



Introduction

- Chinook salmon are important for commercial, sport, subsistence, and personal use fisheries in Upper Cook Inlet, Alaska (annual harvests > 25,000).
- Salmon home to natal streams which results in genetically distinct stocks. Alaska manages fisheries to meet escapement objectives, which requires understanding the productivity of each stock.
- Productivity is measured as the number of fish returning from each stock, including those harvested while migrating to their home stream.
- Most harvested fish are caught as they return to their home stream.
- Genetic data can be used to determine stock composition of harvests.
- Prior to 2008, the genetic baseline for Cook Inlet Chinook salmon consisted of a total of 18 populations and most of these were from the Kenai Peninsula.
- Here we examine a new genetic baseline to determine population structure for insights on potential stock discrimination.



Chinook salmon in Upper Cook Inlet, Alaska: genetic diversity is higher in Southern stocks than in Northern stocks Andy Barclay¹ and Richard Merizon²

¹Gene Conservation Laboratory, Commercial Fisheries Division, Alaska Department of Fish and Game, Anchorage, Alaska ²Sport Fish Division, Alaska Department of Fish and Game, Palmer, Alaska





0 5 10 20 30 40

Within

Collections

Methods From 2008 to 2010, adult Chinook were sampled throughout Cook Inlet and screened for 40 single nucleotide polymorphisms.

Results

An additional 2,199 fish were screened, increasing the size of the baseline to 5,074 fish representing 30 populations.





Southern region

Multidimensional scaling

Methods

Pairwise F_{ST} between populations was calculated and plotted using multidimensional scaling. Populations were assigned to 6 groups based on geography.

Results

Populations cluster into two regions: Northern - Most populations in this region cluster with other populations in the same group. One west Cook Inlet (3) and one Knik Arm (13) population cluster with Susitna **River populations (green).** Southern - The two lower tributary populations in the Kenai and Kasilof rivers (25 & 26) cluster and the mainstem populations from each river cluster as well (20, 24, & 26).



Methods

Genetic variation between and among groups and regions was calculated using hierarchical log-likelihood tests.

Results

There is more within-group and among-group diversity in the Southern region, indicating a greater potential for stock discrimination among Southern stocks than Northern stocks.

Acknowledgements

Funding for this study was provided by the Pacific Coast Salmon Recovery Fund under project 45864, Northern Cook Inlet Chinook GSI. We would like to thank the Chickaloon Village Traditional Council for providing us with an additional two years of samples from Moose Creek.



Hierarchical log-likelihood

