# Genetic structure of chum and pink salmon in Prince William Sound and Southeast Alaska

Gene Conservation Laboratory

Alaska Department of Fish and Game

Alaska Board of Fisheries

March 8, 2019

# Outline

- Background
- Chum results
- Pink results

# 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?

# Understanding Genetic Structure

- Differences between populations:
  - Influenced by: selection, mutation, genetic drift, migration

# Understanding Genetic Structure

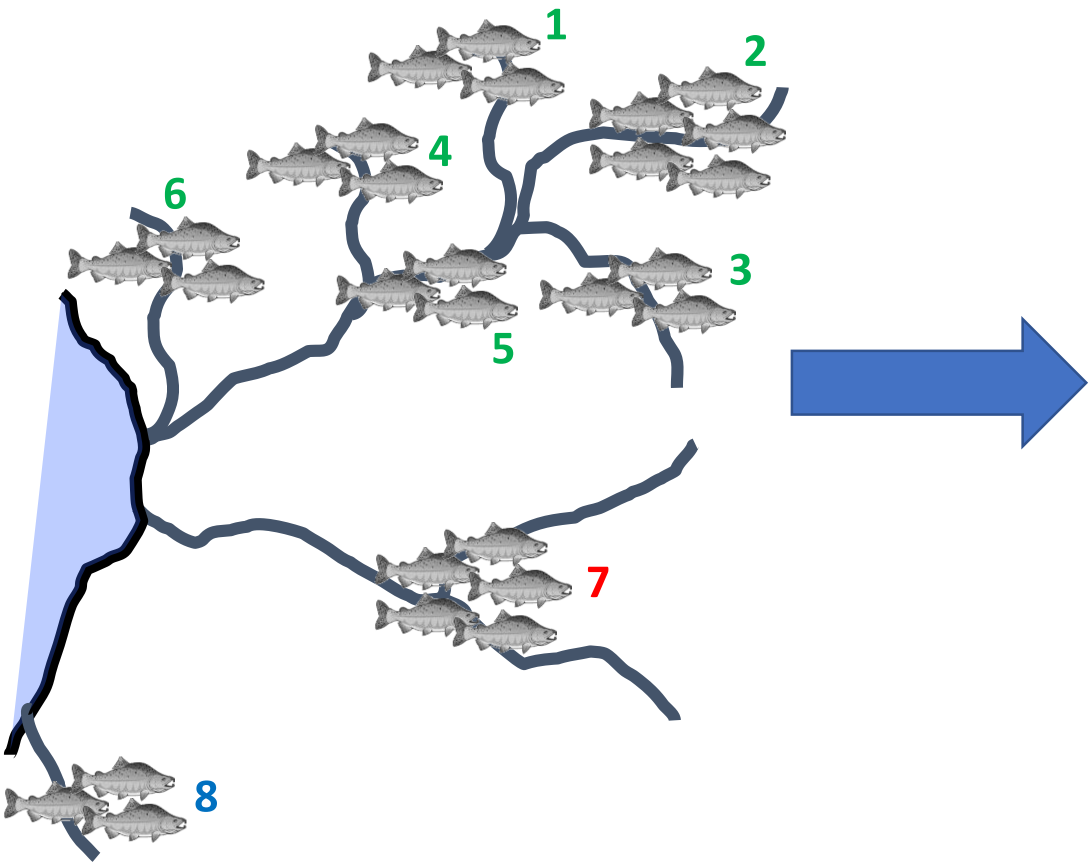
- Differences between populations:
  - Influenced by: selection, mutation, *genetic drift*, *migration*

*genetic drift* ~ ***homing***

*migration* ~ ***straying***

    - *Measuring the balance between these within a species across an area*
  - Measured by quantifying pairwise genetic differences
  - Visualize using genetic trees

# Population Structure: An example



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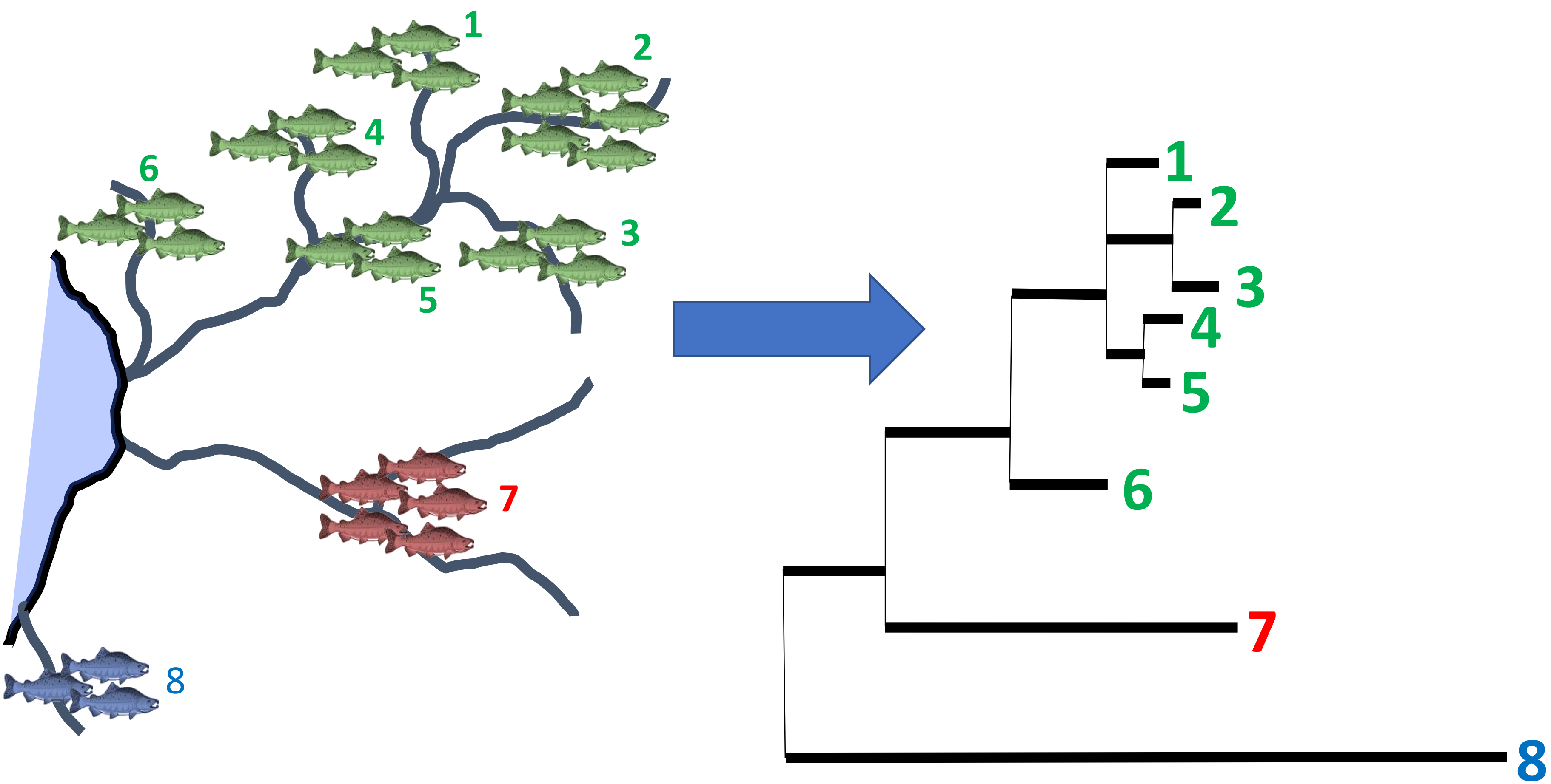

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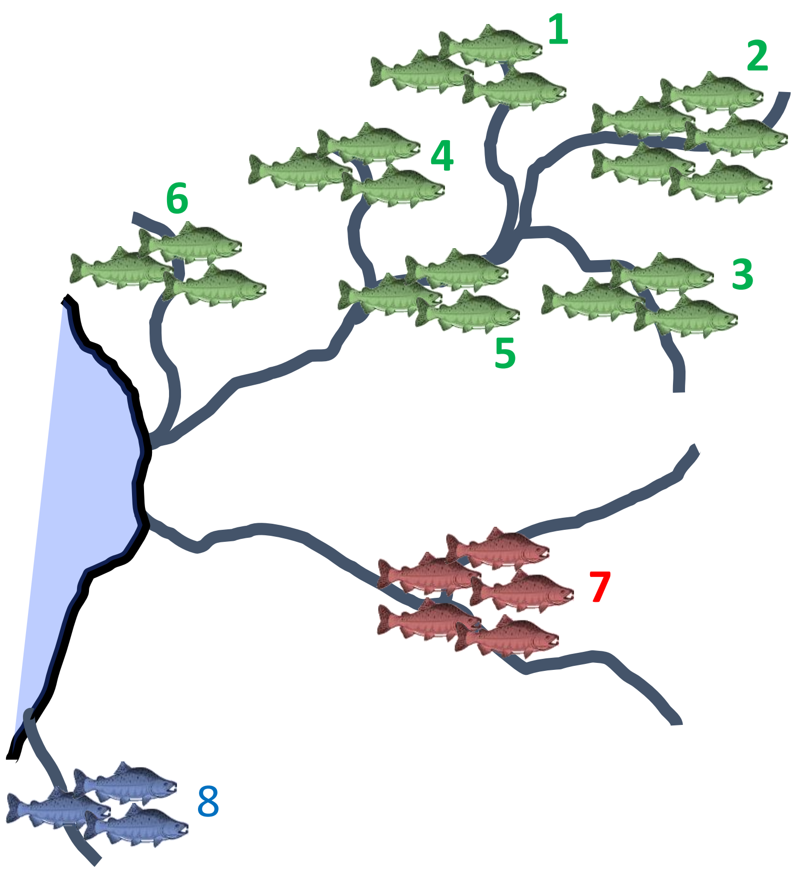
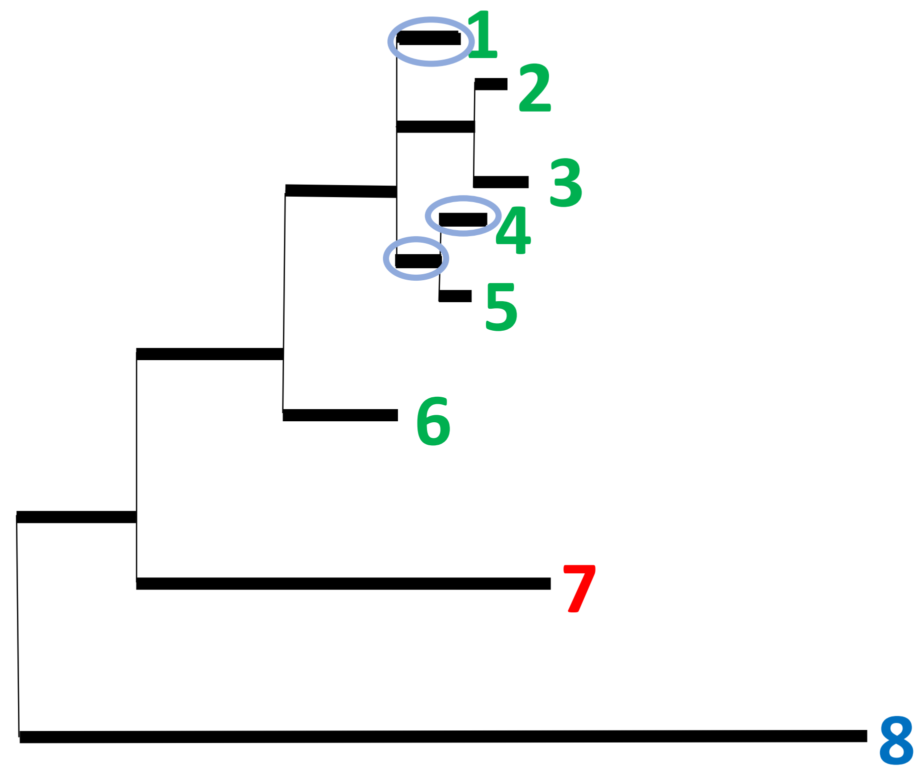
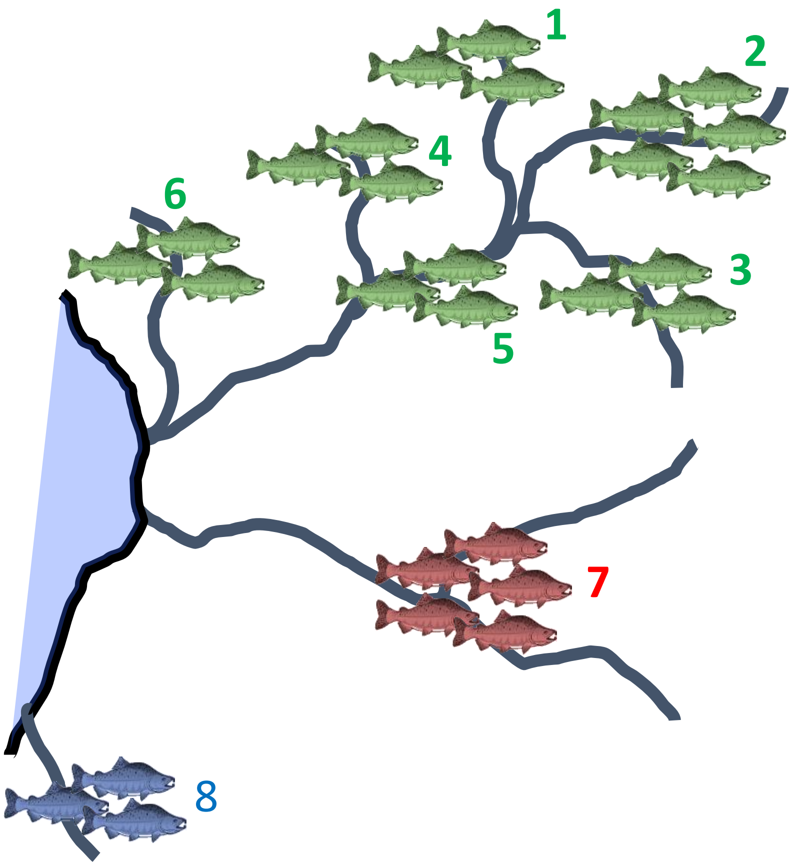
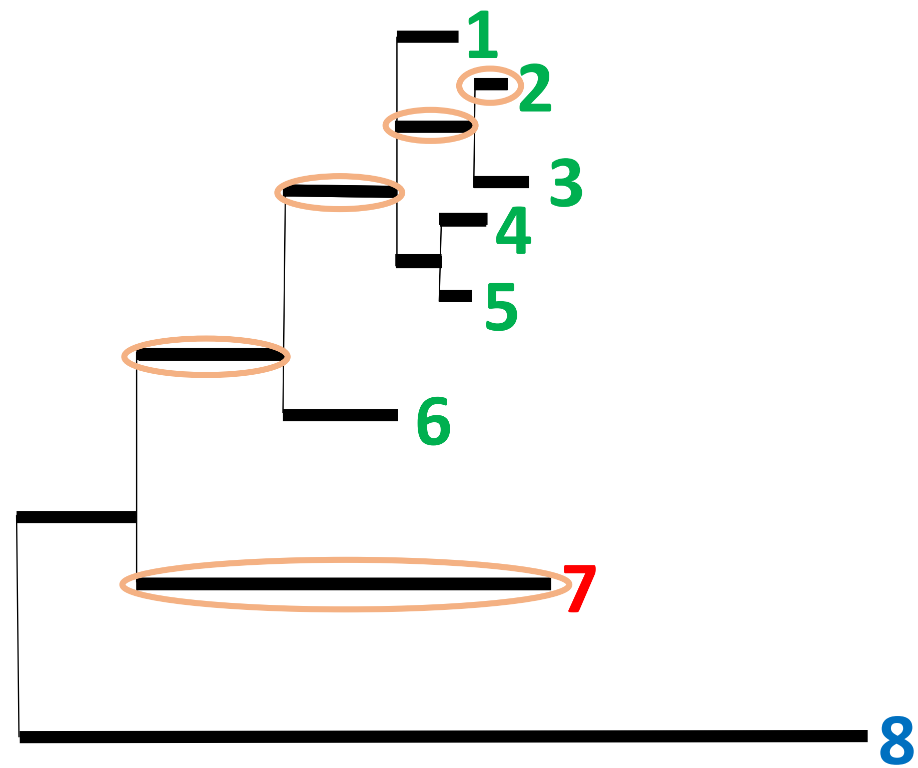



Difference between 1 and 4: + + =

# Population Structure: An example

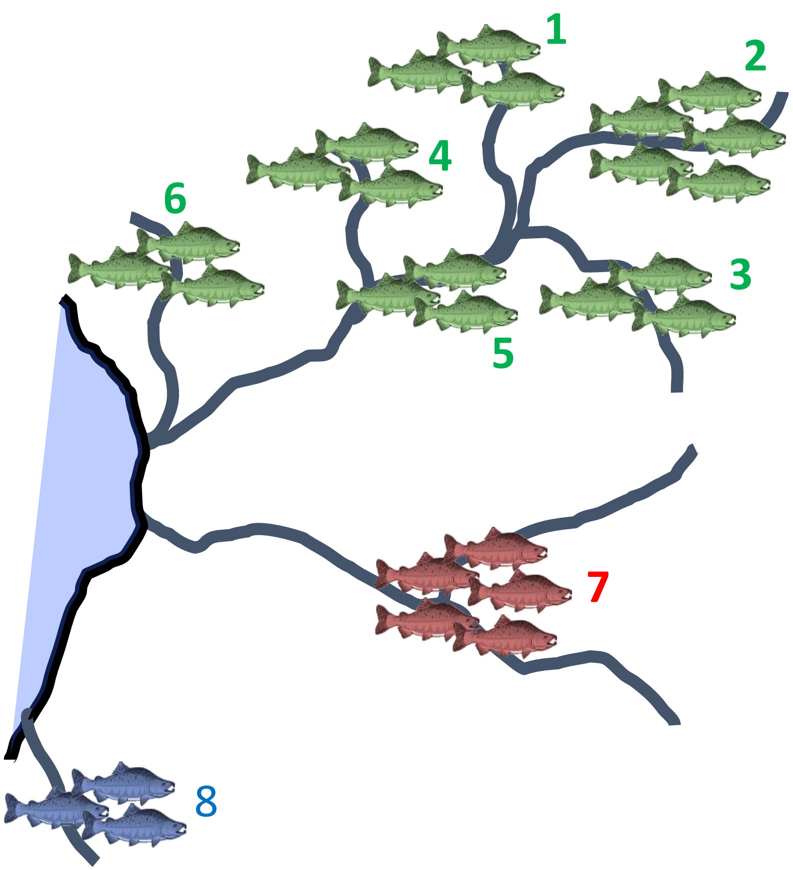


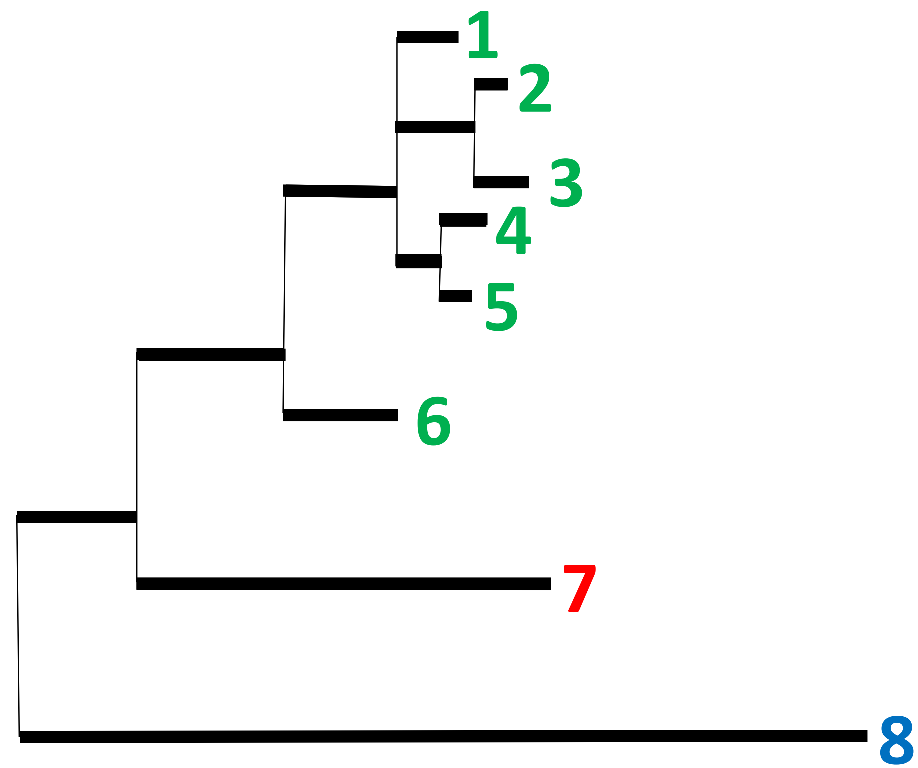




Difference between 1 and 4:

Difference between 2 and 7: + + + + =

# Population Structure: An example

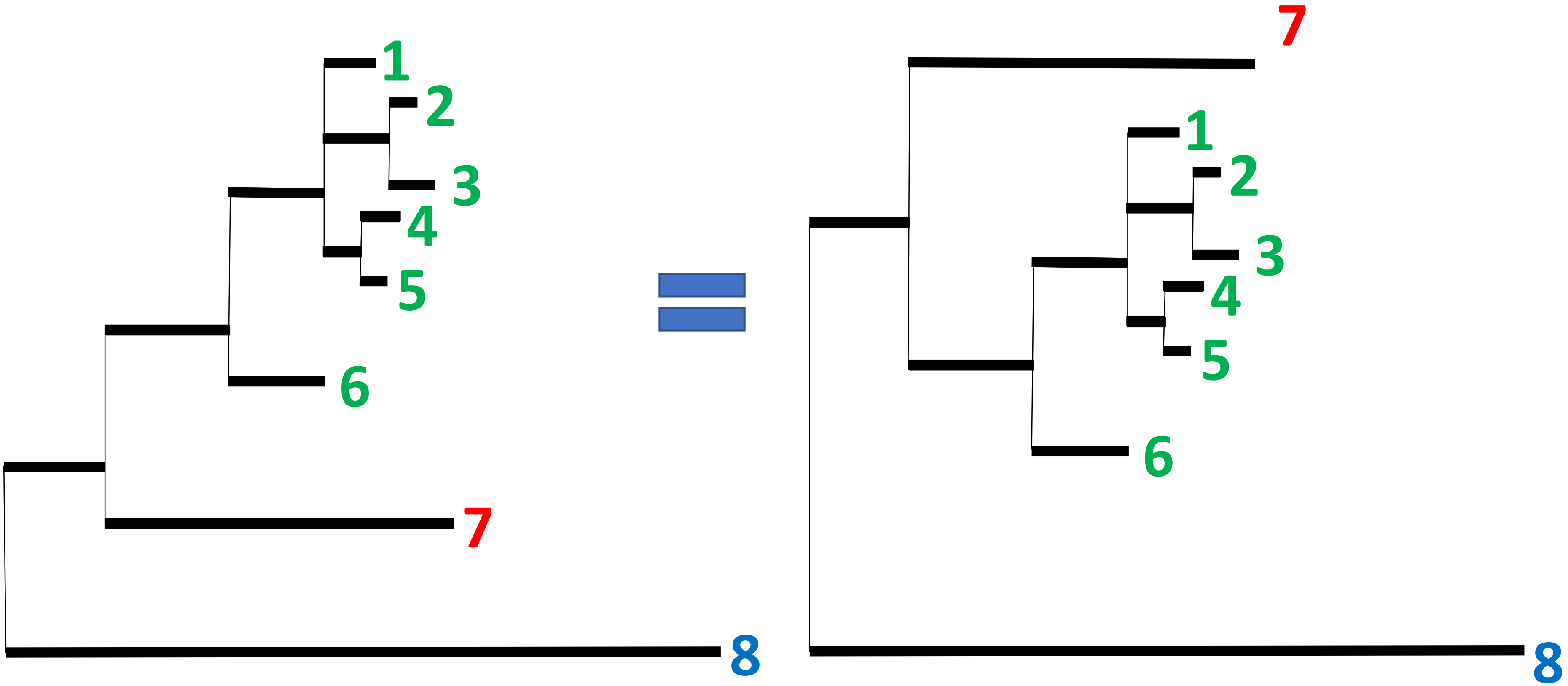



Difference between 1 and 4:

Difference between 2 and 7:

# Population Structure: An example



# Chum salmon in Prince William Sound and Southeast Alaska

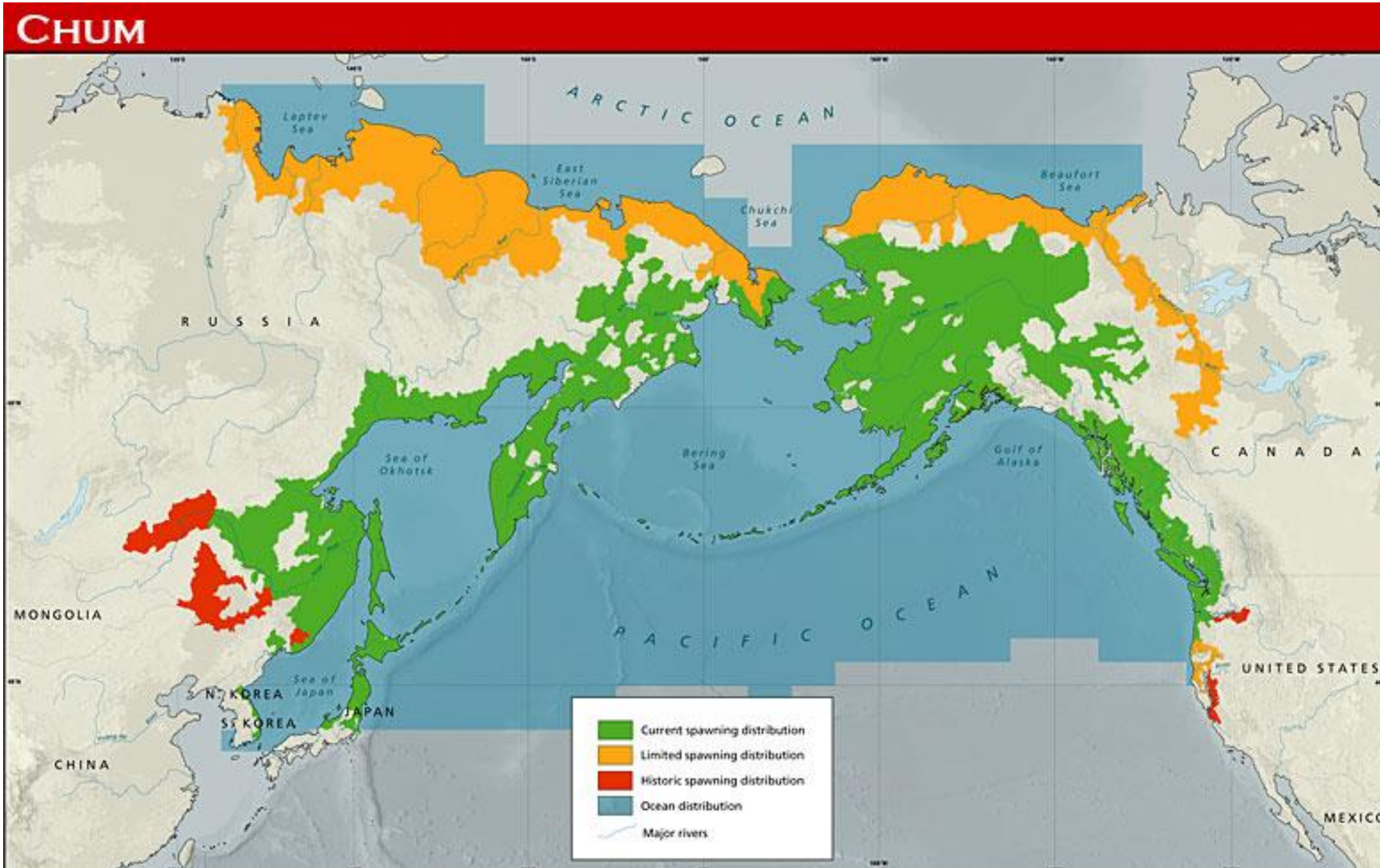
Sara Gilk-Baumer and William D. Templin

Alaska Department of Fish and Game, Gene Conservation Lab

# Life History of Chum Salmon

- Migrate as juveniles to ocean
- Typically 2-4 years spent at sea
- Two run timings: summer & fall

# Distribution of Chum Salmon




*http://www.salmonnation.org/fish/meet_species.html*

# Previous work (a sampling)

**Determining Continent of Origin of Chum Salmon (*Oncorhynchus keta*) Using Genetic Stock Identification Techniques: Status of Allozyme Baseline in Asia**

Gary A. Winans and Paul B. Aebersold
*Northwest Fisheries Science Center, National Marine Fisheries Service, Seattle, WA 98112-2097, USA*
Shigehiko Urawa
*Hokkaido Salmon Hatchery, Fisheries Agency of Japan, Sapporo 062, Japan*
and Nataly V. Varnavskaya
*Kamchatka-TINRO, Petropavlovsk, Russia*

**Population structure and stock identification of chum salmon (*Oncorhynchus keta*) from British Columbia determined with microsatellite DNA variation**

**Terry D. Beacham, Brian Spilsted, Khai D. Le, and Michael Wetklo**

**Microsatellite Stock Identification of Chum Salmon on a Pacific Rim Basis**

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KHAI D. LE AND MICHAEL WETKLO
*Fisheries and Oceans Canada, Pacific Biological Station, 3190 Hammond Bay Road, Nanaimo, British Columbia V9T 6N7, Canada*

**Genetic Relationships Among Chum Salmon Populations in Southeast Alaska and Northern British Columbia**

C.M. Kondzela, C.M. Guthrie, S.L. Hawkins, C.D. Russell, and J.H. Helle
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*School of Fisheries and Ocean Sciences, University of Alaska Fairbanks, 11120 Glacier Highway, Juneau, AK 99801, U.S.A.*

*Environmental Biology of Fishes* **69:** 37–50, 2004.


**Genetic population structure of chum salmon in the Pacific Rim inferred from mitochondrial DNA sequence variation**

Shunpei Sato[a], Hiroyuki Kojima[b], Junko Ando[a], Hironori Ando[a], Richard L. Wilmot[c], Lisa W. Seeb[d], Vladimir Efremov[e], Larry LeClair[f], Wally Buchholz[g], Deuk-Hee Jin[h], Shigehiko Urawa[i], Masahide Kaeriyama[b], Akihisa Urano[a,j] & Syuiti Abe[k,l]
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[c]*Auke Bay Laboratory, Alaska Fisheries Science Center, NOAA, Juneau, U.S.A.*
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[h]*Kangnung National University, Kangnung, Korea*
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Received 17 April 2003 Accepted 27 April 2003

**Chum Salmon Genetic Diversity in the Northeastern Pacific Ocean Assessed with Single Nucleotide Polymorphisms (SNPs): Applications to Fishery Management**

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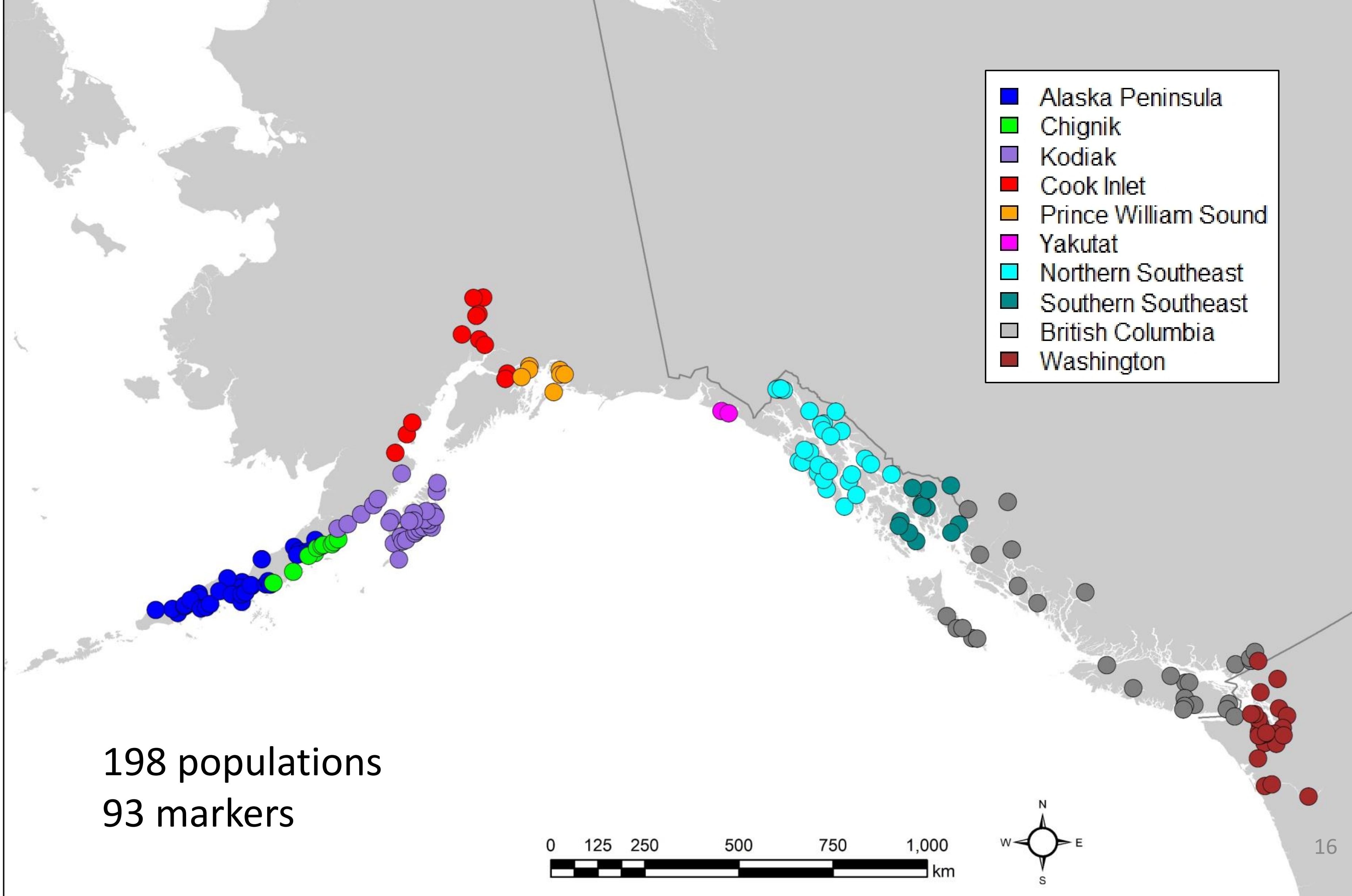
**William Templin**
*Alaska Department of Fish and Game, Division of Commercial Fisheries, Gene Conservation Laboratory, 333 Raspberry Road, Anchorage, Alaska 99518, USA*

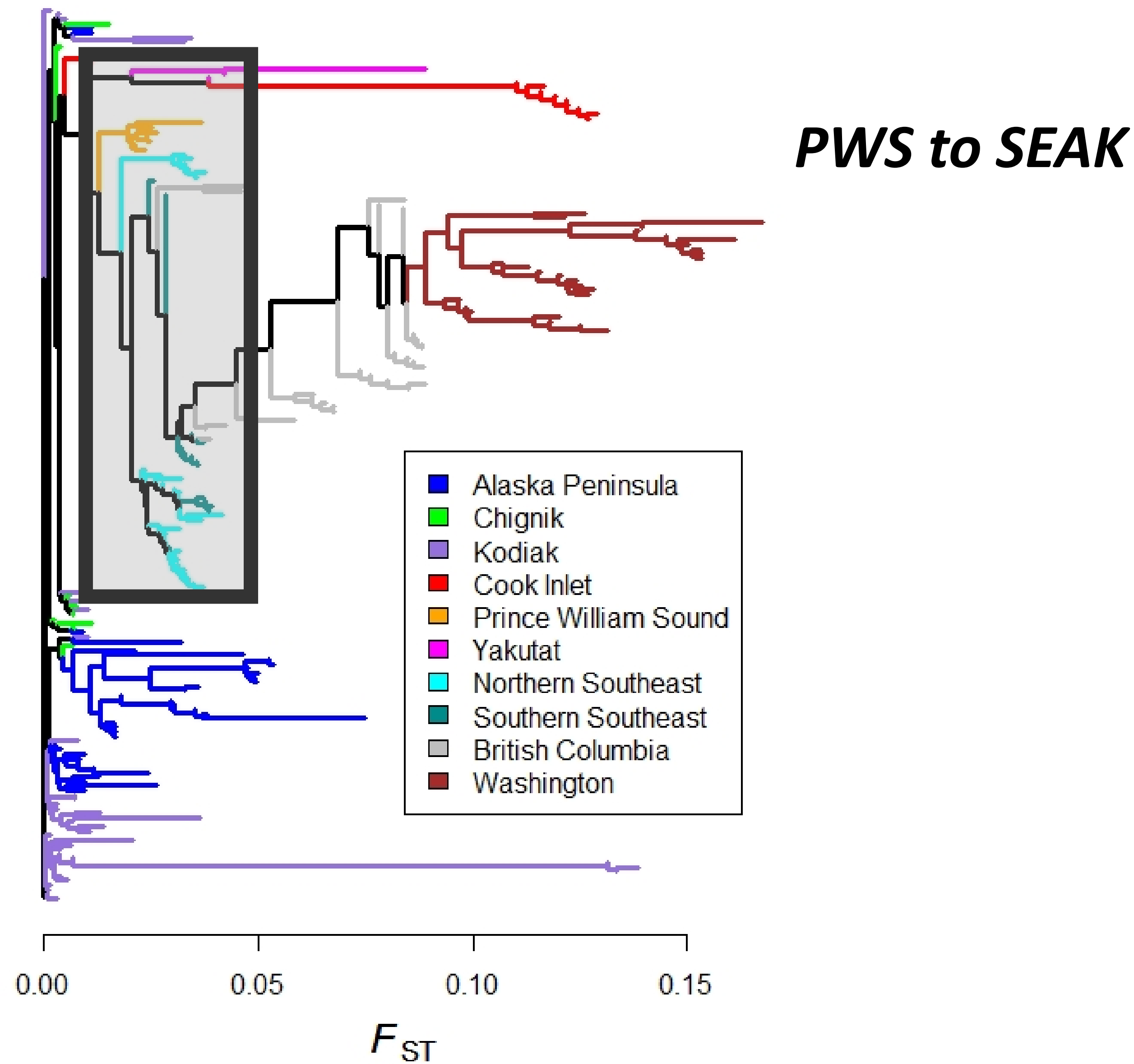
# Chum salmon in the Gulf of Alaska



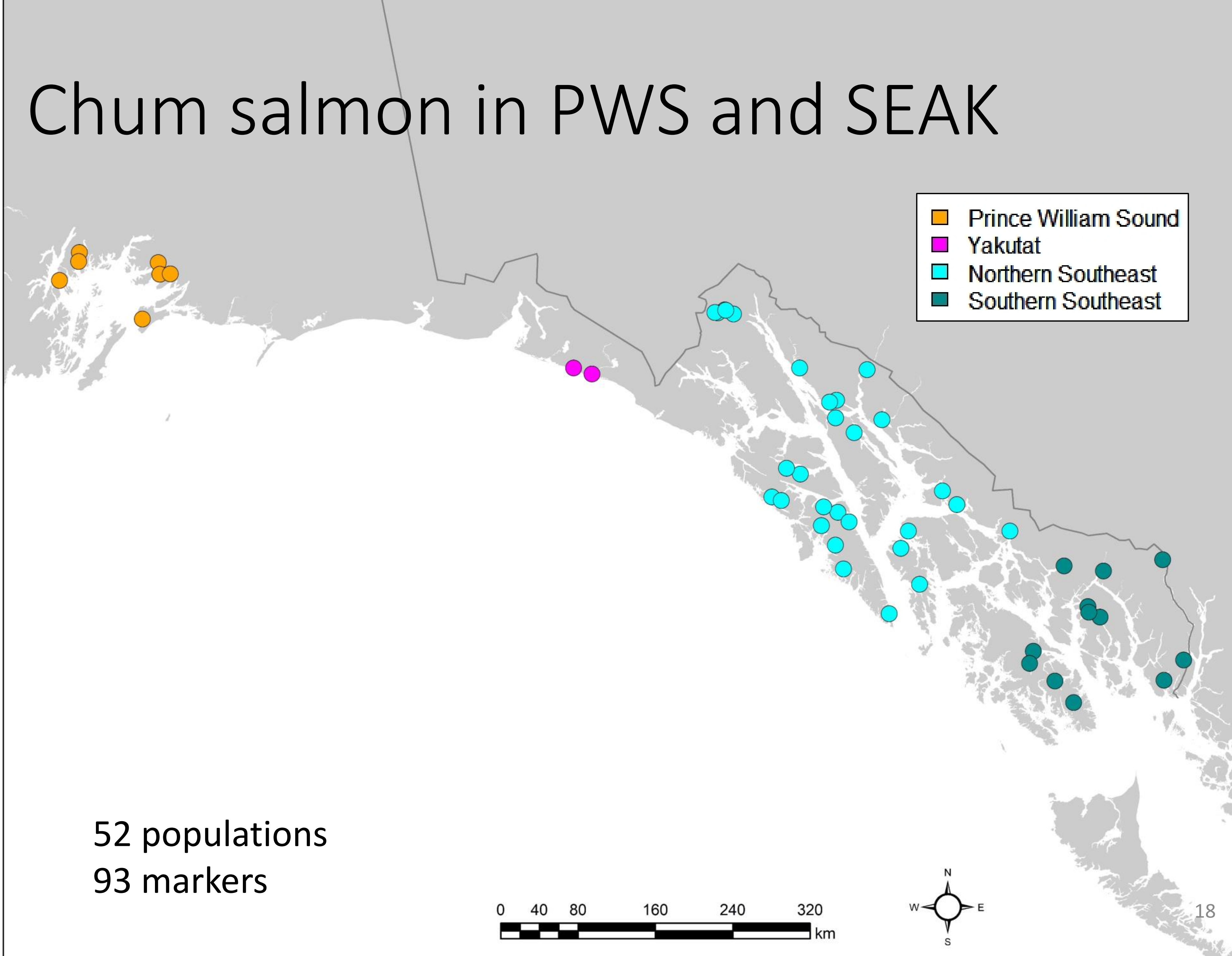

198 populations
93 markers

# Chum salmon in the Gulf of Alaska

198 populations
93 markers



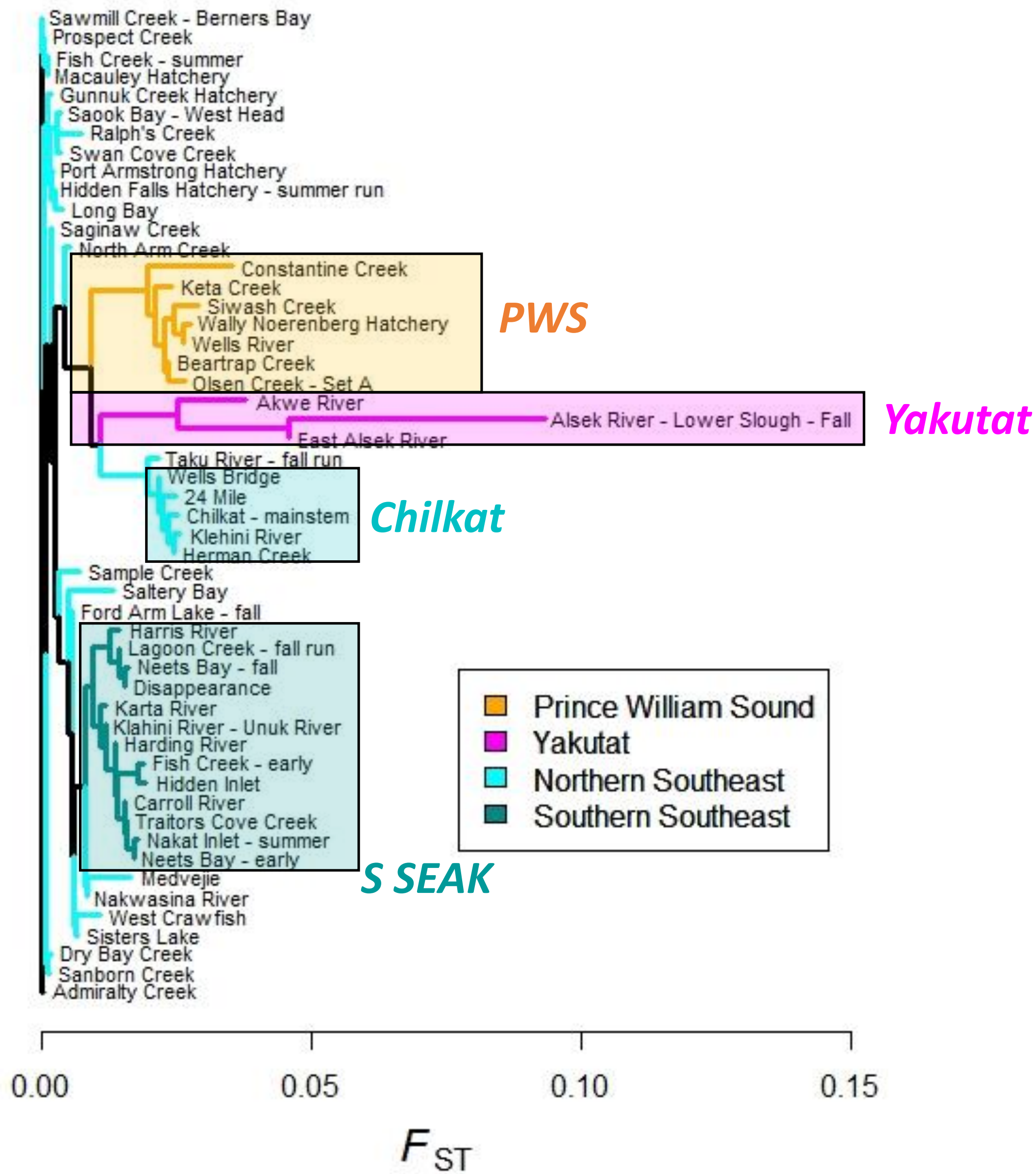
# Chum salmon in PWS and SEAK




52 populations
93 markers

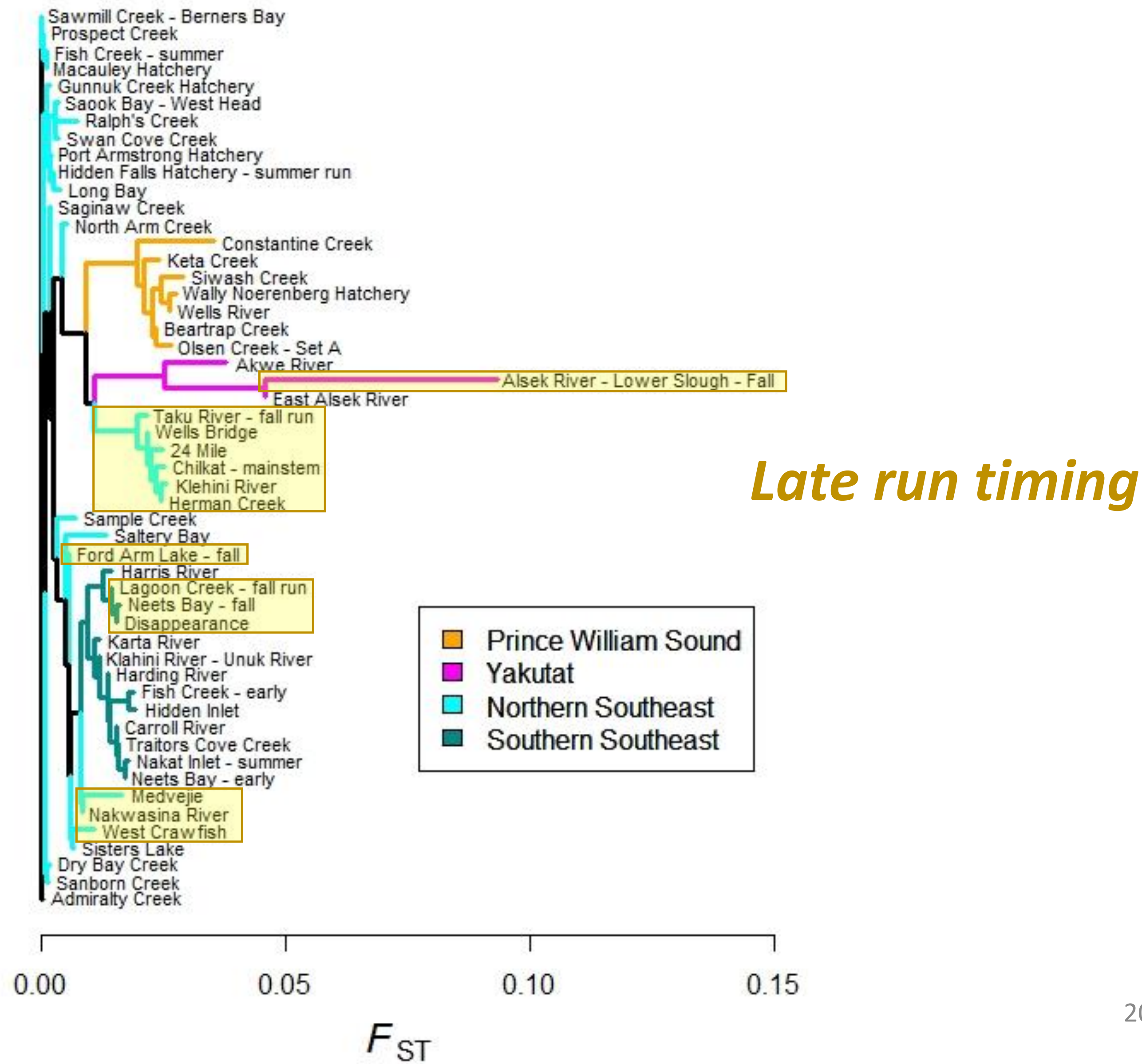
# Chum salmon in PWS and SEAK

52 populations
93 markers



# Chum salmon in PWS and SEAK

52 populations
93 markers



# Conclusions: Chum salmon structure in PWS and SEAK

- Generally correlated with geography
- Some differentiation by run timing
- Similar to other studies

J. Hyde

# Population structure of pink salmon in Prince William Sound

**Wei Cheng[1,2], Christopher Habicht[1], William D. Templin[1], Zachary D. Grauvogel[1], and Anthony J. Gharrett[2]**

**[1]Alaska Department of Fish and Game, Gene Conservation Laboratory**

**[2]University of Alaska Fairbanks, College of Fisheries and Ocean Sciences**

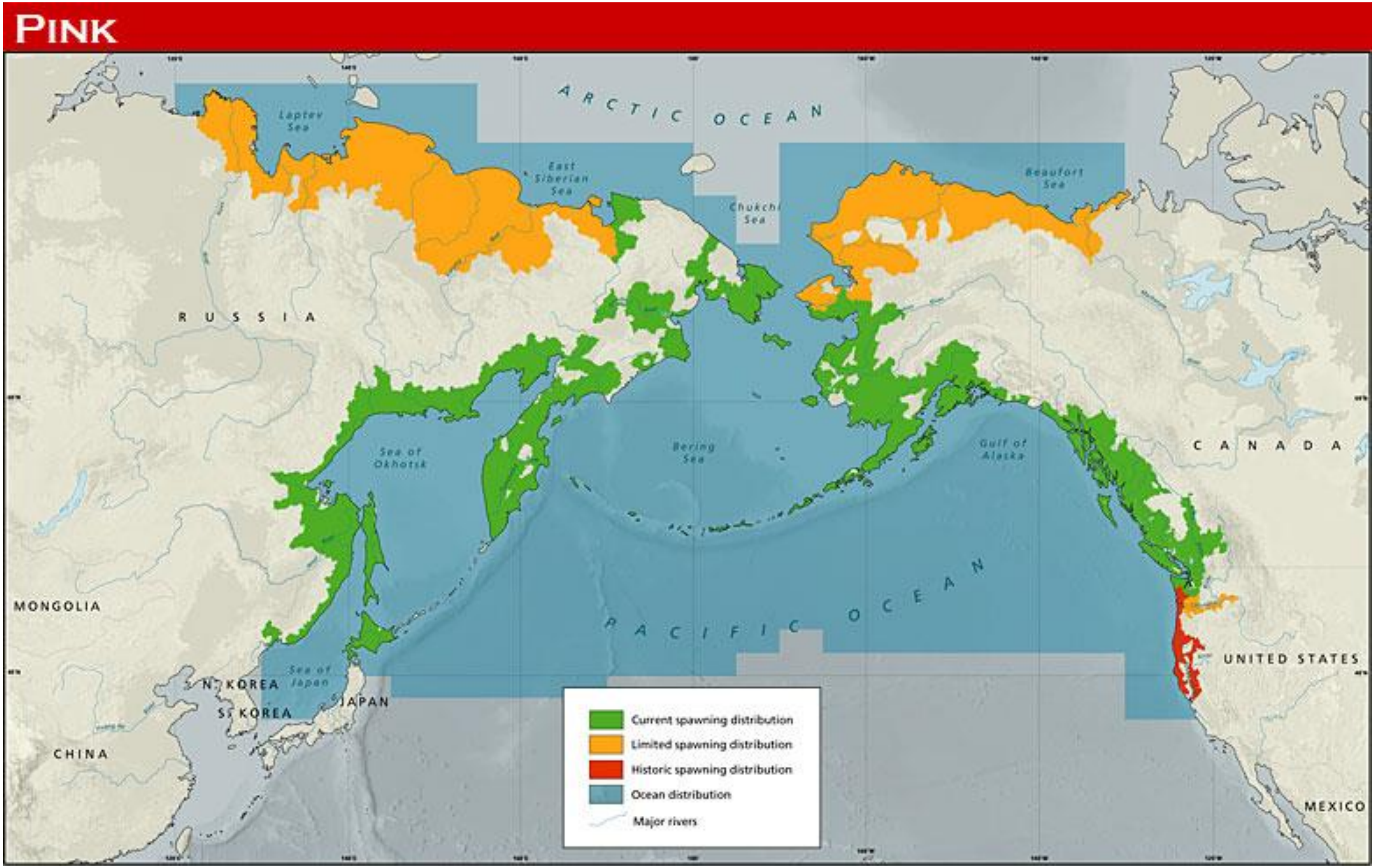
# Life History of Pink Salmon

- **Two-year life cycle**
  - **Odd year**
  - **Even year**

- **Limited freshwater life history**

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

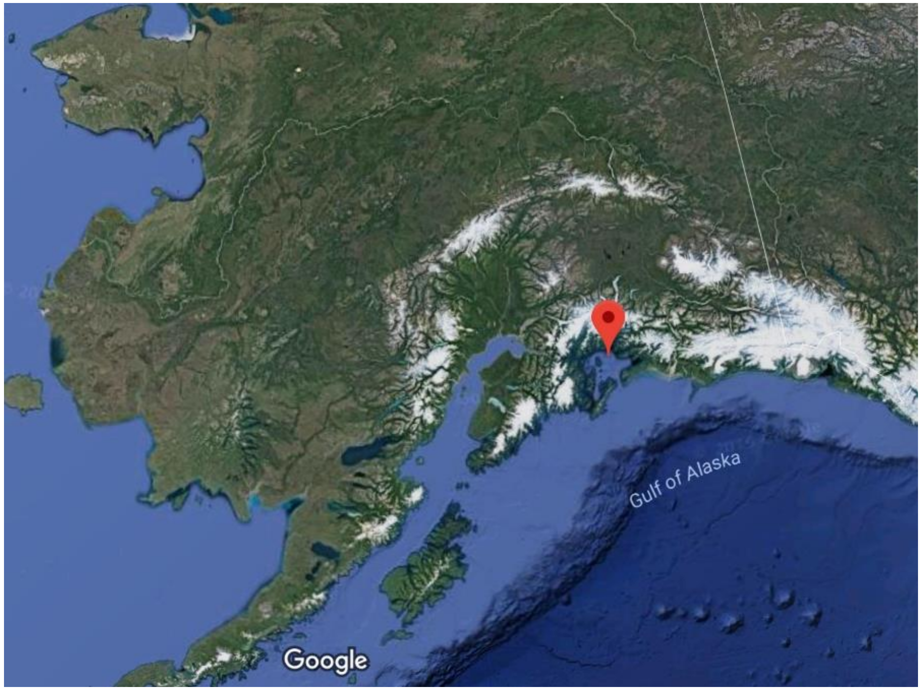
# Distribution of Pink Salmon




***http://www.salmonnation.org/fish/meet_species.html***

# PWS Pink Salmon

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



# Variability in spawning habitat




# 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*
*Printed in Denmark · All rights reserved*



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 ND5/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[1], C. Habicht[1], W. D. Templin[1], L. W. Seeb[1], J. B. Shaklee[2], F. M. Utter[3]**
[1]Alaska Department of Fish & Game, Commercial Fisheries Division, Anchorage, Alaska, [2]Washington Department of Fish & Wildlife, Olympia, [3]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

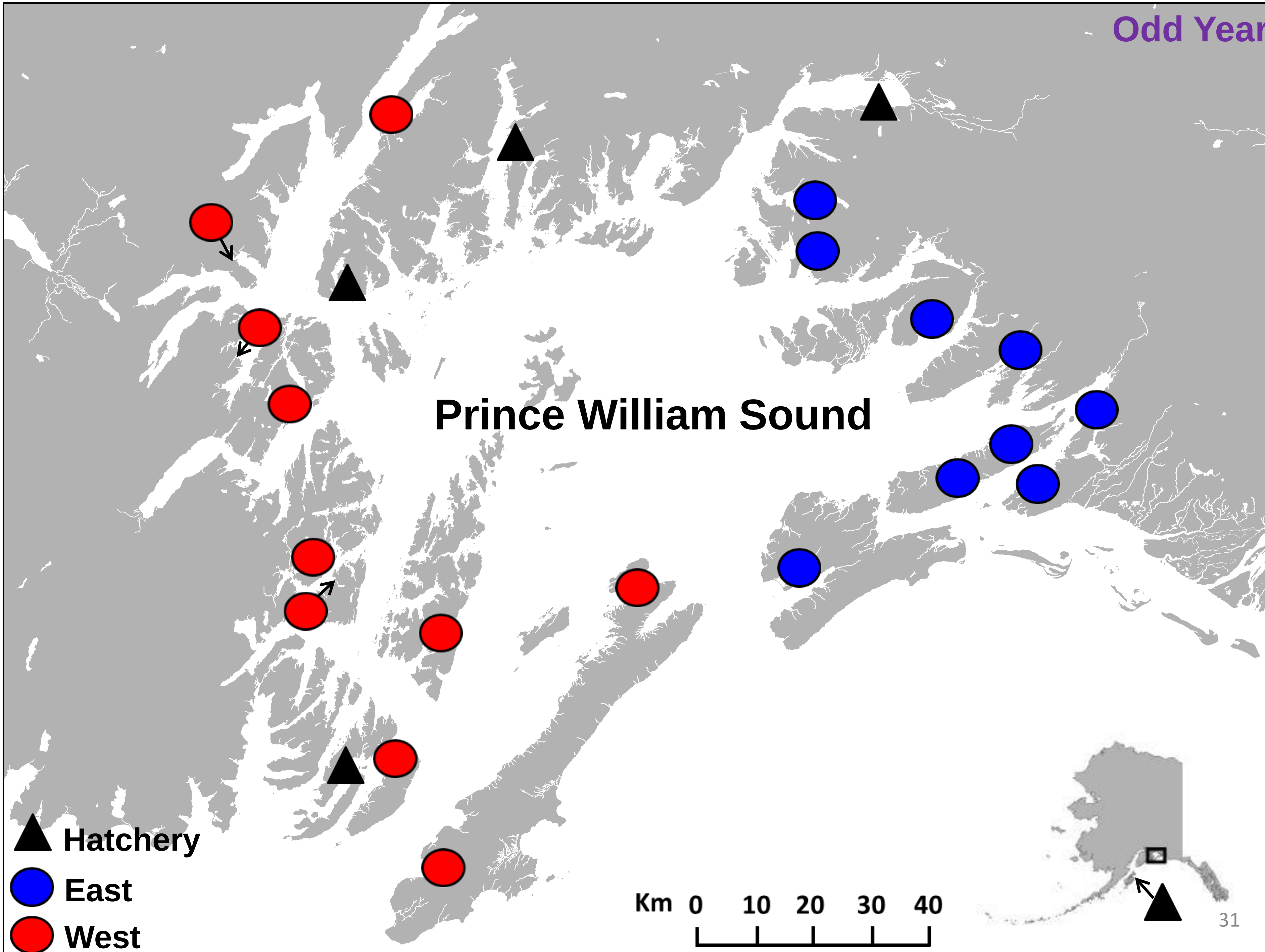
**Un resumen en español se incluye detrás del texto principal de este artículo.**

# Study Design

| | | Contemporary | Historical |
|---|---|---|---|
| Odd Year | Natural | | |
| | Hatchery | | |
| | | | |
| Even Year | Natural | | |
| | Hatchery | | |

# Study Design

| | | Contemporary | Historical |
|---|---|---|---|
| Odd Year | Natural | √ | *(pending)* |
| | Hatchery | √ | *(pending)* |
| | | | |
| Even Year | Natural | | |
| | Hatchery | | |



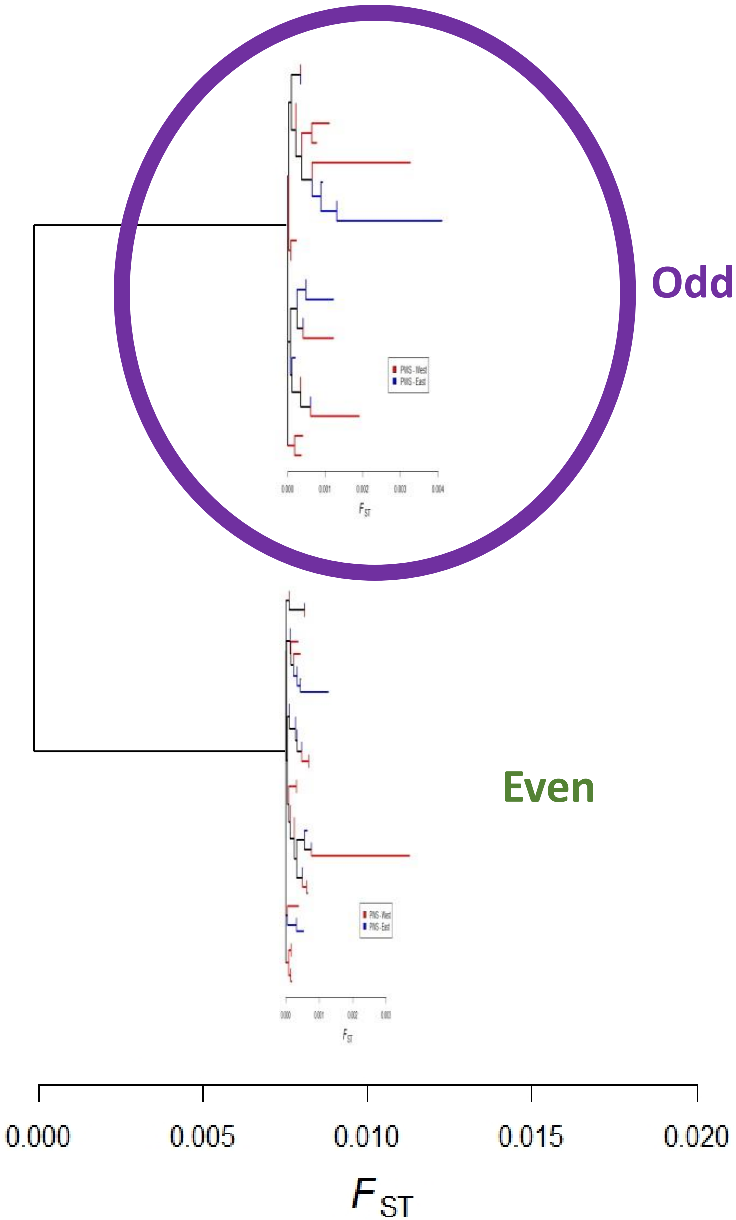
Odd Year
Prince William Sound
Hatchery
East
West
Km 0 10 20 30 40

# Population Structure Analyses

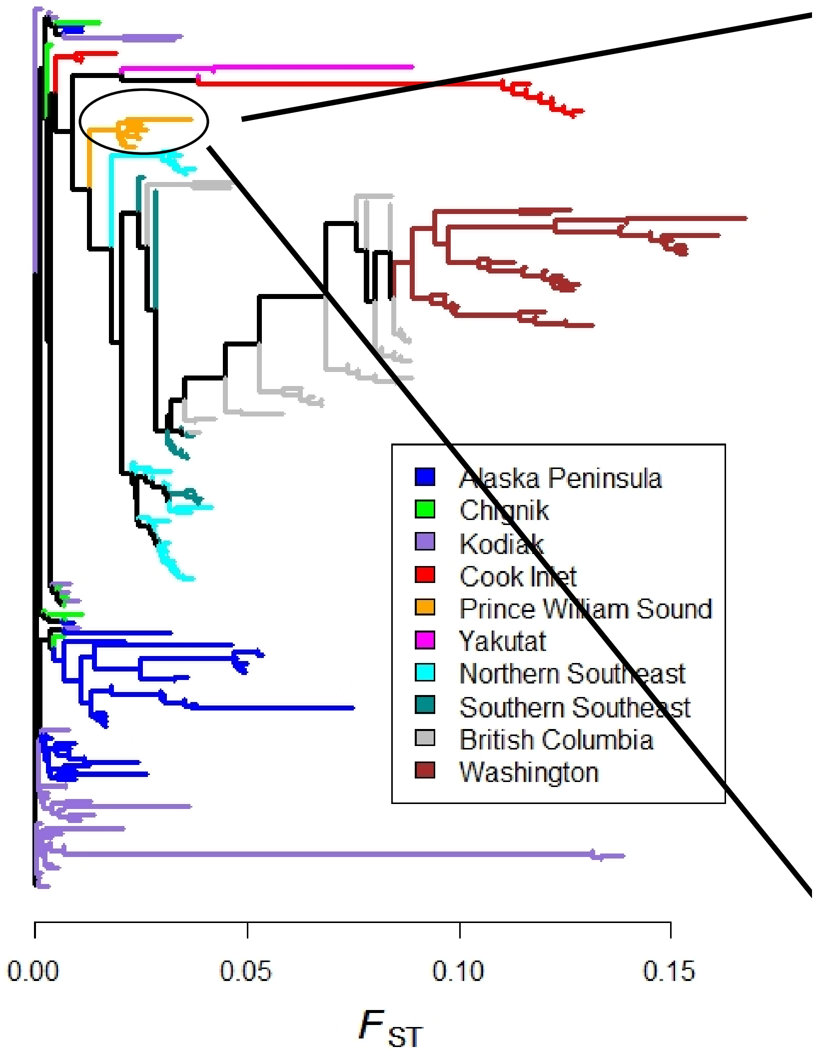
- Calculate genetic differences among collections
- Test for significance of these differences
- Visualize the relationships among collections

# Odd Year

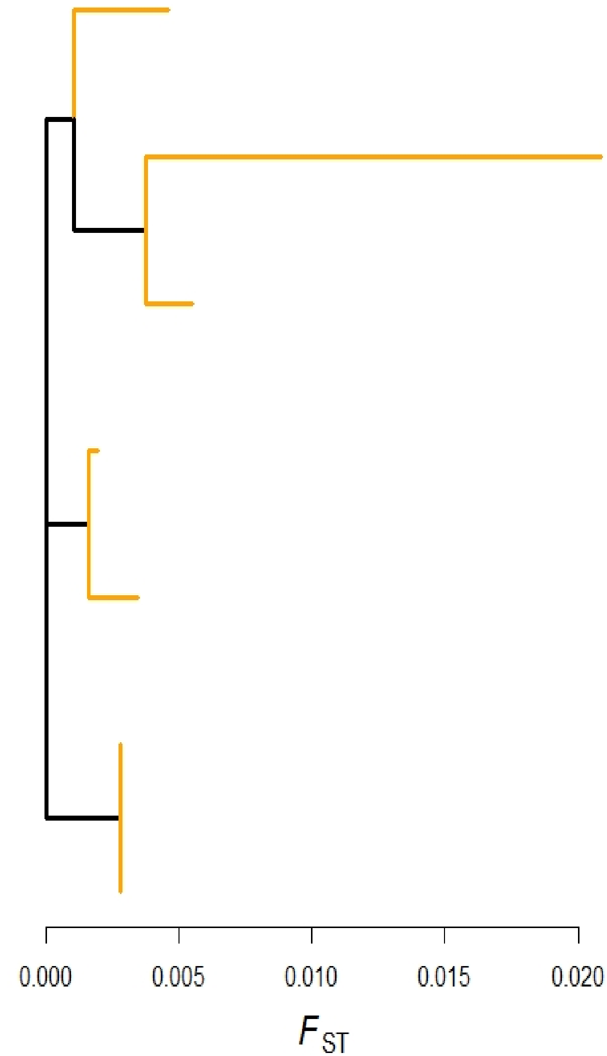
## PWS Pink Salmon



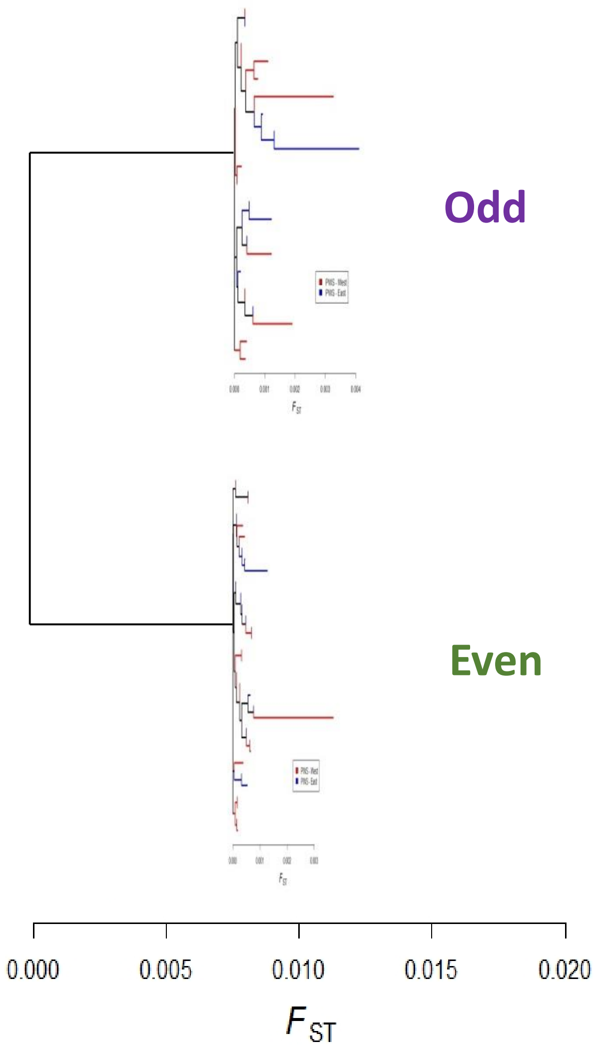
## GOA Chum Salmon



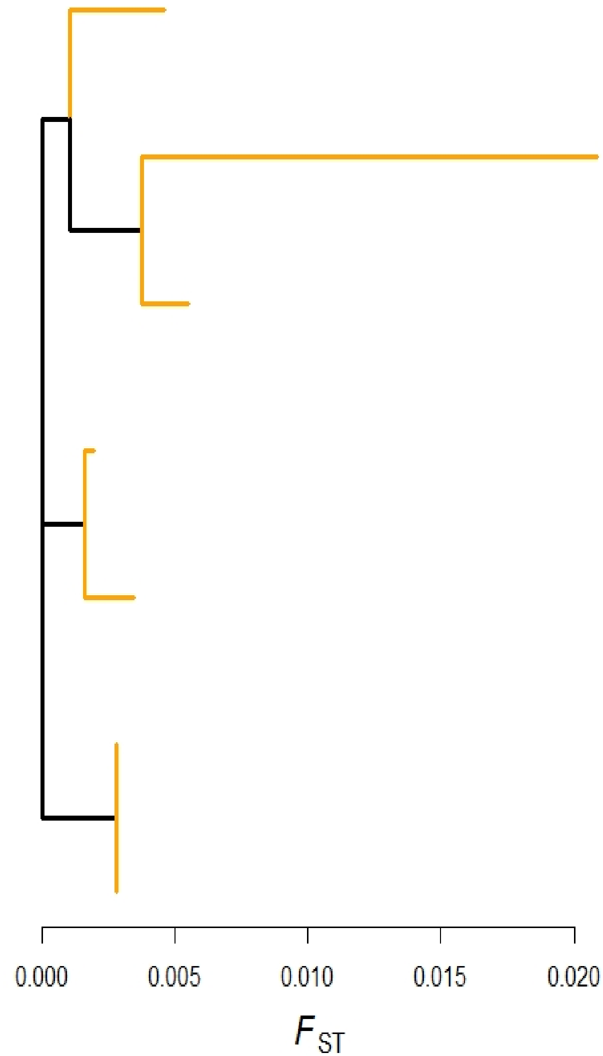

## PWS Chum Salmon



## PWS Pink Salmon




## PWS Chum Salmon



# Odd Year

Alaska Hatchery Research Group

Technical Document:[1] #14

**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. Brenner, 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 (*Ots7e*) 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

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, Auke 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 (× 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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*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 (*One*µ*3*) to 53 (*Ssa85*). 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 $\hat{\theta}$ is a better estimator of intralineage (odd-year × odd-year) population structure, whereas $\hat{\rho}_{ST}$ is best suited for estimating interlineage (odd-year × even-year) population structure. The difference in performance of $\hat{\theta}$ and $\hat{\rho}_{ST}$ 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.

## 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

*Kamchatka Branch of Pacific Research Institute of Fisheries and Oceanography (KoTRINRO), Petropavlovsk-Kamchatsky, 683602, Naberejnaia 18, Russia*

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 $\chi^2$ 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.

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

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

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**Brenda McIntosh**[1]
**Cathy MacConnachie**[1]
**Brian Spilsted**[2]
**Bruce A. White**[3]

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417-2nd Avenue West
Prince Rupert, B. C. Canada V8J 1G8

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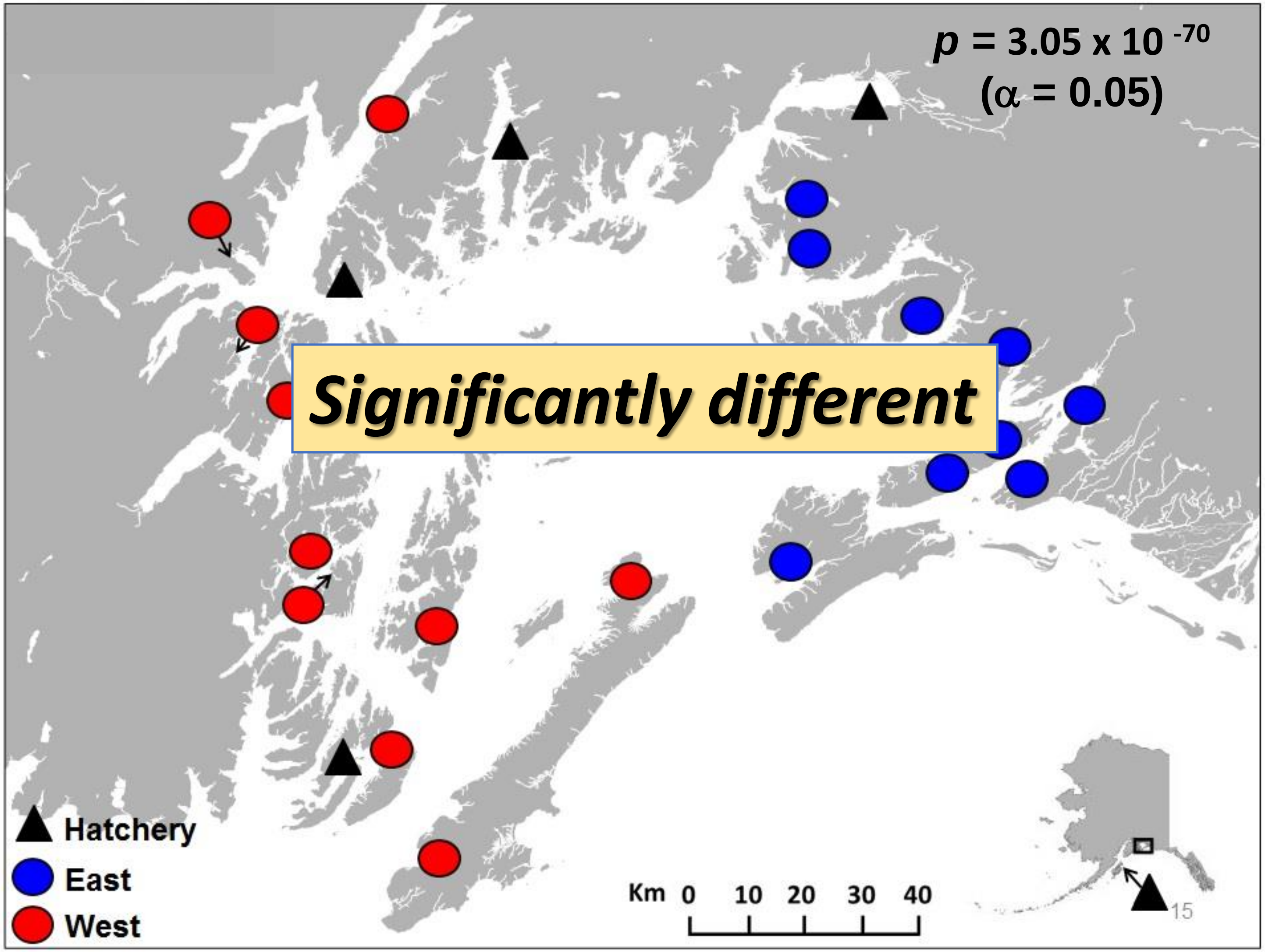
600-1155 Robson Street
Vancouver, B. C., Canada V6E 1B5

# Population Structure Analyses

- Calculate genetic differences among collections

- **Test for significance of these differences**

# Testing for Differences: among Prince Willian Sound

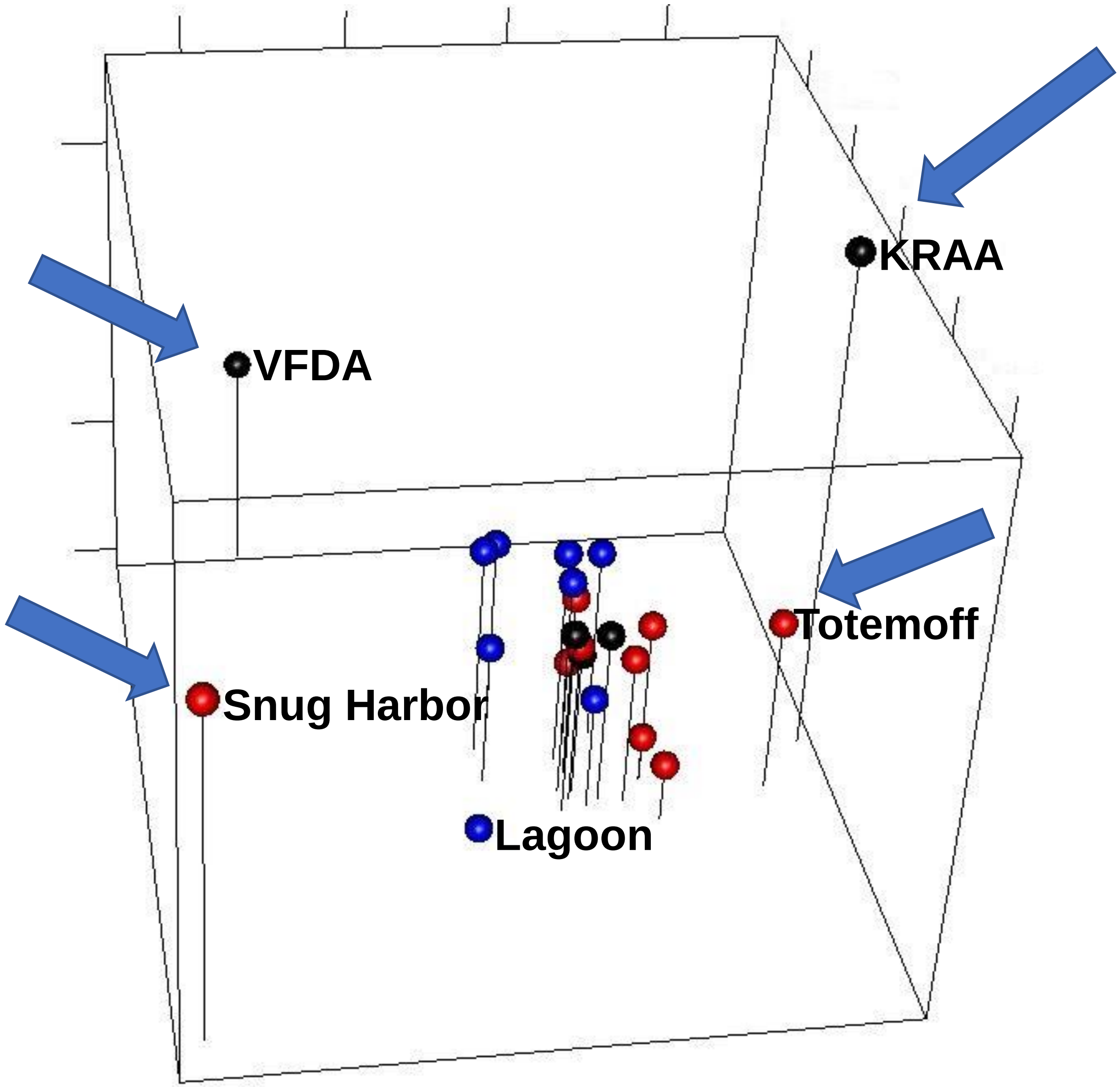


# Population Structure Analyses

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

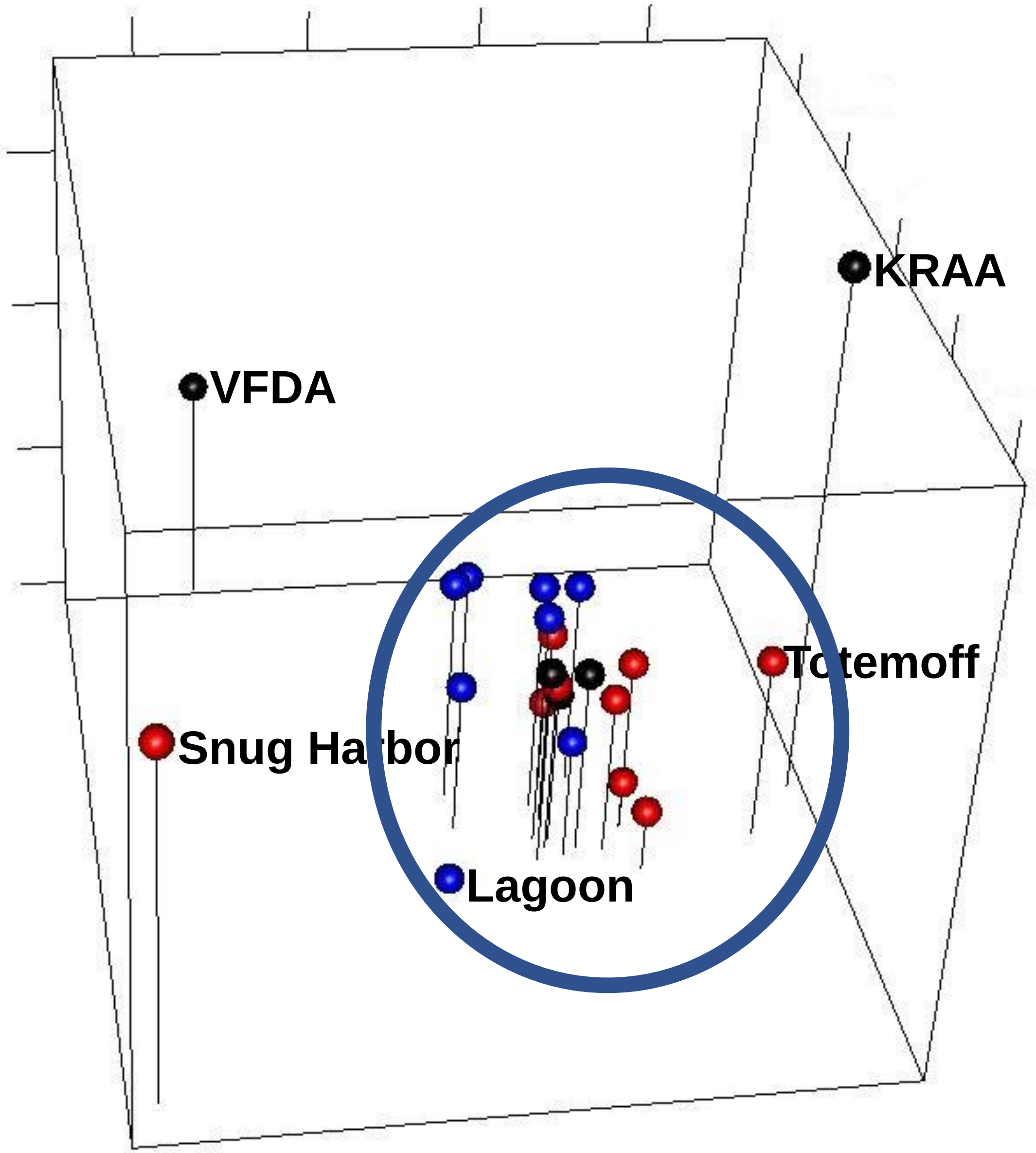
Odd Year

# Visualizing the Relationships among Collections

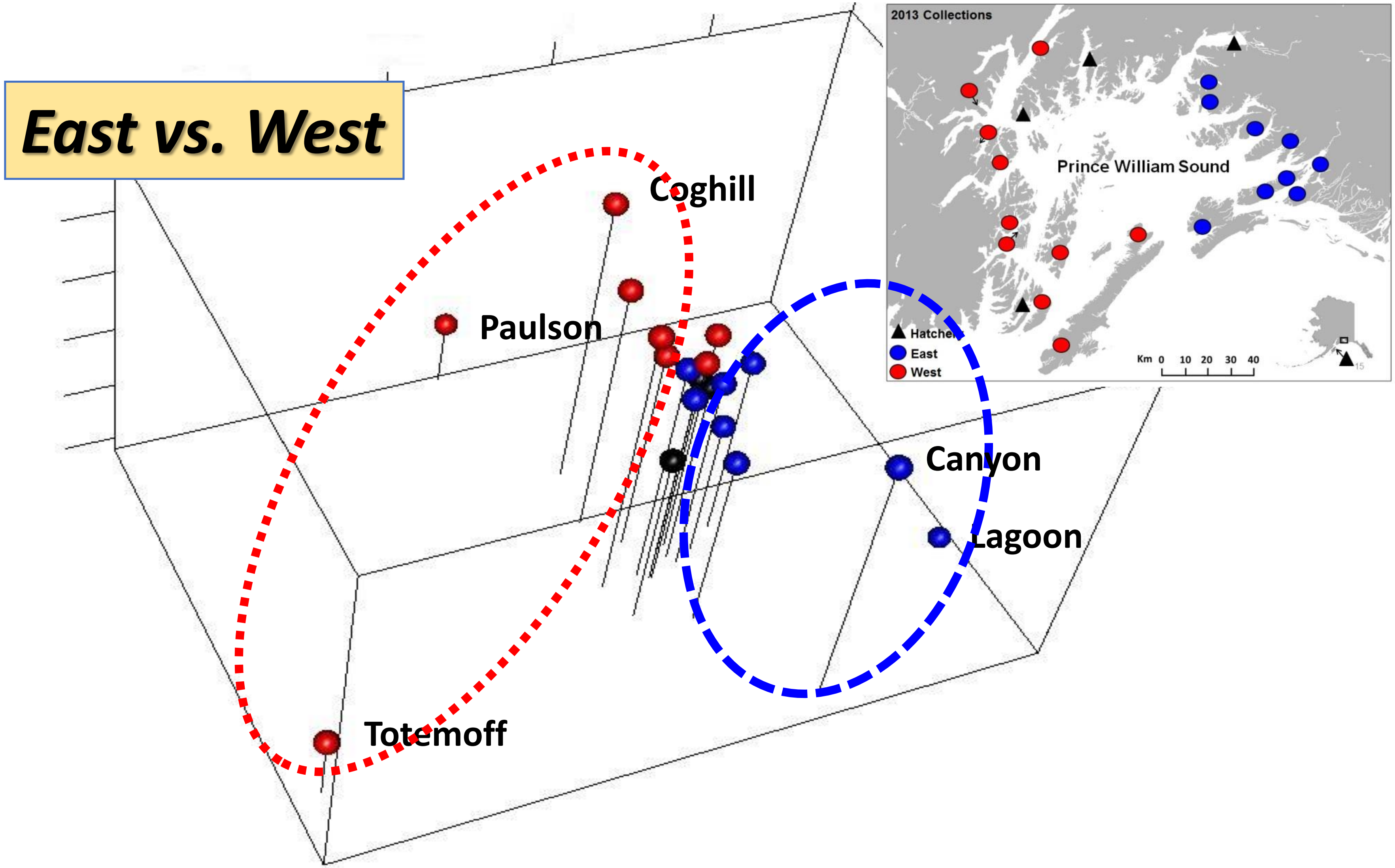


# Visualizing the Relationships among Collections



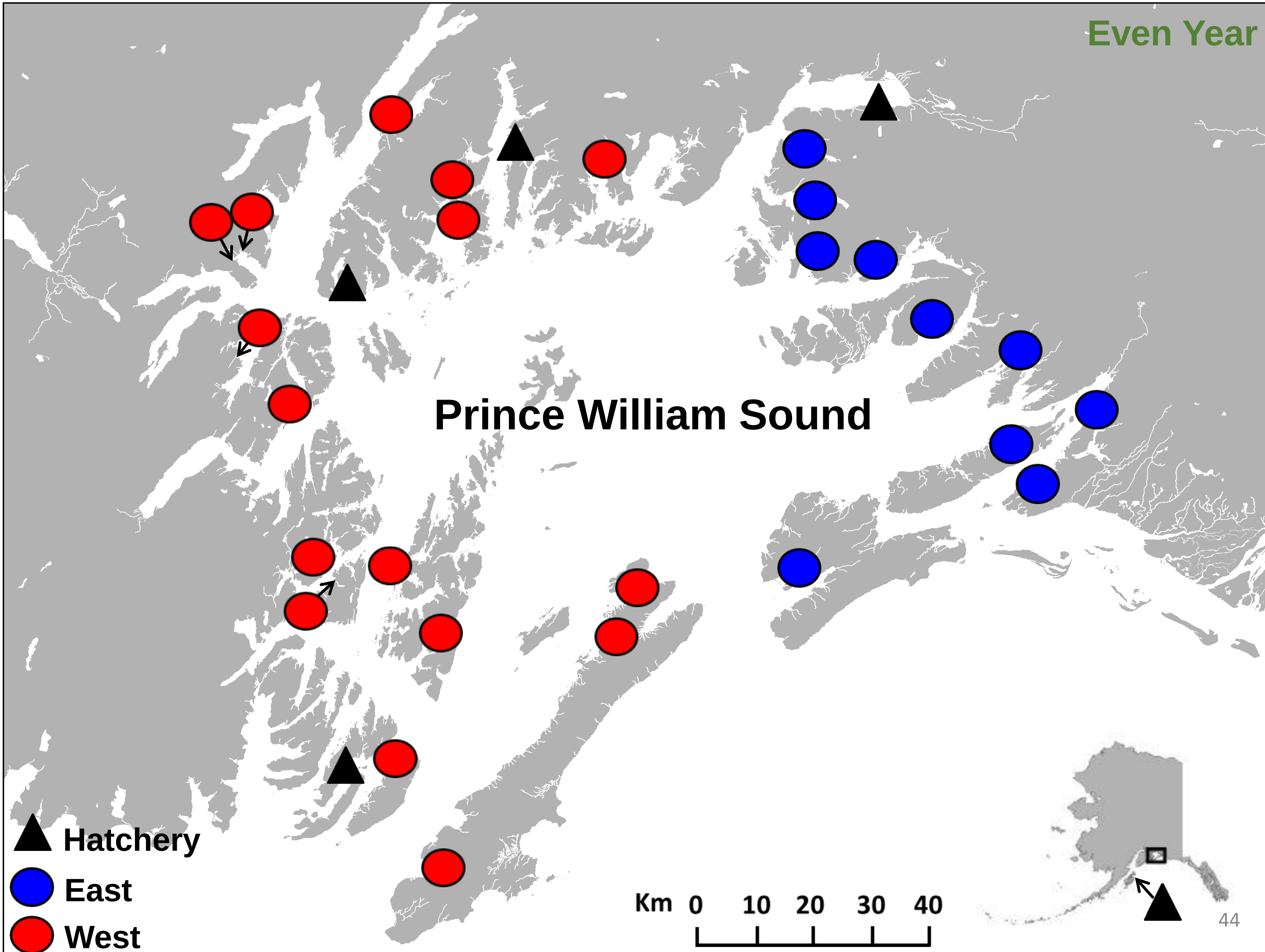


# Visualizing Relationships among Collections – Zooming in

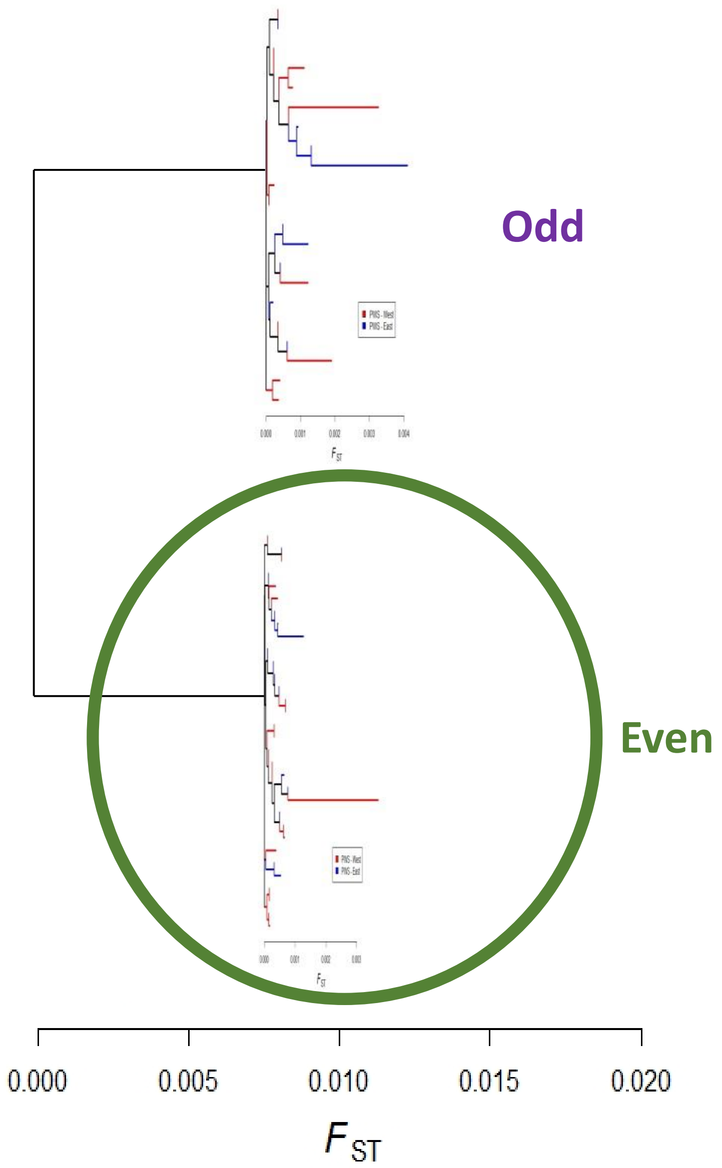


# Study Design

| | | Contemporary | Historical |
|---|---|---|---|
| Odd Year | Natural | √ | *(pending)* |
| | Hatchery | √ | *(pending)* |
| | | | |
| Even Year | Natural | √ | *(pending)* |
| | Hatchery | √ | *(pending)* |


Even Year
Prince William Sound
Hatchery
East
West
Km 0 10 20 30 40

# PWS Pink Salmon



# Even Year

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 ND5/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[1], C. Habicht[1], W. D. Templin[1], L. W. Seeb[1], J. B. Shaklee[2], F. M. Utter[3]**
[1]Alaska Department of Fish & Game, Commercial Fisheries Division, Anchorage, Alaska, [2]Washington Department of Fish & Wildlife, Olympia, [3]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.**

**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

**Date**: XXXX

**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

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

**Terry D. Beacham (contact author)**[1]
**Brenda McIntosh**[1]
**Cathy MacConnachie**[1]
**Brian Spilsted**[2]
**Bruce A. White**[3]

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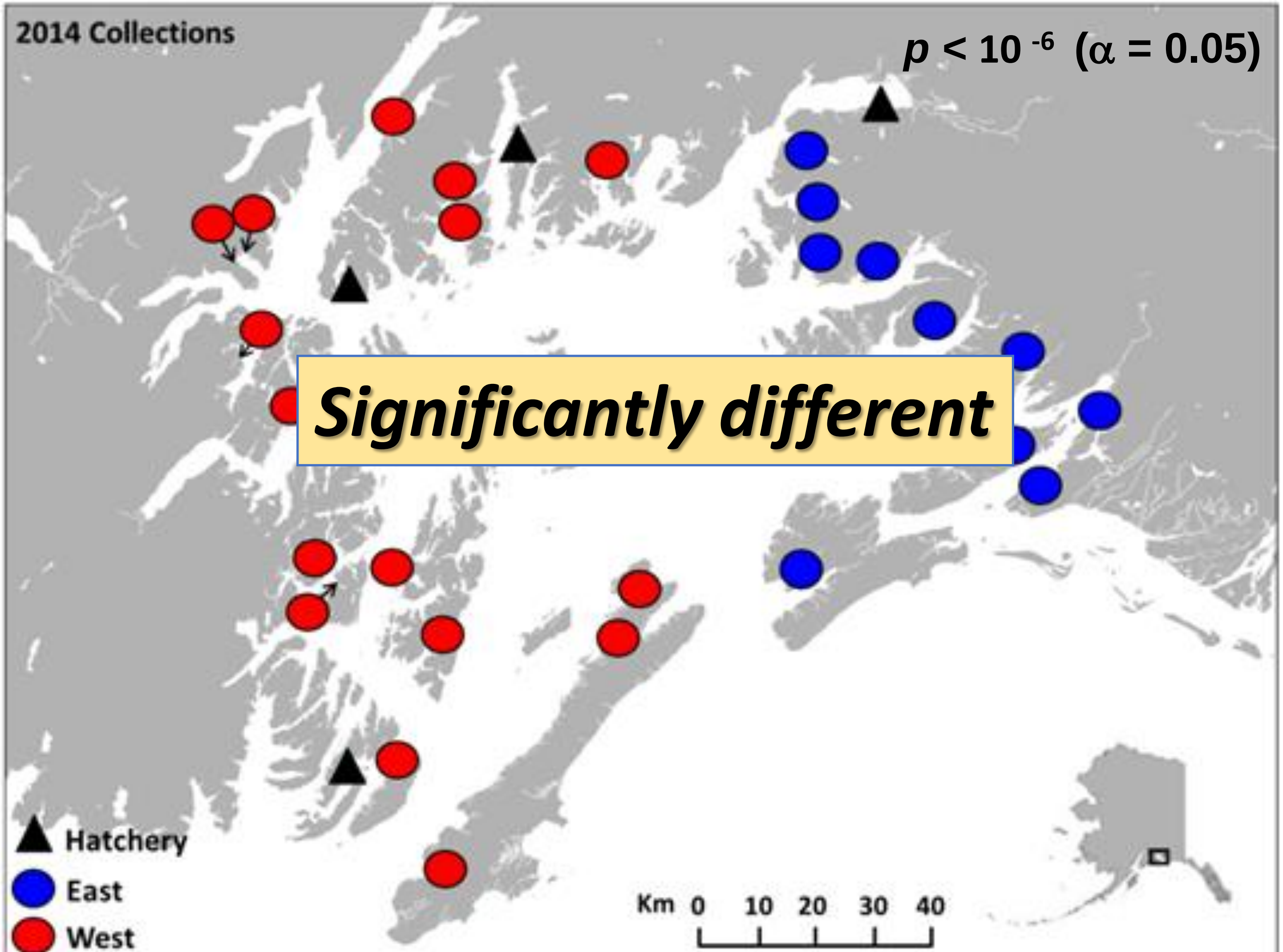
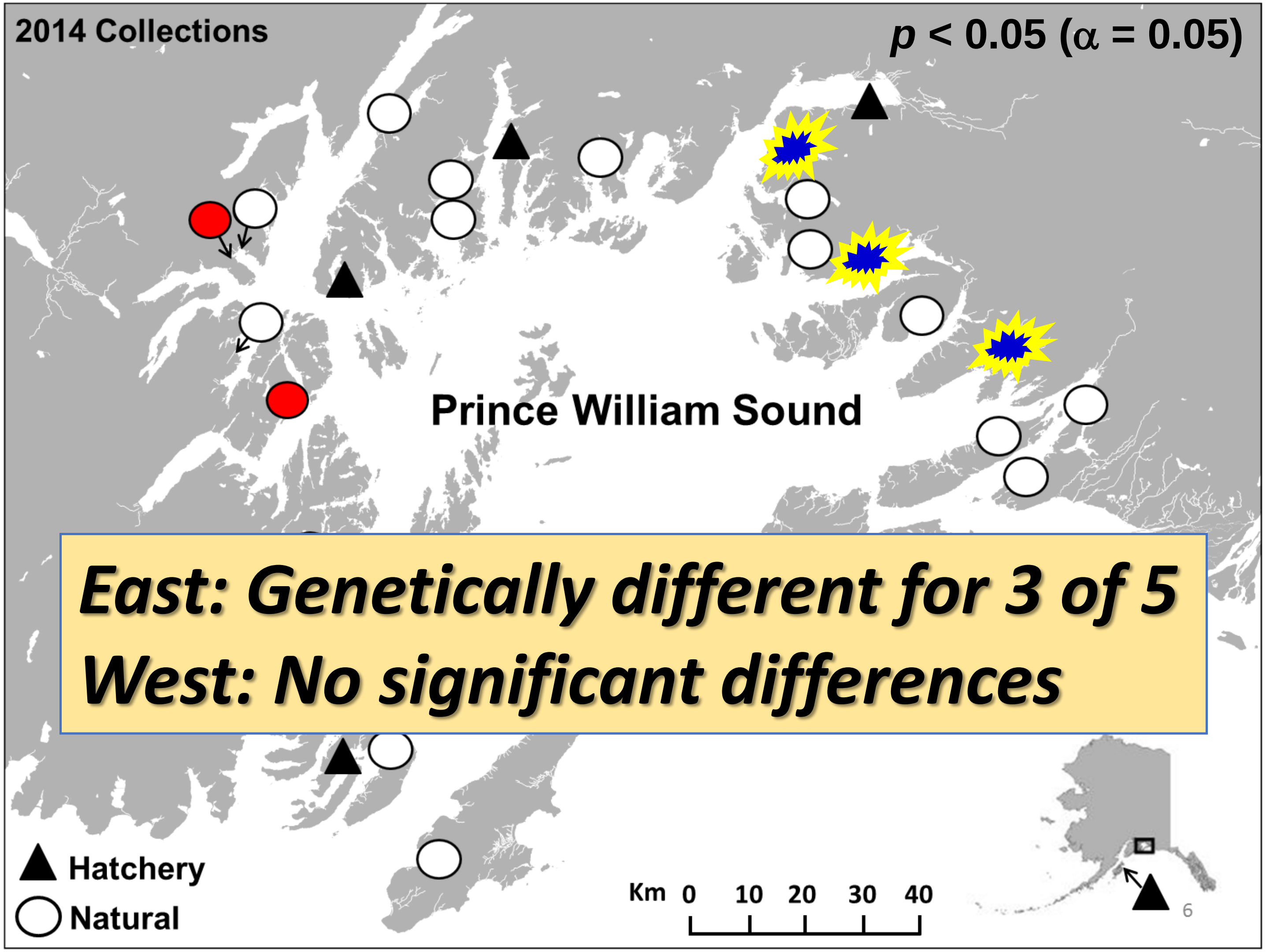
Abstract—Population structure of pink salmon (*Oncorhynchus gorbuscha*) from British Columbia and Washington was examined with a survey of microsatellite variation to describe the distribution of genetic variation. Variation at 16 microsatellite loci was surveyed for approximately 46,500 pink salmon 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

# Testing for Differences: among Prince Willian Sound



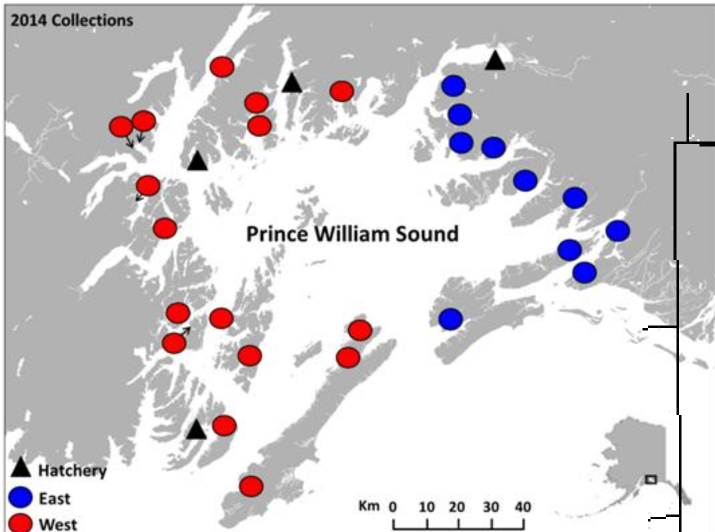
# Testing for Differences: Between Early and Late Collections

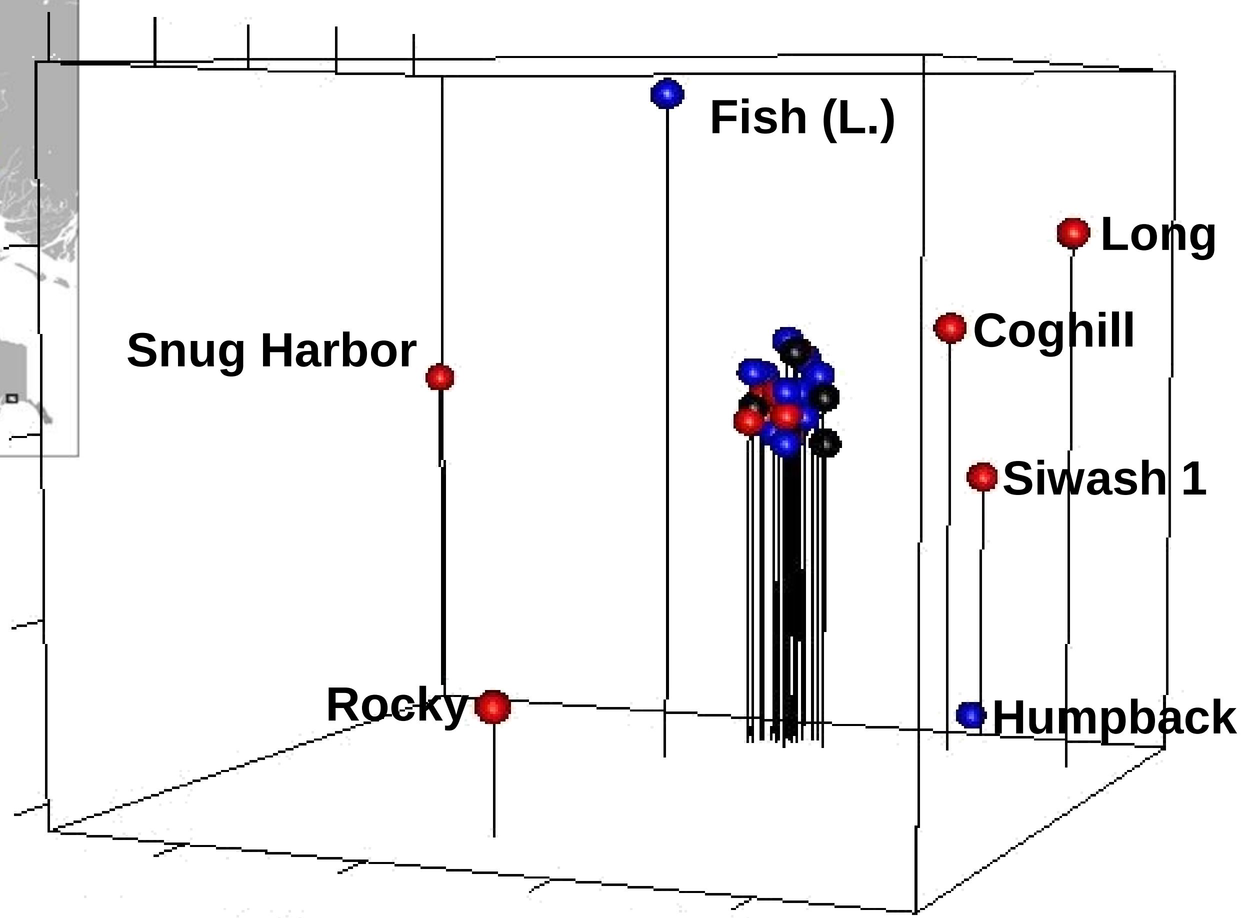



***East: Genetically different for 3 of 5***

***West: No significant differences***

# Visualizing the Relationships among Collections



# Conclusions to date: Pink salmon structure in PWS

- **Genetic variation among pink salmon populations in PWS is very small**
  - ✓ **Odd year – small**
  - ✓ **Even year – even smaller**

- **Kodiak vs. Prince William Sound (PWS)** [data not shown]
  - ✓ **Significantly different in both lineages**

# Conclusions to date: Pink salmon structure in PWS

- **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**

# What is the extent and annual variability of straying?

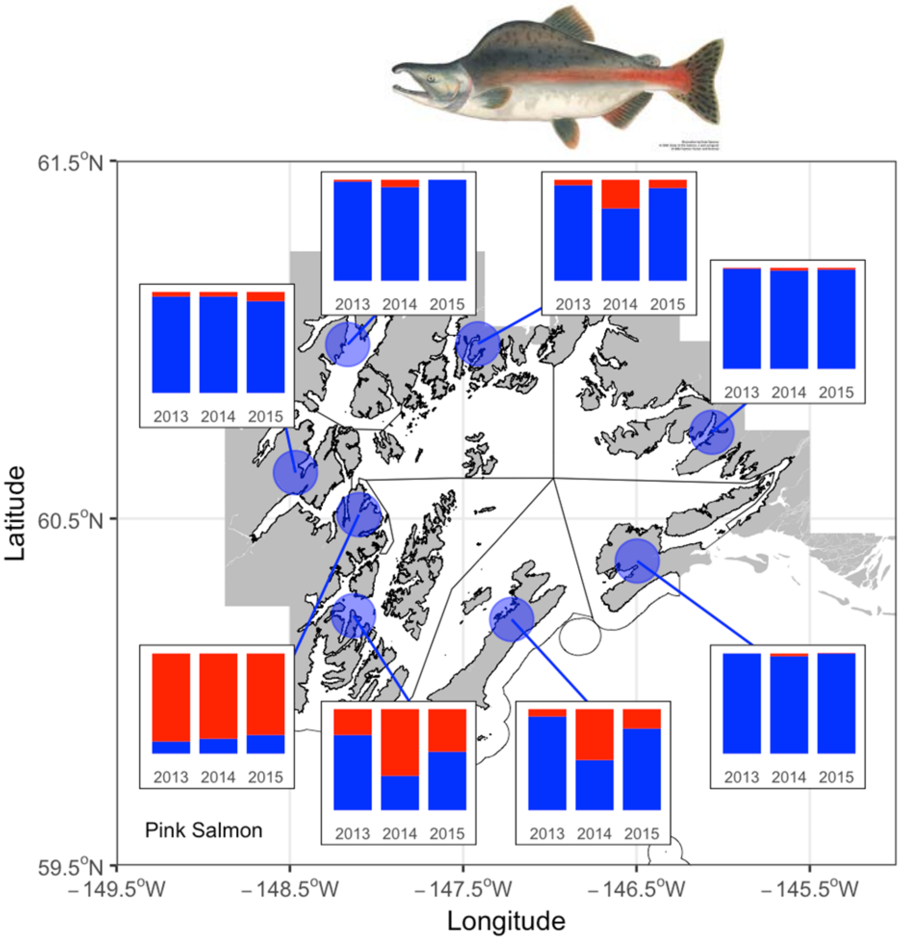
C. Habicht and W. D. Templin

Alaska Department of Fish and Game Gene Conservation Lab

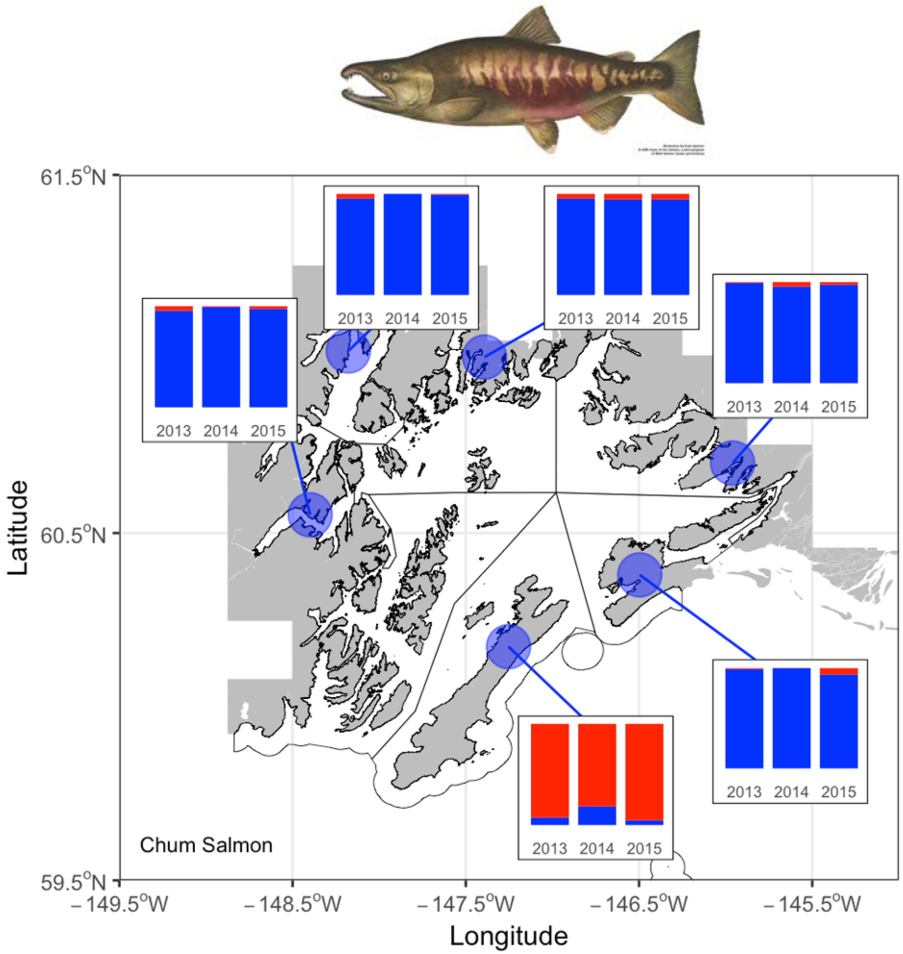
Alaska Board of Fisheries, Hatchery Committee Meeting

March 8, 2019

# PWS: Stream results, district averages




0.1% - 89.9%

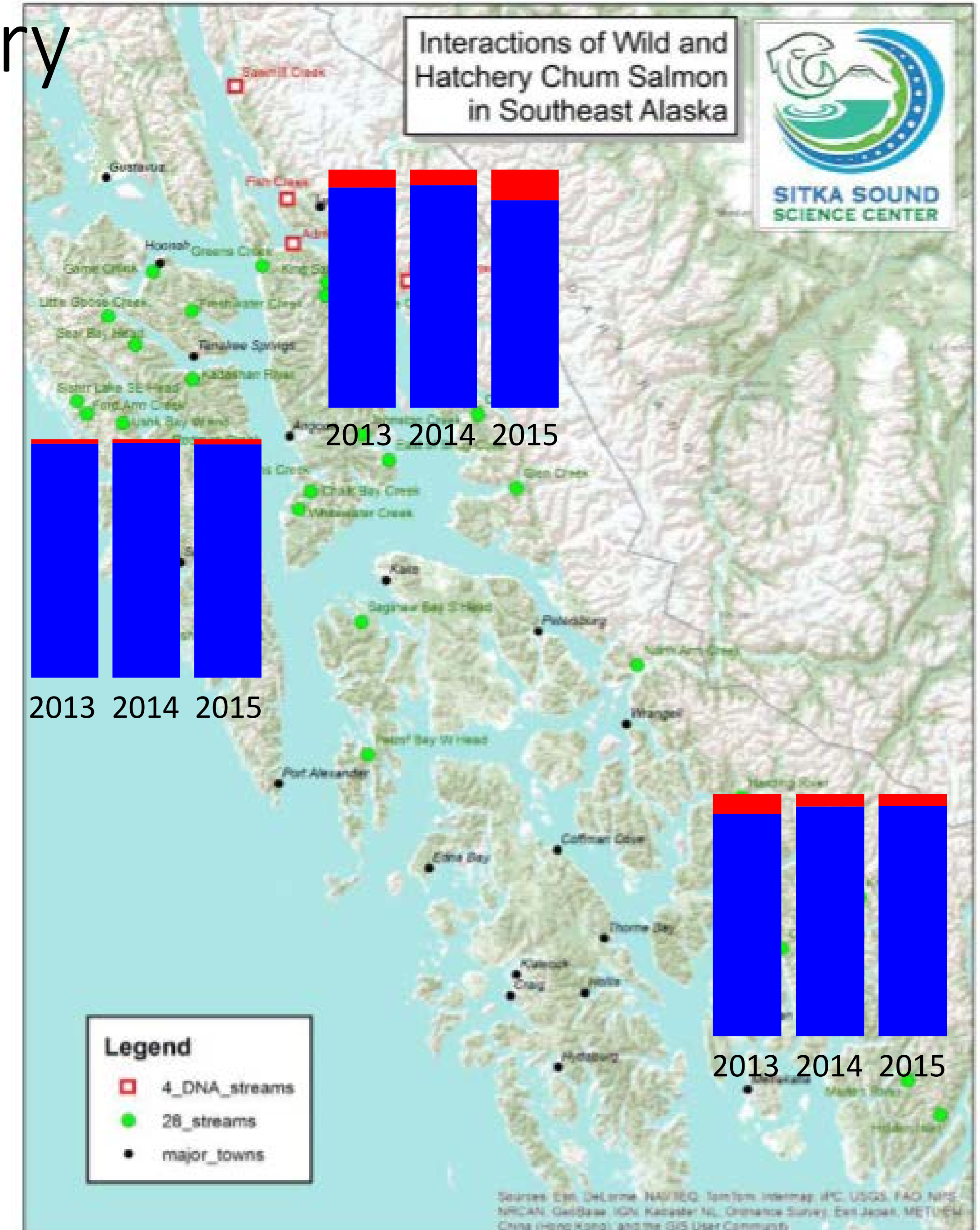



0.0% - 84.6%

# Overall PWS hatchery fractions in spawning streams

| Species | 2013 | 2014 | 2015 |
|---|---|---|---|
| Pink | 4.4% | 14.8% | 9.5% |
| Chum | 2.8% | 3.2% | 3.1% |

# SEAK: Hatchery fraction by stream: 1.5% - 12.7%




# Overall SEAK hatchery fractions in spawning streams

| Species | 2013 | 2014 | 2015 |
|---|---|---|---|
| Chum | 7.3% | 5.4% | 9.2% |

# PWS: Run Size and Harvest Rates

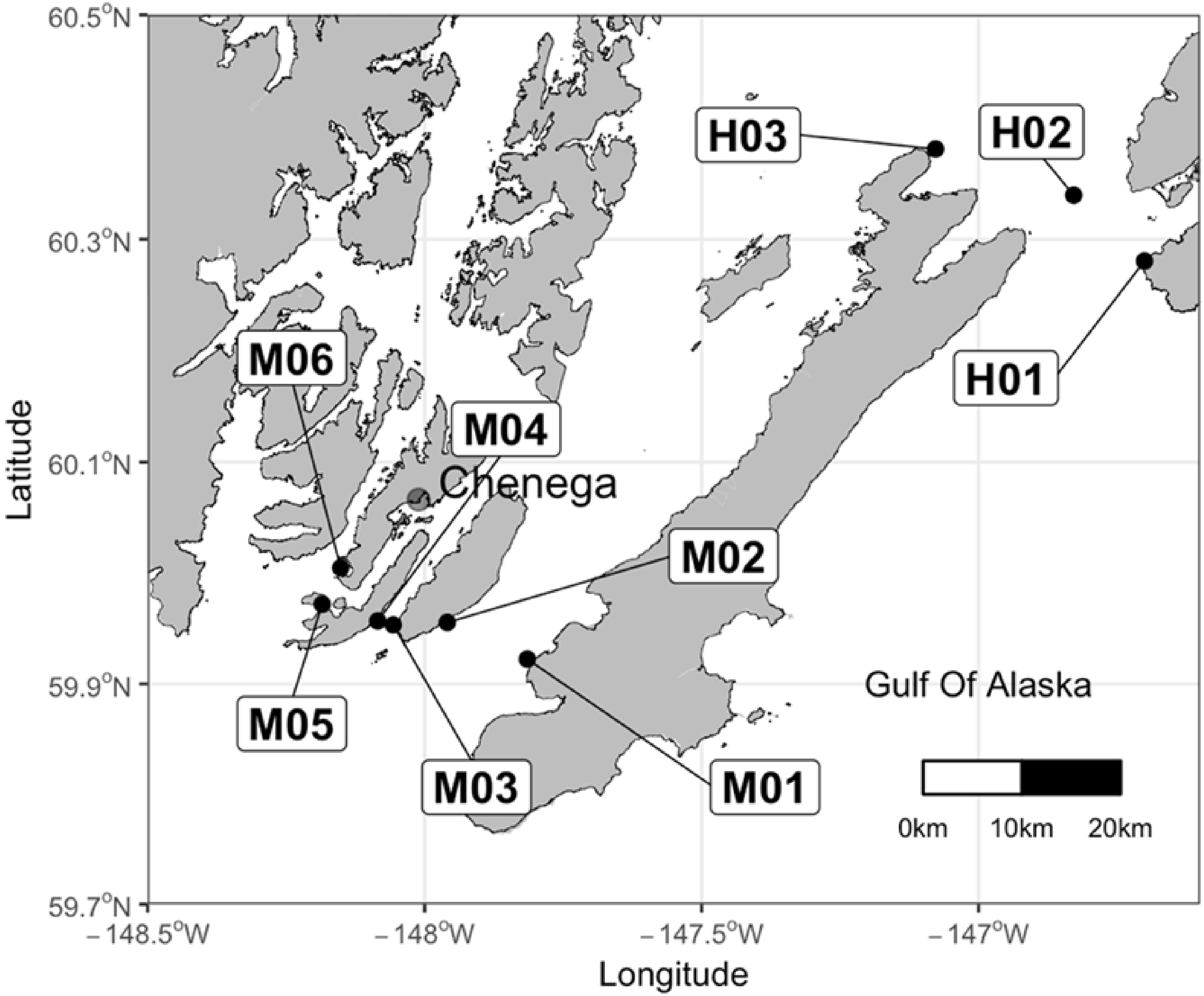
C. Habicht and W. D. Templin

Alaska Department of Fish and Game Gene Conservation Lab

Alaska Board of Fisheries, Hatchery Committee Meeting

March 8, 2019

# Ocean Sampling: PWS



# Ocean sampling 2013–2015 (PWS only)

- Proportions of hatchery fish in **run**
- Results (7,800 samples):
  - Pink salmon: 55 - 86%
  - Chum salmon: 51 - 73%

| Species Common Name | Year | Hatchery Proportion | SE |
|---|---|---|---|
| Pink Salmon | 2013 | 0.679 | .016 |
| | 2014 | 0.864 | .03 |
| | 2015 | 0.549 | .004 |
| Chum Salmon | 2013 | 0.725 | .019 |
| | 2014 | 0.511 | .029 |
| | 2015 | 0.688 | .015 |

Knudsen et al. (2016). Interactions of Wild and Hatchery Pink Salmon and Chum Salmon in Prince William Sound and Southeast Alaska.

# Wild and Hatchery run size estimates

- Preliminary PWS run size estimates; 2013-2015 (Thousands)

| Species Year | Natural spawners | Hatchery strays | Total spawners | Natural run | Hatchery run | Total run |
|---|---|---|---|---|---|---|
| Pink salmon | | | | | | |
| 2013 | 15,698 | 701 | 16,399 | 33,096 | 69,888 | 102,985 |
| 2014 | 5,130 | 741 | 5,872 | 6,960 | 42,757 | 49,718 |
| 2015 | 37,972 | 4,009 | 41,981 | 63,531 | 77,335 | 140,866 |
| Chum salmon | | | | | | |
| 2013 | 894 | 50 | 944 | 1,141 | 3,007 | 4,148 |
| 2014 | 925 | 49 | 975 | 1,175 | 1,228 | 2,404 |
| 2015 | 890 | 28 | 919 | 1,128 | 2,484 | 3,612 |

Knudsen et al. (2016). Interactions of Wild and Hatchery Pink Salmon and Chum Salmon in Prince William Sound and Southeast Alaska.

# Natural and Hatchery harvest rate estimates: PWS pink salmon

| | Estimated Harvest Rates | |
|---|---|---|
| Year | Hatchery | Natural |
| 2013 | 0.99 | 0.53 |
| 2014 | 0.98 | 0.26 |
| 2015 | 0.95 | 0.40 |

# AHRP Fitness Study: PWS Pink Salmon

Emily Lescak, K. Shedd, D. Prince, H. Hoyt, T. Dann, C. Habicht

Alaska Department of Fish and Game Gene Conservation Lab

Alaska Board of Fisheries Hatchery Committee

March 8, 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?

# Hatchery/Natural Fitness

## Steelhead

433

**Differential reproductive success of sympatric, naturally spawning hatchery and wild steelhead trout (*Oncorhynchus mykiss*) through the adult stage**

Jennifer E. McLean, Paul Bentzen, and Thomas P. Quinn

MOLECULAR ECOLOGY
Molecular Ecology (2011) 20, 1860–1869 doi: 10.1111/j.1365-294X.2011.05058.x

Reduced reproductive success of hatchery coho salmon in the wild: insights into most likely mechanisms

VÉRONIQUE THÉRIAULT,* GREGORY R. MOYER,*[1] LAURA S. JACKSON,† MICHAEL S. BLOUIN‡ and MICHAEL A. BANKS*

**Genetic Effects of Captive Breeding Cause a Rapid, Cumulative Fitness Decline in the Wild**

Hitoshi Araki,* Becky Cooper, Michael S. Blouin



Molecular Ecology (2007) 16, 953–966 doi: 10.1111/j.1365-294X.2006.03206.x

Effective population size of steelhead trout: influence of variance in reproductive success, hatchery programs, and genetic compensation between life-history forms

HITOSHI ARAKI,* ROBIN S. WAPLES,† WILLIAM R. ARDREN,‡ BECKY COOPER* and MICHAEL S. BLOUIN*

biology letters
Conservation biology
Biol. Lett. (2009) 5, 621–624
doi:10.1098/rsbl.2009.0315
Published online 10 June 2009

**Carry-over effect of captive breeding reduces reproductive fitness of wild-born descendants in the wild**

Hitoshi Araki*,[†], Becky Cooper and Michael S. Blouin

Transactions of the American Fisheries Society
Publication details, including instructions for authors and subscription information:
http://www.tandfonline.com/loi/utaf20

**Diminished Reproductive Success of Steelhead from a Hatchery Supplementation Program (Little Sheep Creek, Imnaha Basin, Oregon)**

Ewann A. Berntson[a], Richard W. Carmichael[b], Michael W. Flesher[b], Eric J. Ward[c] & Paul Moran[c]

PNAS

Genetic adaptation to captivity can occur in a single generation

Mark R. Christie[a,1], Melanie L. Marine[a], Rod A. French[b], and Michael S. Blouin[a]

## Chinook

North American Journal of Fisheries Management 28:1472–1485, 2008 [Article]

Use of Parentage Analysis to Determine Reproductive Success of Hatchery-Origin Spring Chinook Salmon Outplanted into Shitike Creek, Oregon

JASON BAUMSTEIGER[1]
U.S. Fish and Wildlife Service
DAVID M. HAND* AND DOUGLAS E. OLSON
U.S. Fish and Wildlife Service
ROBERT SPATEHOLTS[2] AND GEOFF FITZGERALD[3]
Confederated Tribes of the Warm Springs Reservation of Oregon
WILLIAM R. ARDREN[4]
U.S. Fish and Wildlife Service

1840

**Factors influencing the relative fitness of hatchery and wild spring Chinook salmon (*Oncorhynchus tshawytscha*) in the Wenatchee River, Washington, USA**

Kevin S. Williamson, Andrew R. Murdoch, Todd N. Pearsons, Eric J. Ward, and Michael J. Ford

MOLECULAR ECOLOGY
Molecular Ecology (2012) 21, 5236–5250 doi: 10.1111/mec.12046

Supportive breeding boosts natural population abundance with minimal negative impacts on fitness of a wild population of Chinook salmon

MAUREEN A. HESS,* CRAIG D. RABE,† JASON L. VOGEL,‡ JEFF J. STEPHENSON,* DOUG D. NELSON† and SHAWN R. NARUM*

Evolutionary Applications
Evolutionary Applications ISSN 1752-4571

ORIGINAL ARTICLE

**Reproductive success of captively bred and naturally spawned Chinook salmon colonizing newly accessible habitat**

Joseph H. Anderson,[1,3,*] Paul L. Faulds,[2] William I. Atlas[1,4] and Thomas P. Quinn[1]

## Coho

2343

**Changes in run timing and natural smolt production in a naturally spawning coho salmon (*Oncorhynchus kisutch*) population after 60 years of intensive hatchery supplementation**

Michael J. Ford, Howard Fuss, Brant Boelts, Eric LaHood, Jeffrey Hard, and Jason Miller

MOLECULAR ECOLOGY
Molecular Ecology (2011) 20, 1860–1869 doi: 10.1111/j.1365-294X.2011.05058.x

Reduced reproductive success of hatchery coho salmon in the wild: insights into most likely mechanisms

VÉRONIQUE THÉRIAULT,* GREGORY R. MOYER,*[1] LAURA S. JACKSON,† MICHAEL S. BLOUIN‡ and MICHAEL A. BANKS*

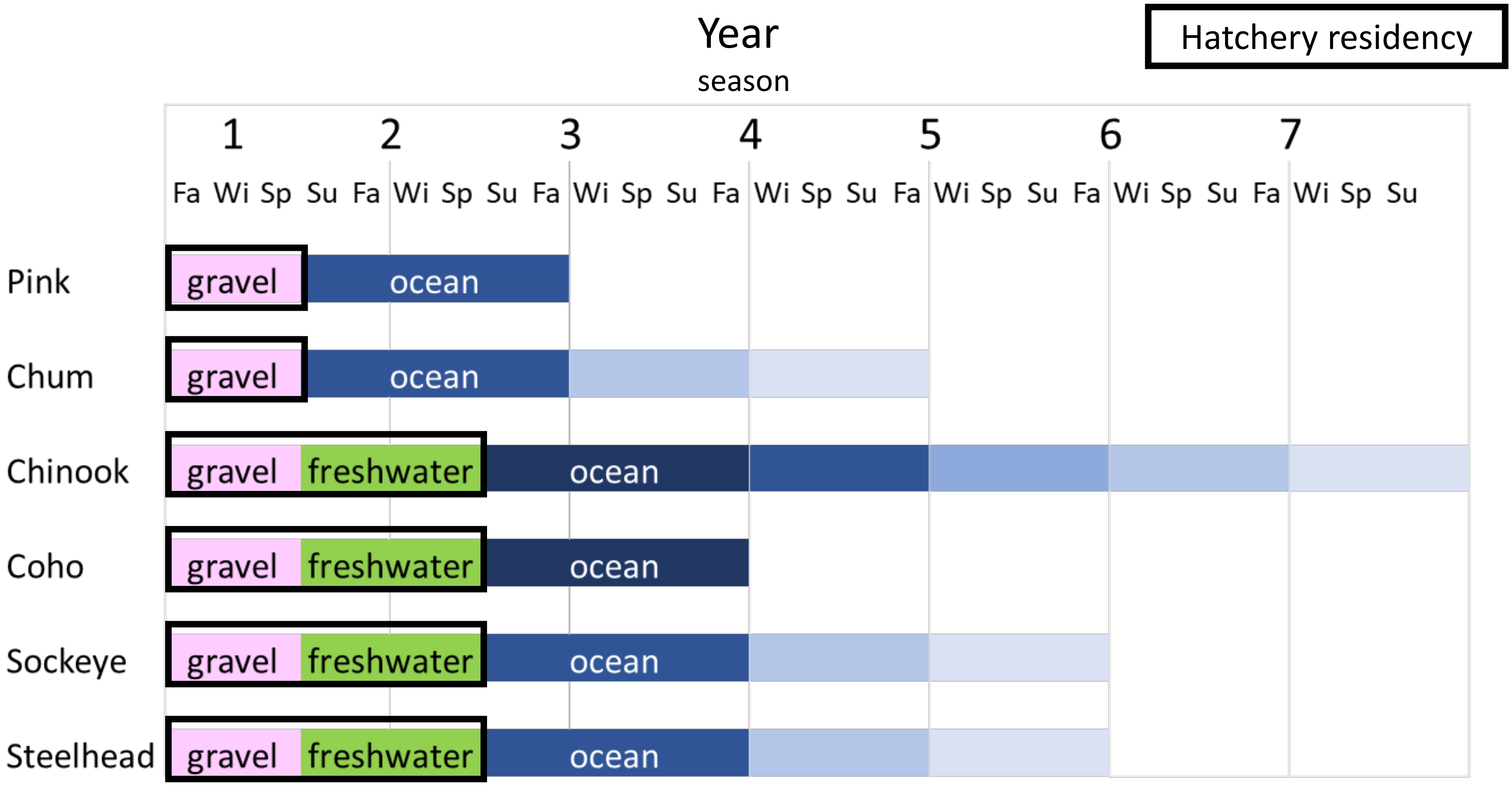
## Chum

781

**Reproductive behavior and relative reproductive success of natural- and hatchery-origin Hood Canal summer chum salmon (*Oncorhynchus keta*)**

Barry A. Berejikian, Donald M. Van Doornik, Julie A. Scheurer, and Richard Bush

# Hatchery/Natural Fitness



# AHRP Streams in PWS

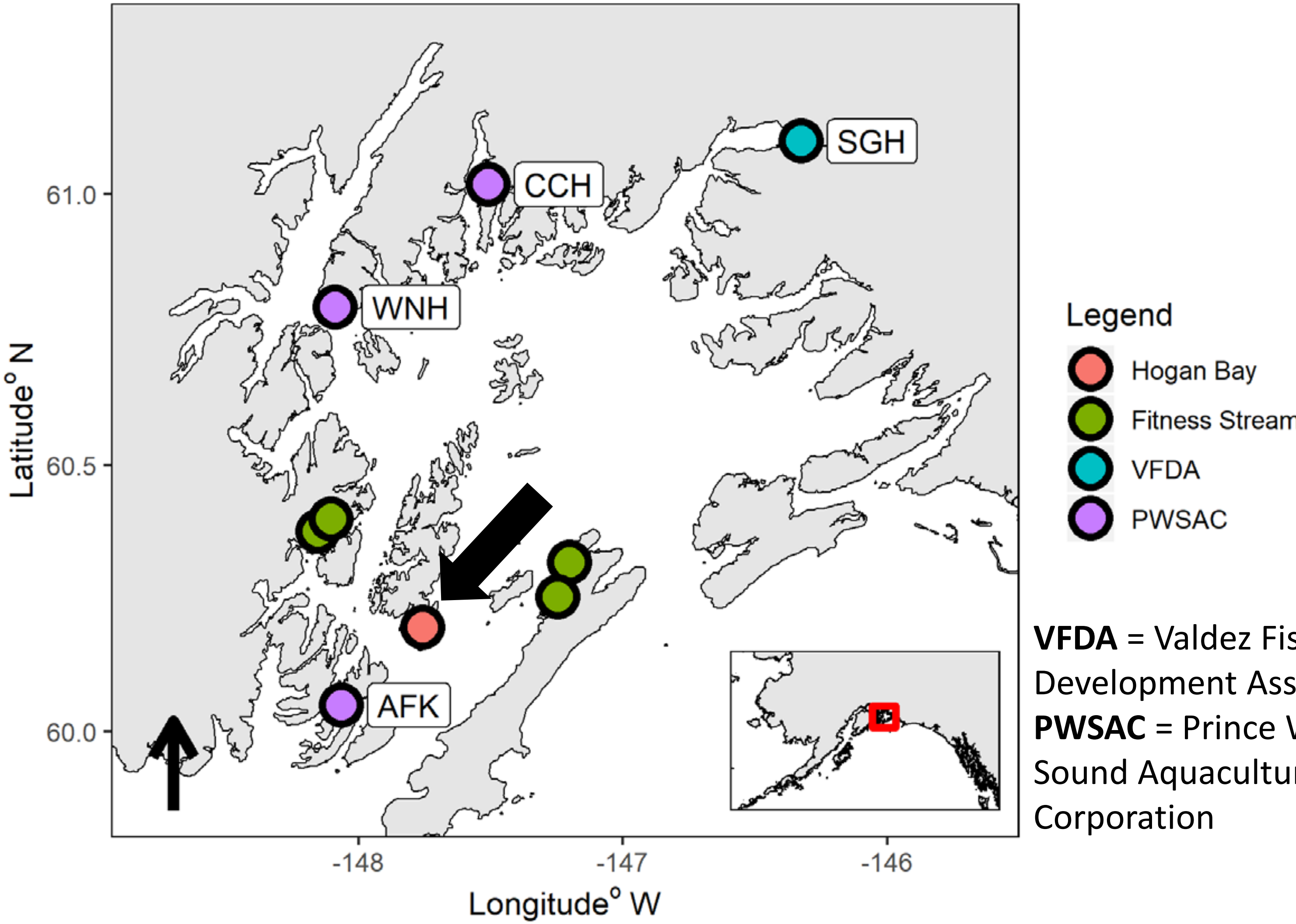



Figure 1 – Lescak et al. *in prep*

**VFDA** = Valdez Fisheries Development Association
**PWSAC** = Prince William Sound Aquaculture Corporation

# Fitness = Reproductive Success

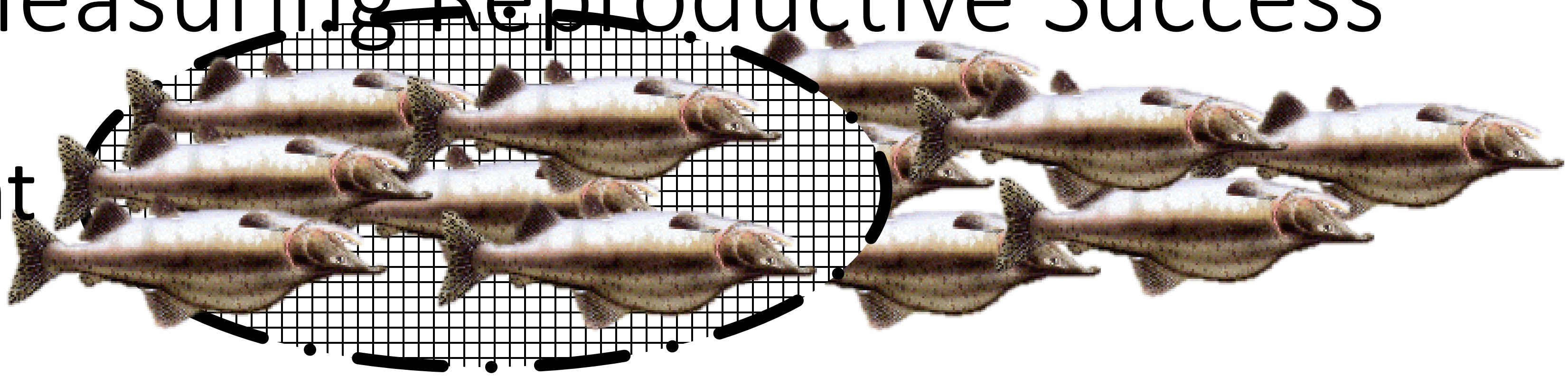
Parent

# Measuring Reproductive Success

Parent

# Measuring Reproductive Success

Parent

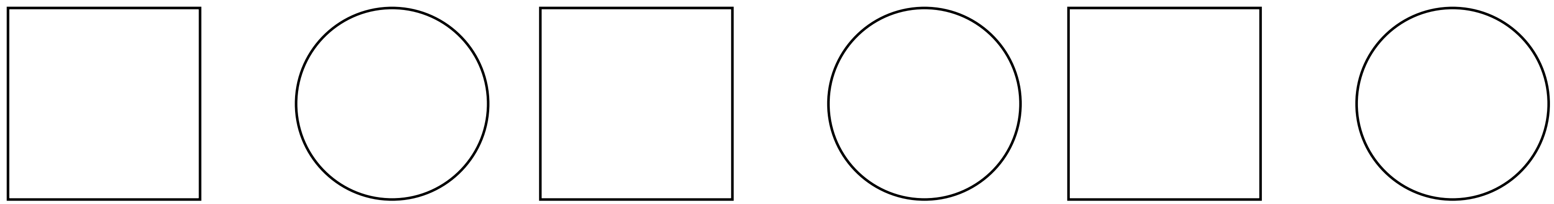


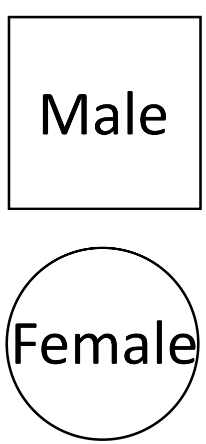
# Measuring Reproductive Success

Parent

# Measuring Reproductive Success

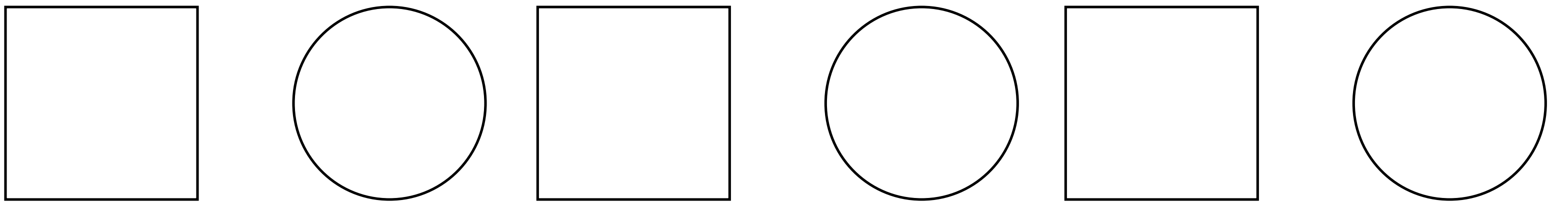
P





# Measuring Reproductive Success

P

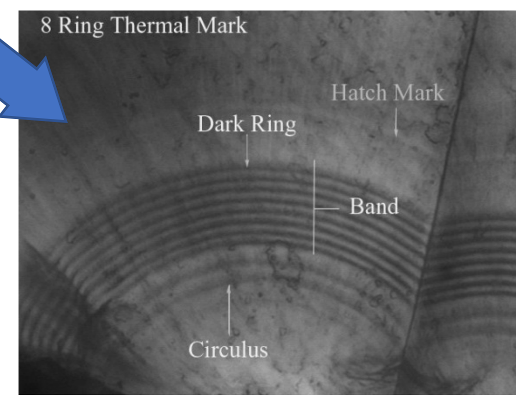


Male

Female

# Measuring Reproductive Success

P

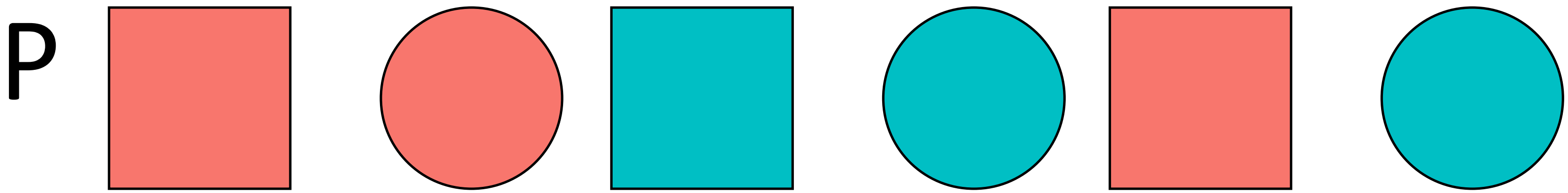


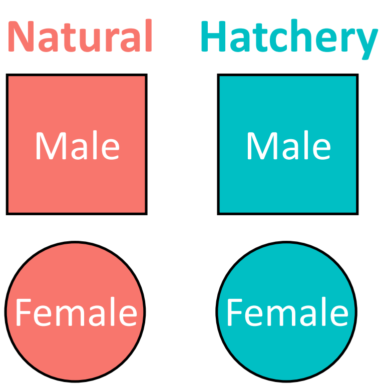

Hatchery-origin

Male

Female

# Measuring Reproductive Success



# Measuring Reproductive Success

P

O

**Natural** | **Hatchery**

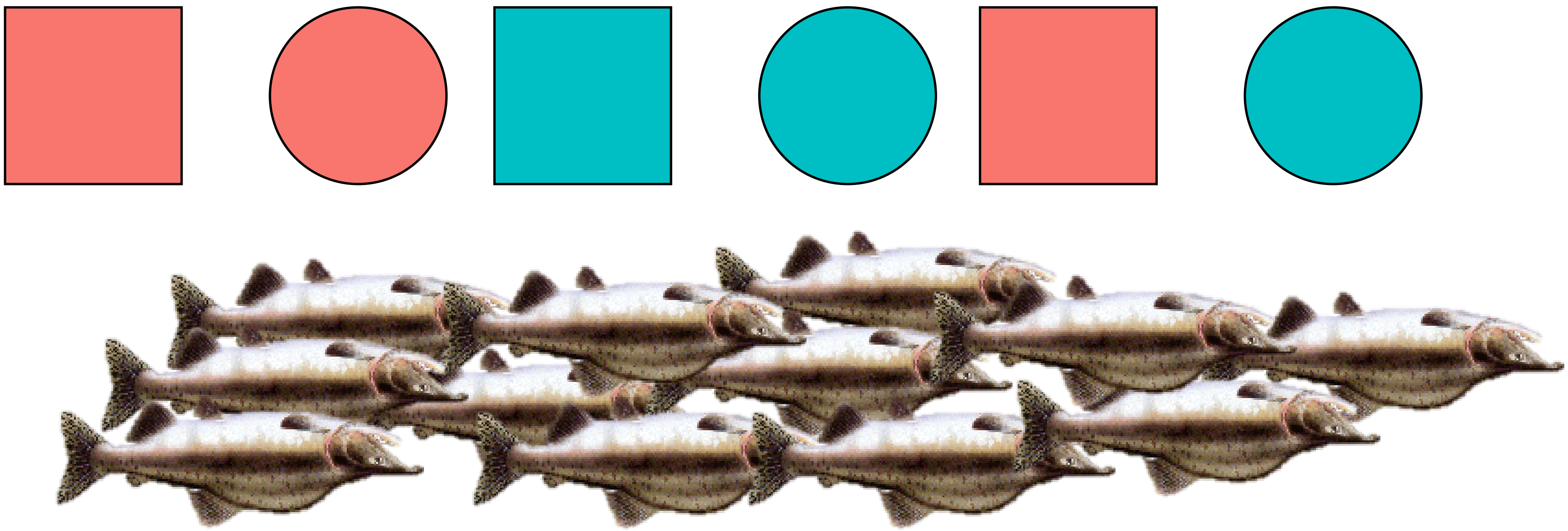
Male | Male

Female | Female

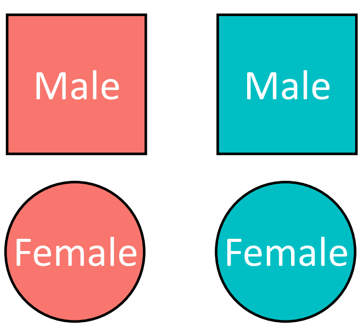
# Measuring Reproductive Success

P

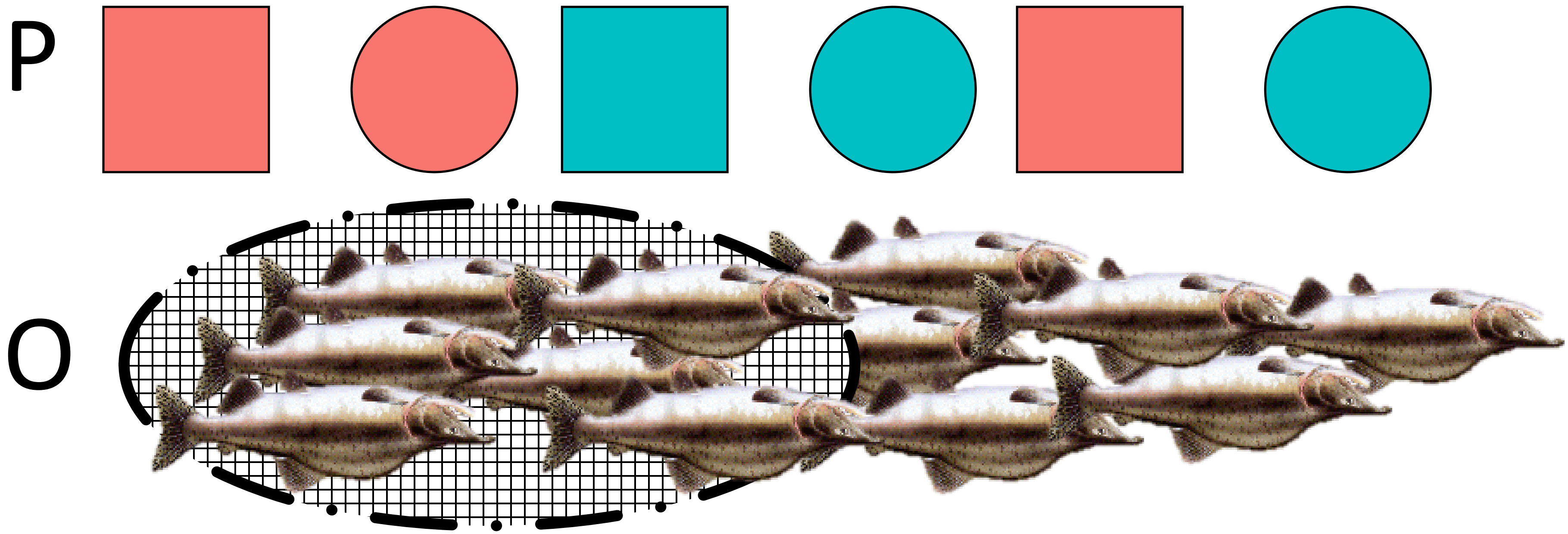
O



Natural Hatchery



# Measuring Reproductive Success

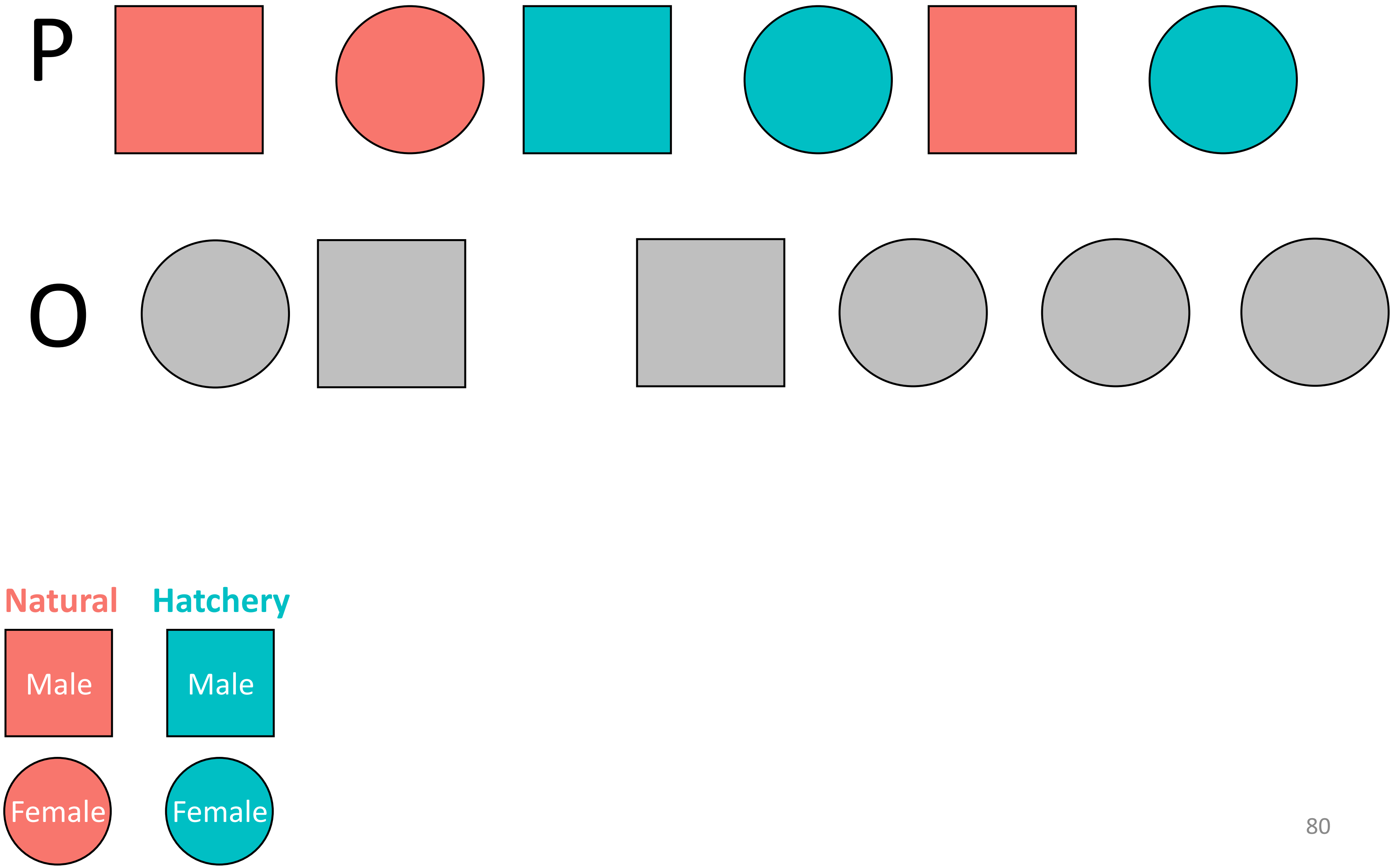



Natural Hatchery

Male Male

Female Female

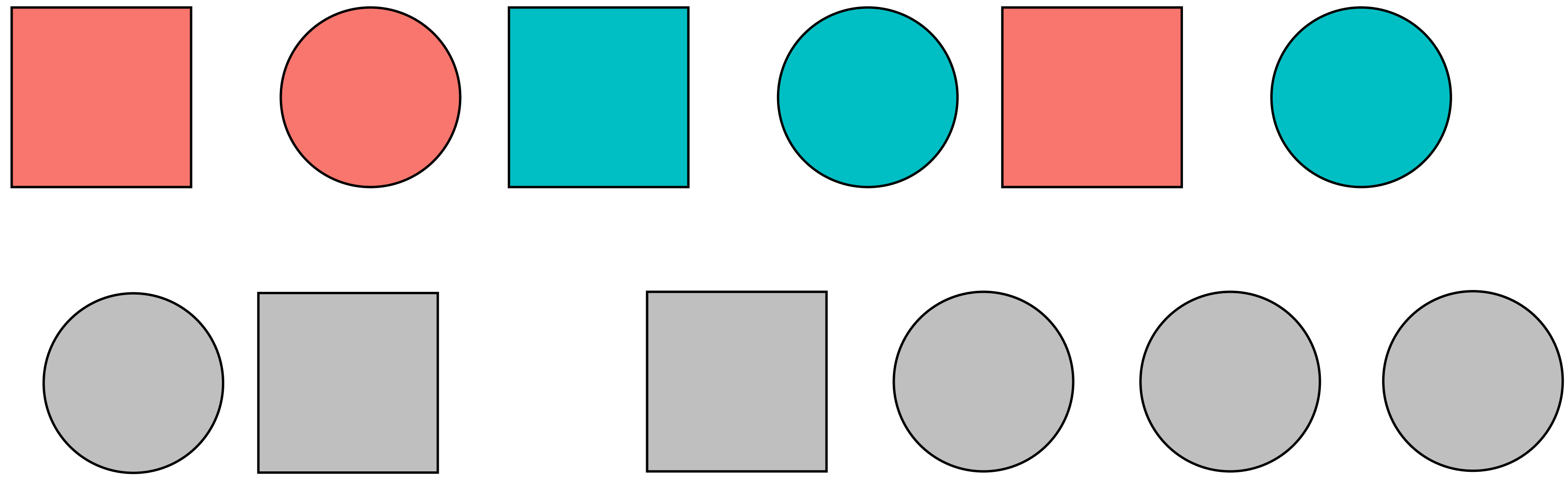
# Measuring Reproductive Success

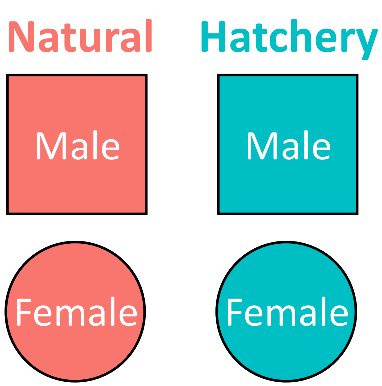


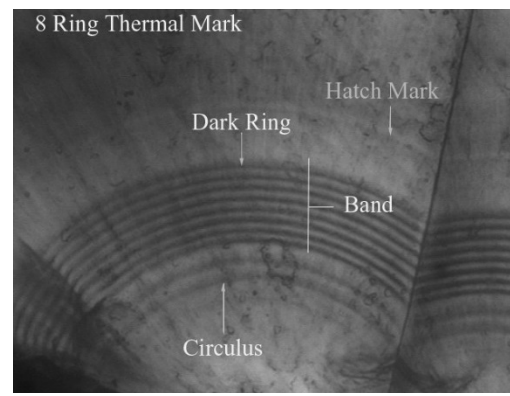
# Measuring Reproductive Success

P

O

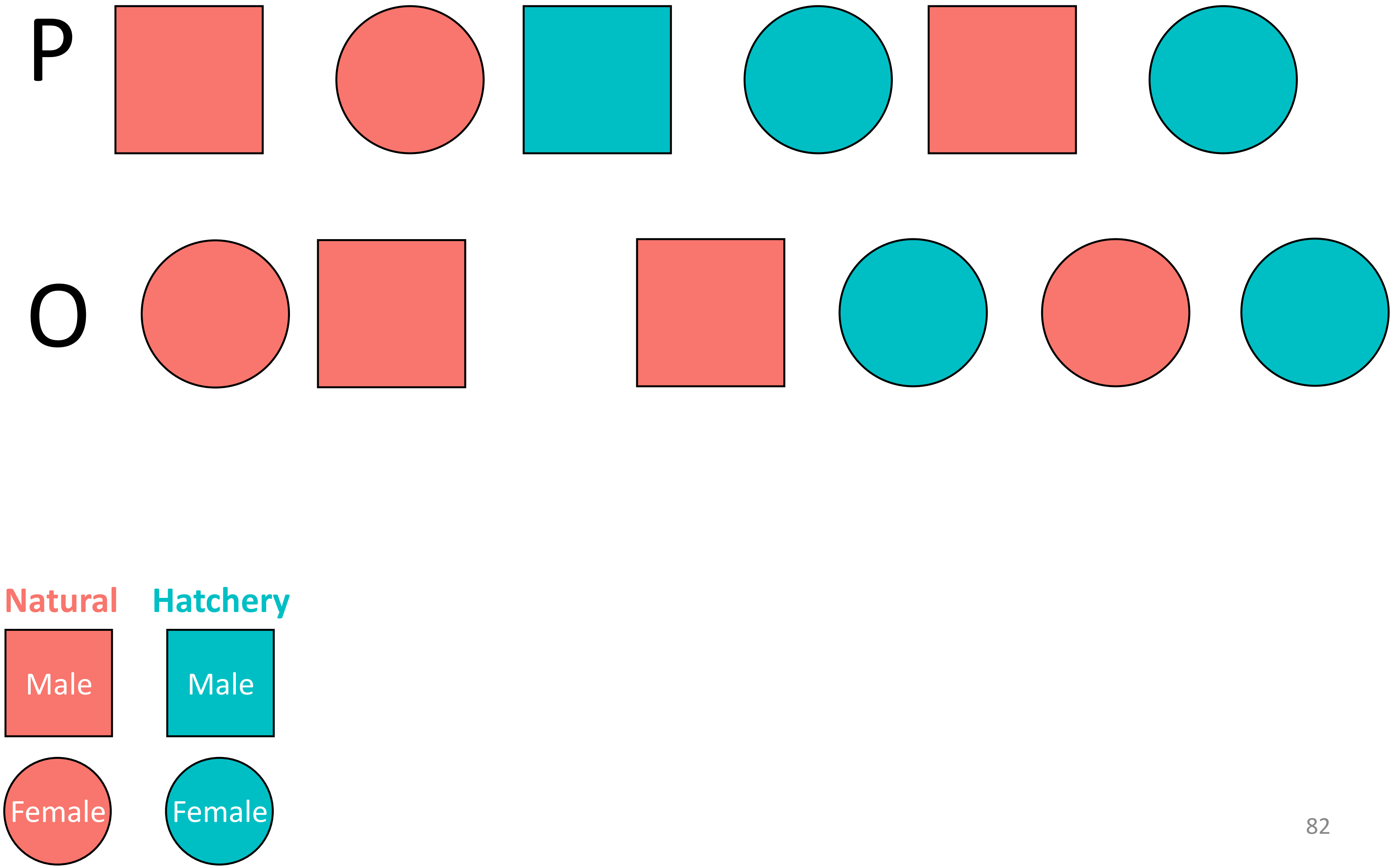


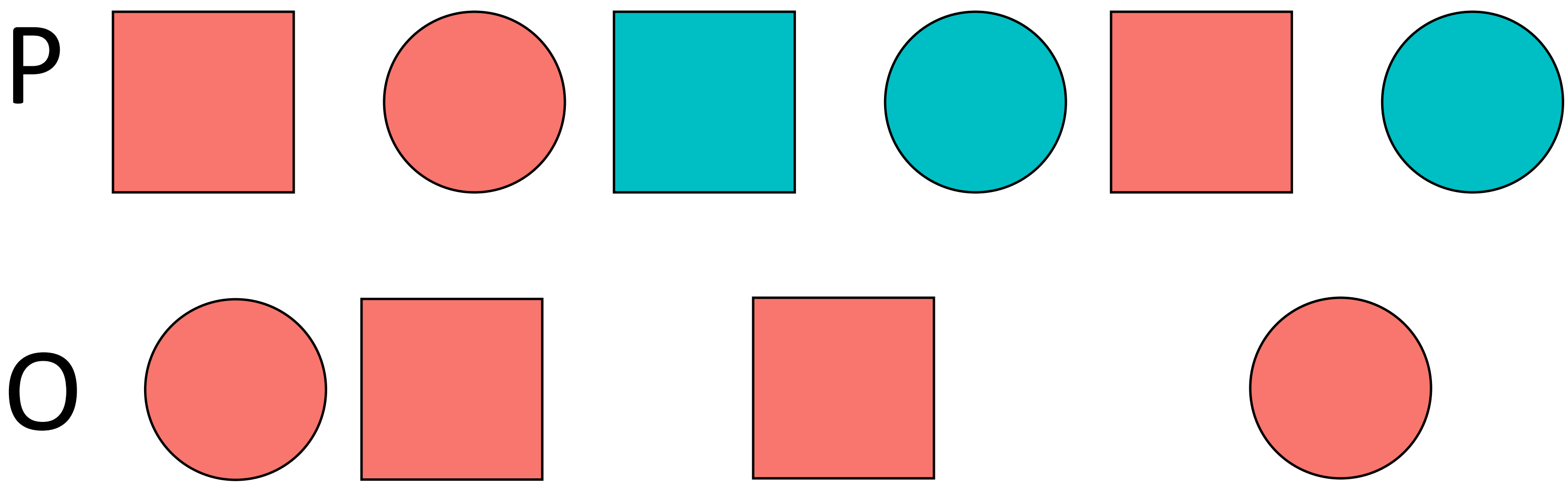



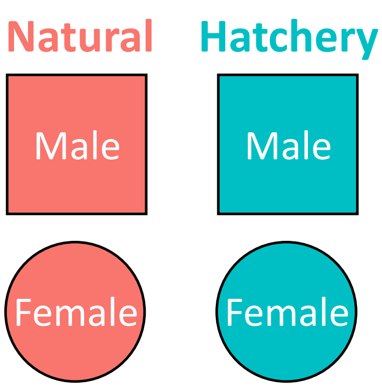

Hatchery-origin

# Measuring Reproductive Success



# Measuring Reproductive Success



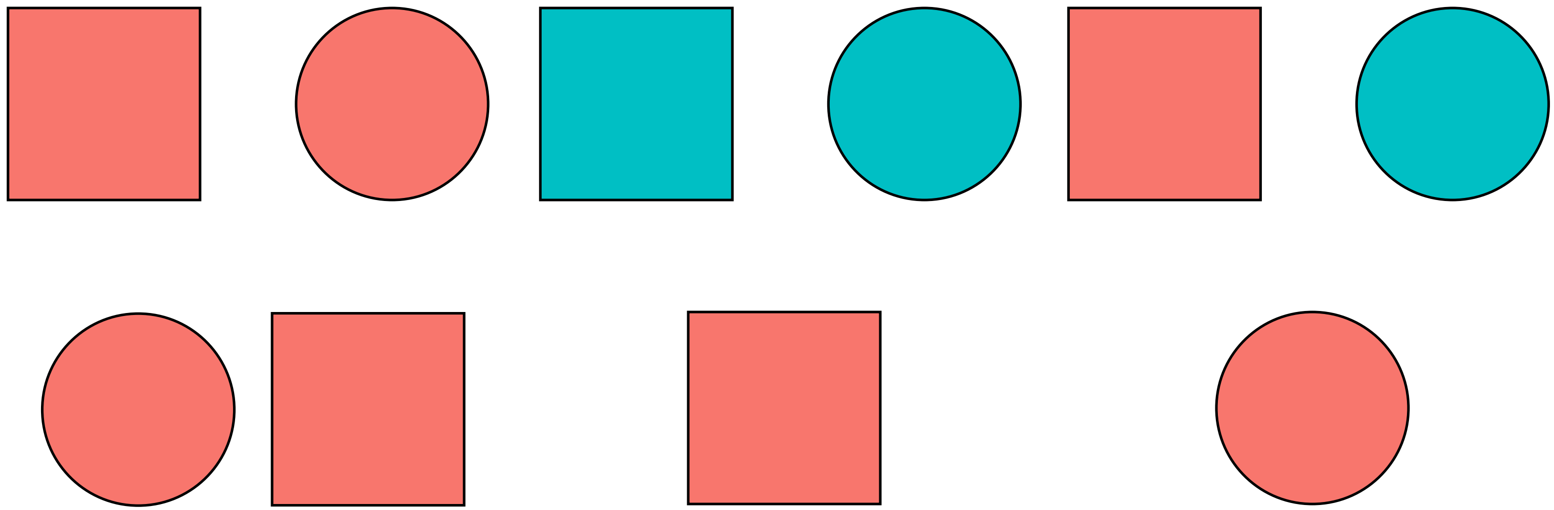



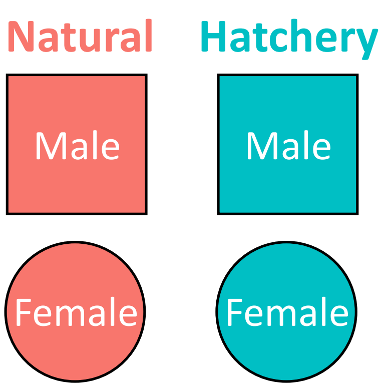

Hatchery-origin fish are not genotyped in the offspring generation because they have a known origin.

# Measuring Reproductive Success

P

O






298 markers

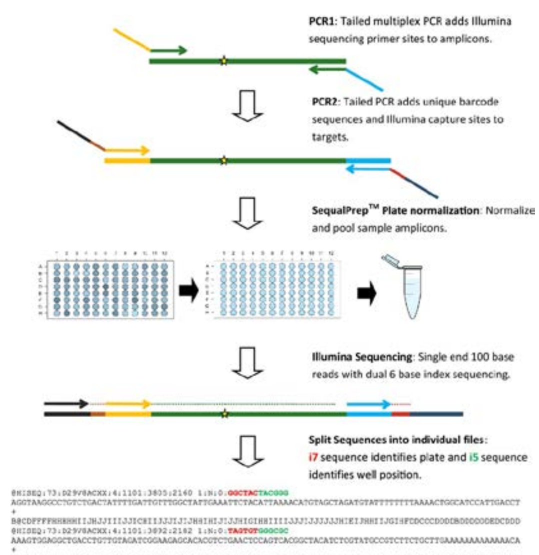
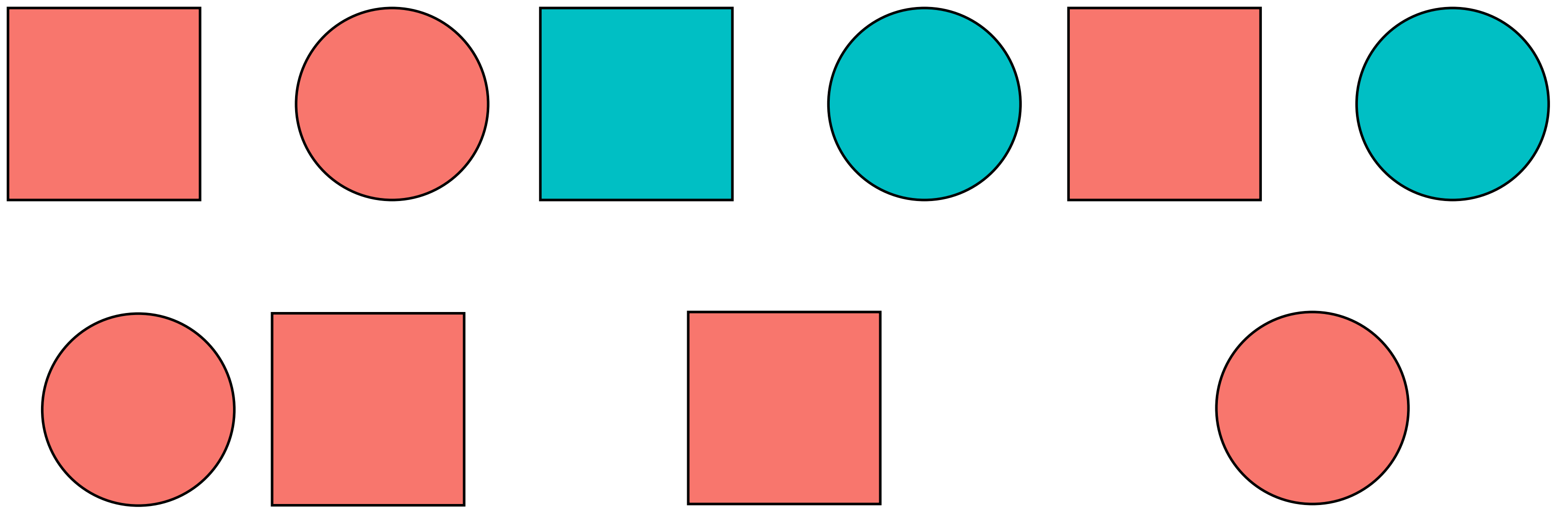


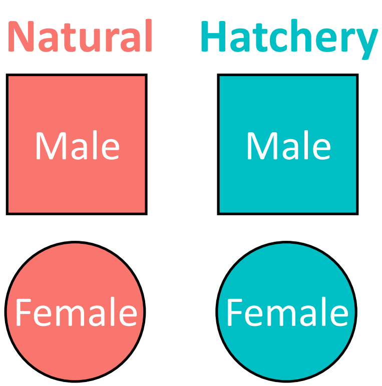

Figure 1 – Campbell et al. 2015

# Measuring Reproductive Success

P

O






298 markers

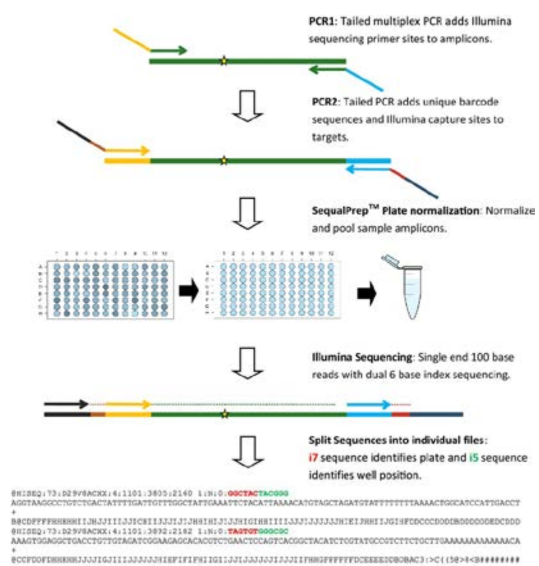


Figure 1 – Campbell et al. 2015

Riester et al. 2009

# Genetic markers for parentage analysis


CTATGTATTAAATGTTAATAATAATAACTAGCTAACC — ***T** allele*
CTATGTAATAAATGTTAATAATAATAACTAGCTAACC — ***A** allele*


CTATGTAATAAATGTTAATAATAATAACTAGCTAACC — ***A** allele*
CTATGTAATAAATGTTAATAATAATAACTAGCTAACC — ***A** allele*


CTATGTAATAAATGTTAATAATAATAACTAGCTAACC — ***A** allele*
CTATGTATTAAATGTTAATAATAATAACTAGCTAACC — ***T** allele*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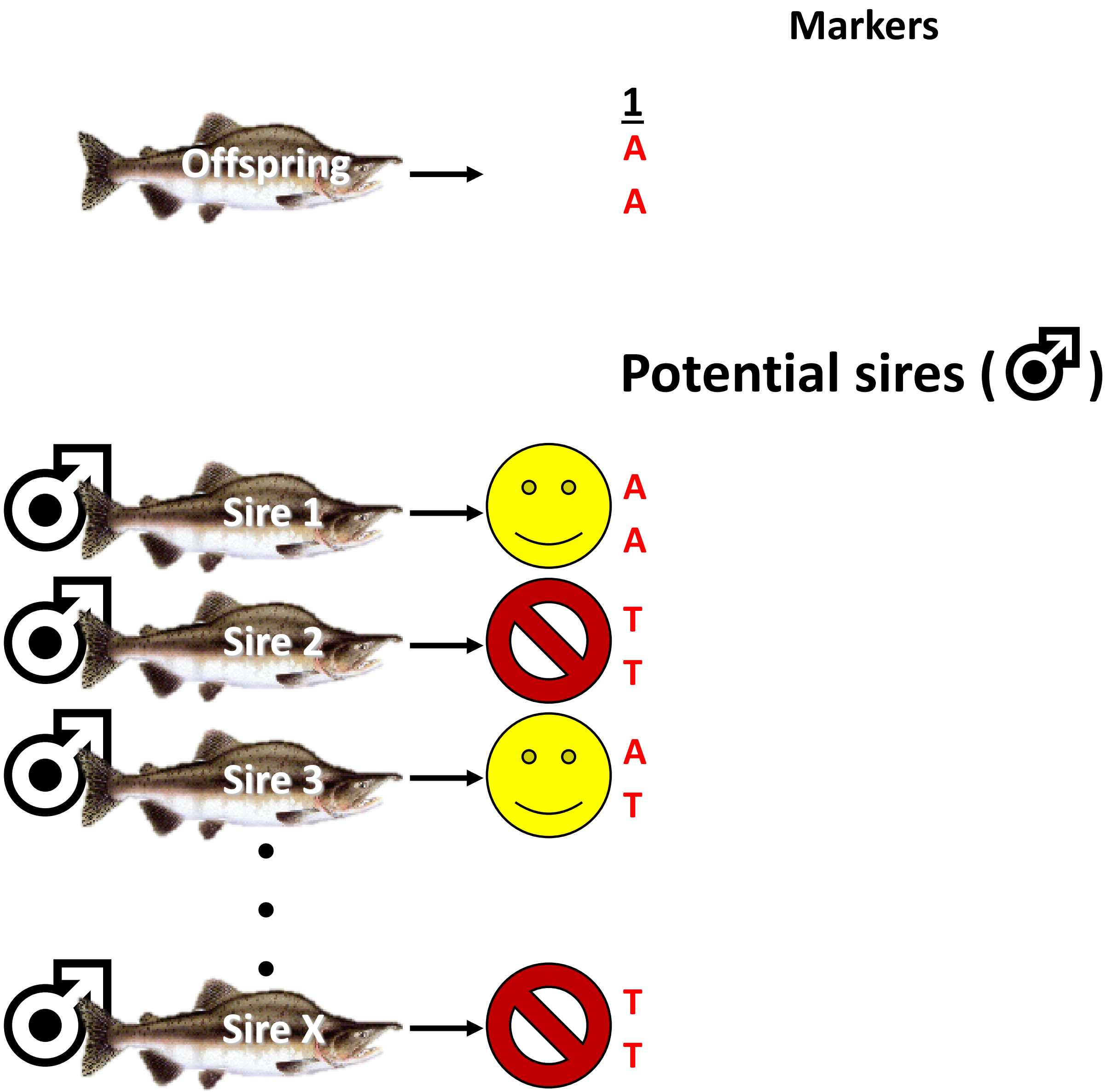
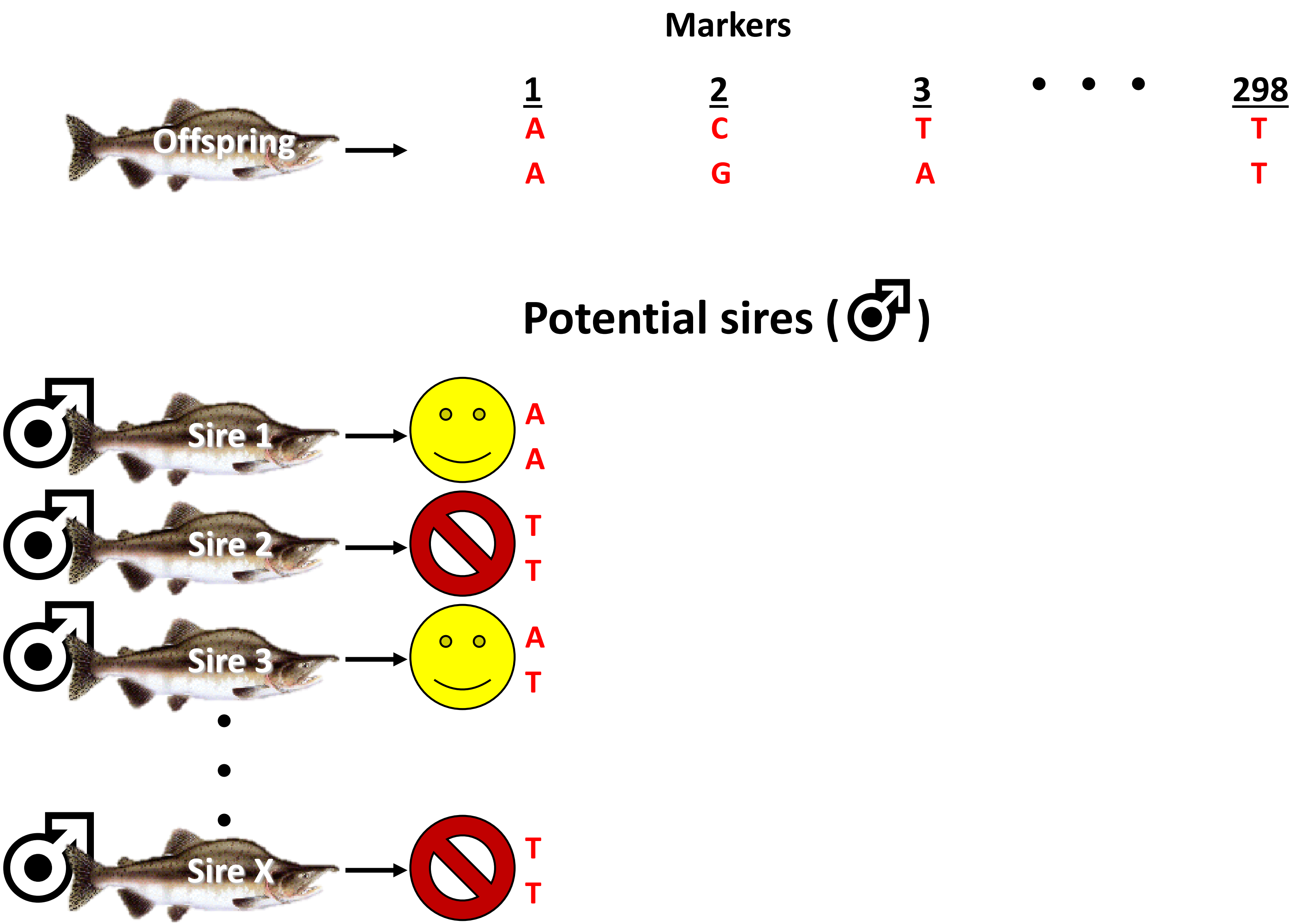
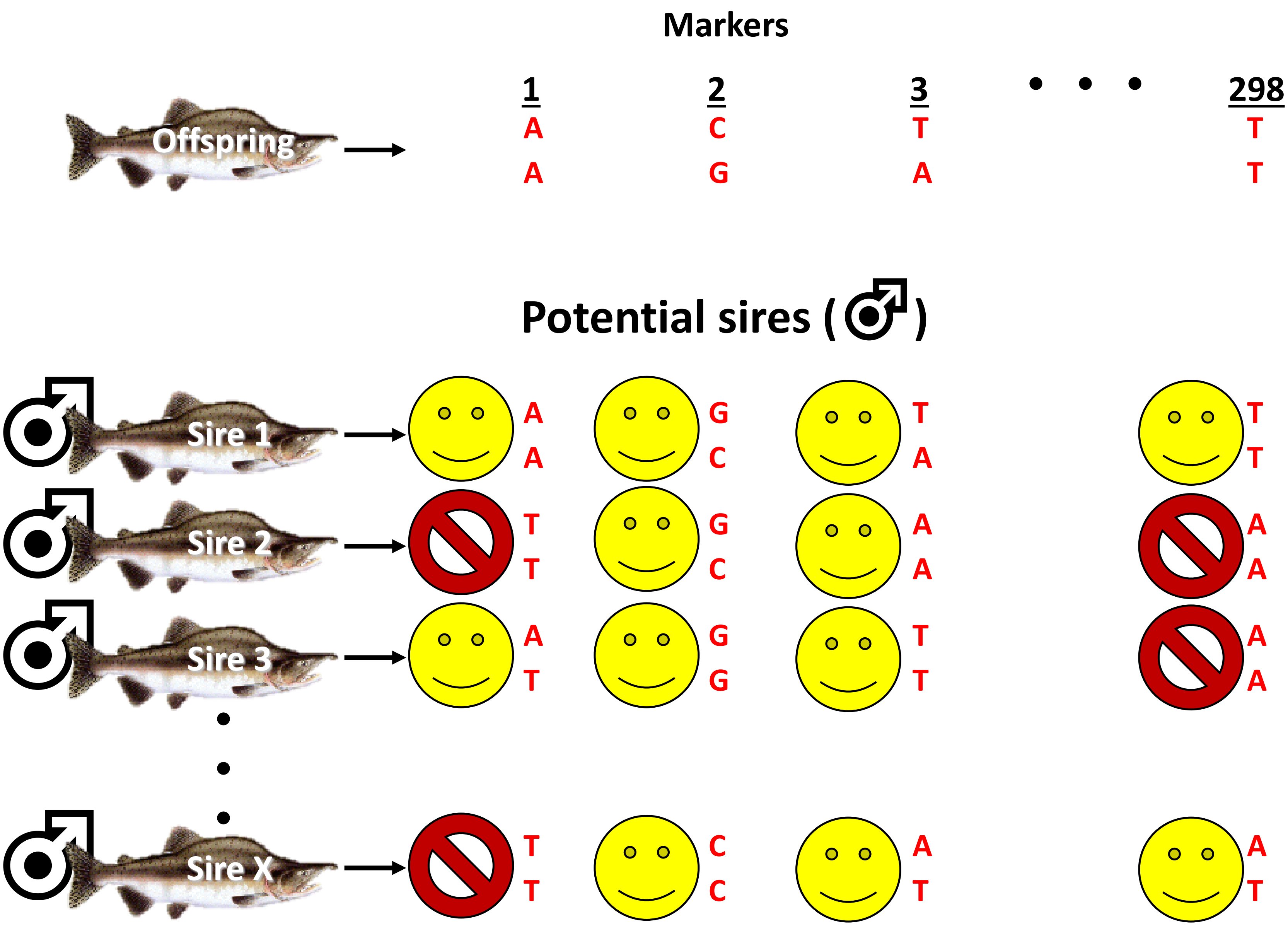
# Genetic markers for parentage analysis



# Genetic markers for parentage analysis



# Genetic markers for parentage analysis



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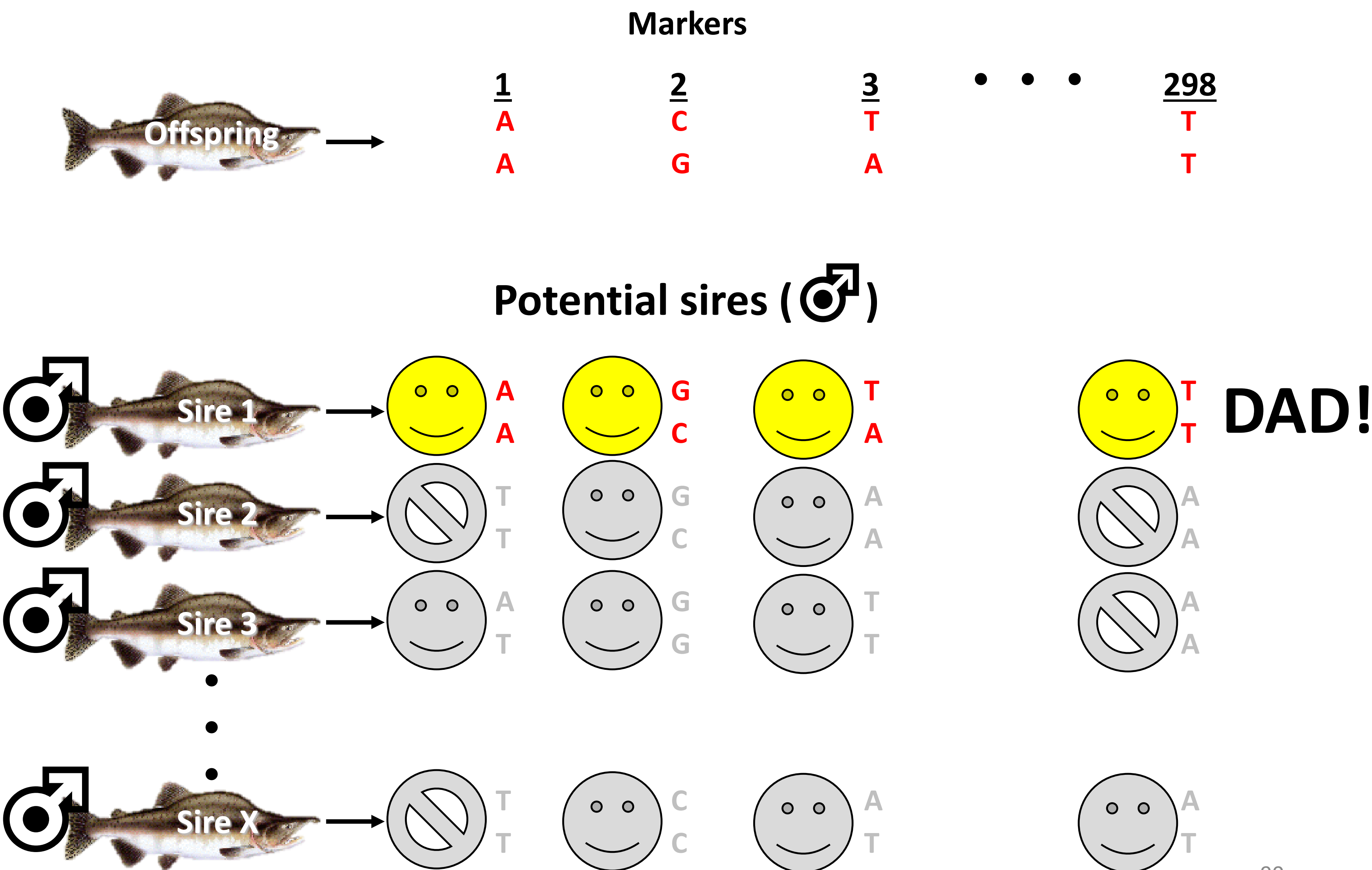
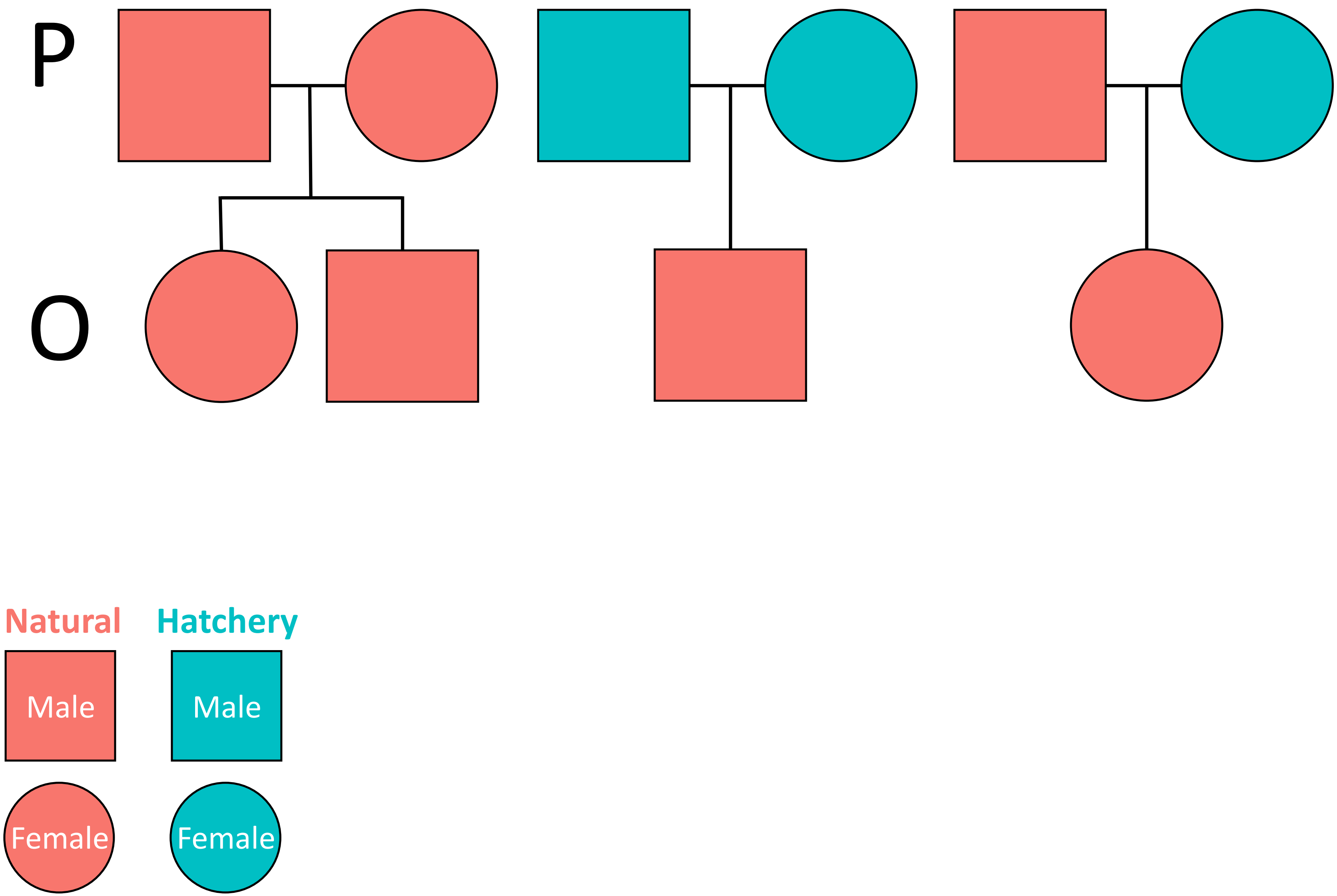
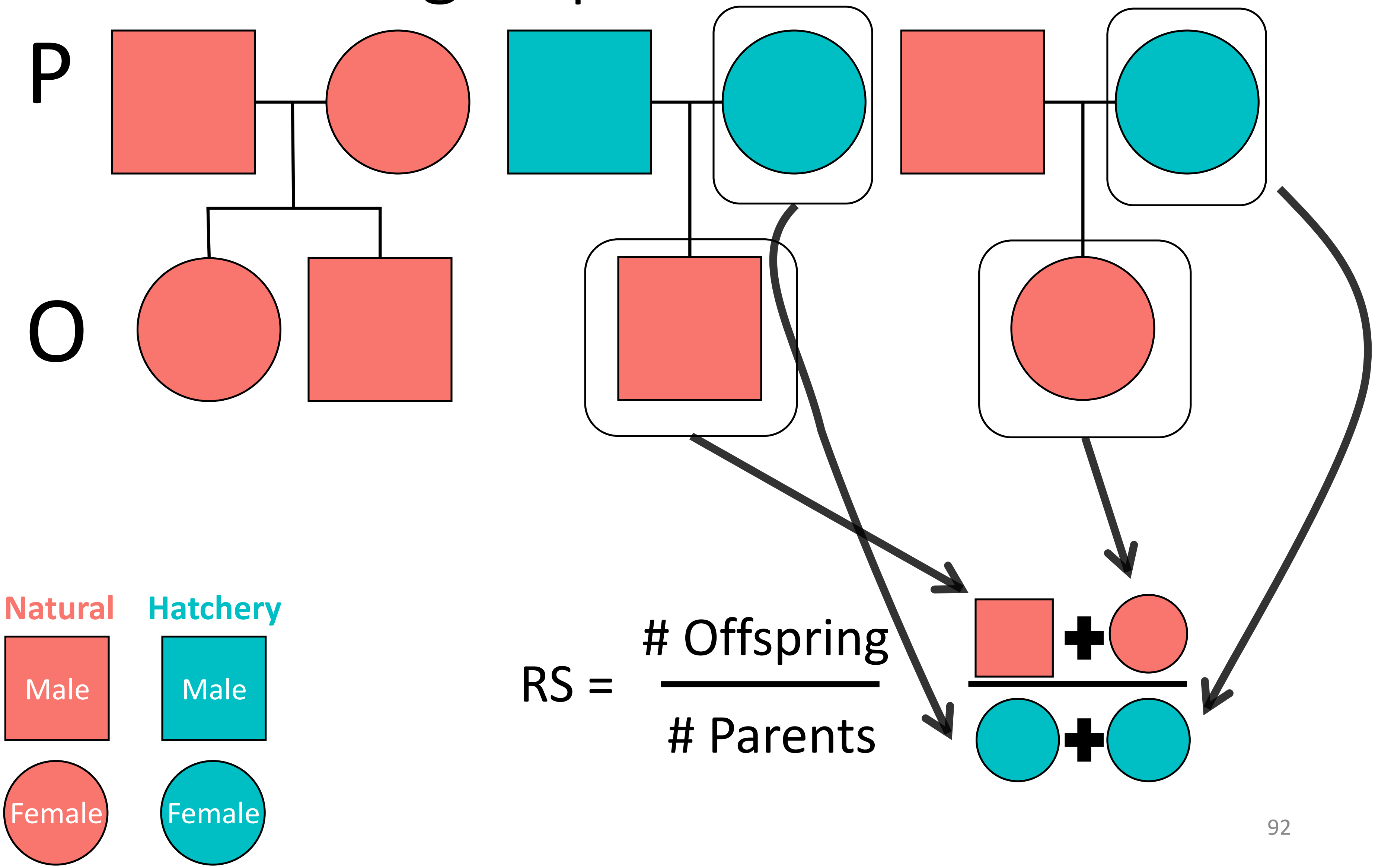


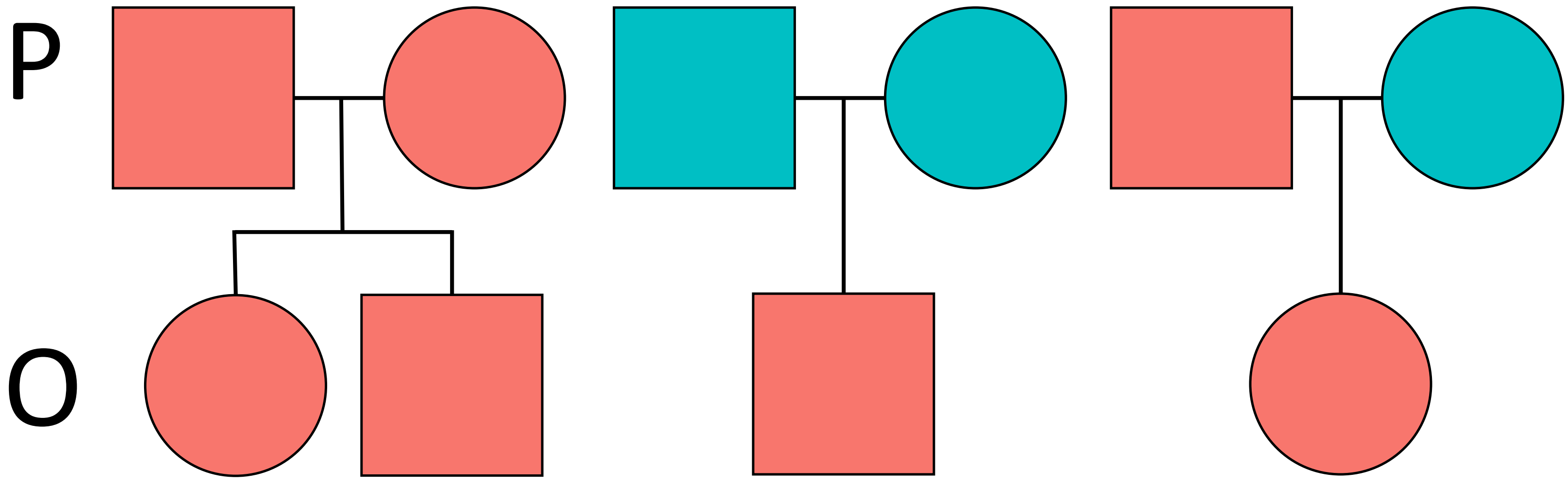
# Measuring Reproductive Success



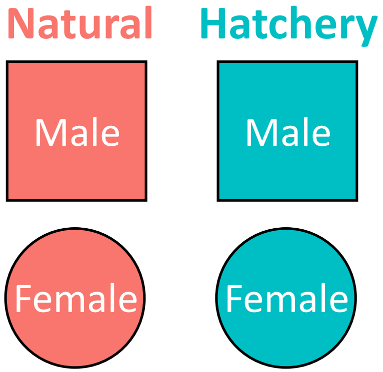
# Measuring Reproductive Success



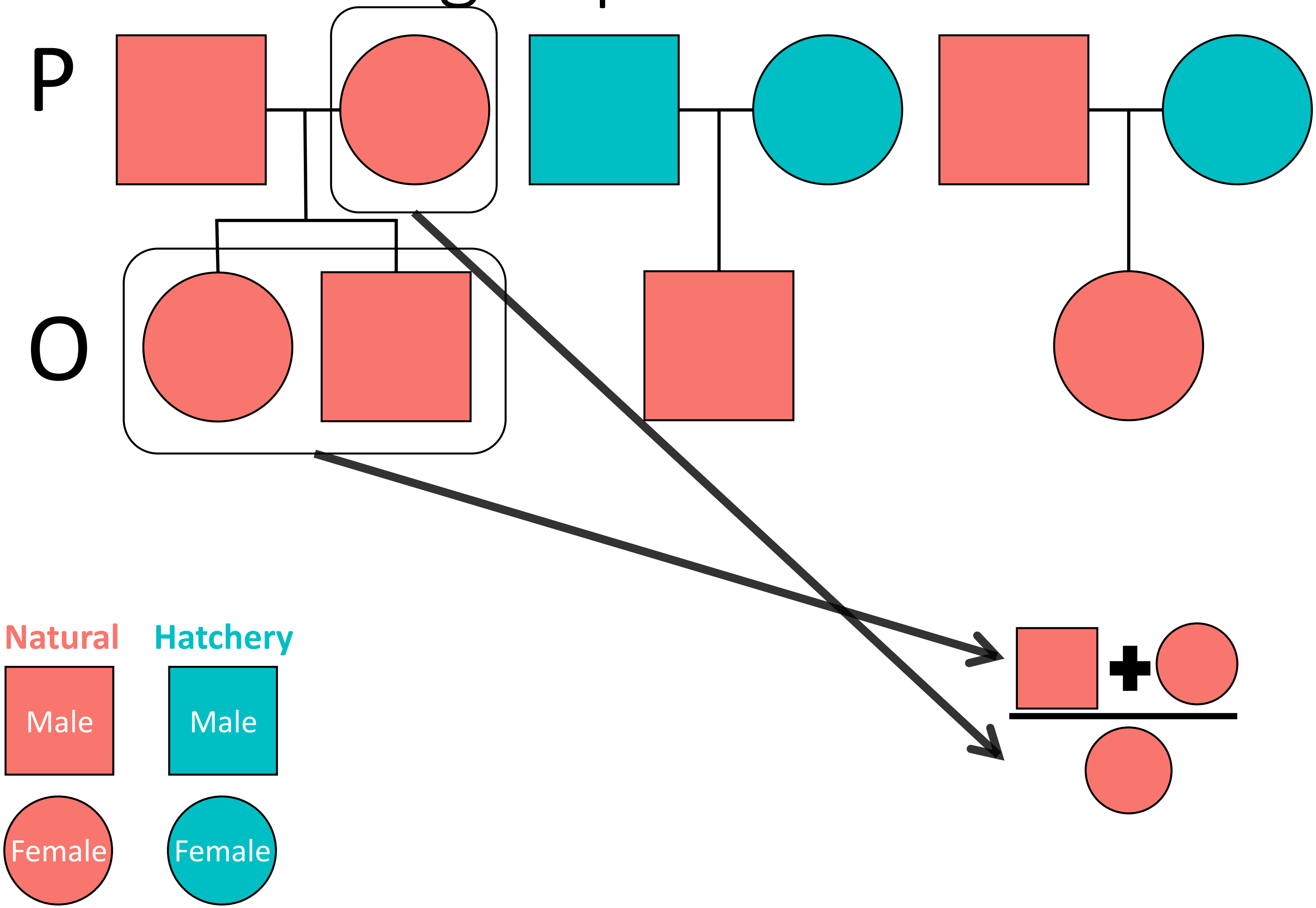
# Measuring Reproductive Success



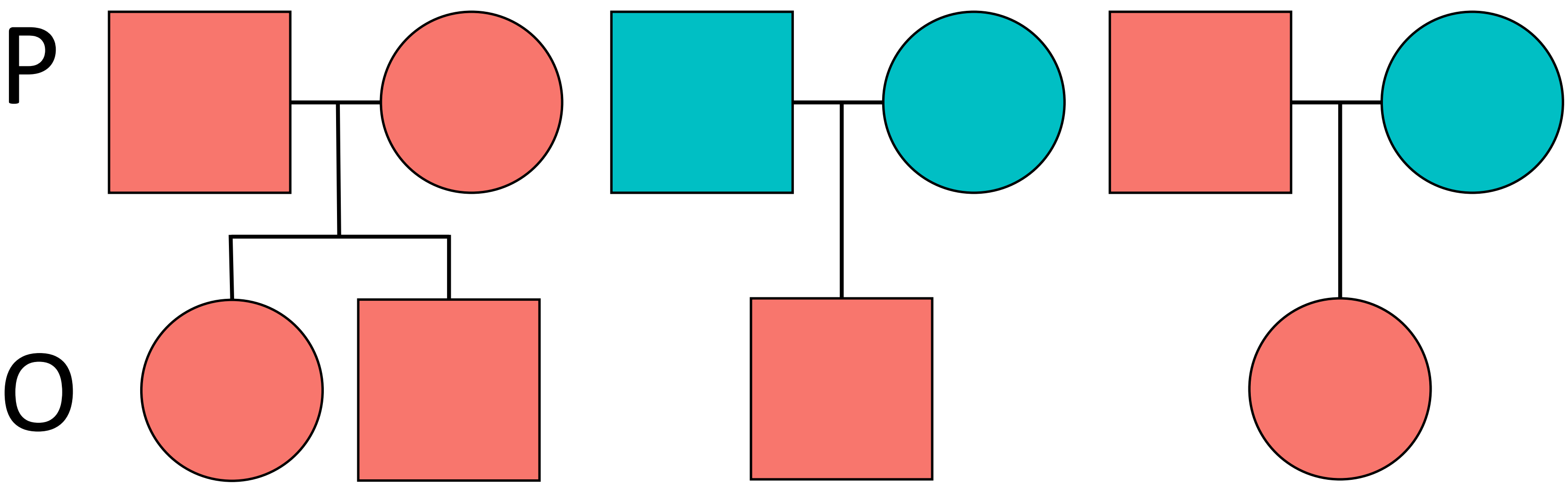

$RS_{H\ Female} = 1$



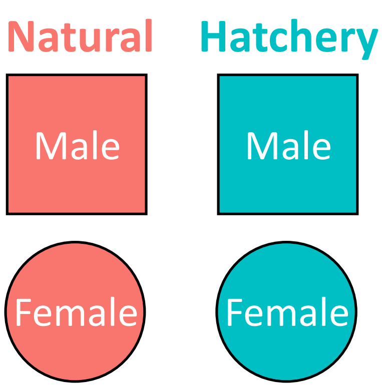
# Measuring Reproductive Success



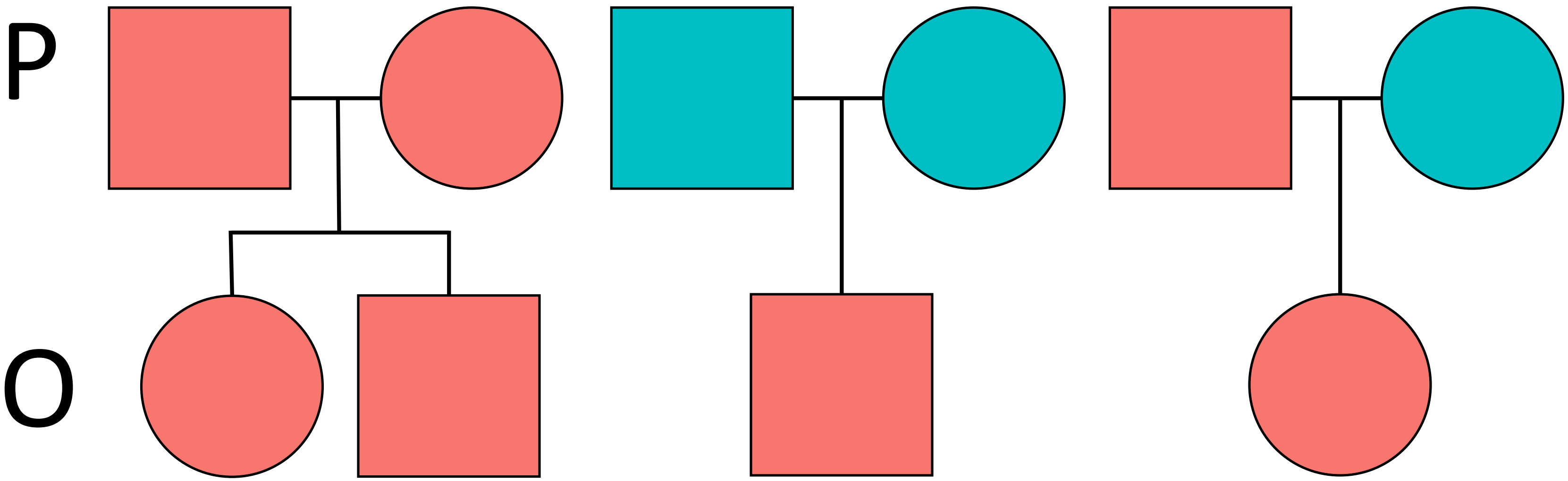
# Measuring Reproductive Success



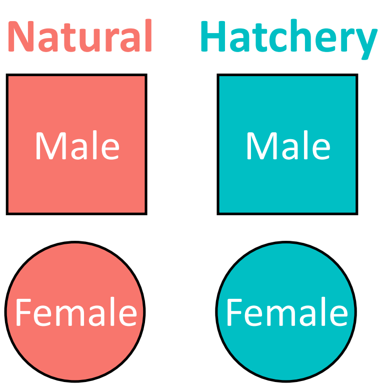

$RS_{N\ Female} = 2$     $RS_{H\ Female} = 1$



# Measuring Reproductive Success



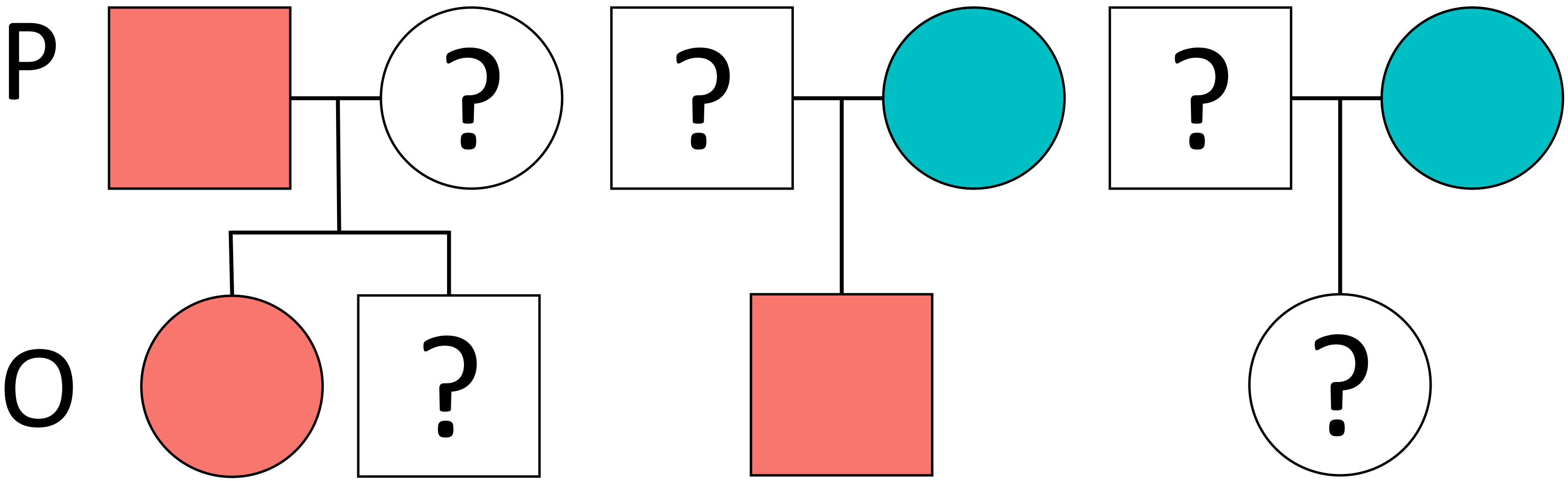

$RS_{N\ Female} = 2$ $\quad$ $RS_{H\ Female} = 1$

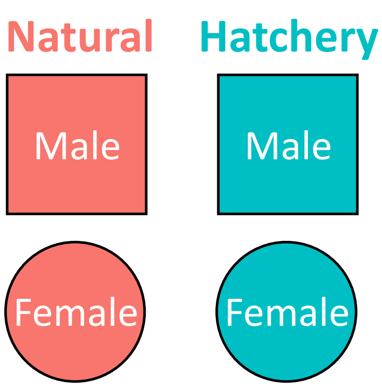



Relative Reproductive Success (RRS)

$$\mathbf{RRS} = \frac{1}{2} = \mathbf{0.5}$$

# Measuring Reproductive Success




Relative Reproductive Success (RRS)

$$RRS = \frac{\overline{RS}_{Hatchery}}{\overline{RS}_{Natural}}$$

# Analyzed Samples: Even-Lineage

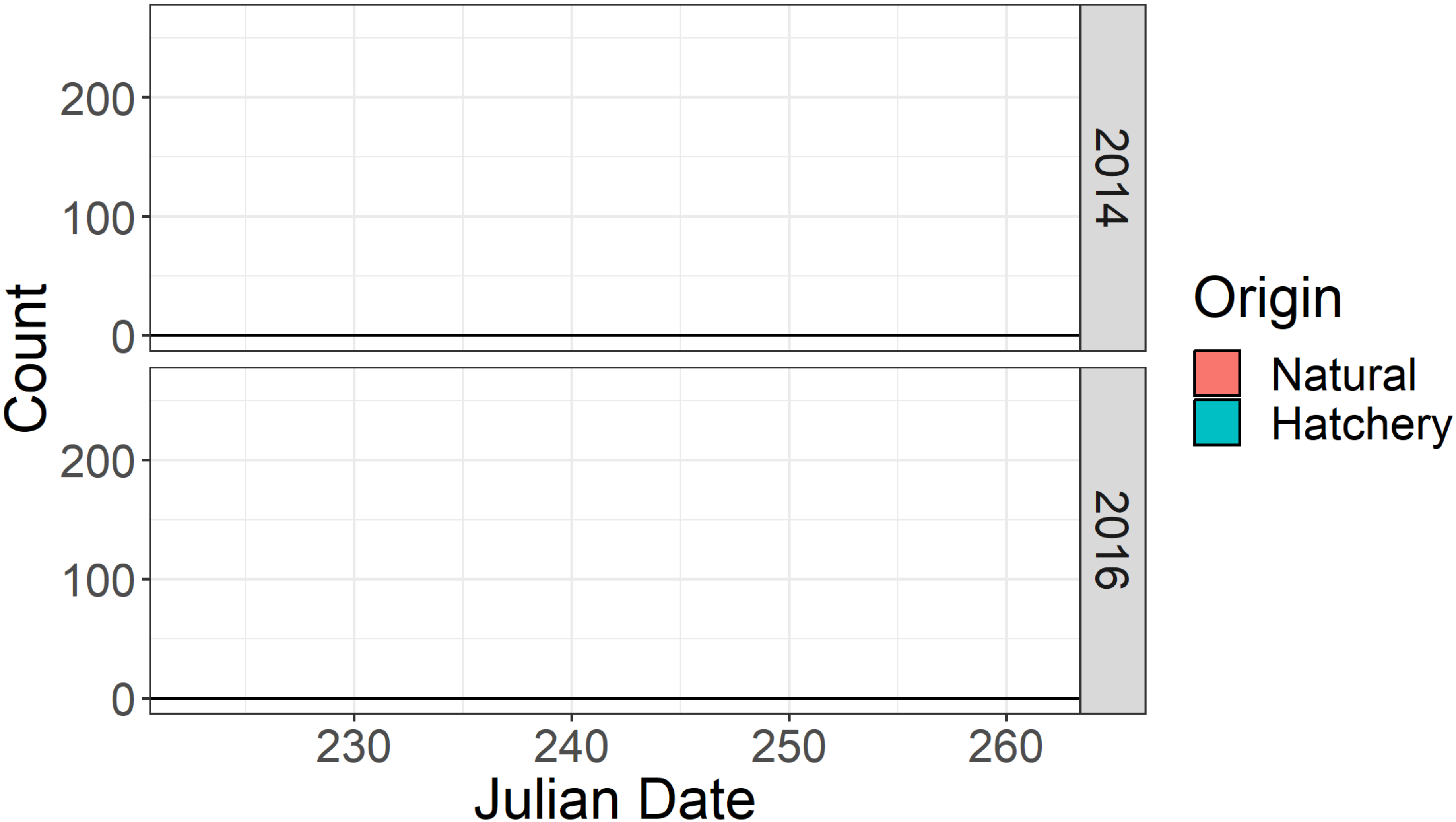



Figure 2b – Lescak et al. *in prep*

# Analyzed Samples: Even-Lineage

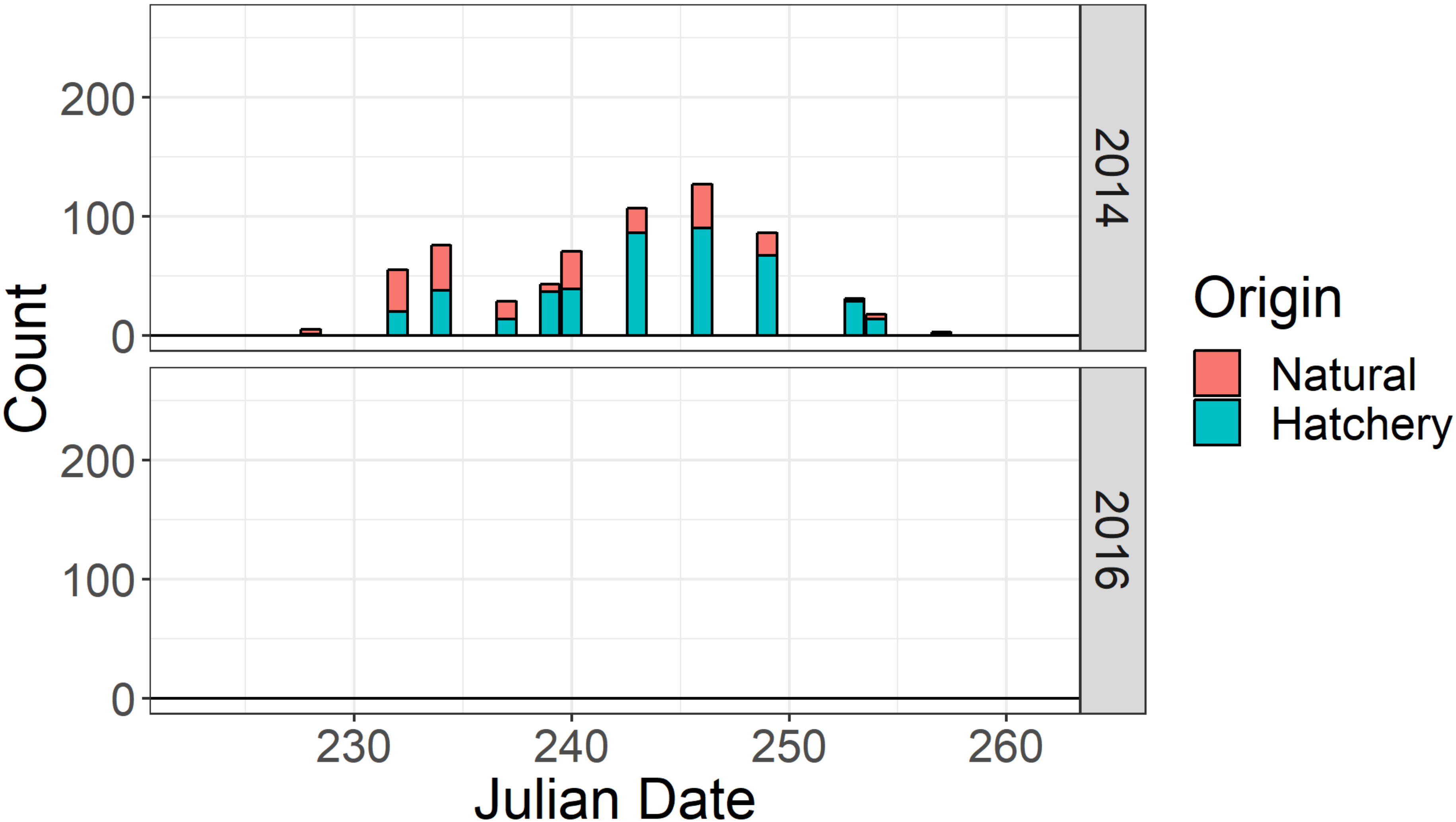



Figure 2b – Lescak et al. *in prep*

# Analyzed Samples: Even-Lineage

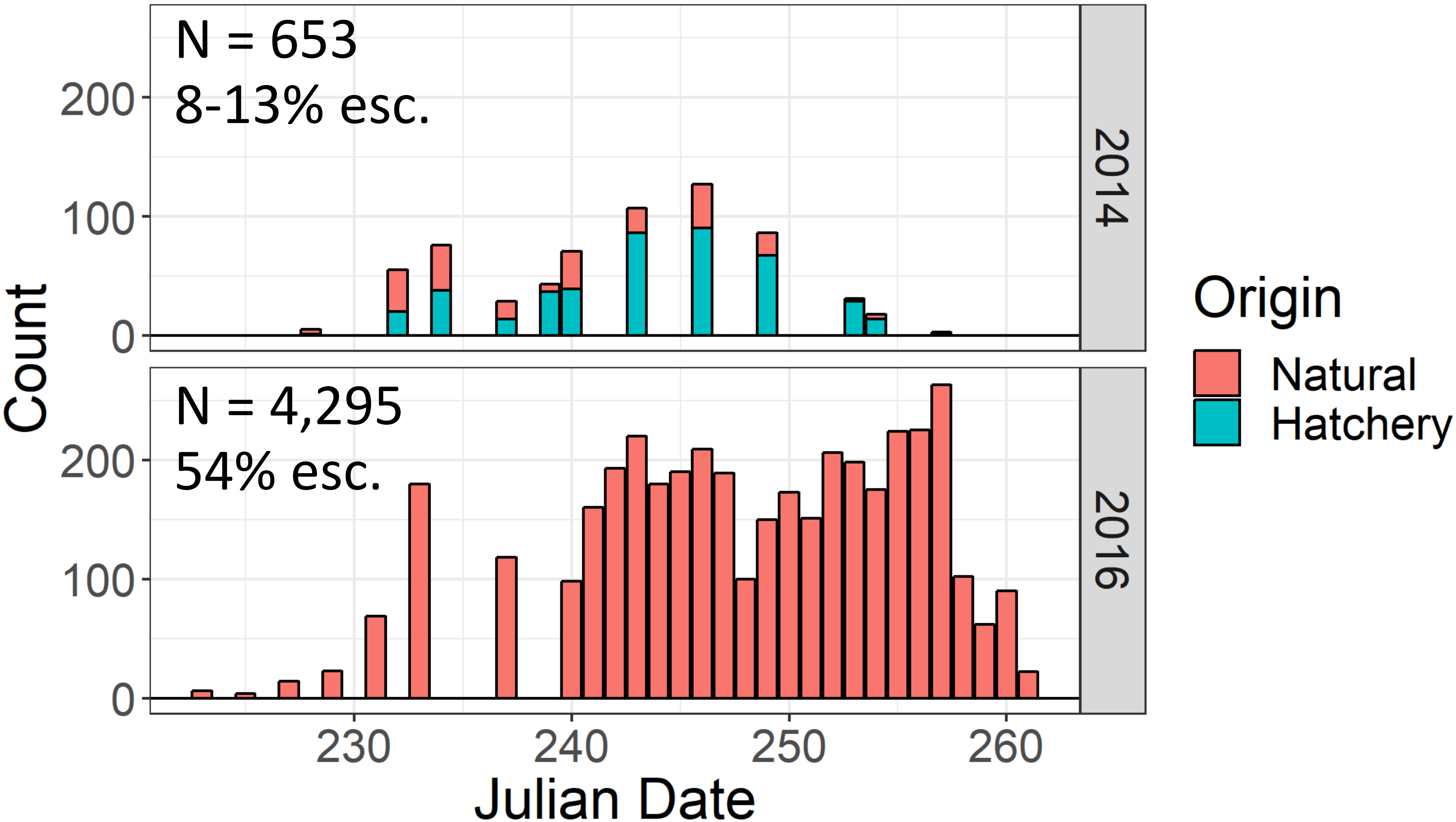



Figure 2b – Lescak et al. *in prep*

# Pedigree Results: Even-Lineage

- 451 offspring (11%) assigned to 184 parents
  - 208 → natural-origin parents
  - 265 → hatchery-origin parents
    - 202 – AF
    - 41 – WN
    - 22 – CCH
    - 0 – SGH

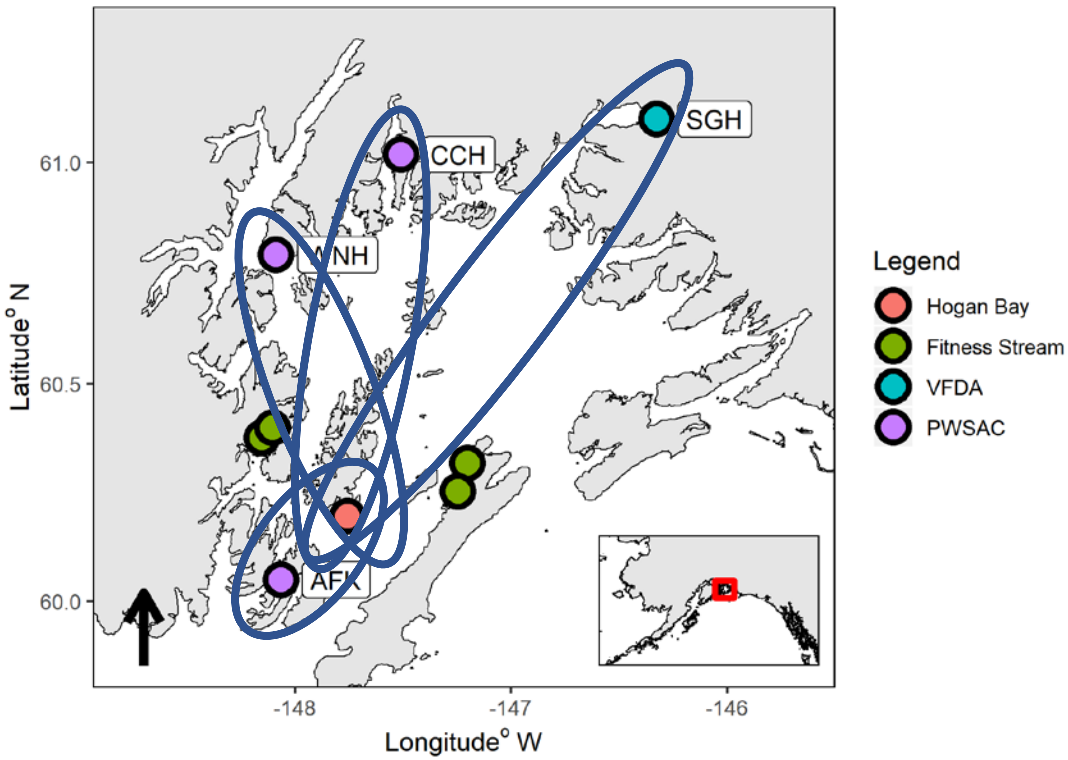



Figure 1 – Lescak et al. *in prep*

# RS Distribution: Even-Lineage

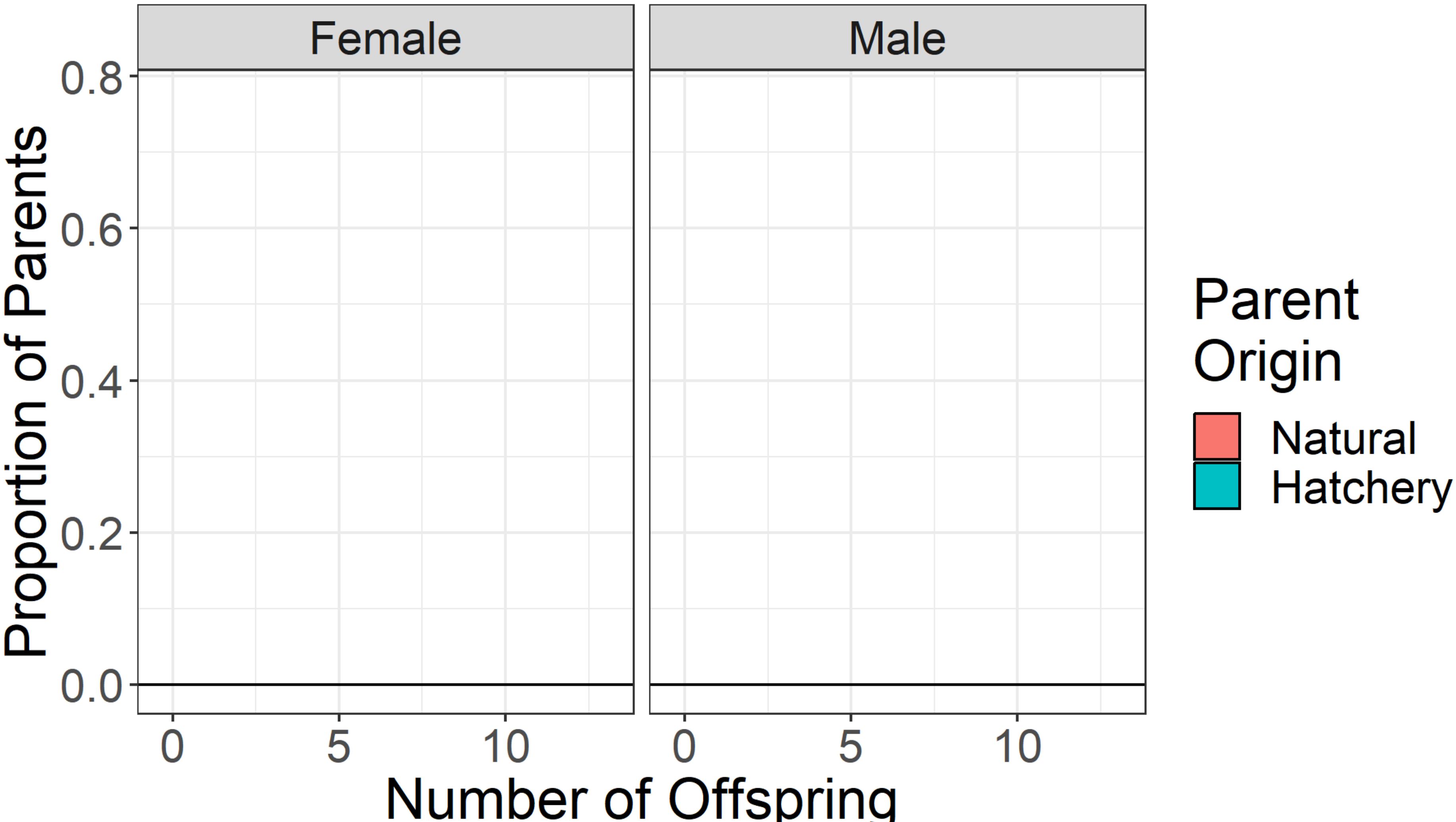



Figure 3b – Lescak et al. *in prep*

# RS Distribution: Even-Lineage

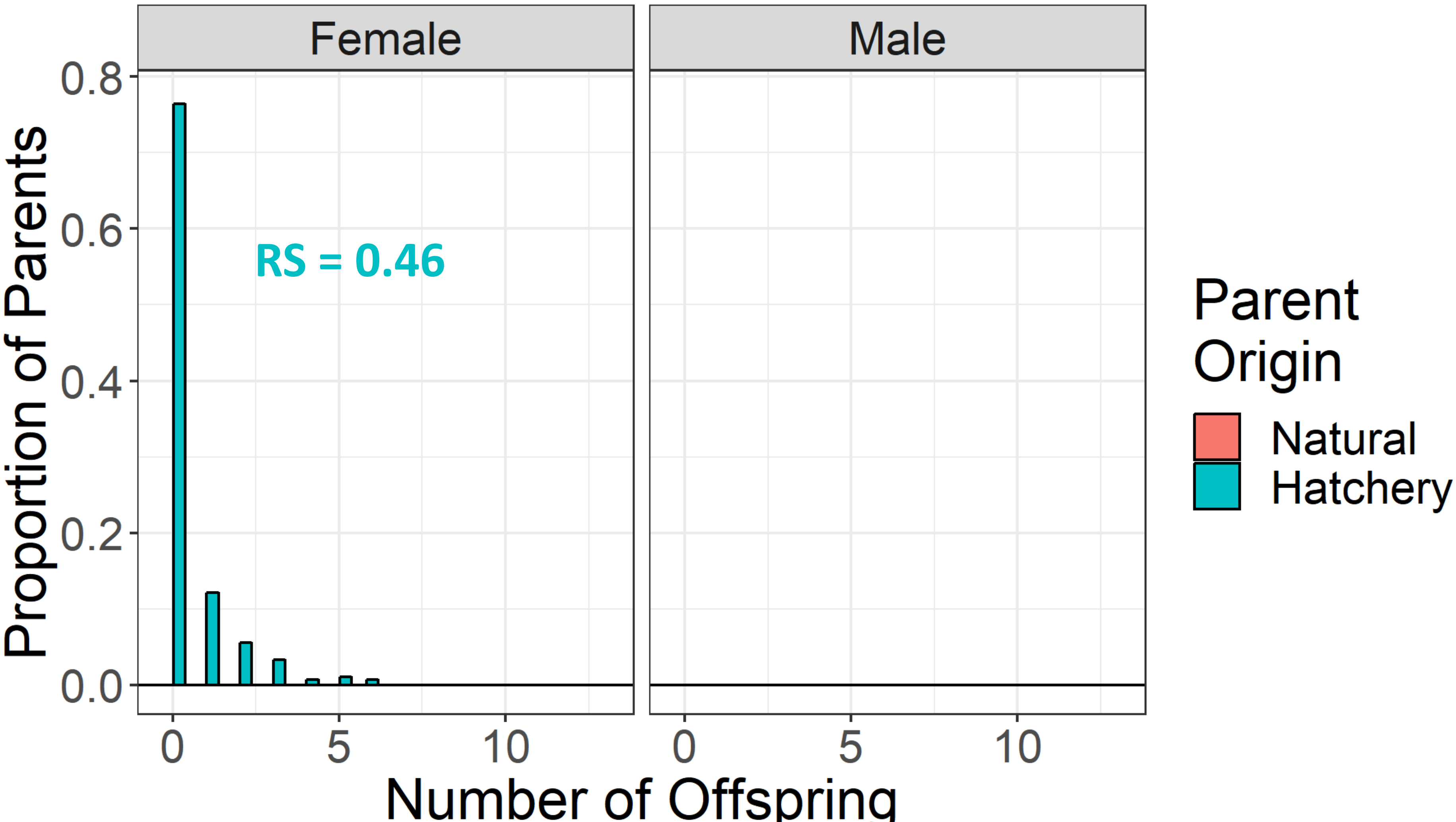



Figure 3b – Lescak et al. *in prep*

# RS Distribution: Even-Lineage

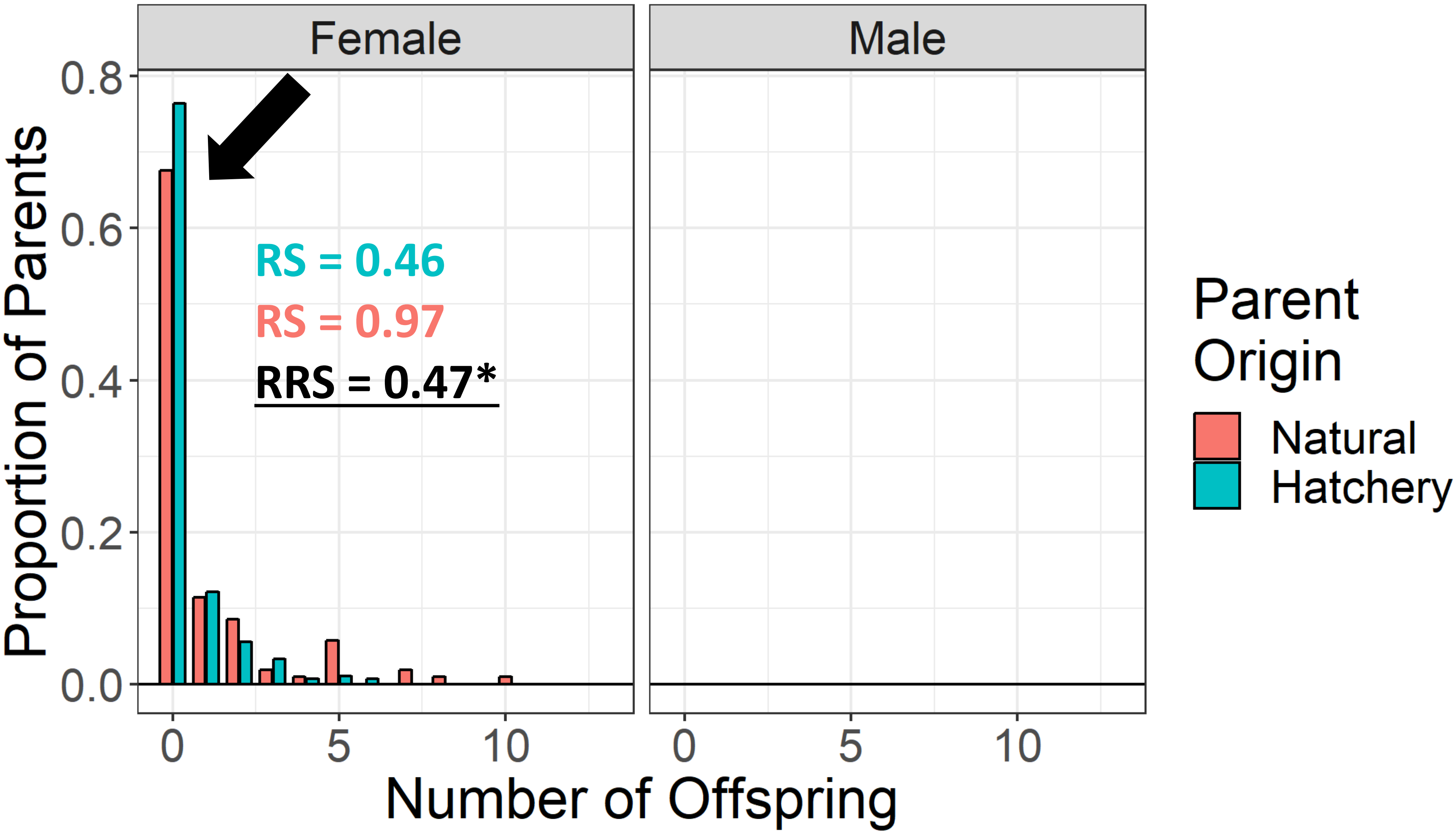



Figure 3b – Lescak et al. *in prep*

# RS Distribution: Even-Lineage

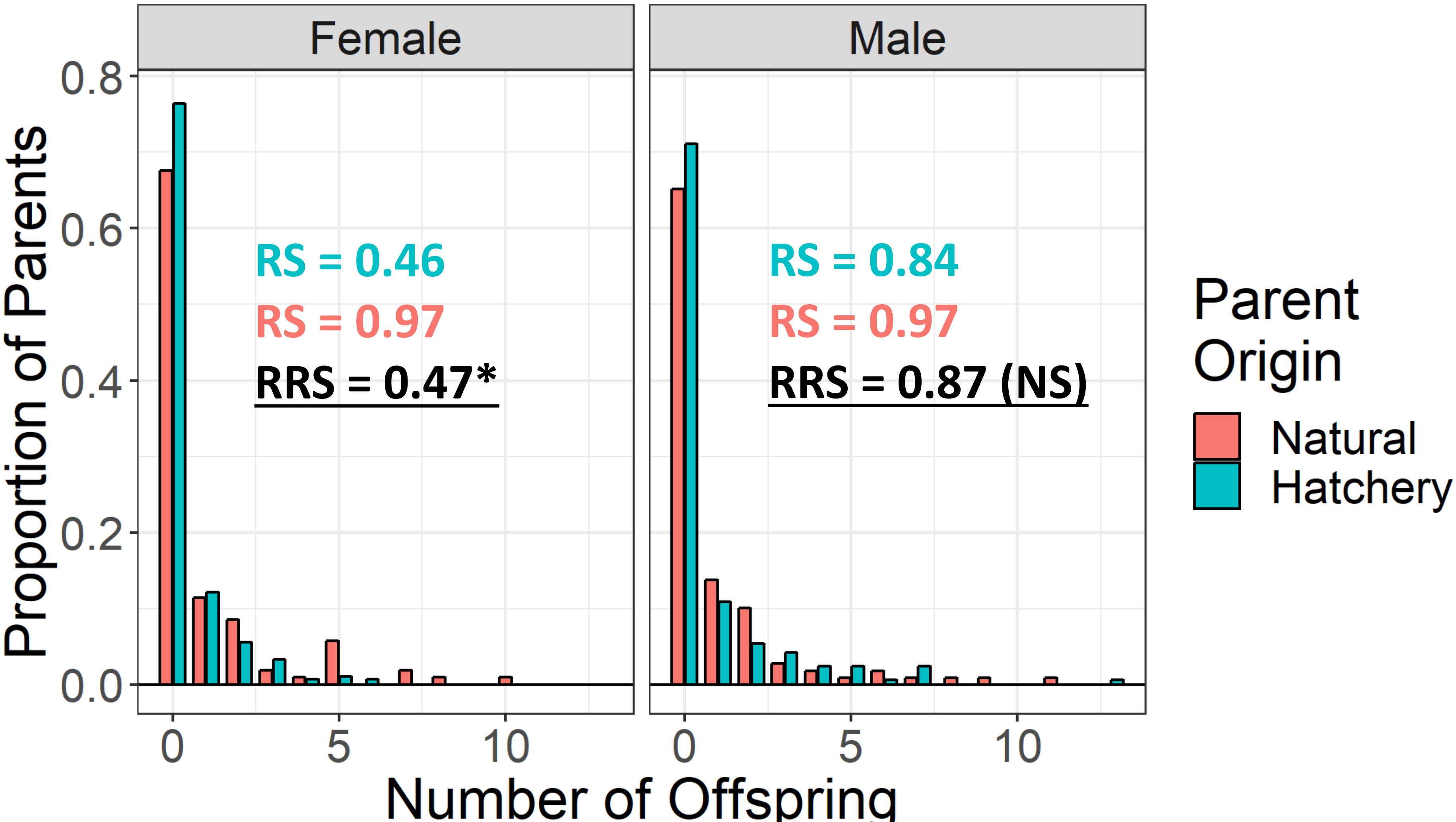
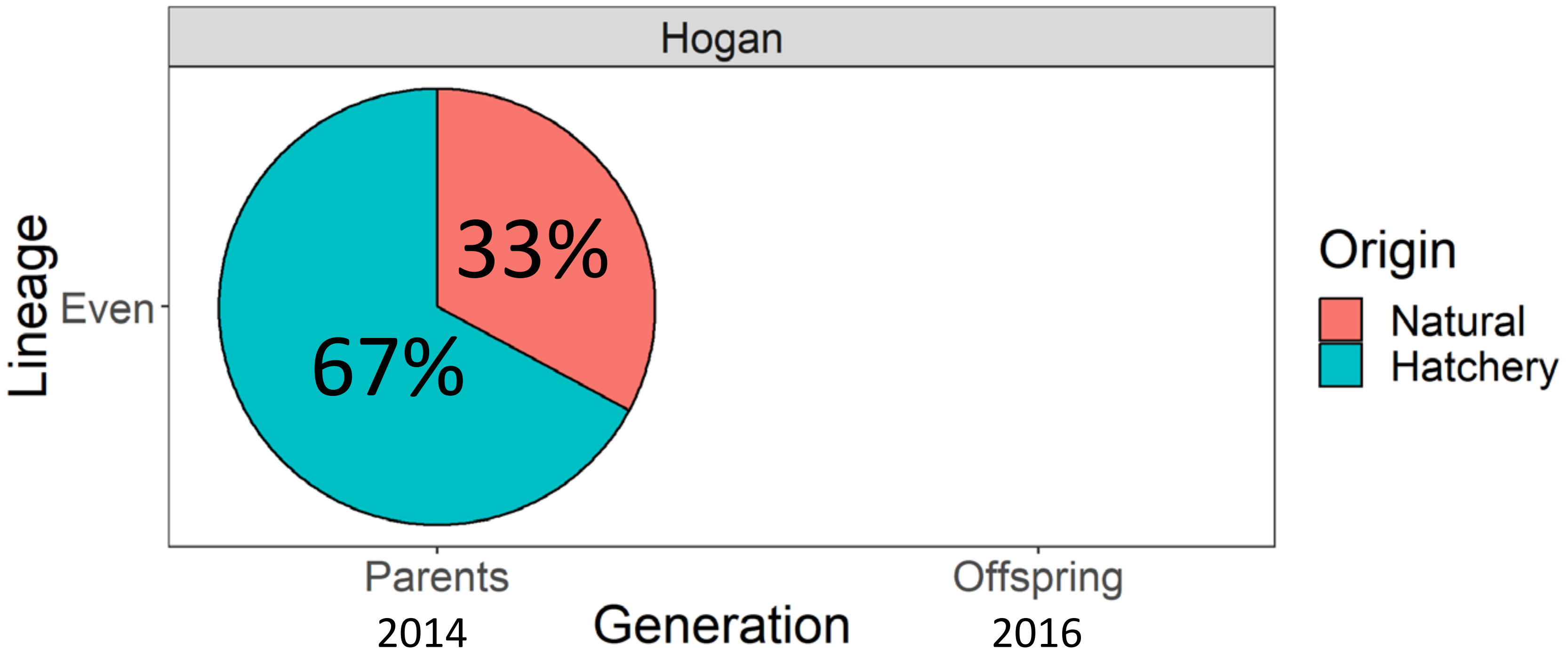
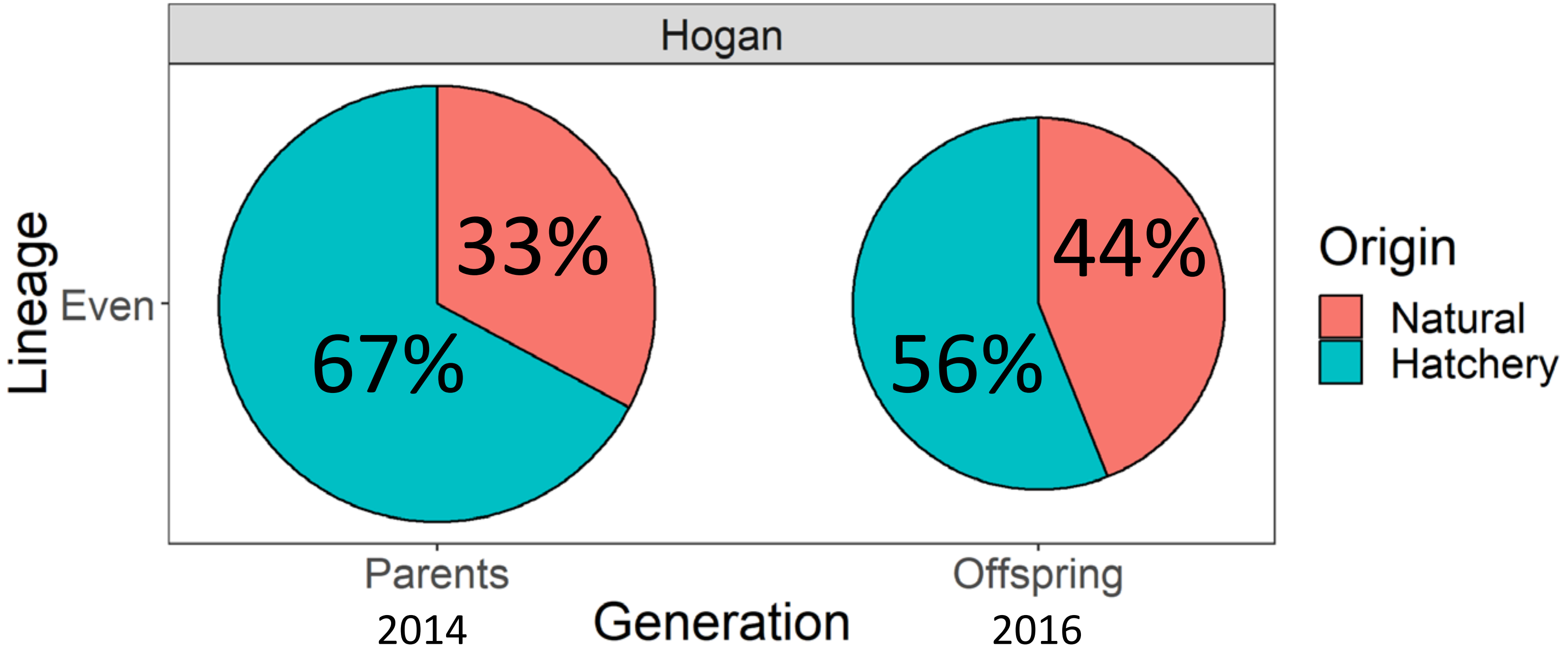



Figure 3b – Lescak et al. *in prep*

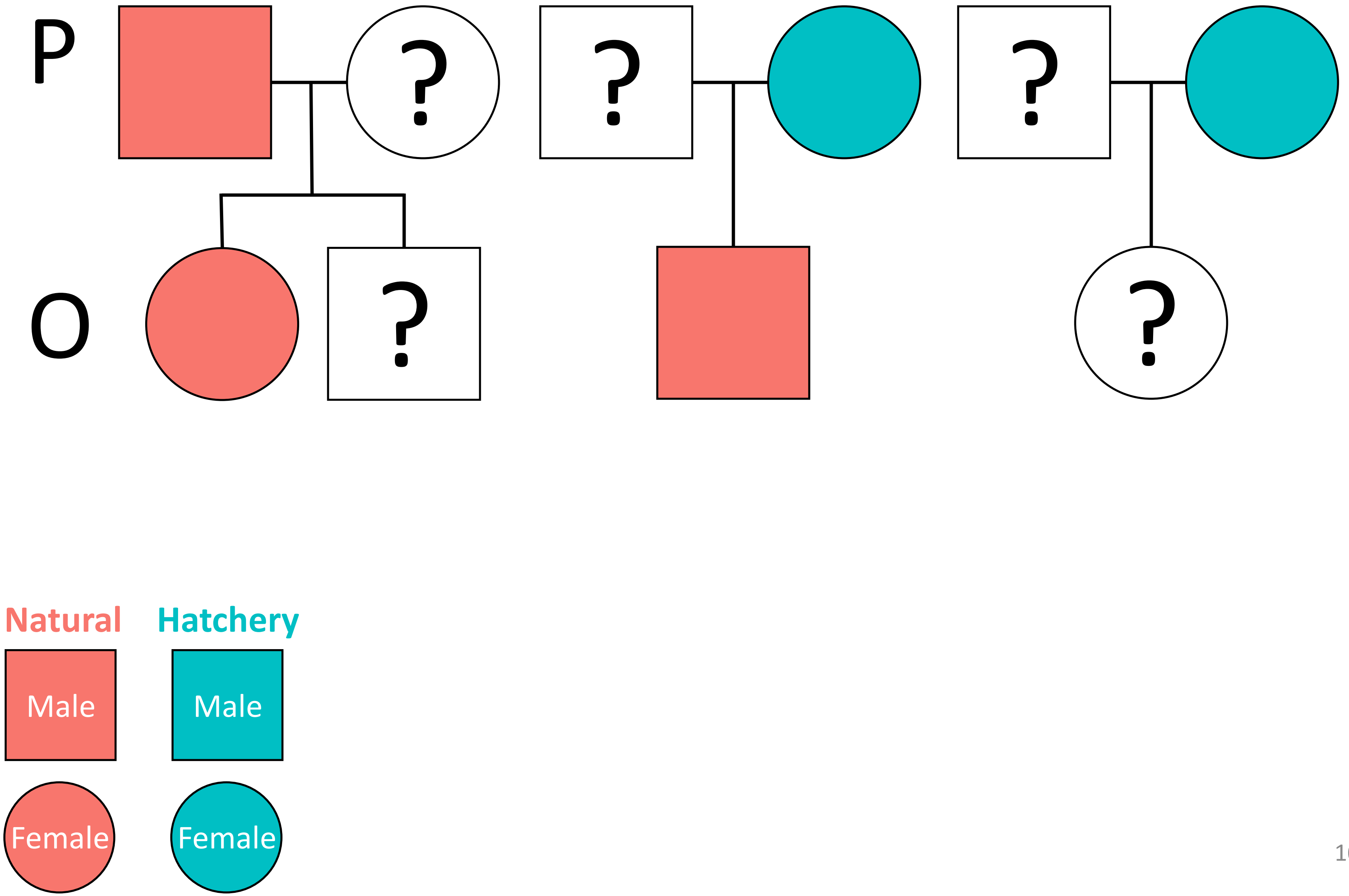
# Proportion Test: Even-Lineage



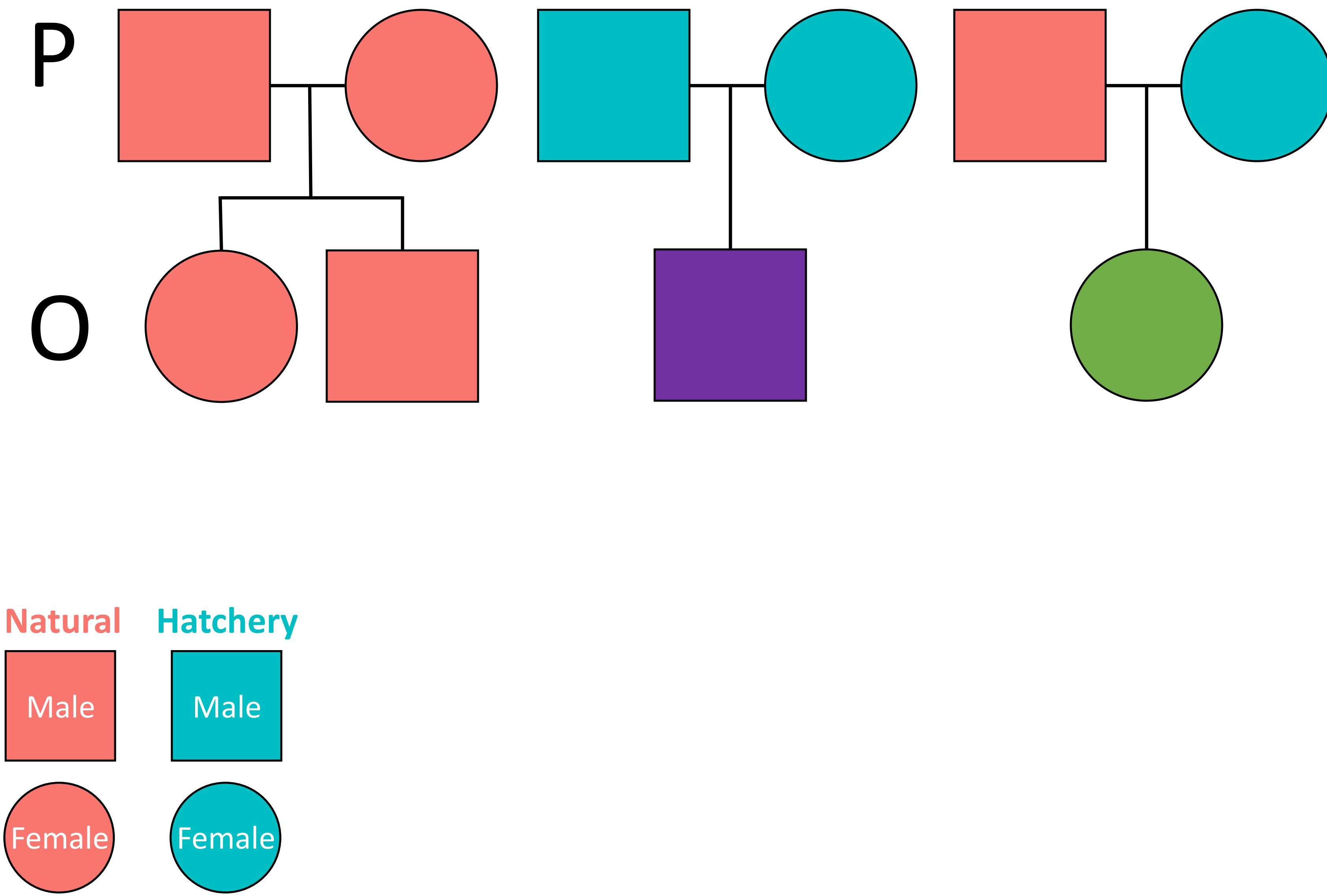
# Proportion Test: Even-Lineage

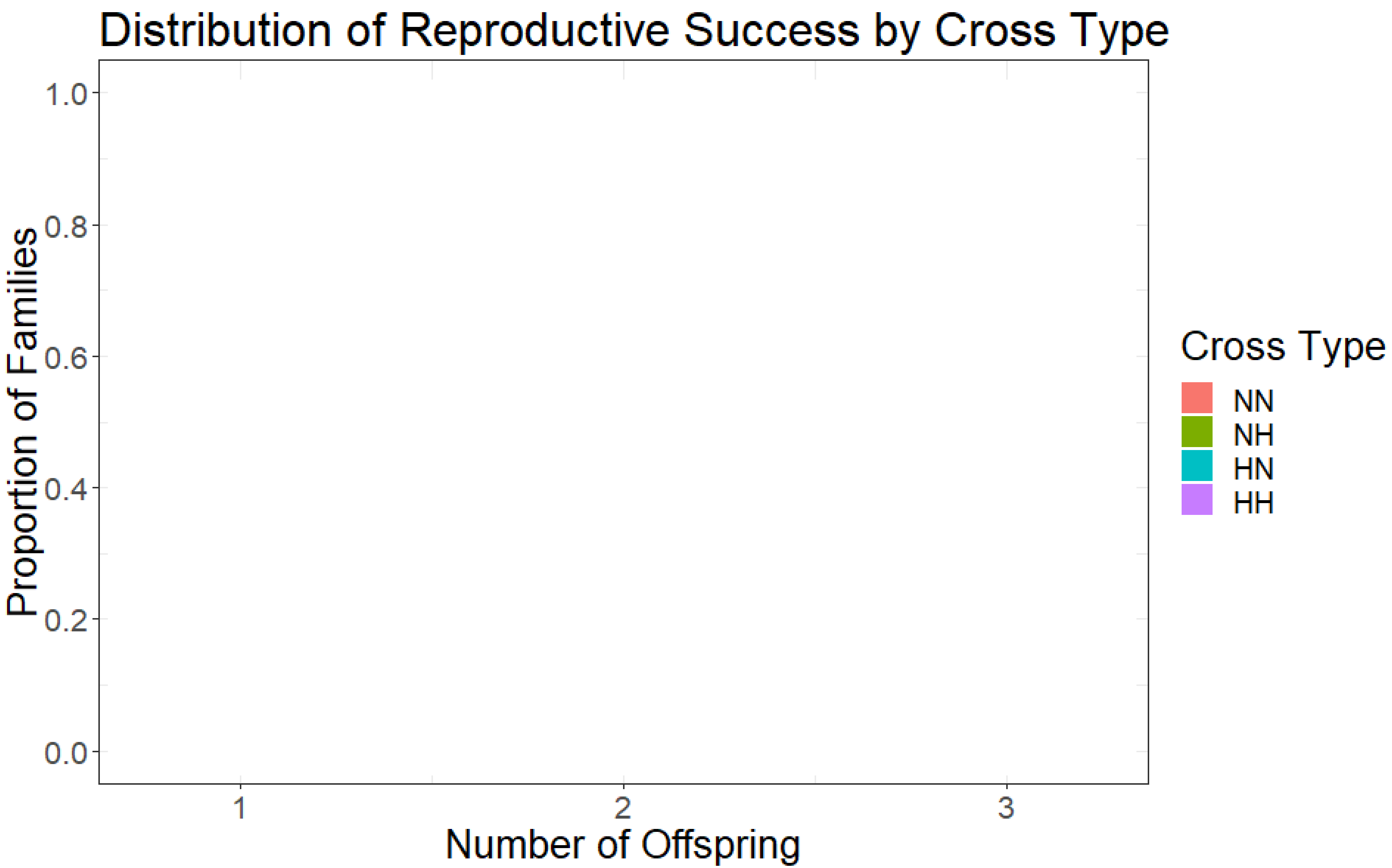


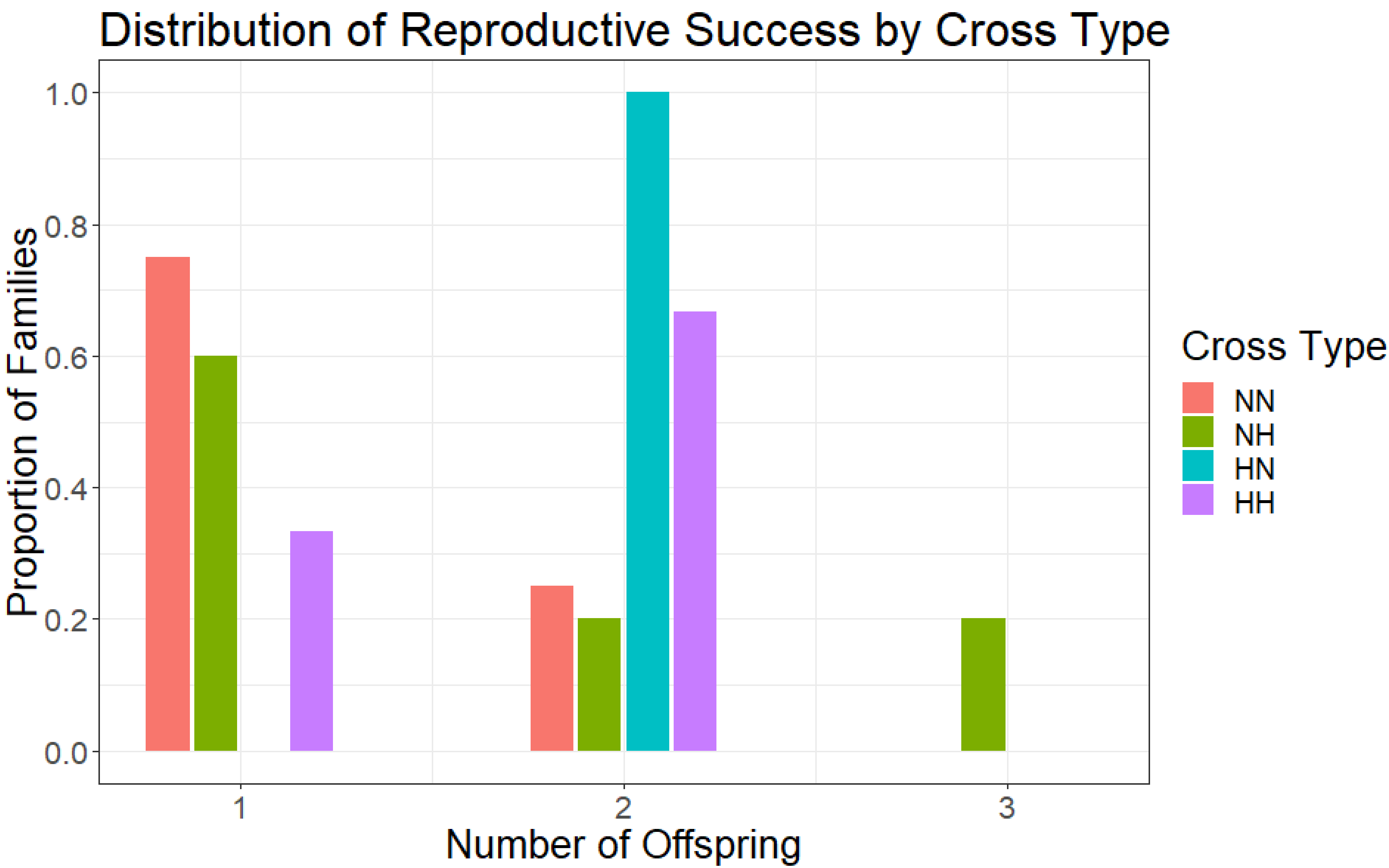
# Parent-Offspring Duos



# Parent-Offspring Trios




Distribution of Reproductive Success by Cross Type
Proportion of Families
1.0
0.8
0.6
0.4
0.2
0.0
1
2
3
Number of Offspring
Cross Type
NN
NH
HN
HH



Distribution of Reproductive Success by Cross Type
Proportion of Families
1.0
0.8
0.6
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0.2
0.0
1
2
3
Number of Offspring
Cross Type
NN
NH
HN
HH

# Analyzed Samples: Odd-Lineage

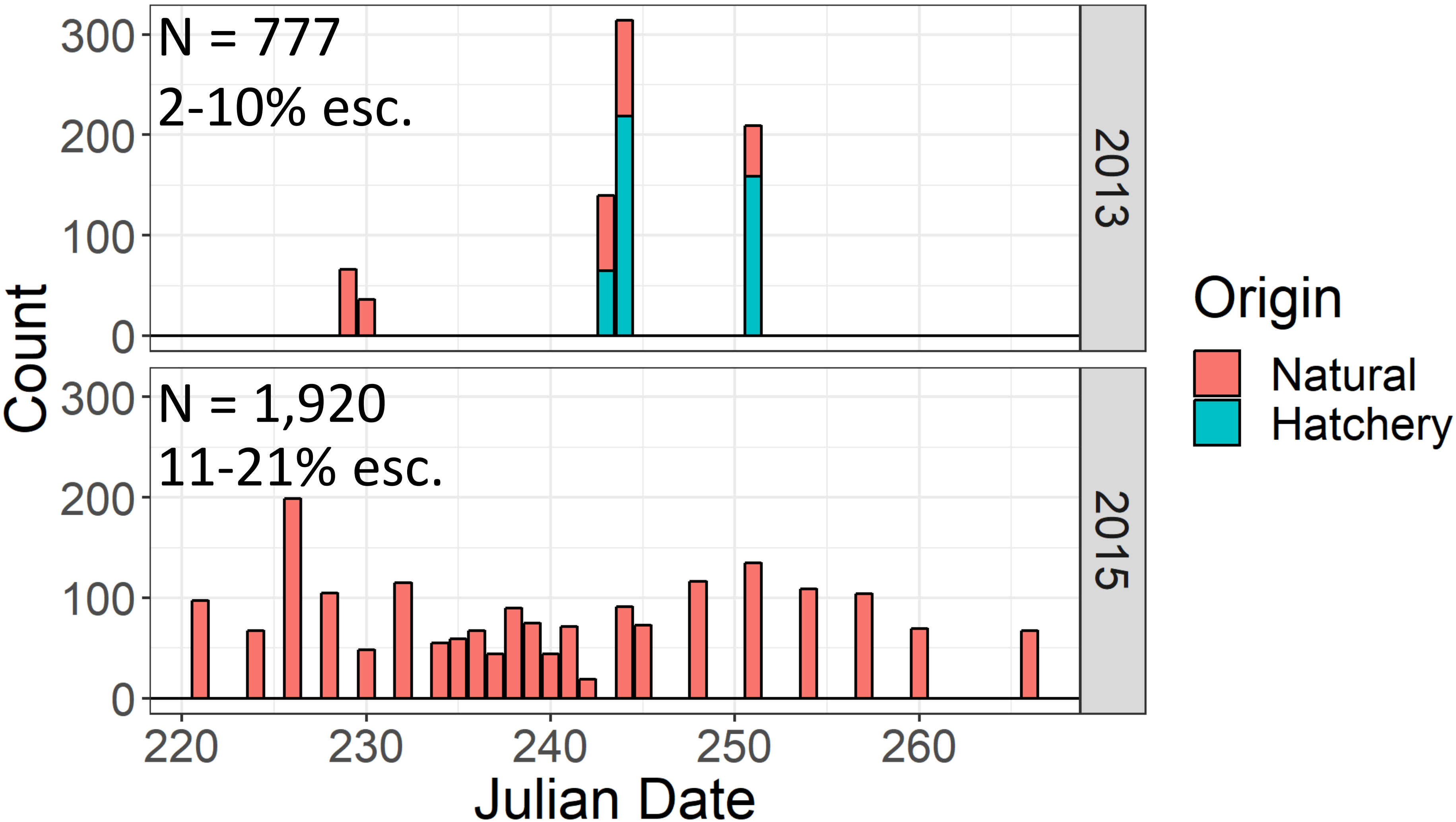



Figure 2a – Lescak et al. *in prep*

# Pedigree Results: Odd-Lineage

- 48 offspring (2.3%) assigned to 20 parents
  - 45 → natural-origin parents
  - 3→ hatchery-origin parents
    - 2 – AFK
    - 1 – WNH
    - 0 – CCH
    - 0 – SGH

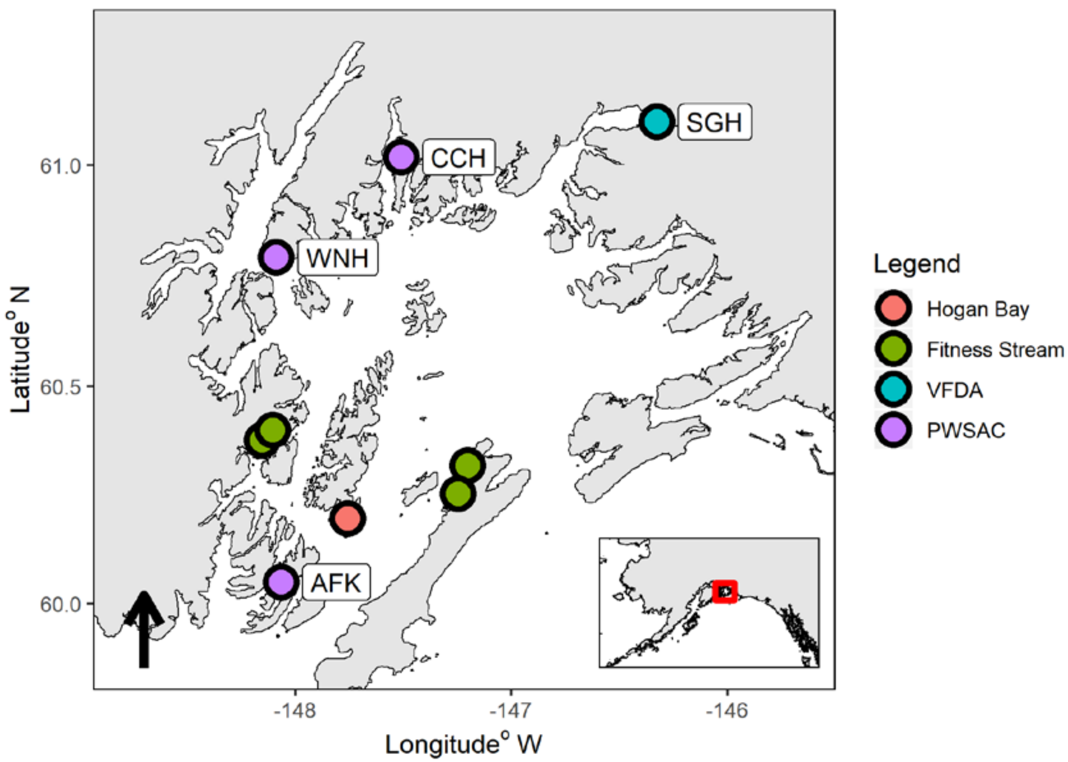



Figure 1 – Lescak et al. *in prep*

# RS Distribution: Odd-Lineage

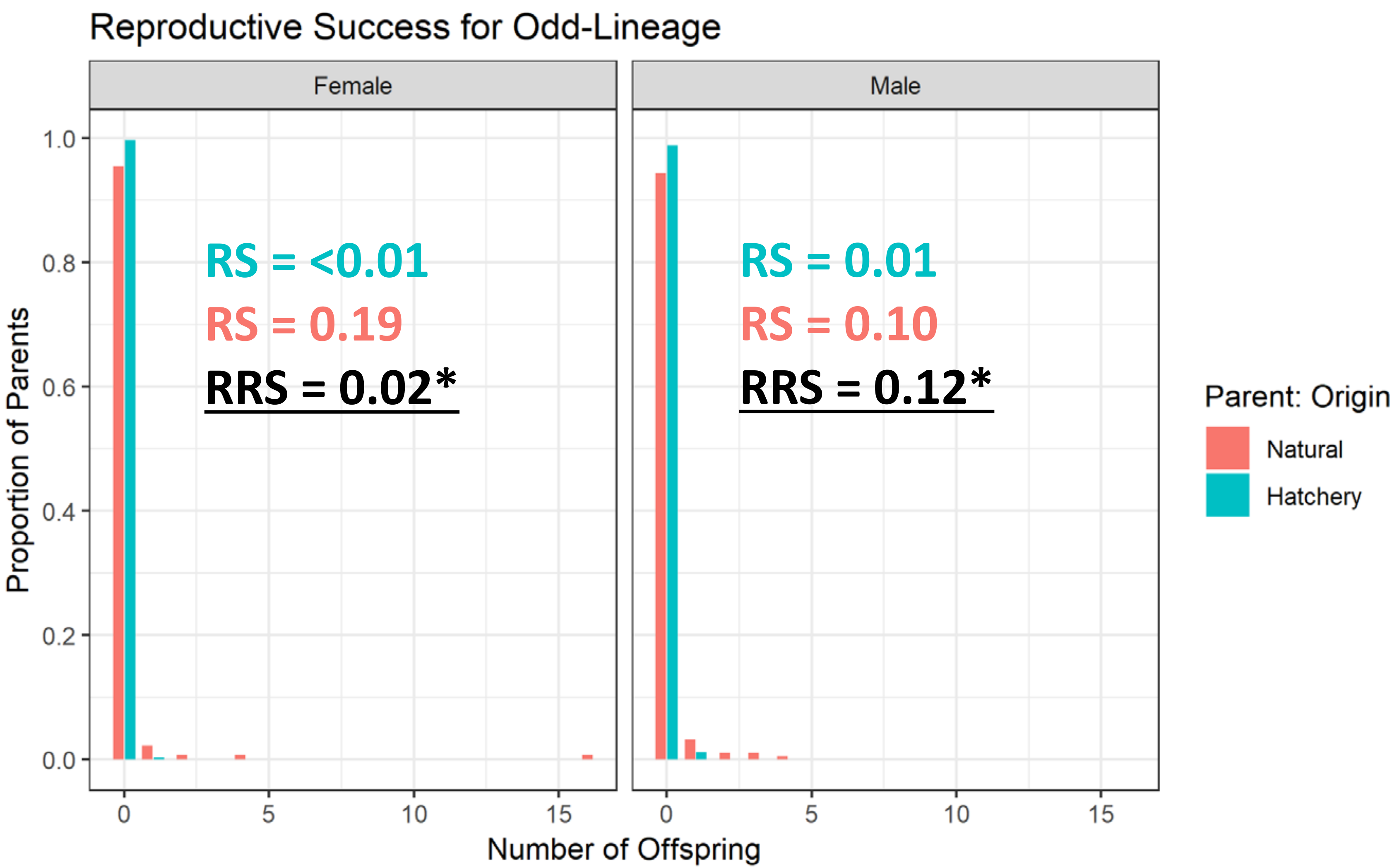
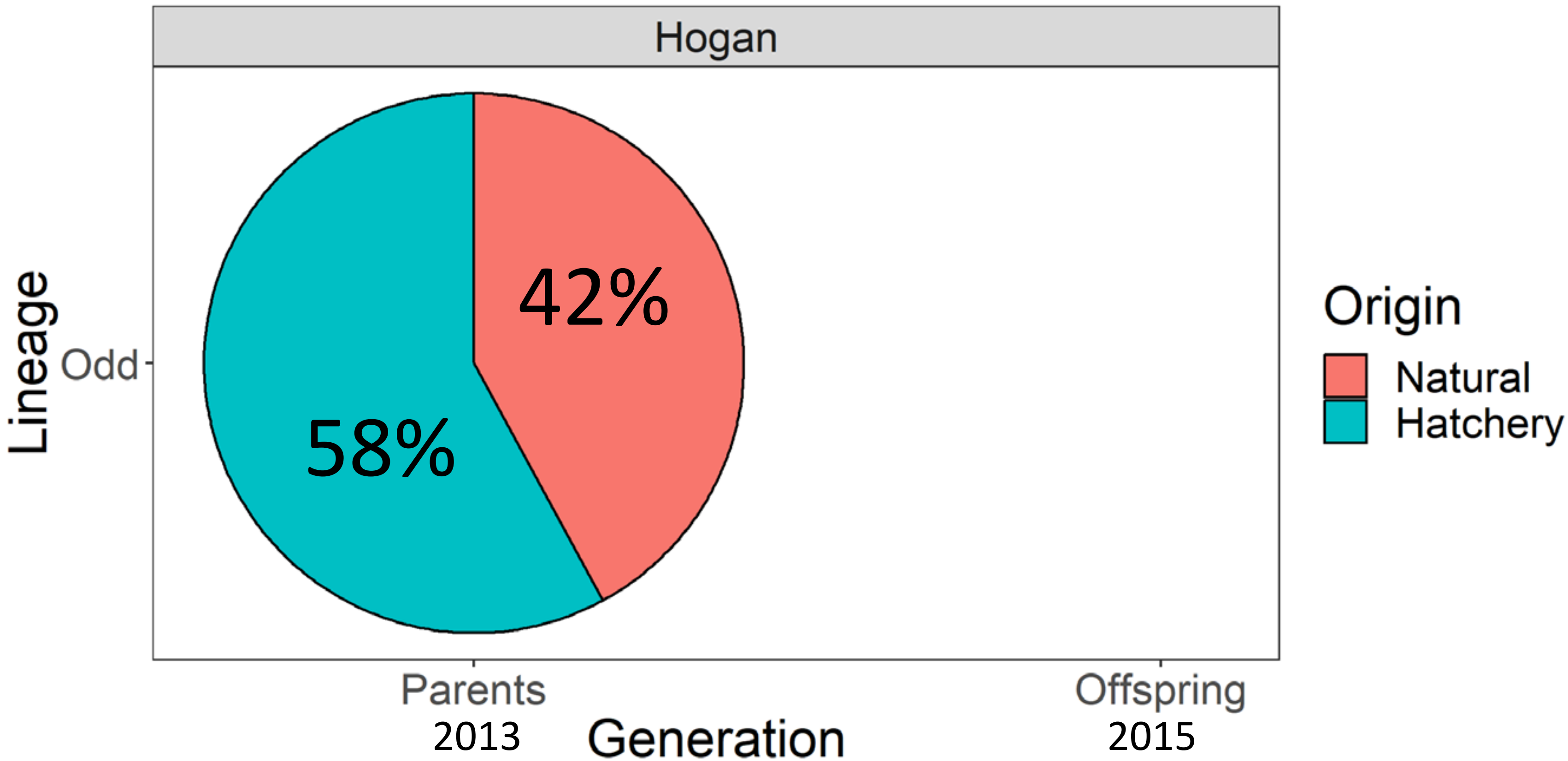
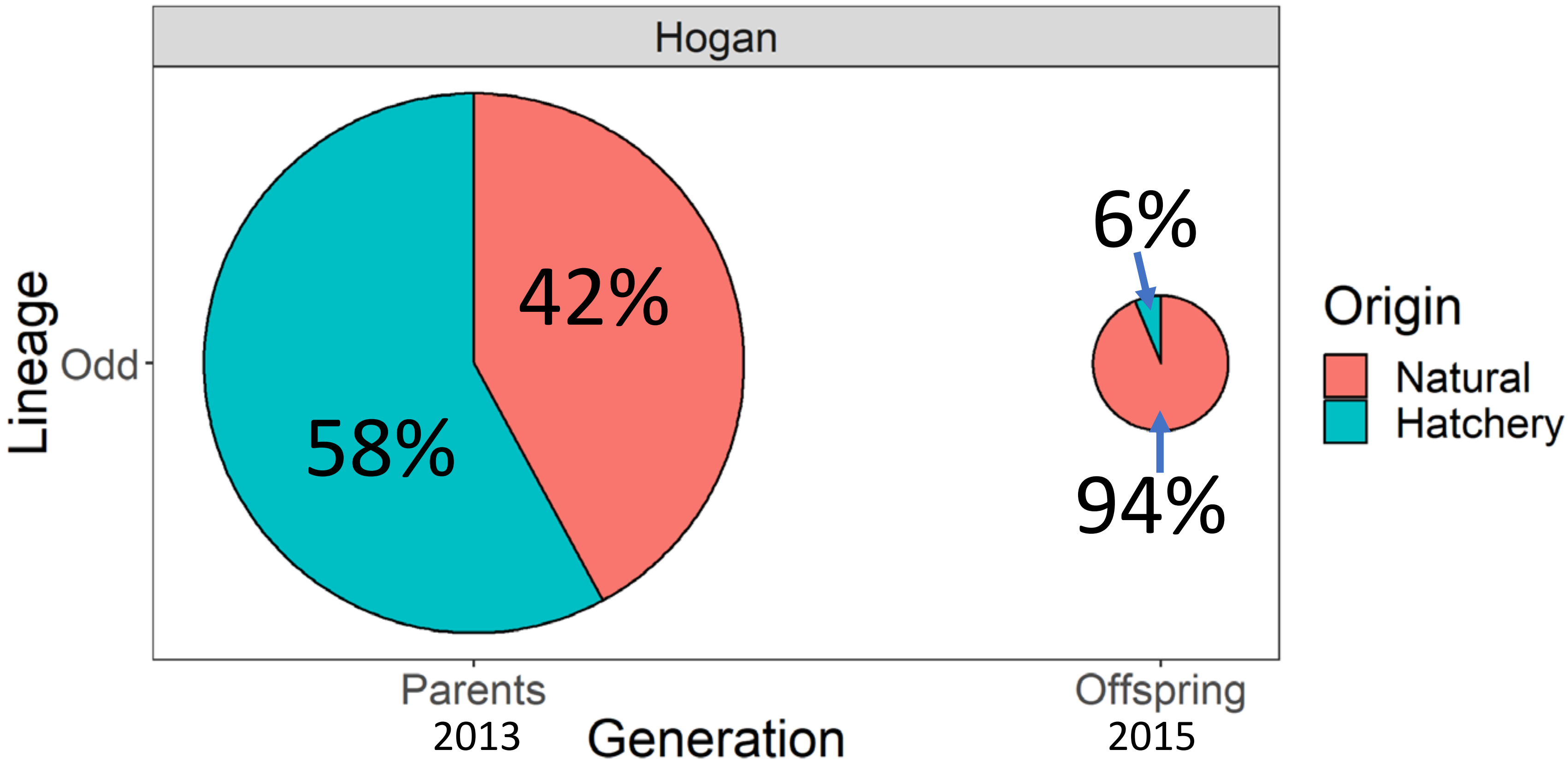



Figure 3b – Lescak et al. *in prep*

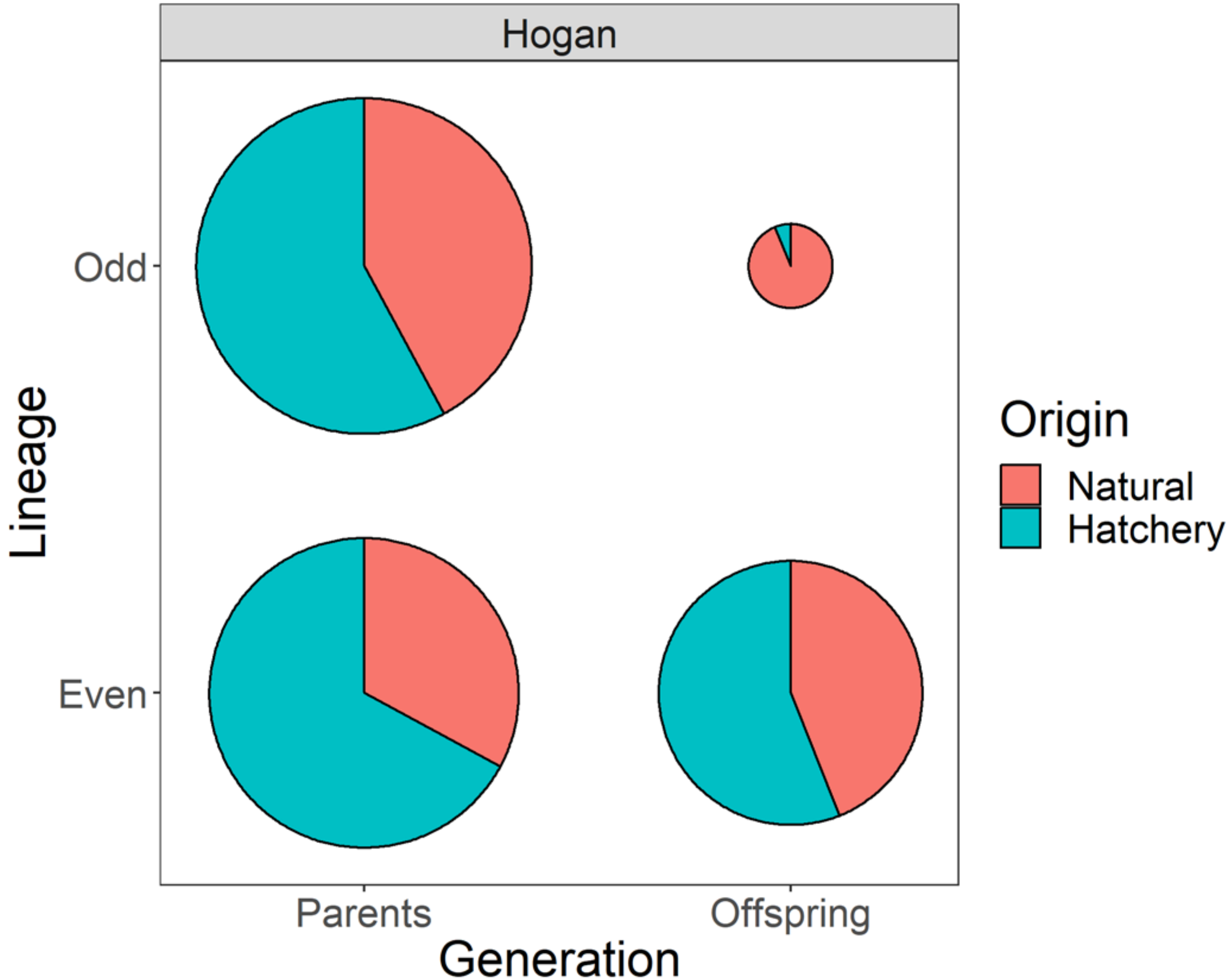
# Proportion Test: Odd-Lineage



# Proportion Test: Odd-Lineage



# Proportions for Both Lineages



# How robust are our pedigrees?

- Simulations
  - No incorrect or missed assignments
- Sensitivity analysis for *FRANz* parameters
  - Results robust to changes in genotyping error rates and maximum numbers of potential parents
- All parentage assignments unequivocal
  - No split pedigrees

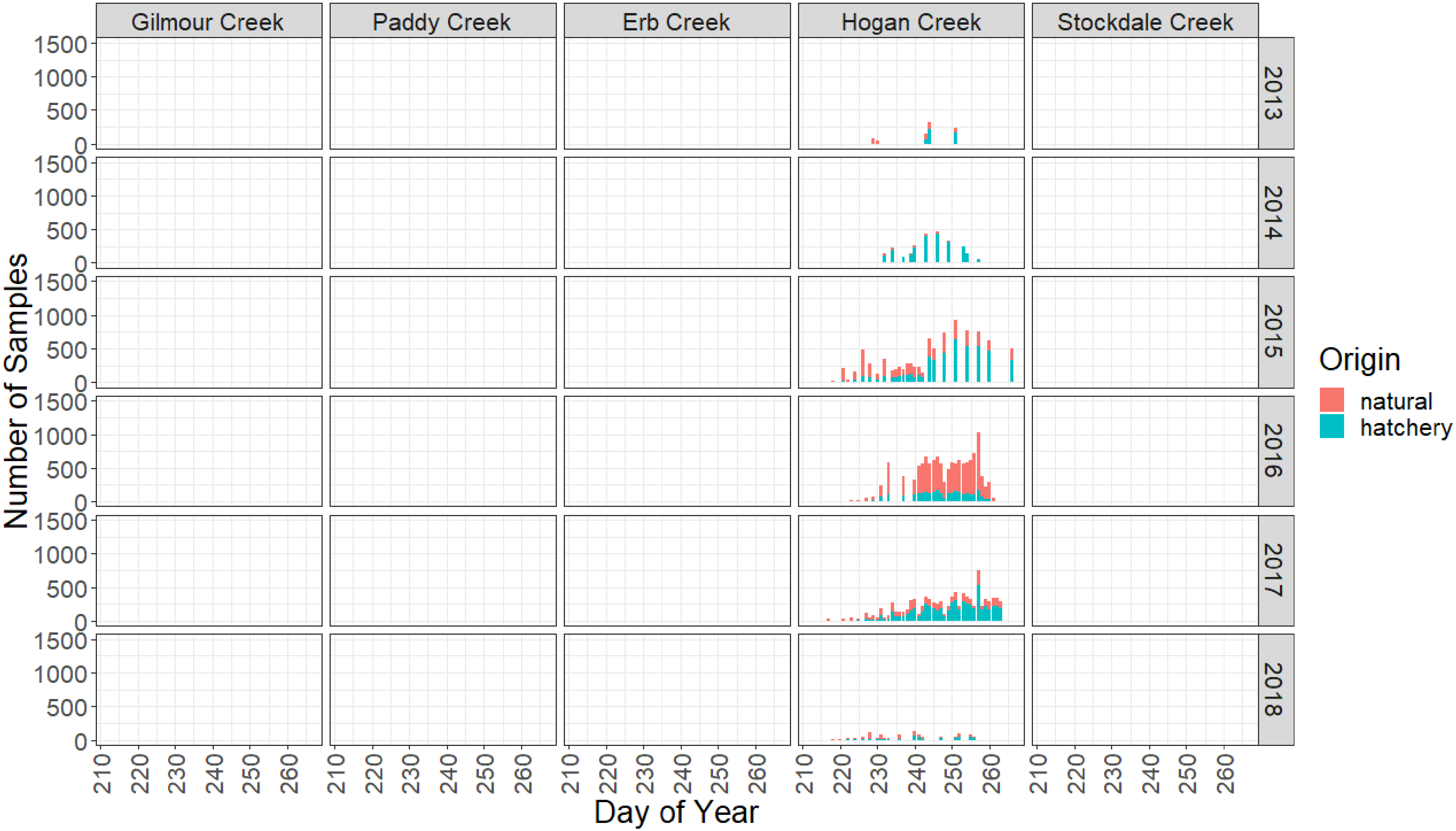
# Results from 1 generation of Hogan

- Pedigree in natural system possible
- Even-lineage
  - 451 offspring to 184 parents
  - Offspring assignment rate 11.0%
  - RRS = **0.47** (significant) for females
  - RRS = **0.87** (not significant) for males
- Odd-lineage
  - 48 offspring to 20 parents
  - Offspring assignment rate 2.5%
- Under-representation of offspring assigned to hatchery-origin parents in both lineages

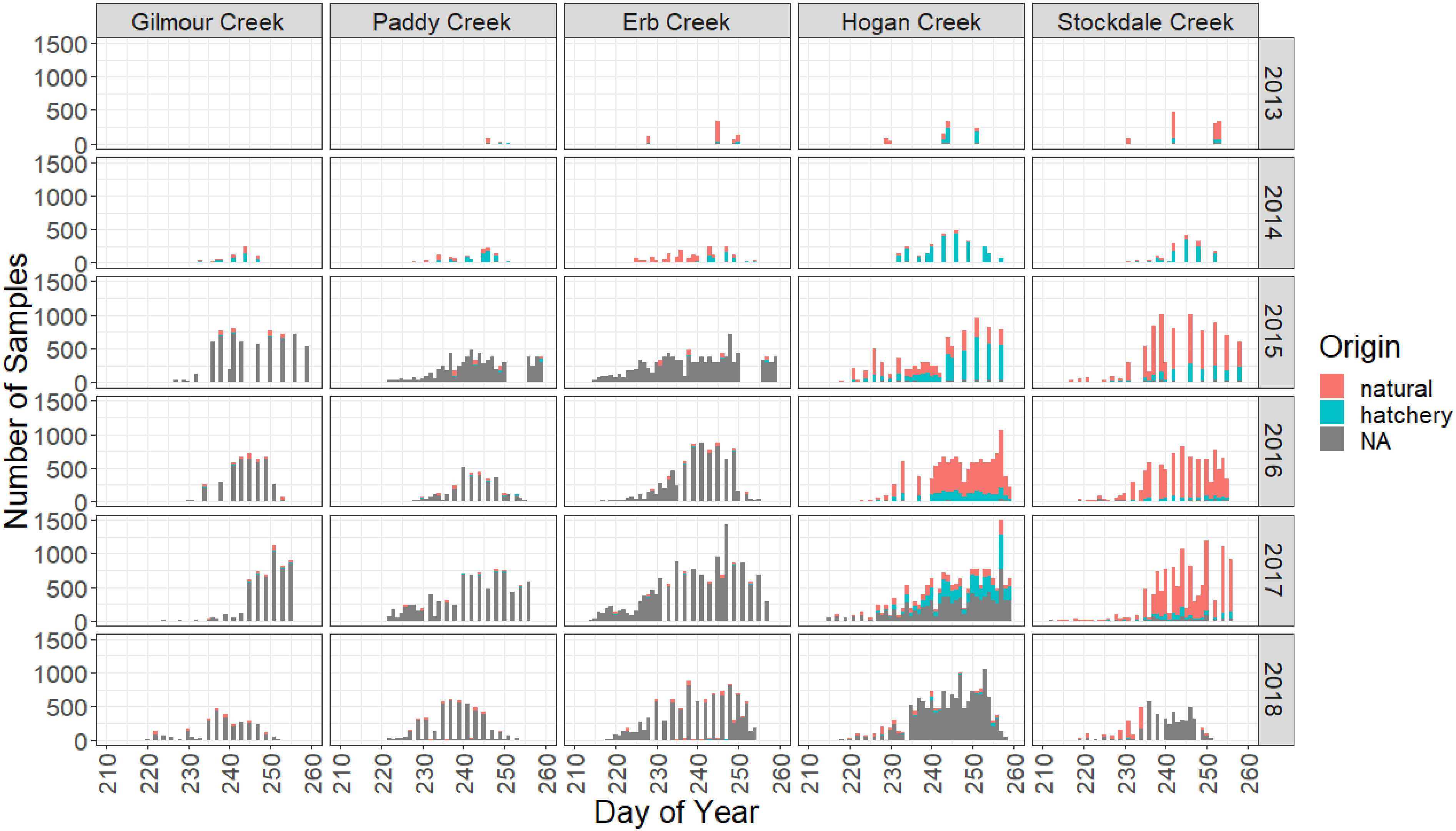
# Conclusions from Hogan Bay

- Hatchery-origin fish spawned and produced adult offspring that were sampled
- Hatchery-origin fish spawned with both other hatchery-origin fish as well as natural-origin fish
- On average, hatchery-origin fish produced fewer adult offspring that returned to Hogan Bay and were sampled than their natural-origin conspecifics
- There are potentially important differences in RS between male and female hatchery-origin fish

# Future Analyses



# Future Analyses



# Acknowledgements


- Alaska Hatchery Research Program
  - State of Alaska
  - Seafood industry
  - Private non-profit hatcheries
- North Pacific Research Board (Project #1619)
  - Funding for Hogan Bay analyses
- Prince William Sound Science Center
  - Field collection
- ADF&G Cordova Otolith Lab
- University of Washington - Seeb Lab
- ADF&G Gene Conservation Laboratory


Questions?
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# AHRP Fitness Study: SEAK Chum Salmon

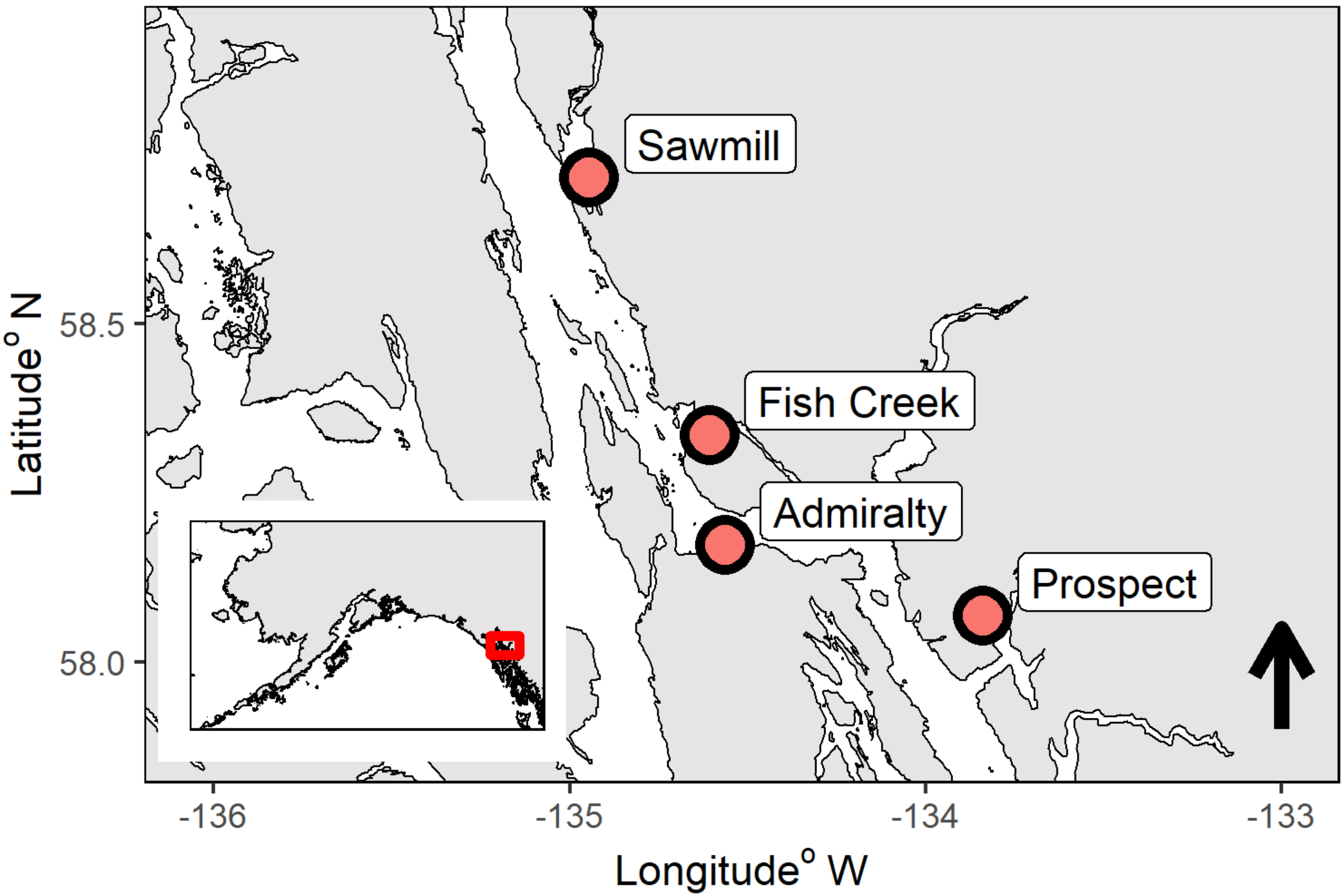
Kyle Shedd, E. Lescak, H. Hoyt, T. Dann, C. Habicht

Alaska Department of Fish and Game Gene Conservation Lab

Alaska Board of Fisheries Hatchery Committee

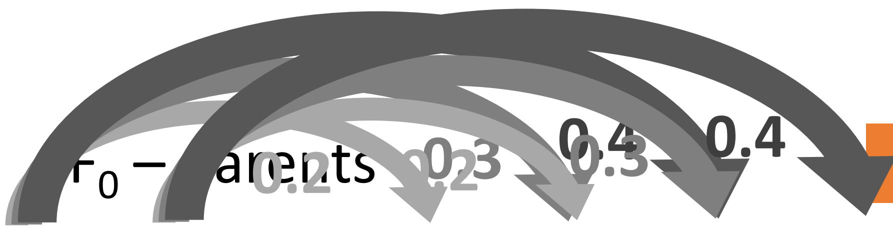
March 8, 2019

# Map of SEAK Chum fitness streams



# Study plan

| Species | 2013 | 2014 | 2015 | 2016 | 2017 | Sampling year 2018 | 2019 | 2020 | 2021 | 2022 | 2023 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Chum (BY 1) | $F_0$ | $F_1$ | [hatched] | $F_1$ | $F_1$ | $F_1/F_2$ | $F_1/F_2$ | $F_2$ | $F_2$ | $F_2$ | [hatched] |
| Chum (BY 2) | | $F_0$ | $F_1$ | [hatched] | $F_1$ | $F_1/F_2$ | $F_1/F_2$ | $F_2$ | $F_2$ | $F_2$ | $F_2$ |




| Species | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Chum (BY1) | $F_0$ | | | | $F_1$ | $F_1$ | | | | | |
| Chum (BY2) | | $F_0$ | | | $F_1$ | $F_1$ | $F_1$ | | | | |

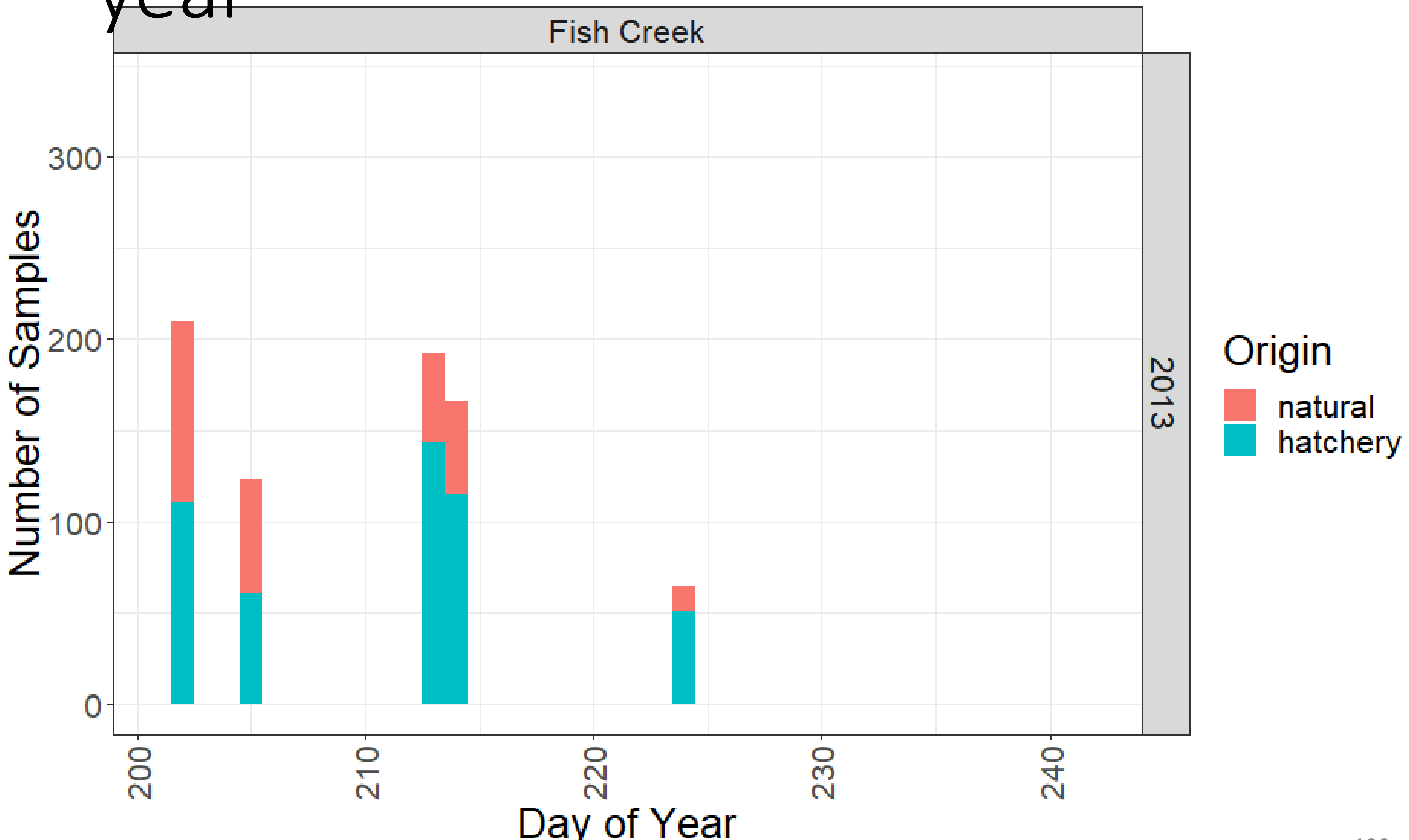
Adult

Adult + Alevin

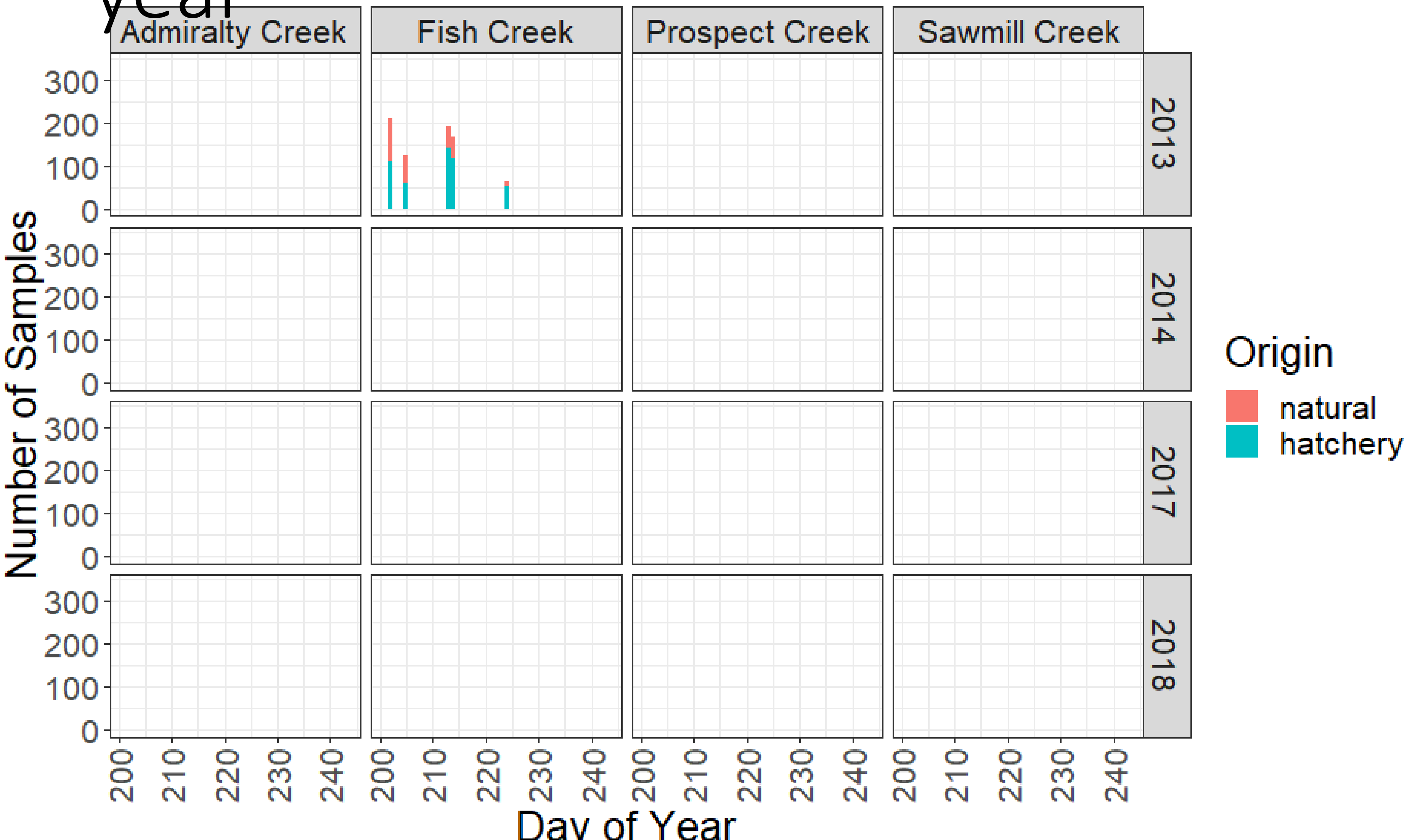
# Statistical power of study plan

- Need minimum ~100 parents of each sex/origin
- Ideally a high proportion of parents
  - Hogan Bay 2013/2015
    - Low sampling rate = few parent-offspring assignments
- Sample high proportion of offspring
  - Consistent proportion for all return years
  - Differences in age at return?

# Samples by origin, stream, and year



# Samples by origin, stream, and year



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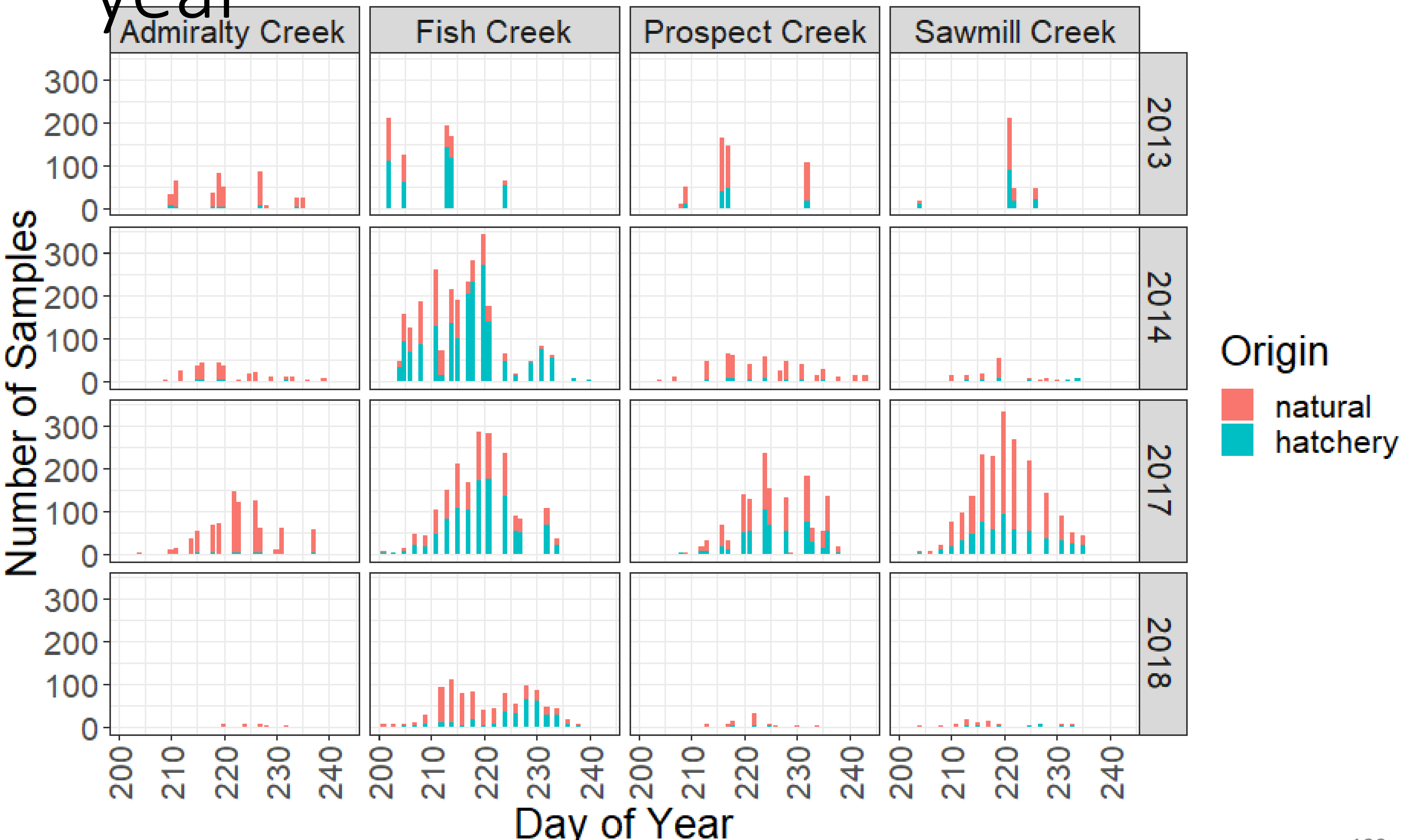

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- Sitka Sound Science Cente
  - Field collection
- ADF&G Mark, Tag and Age Lab
- ADF&G Gene Conservation Laboratory


Questions?