# Chum Salmon progress on genetic markers



Kristen Gruenthal Gene Conservation Laboratory Alaska Department of Fish and Game AHRP Informational Meeting March 9, 2022

## Alaska Hatchery Research Program

- 1) What is the genetic structure of pink and chum in PWS and SEAK?
- 2) What is the extent and annual variability of straying?
- 3) What is the impact on <u>fitness</u> (productivity) of natural pink and chum stocks due to straying hatchery pink and chum salmon?

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- Ideally compatible with newer high-throughput GTseq chemistry



CCFDDFDHHHHHJJJJIGJIIIJJJJJHIEFIFIFIGIIJJJJJJJJJJJJJIJFHHGFFFFFDCEEEEDDBDBAC3:>C((50>8<B###########

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  - 61 SNPs overlap with WASSIP baseline
  - MAF > 0.3 for 137 SNPs
  - No microhaplotypes identified

*Insufficient for our incomplete pedigrees* 



#### Progress and next steps

- Purpose-build a chum GT-seq panel for parentage
  - 300-400 markers
  - Single-SNP MAF > 0.3
  - Microhaplotypes, if possible
- Progress to date
  - Restriction site-associated DNA sequencing (RADseq) completed Fall 2021
    - 48 natural-origin chum from each of Fish, Sawmill, and Prospect Creeks
    - 24 DIPAC broodstock
    - 24 DIPAC hatchery strays in Fish Creek
  - SNP discovery and genotyping in progress
- Next steps
  - Filter data for high MAF loci (preferentially retaining microhaplotypes)
  - Rank loci by information content
  - Design primer sets for top ~500 loci
    - Optional: include the Best 96 and/or 137 high MAF Oke.350 SNPs (crosscompatibility)
  - Optimize panel in lab (iteratively cull loci)

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- Alaska Hatchery Research Program
  - State of Alaska
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  - Private non-profit hatcheries
- Pacific Salmon Commission
  - Northern Endowment Fund
- Sitka Sound Science Center
  - Field collection
- ADF&G Mark, Tag and Age Lab
- ADF&G Gene Conservation Laboratory



## Questions?