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*

  \[ \text{genetic drift} \sim \text{homing} \]  
  \[ \text{migration} \sim \text{straying} \]

  • 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
Population Structure: An example
Population Structure: An example

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 98112-2102, USA
Shigehiko Urawa
Hokkaido Salmon Hatchery, Fisheries Agency of Japan, Sapporo 062, Japan
and Nataly V. Varnavskaya
Kamchatka FNRIP, Petropavlovsk, Russia

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

C.M. Kondzeila, C.M. Guthrie, S.L. Hawkins, C.D. Russell, and J.H. Helle
Auke Bay Laboratory, Alaska Fisheries Science Center, National Marine Fisheries Service, National Oceanographic and Atmospheric Administration, 11303 Glacier Highway, Juneau, AK 99801-0626, U.S.A.
and A.J. Gharrett
School of Fisheries and Ocean Sciences, University of Alaska Fairbanks, 11120 Glacier Highway, Juneau, AK 99801, U.S.A.

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

Maureen P. Small*
Washington Department of Fish and Wildlife, Molecular-Genetics Lab, 1113 Washington Street Southeast, Olympia, Washington 98504, USA
Serena D. Rogers Olive
Alaska Department of Fish and Game, Division of Commercial Fisheries, Gene Conservation Laboratory, 333 Raspberry Road, Anchorage, Alaska 99518, USA
Lisa W. Seeb, James E. Seeb, and Carita E. Pascal
School of Aquatic and Fishery Sciences, University of Washington, 1122 Northeast Boat Street, Box 355020, Seattle, Washington 98195, USA
Kenneth J. Warbuit
Washington Department of Fish and Wildlife, Molecular-Genetics Lab, 1111 Washington Street, Olympia, Washington 98504, USA; and School of Aquatic and Fishery Sciences, University of Washington, 1122 Northeast Boat Street, Box 355020, Seattle, Washington 98195, USA
William Tempkin
Alaska Department of Fish and Game, Division of Commercial Fisheries, Gene Conservation Laboratory, 333 Raspberry Road, Anchorage, Alaska 99518, USA

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

Terry D. Beacham, Brian Splittstoesser, Kahl D. Le, and Michael Wettko

Microsatellite Stock Identification of Chum Salmon on a Pacific Rim Basis

TERRY D. BEACHAM,* JOHN R. CANDY, AND C. WALLACE
Fisheries and Oceans Canada, Pacific Biological Station, 3190 Hammond Bay Road, Nanaimo, British Columbia V9T 6N7, Canada
SHIGEHIKO URAWA† AND SHUNPEI SATO
National Salmon Resources Center, Fisheries Research Agency, Toyohira-ku, Sapporo 062-0043, Japan
NATALYA V. VARNAVSKAYA
Kamchatka Fishery and Oceanography Research Institute, 18 Naberezhnaya Street, Petropavlovsk-Kamchatsky 683000, Russia
KHAL D. LE AND MICHAEL WETTKO
Fisheries and Oceans Canada, Pacific Biological Station, 3190 Hammond Bay Road, Nanaimo, British Columbia V9T 6N7, Canada

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

Shunpei Sato†, Hiroyuki Kojima†, Junko Ando†, Hiroori Ando†, Richard L. Wilman*, Lisa W. Seeb‡, Vladimir Eremov*, Larry LeClair*, Wally Buchholz†, Deuk-Hee Jim†, Shigehiko Urawa†, Masahide Kaeriyama‡, Akhisa Urano‡ & Syoiti Abe‡
*Division of Biological Science, Graduate School of Science, Hokkaido University, Sapporo 060-0010, Japan
†Graduate School of Science and Engineering, Hokkaido Tokai University, Sapporo 005-8601, Japan
‡Auke Bay Laboratory, Alaska Fisheries Science Center, NOAA, Juneau, USA
§Alaska Department of Fish and Game, Anchorage, USA
®Russian Academy of Science, Vladivostok, Russia
†Washington Department of Fish and Wildlife, Olympia, Washington, USA
‡U.S. Fish and Wildlife Service, Anchorage, AK, USA
§Kangnai National University, Kangnung, Korea
¶Salmon Resources Center, Sapporo 062-0922, Japan
||Field Science Center, Hokkaido University, Sapporo 060-0811, Japan
*Laboratory of Animal Cytogenetics, Center for Advanced Science and Technology, Hokkaido University, Sapporo 060-0810, Japan (e-mail: sato@ees.hokudai.ac.jp)
‡Laboratory of Breeding Science, Graduate School of Fisheries Sciences, Hokkaido University, Hakodate 041-8611, Japan

Received 17 April 2003 Accepted 27 April 2003
Chum salmon in the Gulf of Alaska

198 populations
93 markers
Chum salmon in the Gulf of Alaska

198 populations
93 markers

PWS to SEAK
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
Population structure of pink salmon in Prince William Sound

Wei Cheng\textsuperscript{1,2}, Christopher Habicht\textsuperscript{1}, William D. Templin\textsuperscript{1}, Zachary D. Grauvogel\textsuperscript{1}, and Anthony J. Gharrett\textsuperscript{2}

\textsuperscript{1}Alaska Department of Fish and Game, Gene Conservation Laboratory

\textsuperscript{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

Swanson Creek

McCleod Creek

Rocky Creek

Duck River
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

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


Abstract - Allozyme and mitochondrial DNA (mtDNA) data were obtained from pink salmon throughout Prince William Sound, Alaska, from two hatchery, live upstream, and 20 tidal locations distributed among five management regions collected during 1994. Screening for allozymes included 65 loci for 50 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 Koppea 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 Arrhin F. Koenig 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.

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 3, 1996

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

<table>
<thead>
<tr>
<th></th>
<th>Contemporary</th>
<th>Historical</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Odd Year</strong></td>
<td>Natural</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Hatchery</td>
<td></td>
</tr>
<tr>
<td><strong>Even Year</strong></td>
<td>Natural</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Hatchery</td>
<td></td>
</tr>
</tbody>
</table>
# Study Design

<table>
<thead>
<tr>
<th></th>
<th>Contemporary</th>
<th>Historical</th>
</tr>
</thead>
<tbody>
<tr>
<td>Odd Year</td>
<td>Natural</td>
<td>✓</td>
</tr>
<tr>
<td></td>
<td>Hatchery</td>
<td>✓</td>
</tr>
<tr>
<td>Even Year</td>
<td>Natural</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Hatchery</td>
<td></td>
</tr>
</tbody>
</table>
Population Structure Analyses

• Calculate genetic differences among collections

• Test for significance of these differences

• Visualize the relationships among collections
PWS Pink Salmon

Odd Year

Odd

Even

$F_{ST}$
Population structure of odd-broodline Asian pink salmon and its contrast to the even-broodline structure


*National Marine Fisheries Service, Auke Bay Laboratory, 11805 Glacier Hwy, Juneau, AK 99801-5876, U.S.A.; **Kamchatka Scientific Research Institute of Fisheries and Oceanography, Kamchatka NIKO, Petropavlovsk-Kamchatsky 683602, Kamchatka, Russia; **Kamchatka Branch of Pacific Research Institute of Fisheries and Oceanography (KoTRINO), A-1100000, 14 Vvedenskaya Alley, Vladivostok 690000, Russia; #Russian Academy of Sciences, Far Eastern Branch, Institute of Marine Biology, Vladivostok 690041, Russia, #Pacific Salmon Resource Center, Naknek, Alaska, USA; †Hokkaido University, Laboratory of Genetics and Embryology, Faculty of Fisheries, Hokkaido 041, Japan and JBird Watch, 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 (645) totally allozyme loci from 35 populations, occurred within populations. The remaining inter-population variability was attributed to: (1) differences between northern (the northern Sea of Okhotsk), eastern Kamchatka Peninsula and western Kamchatka Peninsula and southern (Kuril Islands, Sakhalin Islands and Hokkaido Island) populations; (2) differences between the southern areas; and (3) low variation among populations within areas. The patterns contrasted strongly with those observed for Asian even-broodline populations. In this case, it would therefore appear that migration-drift equilibrium has not yet obtained in either population. Structural differences were also significant and that the even- and odd-broodline populations are of different ages and that one is derived from the other. Allozyme data do not provide a complete picture for identifying the ancestral lineage.

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

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

James B. Shaklee
Washington Department of Fish and Wildlife, 600 Capitol Way N, Olympia, WA 98501-1091, U.S.A.

and Natalya V. Varnavskaya
Kamchatka Branch of Pacific Research Institute of Fisheries and Oceanography (KoTRINO), Petropavlovsk-Kamchatsky, 683602, Naberezhnaya 18, Russia


We collected and electrophoretically analyzed a total of 358 fish from eight locations along the Pacific Coast of Russia. We successfully screened 44 electrophoretic loci: 14 loci were polymorphic. All loci of the 3.99 level and the remaining 22 were either monomorphic or exhibited very rare variation in these collections. Contingency tests using the most variable loci revealed significant heterogeneity among all eight collections (p=0.0028) 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=0.077). Multidimensional scaling and minimum spanning tree analyses using genetic distances among populations indicated that geographic proximity of spawning sites was not associated with genetic similarity. The eight odd-year pink salmon (Oncorhynchus gorbuscha) populations from Russia were compared with 16 collections from North America (southeastern Alaska, British Columbia, and Washington) using data for 13 loci. The Russian populations differed significantly 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 Analyses

• Calculate genetic differences among collections

• Test for significance of these differences
Testing for Differences: among Prince Willian Sound

$p = 3.05 \times 10^{-70}$

(\(\alpha = 0.05\))

Significantly different

Odd Year
Population Structure Analyses

• Calculate genetic differences among collections

• Test for significance of these differences

• Visualize the relationships among collections
Visualizing the Relationships among Collections
Visualizing the Relationships among Collections

- Snug Harbor
- VFDA
- KRAA
- Totemoff
- Lagoon
Visualizing Relationships among Collections – Zooming in

*East vs. West*

- Coghill
- Paulson
- Totemoff
- Canyon
- Lagoon

Odd Year
## Study Design

<table>
<thead>
<tr>
<th></th>
<th>Contemporary</th>
<th>Historical</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Odd Year</strong></td>
<td>Natural</td>
<td>✓ (pending)</td>
</tr>
<tr>
<td></td>
<td>Hatchery</td>
<td>✓ (pending)</td>
</tr>
<tr>
<td><strong>Even Year</strong></td>
<td>Natural</td>
<td>✓ (pending)</td>
</tr>
<tr>
<td></td>
<td>Hatchery</td>
<td>✓ (pending)</td>
</tr>
</tbody>
</table>
PWS Pink Salmon

Even Year

Odd

Even

\( F_{ST} \)
Allozyme and mitochondrial DNA variation describe ecologically important genetic structure of even-year pink salmon inhabiting Prince William Sound, Alaska


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 alleles (experiences >0.01 in one or more collections and were used for population analyses. Eight haplotypes were detected after screening 46 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 panmictic support and managing native populations in Prince William Sound at the regional level. Distinctions between upstream and tidal collections were detected within Lagoon Creek (allozymes) and Koppes 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 distance from Alaskan P. Kent Hughes 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.

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. Gravvovg, 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 fisheries. 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 (Fst), a measure of population divergence, was 0.001 over all loci and the Fst 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 Fst 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 McIntosh1
Cathy MacConachie1
Brian Spils4
Bruce A. White3

E-mail address for contact author: Terry.Beacham@di.e.mpo.gc.c

1 Fisheries and Oceans Canada
Pacific Biological Station
3190 Hammond Bay Road
Nanaimo, B. C., Canada V9T 5N7
2 Fisheries and Oceans Canada
417-2nd Avenue West
Prince Rupert, B. C., Canada V8J 1G8
3 Pacific Salmon Commission
600-1155 Robson Street
Vancouver, B. C., Canada V6E 1B5
Testing for Differences: among Prince Willian Sound

Even Year

$p < 10^{-6} (\alpha = 0.05)$
Testing for Differences: Between Early and Late Collections

East: Genetically different for 3 of 5
West: No significant differences

$p < 0.05 (\alpha = 0.05)$
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

<table>
<thead>
<tr>
<th>Species</th>
<th>2013</th>
<th>2014</th>
<th>2015</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pink</td>
<td>4.4%</td>
<td>14.8%</td>
<td>9.5%</td>
</tr>
<tr>
<td>Chum</td>
<td>2.8%</td>
<td>3.2%</td>
<td>3.1%</td>
</tr>
</tbody>
</table>
SEAK: Hatchery fraction by stream: 1.5% - 12.7%
Overall SEAK hatchery fractions in spawning streams

<table>
<thead>
<tr>
<th>Species</th>
<th>2013</th>
<th>2014</th>
<th>2015</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chum</td>
<td>7.3%</td>
<td>5.4%</td>
<td>9.2%</td>
</tr>
</tbody>
</table>
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%

<table>
<thead>
<tr>
<th>Species Common Name</th>
<th>Year</th>
<th>Hatchery Proportion</th>
<th>SE</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pink Salmon</td>
<td>2013</td>
<td>0.679</td>
<td>.016</td>
</tr>
<tr>
<td></td>
<td>2014</td>
<td>0.864</td>
<td>.03</td>
</tr>
<tr>
<td></td>
<td>2015</td>
<td>0.549</td>
<td>.004</td>
</tr>
<tr>
<td>Chum Salmon</td>
<td>2013</td>
<td>0.725</td>
<td>.019</td>
</tr>
<tr>
<td></td>
<td>2014</td>
<td>0.511</td>
<td>.029</td>
</tr>
<tr>
<td></td>
<td>2015</td>
<td>0.688</td>
<td>.015</td>
</tr>
</tbody>
</table>

Wild and Hatchery run size estimates

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

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

Natural and Hatchery harvest rate estimates: PWS pink salmon

<table>
<thead>
<tr>
<th>Year</th>
<th>Estimated Harvest Rates</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Hatchery</td>
</tr>
<tr>
<td>2013</td>
<td>0.99</td>
</tr>
<tr>
<td>2014</td>
<td>0.98</td>
</tr>
<tr>
<td>2015</td>
<td>0.95</td>
</tr>
</tbody>
</table>
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
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**

**Chinook**

**Coho**

**Chum**
Hatchery/Natural Fitness

<table>
<thead>
<tr>
<th>Year</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Fa</td>
<td>Wi</td>
<td>Sp</td>
<td>Su</td>
<td>Fa</td>
<td>Wi</td>
<td>Sp</td>
</tr>
<tr>
<td>Pink</td>
<td>gravel</td>
<td>ocean</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Chum</td>
<td>gravel</td>
<td>ocean</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Chinook</td>
<td>gravel</td>
<td>freshwater</td>
<td>ocean</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Coho</td>
<td>gravel</td>
<td>freshwater</td>
<td>ocean</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sockeye</td>
<td>gravel</td>
<td>freshwater</td>
<td>ocean</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Steelhead</td>
<td>gravel</td>
<td>freshwater</td>
<td>ocean</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Hatchery residency
AHRP Streams in PWS

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

Figure 1 – Lescak et al. in prep
Fitness = Reproductive Success

Parent
Measuring Reproductive Success

Parent
Measuring Reproductive Success

Parent
Measuring Reproductive Success

Parent
Measuring Reproductive Success

P

Male

Female
Measuring Reproductive Success

Male  Female

P □   □   □   □   □   □
Measuring Reproductive Success

Male  Female  75

Hatchery-origin
Measuring Reproductive Success

P

Natural

Male

Female

Hatchery

Male

Female
Measuring Reproductive Success

Natural
- Male
- Female

Hatchery
- Male
- Female
Measuring Reproductive Success

Natural
Male
Female

Hatchery
Male
Female
Measuring Reproductive Success

Natural
Male
Female

Hatchery
Male
Female
Measuring Reproductive Success

Natural
Male
Female

Hatchery
Male
Female
Measuring Reproductive Success

Natural Male

Natural Female

Hatchery Male

Hatchery Female

Hatchery-origin

8 Ring Thermal Mark
Dark Ring
Hatch Mark
Band
Circulus
Measuring Reproductive Success

Natural| Hatchery
Male    | Male
Female  | Female
Hatchery-origin fish are not genotyped in the offspring generation because they have a known origin.
Measuring Reproductive Success

298 markers

Figure 1 – Campbell et al. 2015
Measuring Reproductive Success

<table>
<thead>
<tr>
<th>Natural Male</th>
<th>Hatchery Male</th>
<th>Female</th>
<th>Female</th>
</tr>
</thead>
<tbody>
<tr>
<td>Male</td>
<td>Female</td>
<td>Male</td>
<td>Female</td>
</tr>
</tbody>
</table>

298 markers

Figure 1 – Campbell et al. 2015

Riester et al. 2009
Genetic markers for parentage analysis

Fish 1
- CTATGTA\(\text{T}\)AAATGTTAATAATAAACTAGCTAACC
- CTATGTA\(\text{A}\)AAATGTTAATAATAAACTAGCTAACC

Fish 2
- CTATGTA\(\text{A}\)AAATGTTAATAATAAACTAGCTAACC
- CTATGTA\(\text{A}\)AAATGTTAATAATAAACTAGCTAACC

Fish 3
- CTATGTA\(\text{A}\)AAATGTTAATAATAAACTAGCTAACC
- CTATGTA\(\text{T}\)AAATGTTAATAATAAACTAGCTAACC

Fish 4
- CTATGTA\(\text{T}\)AAATGTTAATAATAAACTAGCTAACC
- CTATGTA\(\text{T}\)AAATGTTAATAATAAACTAGCTAACC

Legend:
- T allele
- A allele
Genetic markers for parentage analysis

Markers

Potential sires (♂)

Offspring

1
A
A

Sire 1

A
A

Sire 2

T
T

Sire 3

A
T

Sire X

T
T
Genetic markers for parentage analysis

<table>
<thead>
<tr>
<th>Markers</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>•</th>
<th>•</th>
<th>•</th>
<th>298</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>A</td>
<td>C</td>
<td>T</td>
<td></td>
<td></td>
<td></td>
<td>T</td>
</tr>
<tr>
<td></td>
<td>A</td>
<td>G</td>
<td>A</td>
<td></td>
<td></td>
<td></td>
<td>T</td>
</tr>
</tbody>
</table>

Potential sires (♂)

- **Sire 1**: A A
- **Sire 2**: T T
- **Sire 3**: A T
- **Sire X**: T T

Offspring →
Genetic markers for parentage analysis

Potential sires (♂)

Sire 1

Sire 2

Sire 3

Sire X

Offspring

Markers

1  2  3  •  •  •  298
A  C  T  A
A  G  A  T
A  C  T

89
Genetic markers for parentage analysis

Potential sires (♂)

Offspring

Markers

1
A
2
C
3
T
•
•
•
298
T
T

Sire 1
A
A

Sire 2
T
T

Sire 3
A
T

Sire X
T
T

DAD!
Measuring Reproductive Success

RS = \frac{\text{# Offspring}}{\text{# Parents}}

Natural
Male
Female

Hatchery
Male
Female

P
O
Measuring Reproductive Success

\[ RS_H \text{ Female} = 1 \]
Measuring Reproductive Success

Natural Male
Female
Hatchery Male
Female
Measuring Reproductive Success

\[ RS_N \text{ Female} = 2 \]

\[ RS_H \text{ Female} = 1 \]
Measuring Reproductive Success

Relative Reproductive Success (RRS)

\[ \text{RRS} = \frac{1}{2} = 0.5 \]

\[ \text{RS}_N \text{ Female} = 2 \]
\[ \text{RS}_H \text{ Female} = 1 \]

Natural | Hatchery
--- | ---
Male | Male
Female | Female
Measuring Reproductive Success

Relative Reproductive Success (RRS)

\[
RRS = \frac{RS_{\text{Hatchery}}}{RS_{\text{Natural}}}
\]
Analyzed Samples: Even-Lineage

Figure 2b – Lescak et al. *in prep*
Figure 2b – Lescak et al. *in prep*
Analyzed Samples: Even-Lineage

N = 653
8-13% esc.

N = 4,295
54% esc.

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 – WNI
    - 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

RS = 0.46

Figure 3b – Lescak et al. *in prep*
RS Distribution: Even-Lineage

**Female**
- RS = 0.46
- RS = 0.97
- RRS = 0.47*

**Male**

**Parent Origin**
- Natural
- Hatchery

Figure 3b – Lescak et al. *in prep*
RS Distribution: Even-Lineage

Female

- RS = 0.46
- RS = 0.97
- RRS = 0.47*

Male

- RS = 0.84
- RS = 0.97
- RRS = 0.87 (NS)

Parent Origin
- Natural
- Hatchery

Figure 3b – Lescak et al. in prep
Proportion Test: Even-Lineage

Hogan

Origin
- Natural
- Hatchery

Lineage
- Even

Parents 2014

Generation

Offspring 2016

33%

67%
Proportion Test: Even-Lineage

Hogan

<table>
<thead>
<tr>
<th>Lineage</th>
<th>Even</th>
<th>Parents 2014</th>
<th>Generation</th>
<th>Offspring 2016</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>67%</td>
<td></td>
<td>56%</td>
</tr>
<tr>
<td>Origin</td>
<td></td>
<td>Natural</td>
<td>Hatchery</td>
<td>Natural</td>
</tr>
<tr>
<td></td>
<td>33%</td>
<td></td>
<td>44%</td>
<td></td>
</tr>
</tbody>
</table>

2014 2016
Parent-Offspring Duos

P

O

Natural Hatchery

Male Female Male Female
Parent-Offspring Trios

Natural Hatchery

Male Female

Male Female

Male Female
Analyzed Samples: Odd-Lineage

N = 777
2-10% esc.

N = 1,920
11-21% esc.

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

Reproductive Success for Odd-Lineage

<table>
<thead>
<tr>
<th>Female</th>
<th>Male</th>
</tr>
</thead>
<tbody>
<tr>
<td>RS = &lt;0.01</td>
<td>RS = 0.01</td>
</tr>
<tr>
<td>RS = 0.19</td>
<td>RS = 0.10</td>
</tr>
<tr>
<td>RRS = 0.02*</td>
<td>RRS = 0.12*</td>
</tr>
</tbody>
</table>

Figure 3b – Lescak et al. *in prep*
Proportion Test: Odd-Lineage

- **Lineage**: Odd
  - Parents 2013: 58%
  - Offspring 2015: 42%

- **Origin**:
  - Natural
  - Hatchery
Proportion Test: Odd-Lineage

**Lineage**
- **Odd**: 58%
- **Hogan**: 42%

**Generation**
- **Parents 2013**
- **Offspring 2015**

**Origin**
- Natural: 94%
- Hatchery: 6%
Proportions for Both Lineages

- **Lineage**
  - Odd
  - Even

- **Generation**
  - Parents
  - Offspring

- **Origin**
  - Natural
  - Hatchery

The diagram shows the proportions for both lineages (Odd and Even) across generations (Parents and Offspring) for the Hogan origin, with the natural and hatchery origin categories.
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
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?
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

- **F0** – parents
- **F1** – offspring
- **F2** – grand-offspring
- **Adult**
- **Alevin**


- **Chum (BY1)**
  - F0
  - F1
  - F1

- **Chum (BY2)**
  - F0
  - F1
  - F1
  - F1

- **Sampling year**
  - 0.2
  - 0.3
  - 0.4
  - 0.4
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.
## Samples by origin, stream, and year

<table>
<thead>
<tr>
<th>Stream</th>
<th>2013</th>
<th>2014</th>
<th>2017</th>
<th>2018</th>
</tr>
</thead>
<tbody>
<tr>
<td>Admiralty Creek</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Fish Creek</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Prospect Creek</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sawmill Creek</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

### Number of Samples

- **Origin**: natural, hatchery

### Day of Year

- Ranges: 200 to 240
Acknowledgements

• Alaska Hatchery Research Program
  • State of Alaska
  • Seafood industry
  • Private non-profit hatcheries

• Sitka Sound Science Center
  • Field collection

• ADF&G Mark, Tag and Age Lab
• ADF&G Gene Conservation Laboratory
Questions?