

An overview of genetic stock identification of salmon captured in Alaska groundfish fisheries

Wes Larson
Program Manager, Genetics Group
NOAA Alaska Fisheries Science Center
wes.larson@noaa.gov

Goals of salmon bycatch stock identification

Primary goals

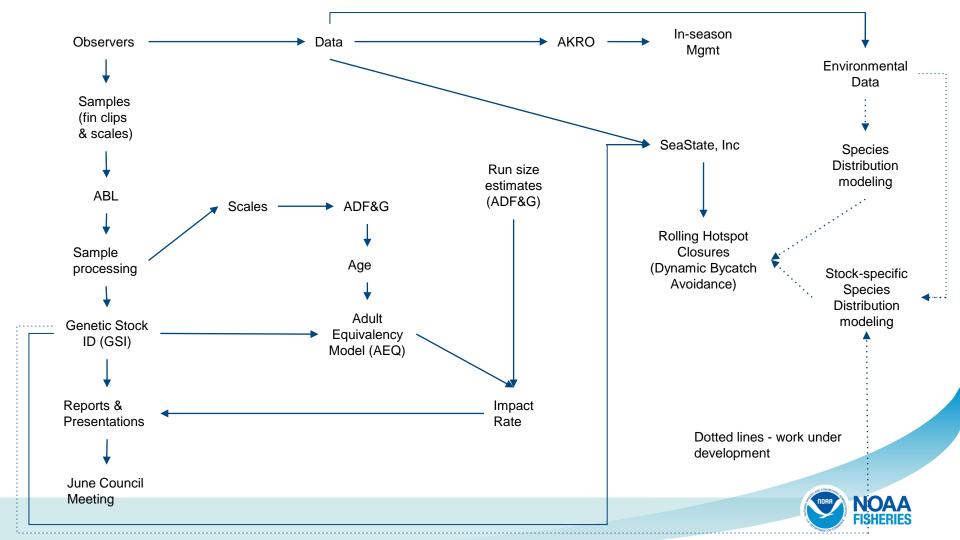
- •(1) Determine the geographic origin of salmon caught in federally managed groundfish fisheries to determine stock-specific impacts (current)
- •(2) Merge stock ID with other data to predict stock-specific distributions and potentially avoid certain stocks (future)
- Today
 - Overview of the program
 - Higher level results from Chinook Salmon & Chum Salmon



Genetic sampling from the observer program

- BSAI pollock: Systematic random sampling
 - All salmon counted
 - •Chinook 1 in 10 sampled
 - •Chum 1 in 30 with further subset analyzed for genetics (½ to ¼ of samples depending on number)
- GOA pollock: Simple random sampling with respect to trip (few chum caught)
- Data collected for each sampled salmon
 - Basic information (length and sex)
 - Scale samples for aging
 - Genetic Samples





Genetic Methods - Genetic stock identification (GSI)

• Objective: Estimate the proportion of the bycatch that is from different regional groups

 Method: Compare genetic composition of bycatch (mixture) to known spawning aggregations (baseline)



Genetic stock identification: a visual

Bycatch Mixture - Genetically sample salmon



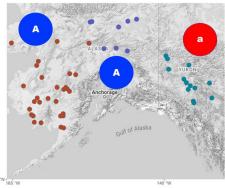
What proportion comes from major drainages?

Think about the individual



Genotype = AA

Baseline -3 Reporting Groups
Fixed for genetic marker



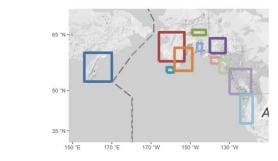
Compare to known spawning populations.

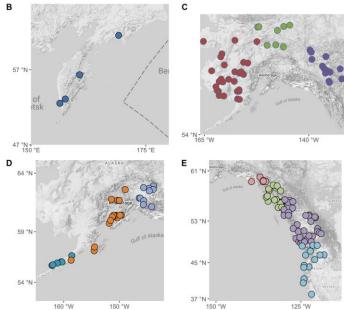


Baseline -Chinook Salmon

11 reporting groups

- ь. Russia
- c. Coastal Western Alaska, Middle Yukon, Upper Yukon
- d. North Alaska Peninsula, NW Gulf of Alaska, Copper, NE Gulf of Alaska,
- e. Southeast Alaska, British Columbia, West coast US



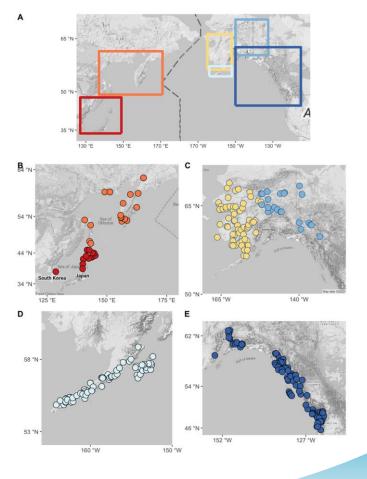




Baseline - Chum Salmon

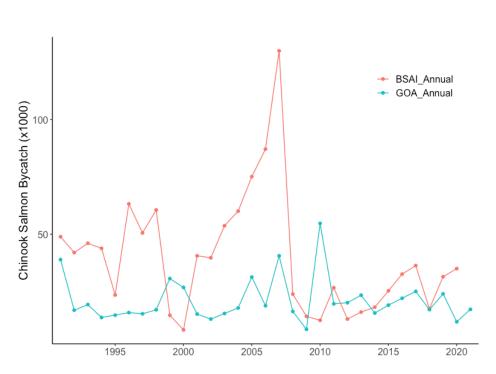
6 reporting groups:

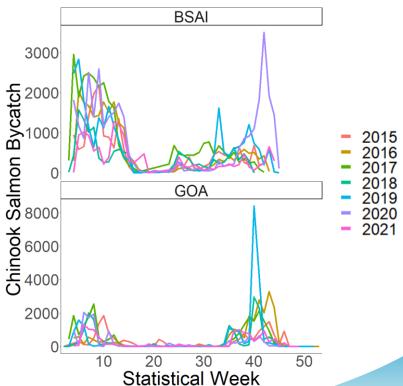
- b. SE Asia & NE Asia
- c. Upper/Middle Yukon, Western Alaska,
- d. Southwest Alaska
- e. Gulf of Alaska / Pacific Northwest





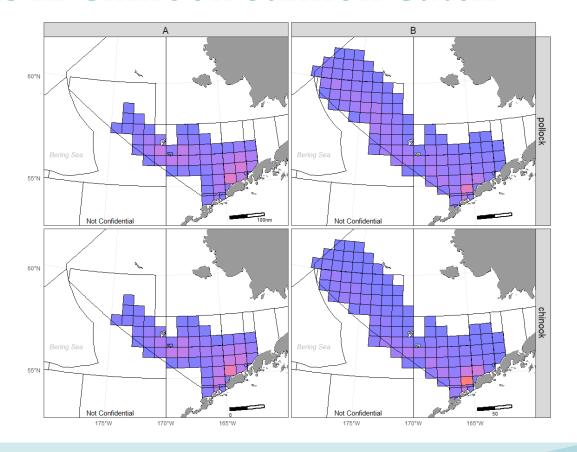
Trends in Chinook Salmon Bycatch





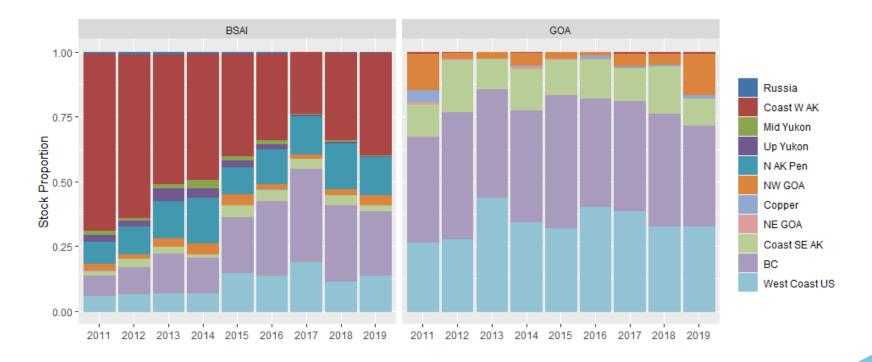


Trends in Chinook Salmon Catch



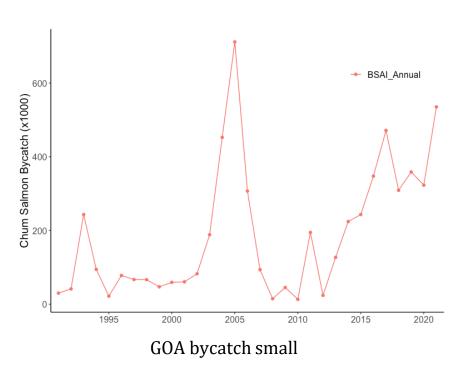


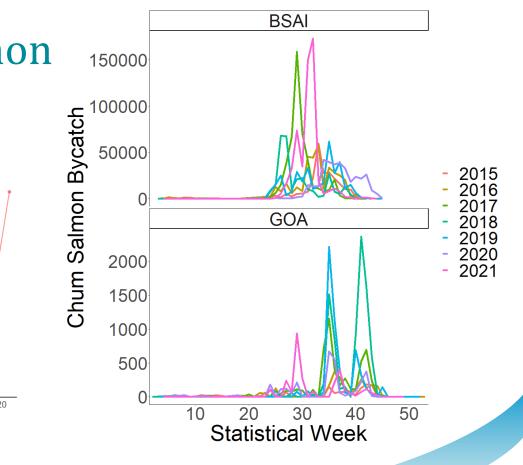
Trends in Chinook Salmon Stock Composition





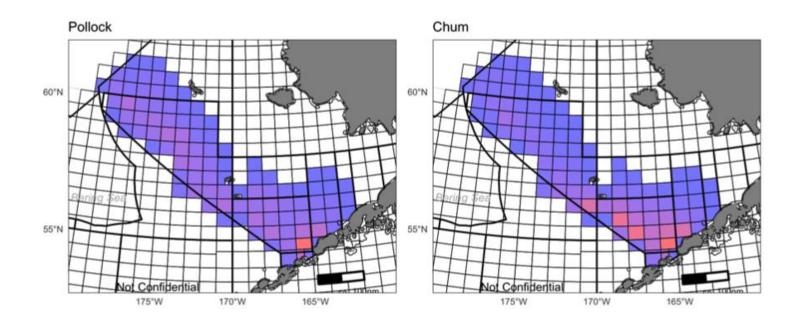
Trends in Chum Salmon





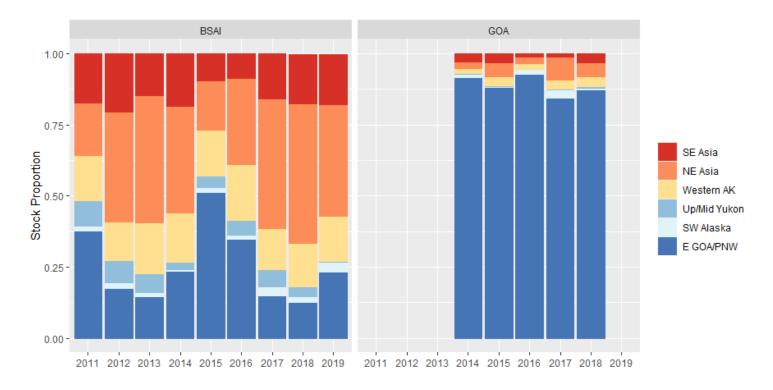


Trends in Chum Salmon





Trends in Chum Salmon Stock Composition - BSAI





Future Directions: updating workflow

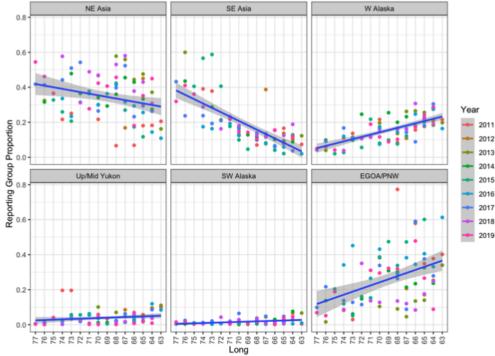
- New genotyping chemistry and analysis method
- Ages for all samples
- Database integration
- Collaboration with quantitative ecologists
- Automated workflow





Future Directions: benefits of increased efficiency

- Reduce turnaround by a year for chum
- Leverage new database capabilities
- Retrospective analyses
- Distribution modeling
 - Stock proportions, ages, environmental covariates
 - Goal: better avoid certain stocks



As you move west, proportion of Asian stocks increase and WAK and southern stocks decrease



Collaborative Research

- <u>AFSC ABL</u> C. Guthrie, C. Kondzela, J. Whittle, K. Karpan, Hv. T. Nguyen, E. Yasumiishi, K. D'Amelio, J. Watson, P. Barry
- AFSC REFM J. Ianelli
- <u>AFSC FMA</u> M. Concepcion, B. Mason, J. Cahalan, and a village
- AKFIN C. Kohler, R. Ames, R. Ryznar, M. Callahan
- · ADFG GCL C. Habicht, K. Shedd, C. Jalbert, E. Lee
- ADFG MTAL J. Neil, D. Oxman, B. Agler, T. Frawley
- <u>Funding-PCCRC</u>, NOAA, additional proposals in progress (AYKSSI)

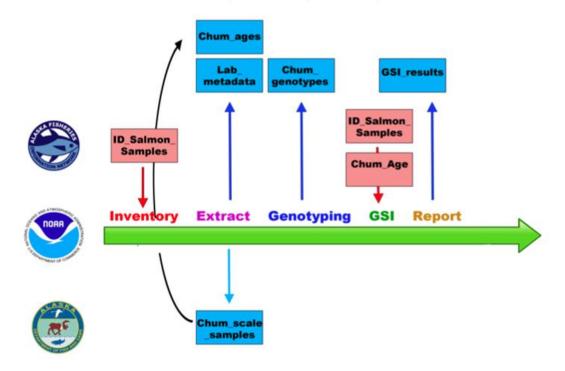


Questions wes.larson@noaa.gov



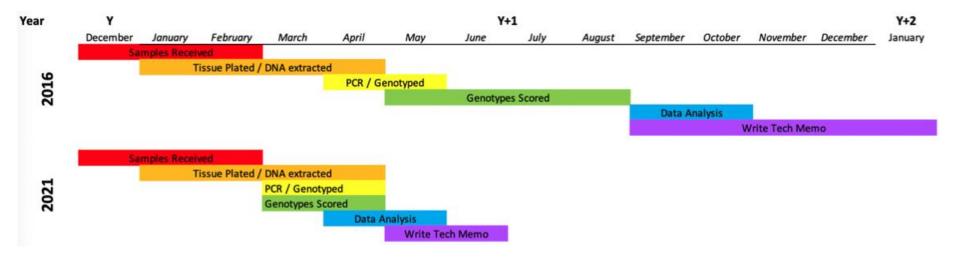
Pipeline Development

NOAA, ADF&G, AKFIN, UAF



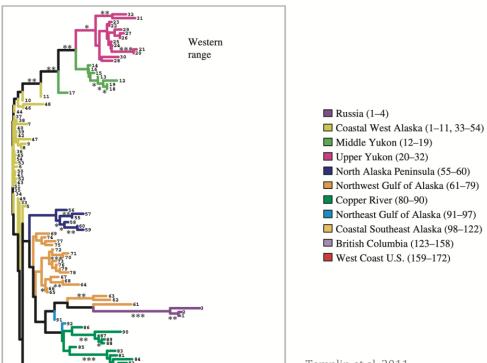


Accelerated GSI timelines





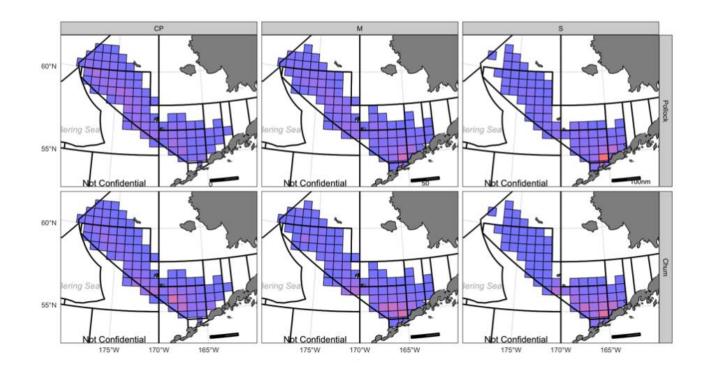
Genetic Differentiation of Yukon





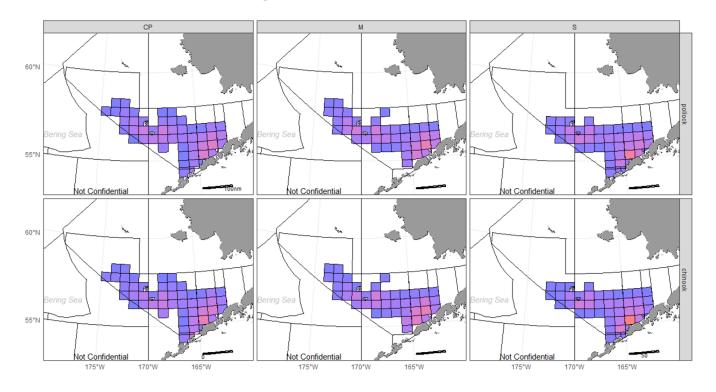


Chum Catch By Sector



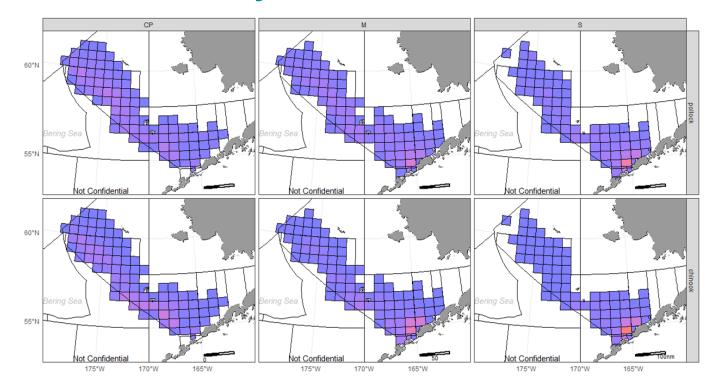


Chinook Catch By Sector A Season



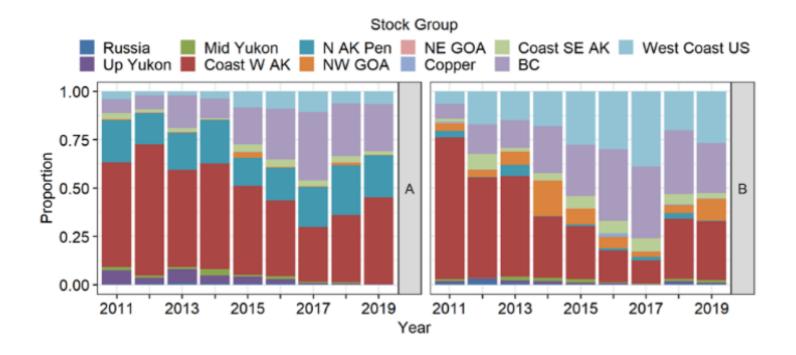


Chinook Catch By Sector B Season



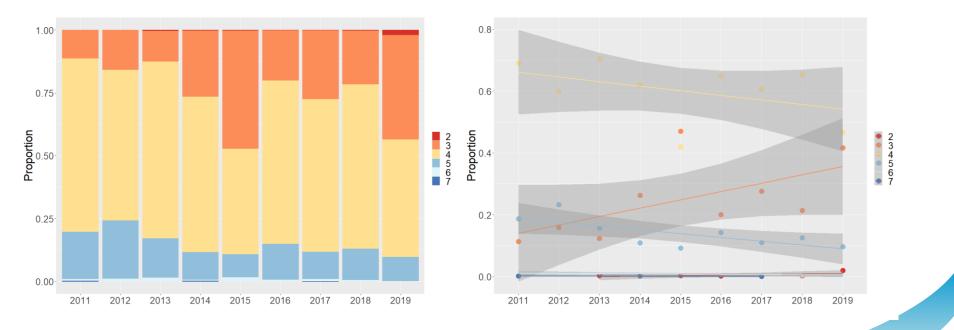


Chinook: A vs B season





Changes in Chum Age Distribution





Genetic Marker & Baseline Development - Chum Salmon

- · 1994-1996(?)
 - 20 Protein (Allozymes) markers
 - 4-5 regional reporting groups
- · 2005 2019
 - 11 DNA (microsatellite) markers
 - Baseline development DFO
 - 6 regional reporting groups
- 2020
 - 84 DNA (single nucleotide polymorphims) markers
 - WASSIP panel development ADFG
- Existing larger panels require baseline development

