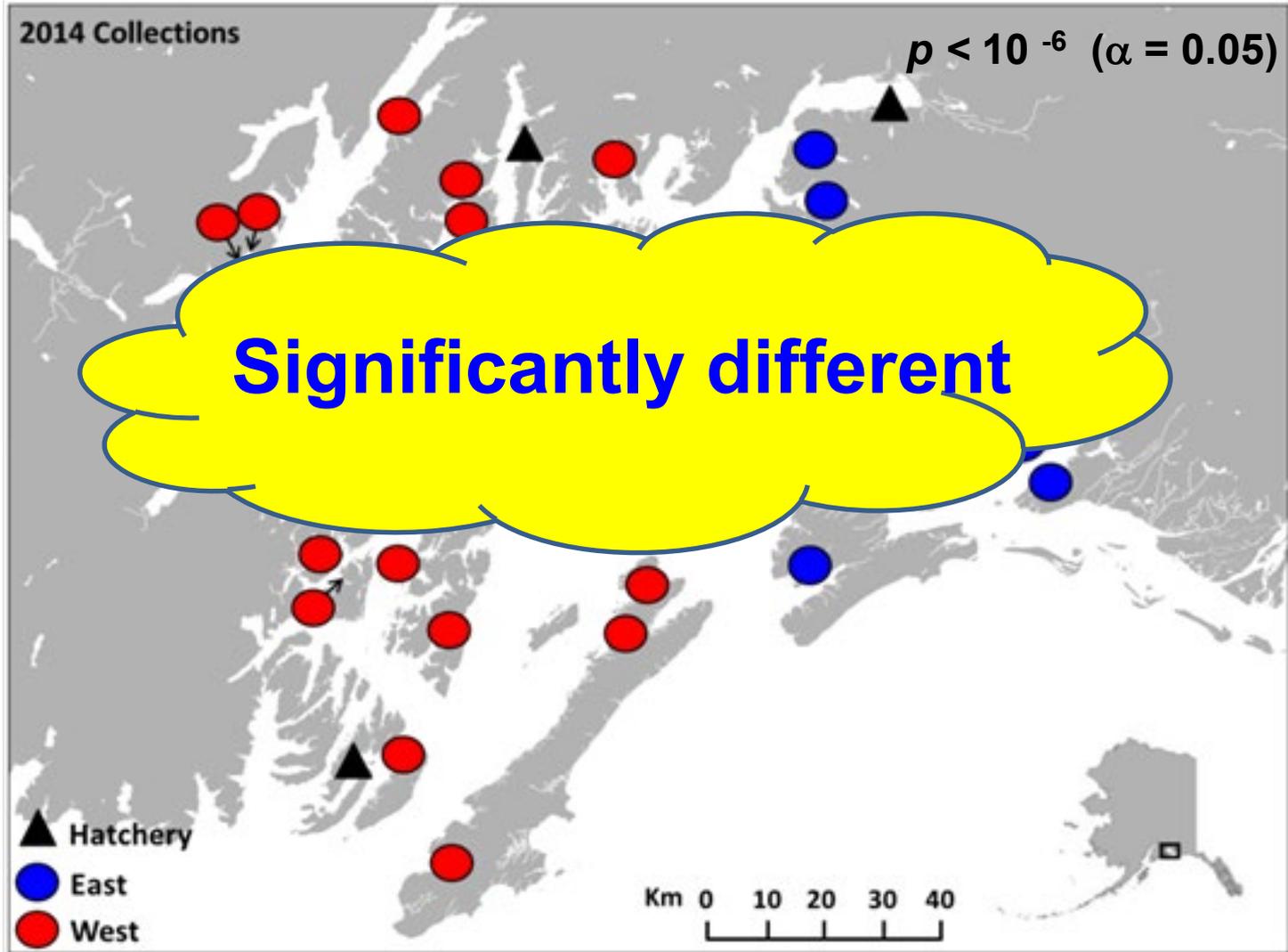
Pink salmon (*Oncorhynchus gorbuscha*) are commercially and ecologically important. In Prince William Sound (PWS), Alaska, pink salmon are the most abundant Pacific salmon species and generate the highest total value for commercial fishery. Pink salmon have a fixed two-year life cycle, which has created reproductively separate broodlines in even- and odd- years. 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 26 natural spawning areas in PWS and one hatchery in Kodiak Management Area (KMA) by genotyping 16 microsatellite loci for nearly 6,554 pink salmon sampled in 2014. The fixation index (F_{ST}), a measure of population divergence, was 0.001 over all loci and the F_{ST} of individual loci ranged from 0.001 to 0.002. Significant differences were detected among those populations from PWS, which meant that pink salmon in PWS were not from a single large homogeneous population. The early fish collection from Snug Harbor Creek was the most divergent. The KMA collection was the second most divergent. Solomon Gulch Hatchery in the northeastern PWS was distinct from collections from other PWS districts, which suggested that it had not exchanged many migrants with other districts. The population structure of even-year pink salmon collected in 2014 was not as strong as odd-year pink salmon collected in 2013, where the F_{ST} over all loci was an order of magnitude higher.

Key words: Pink salmon, even-year, hatchery, Prince William Sound, population genetic

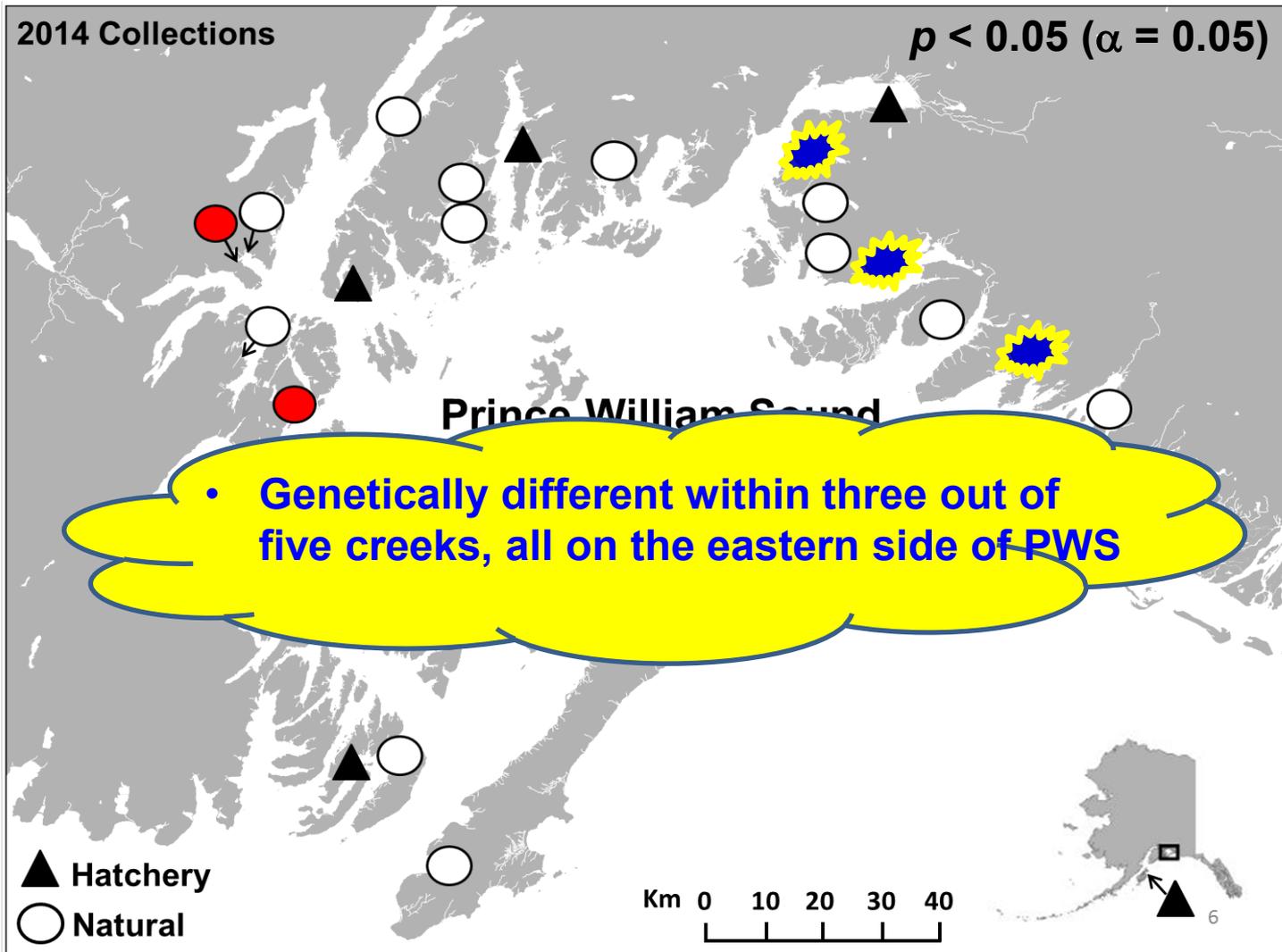
Testing for Difference: Kodiak vs. Prince William Sound



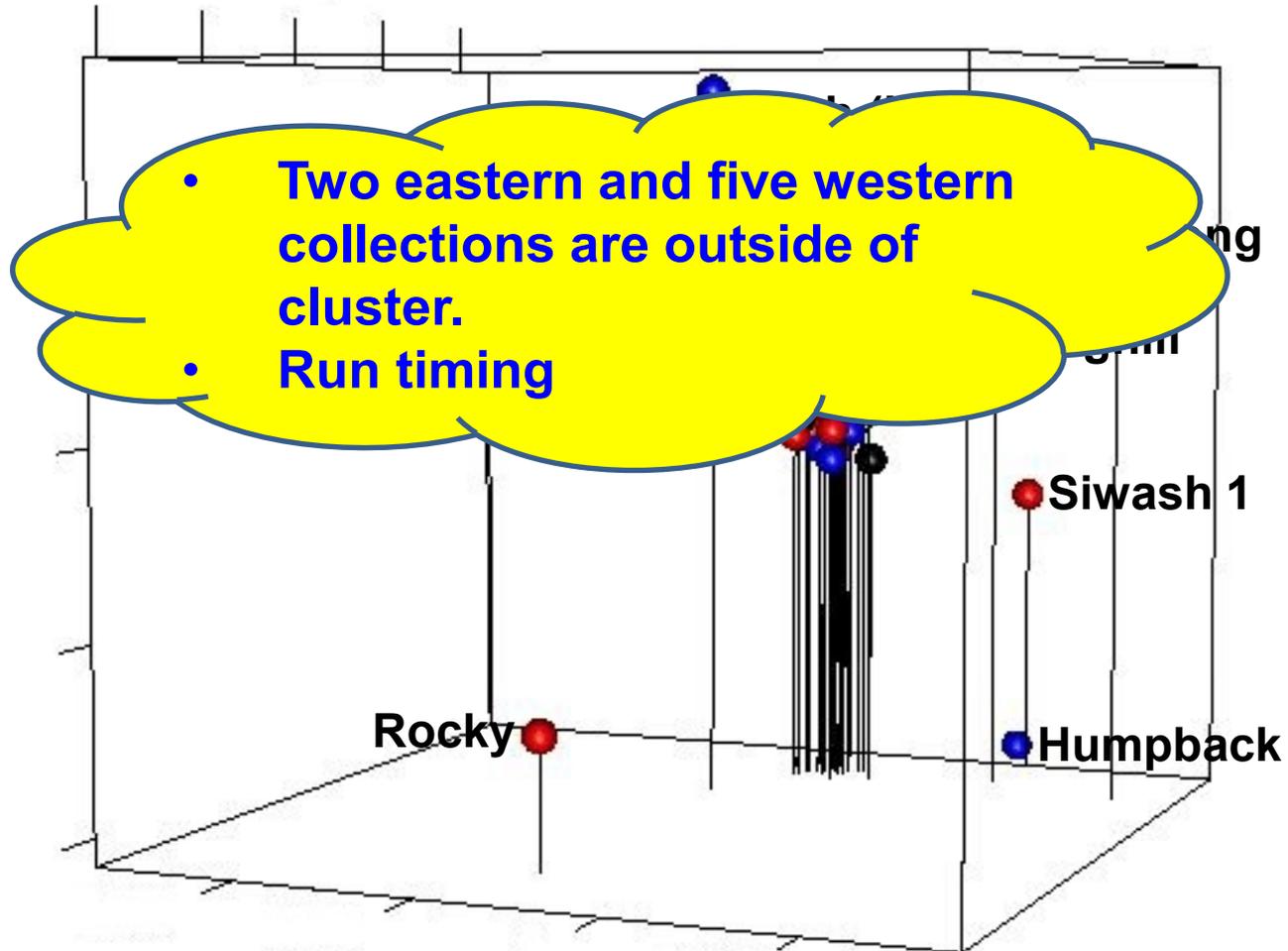
Testing for Differences: among Prince Willian Sound



Testing for Differences: Between Early and Late Collections



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**