Genetic Studies of Chinook Salmon in the Kuskokwim River, Alaska

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Introduction

The subsistence fishery for Chinook salmon in the Kuskokwim River region is one of the largest and most significant in Alaska. The average annual subsistence harvest between 1991 and 2000 was approximately 85,000 Chinook salmon. Low returns in recent years have yielded shortfalls in escapements basin-wide and lead to fishing restrictions, which have directly affected local communities. Sustained productivity of salmon is only possible if genetic diversity and population structure are maintained. We investigated the genetic diversity of Chinook salmon from the Kuskokwim River using three different types of genetic markers: Allozymes, microsatellites and single nucleotide polymorphisms (SNPs). Markers were used to develop a baseline that will be useful for estimating stock composition of commercial and subsistence harvests, investigating run timing and entry patterns within the river, and examining the effectiveness of management actions for the conservation of the resource.

Kuskokwim River Chinook Sampling Sites

1 Salmon River
2 Takotna River
3 Tatlawitsuk River
4 Cheneetnuk River
5 Stony River
6 Kogrukluk River
7 George River
8 Aniak River
9 Tuluksak River
10 Kisaralik River
11 Kwethluk River
12 Eek River
13 Kanektok River
14 Goodnews River

Baseline Collections

Crews from Alaska Department of Fish and Game, US Fish and Wildlife Service, Kuskokwim Native Association, and subsistence users collected samples from Chinook salmon at 14 locations including weir sites, subsistence fisheries near spawning grounds, and on the spawning grounds. The target sample size was 100 adults per collection.

Clipping a piece of fin

Samples stored in liquid nitrogen

Removing salmon from net

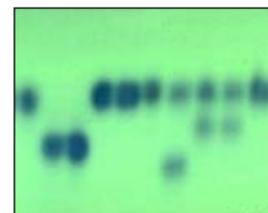Sampling cheek muscle

Laboratory analysis

1) Allozyme

Explanation
Examines variation in protein structure caused by differences in the genetic code.

Advantages
- Over 30 years of experience with this technique
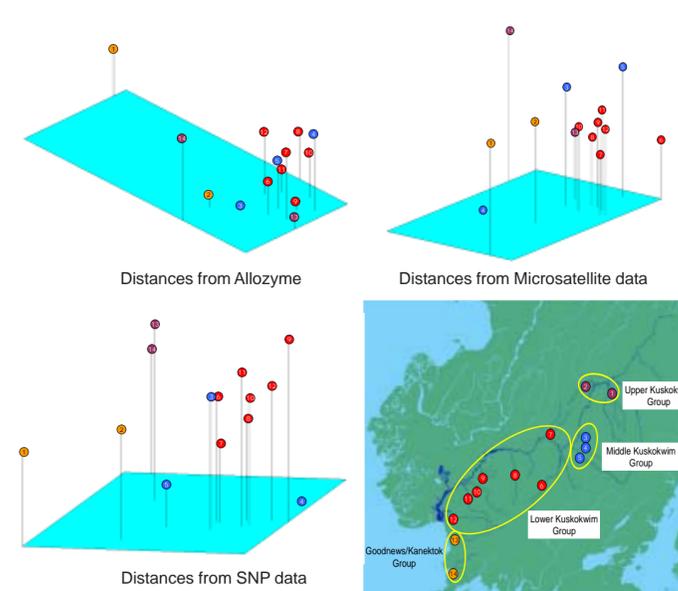- Extensive databases available

Disadvantages
- Requires expensive and hazardous handling in the field and laboratory
- Sampling is generally lethal
- Limited coverage of the genome

2) Microsatellites

Explanation
Examines repeated segments in the noncoding regions of the genetic code.

Advantages
- Sampling does minimal damage to the salmon
- Easier to handle the samples in the field
- High variability improves sensitivity

Disadvantages
- High variability requires larger sample sizes
- Limited coverage of the genome
- Difficult to repeat analyses between laboratories

3) Single Nucleotide Polymorphisms (SNPs)

Explanation
Examines changes at a single position in the genetic code.

Advantages
- Sampling does minimal damage to the salmon
- Easier to handle the samples in the field
- Laboratory analysis is least expensive and rapid
- Can occur anywhere in the genome
- Easy to duplicate analyses between laboratories

Disadvantages
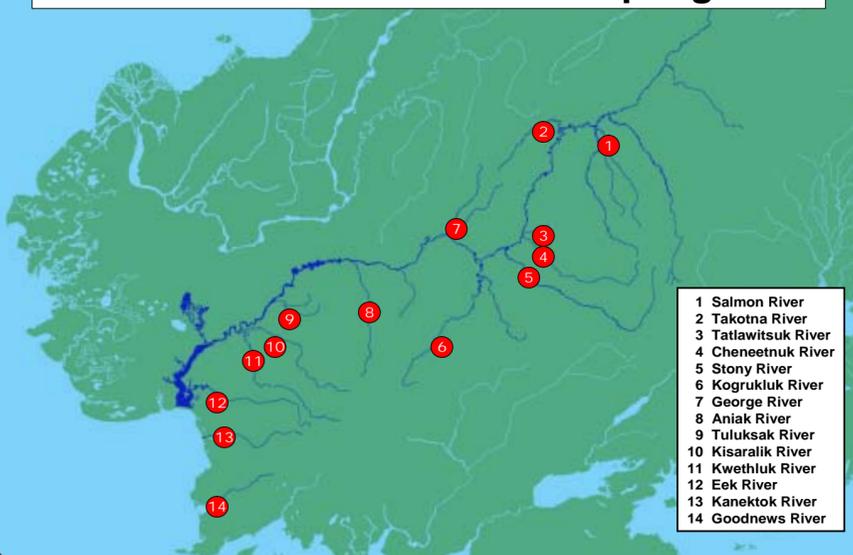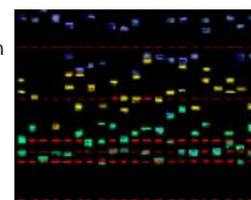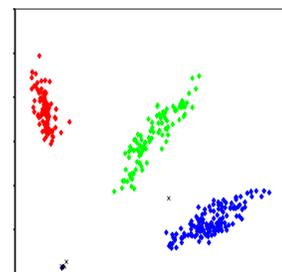- Limited to two potential forms at each marker

Population Structure Investigation

One method used to investigate the similarity between populations was to calculate the genetic distance between populations using each of the three types of genetic marker. These distances were drawn in three dimensions to display relationships between populations (The further apart two dots are, the less similar the populations.) The dots and numbers match the populations on the map. The populations were divided into four groups based on genetic and geographic factors. Group membership is indicated by the color of the dot. All three types of markers separate the Upper Kuskokwim and Goodnews/Kanektok populations, but differ in their ability to distinguish the Lower and Middle Kuskokwim groups.

Distances from Allozyme

Distances from Microsatellite data

Distances from SNP data

Upper Kuskokwim Group

Middle Kuskokwim Group

Lower Kuskokwim Group
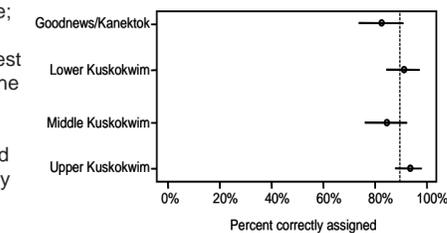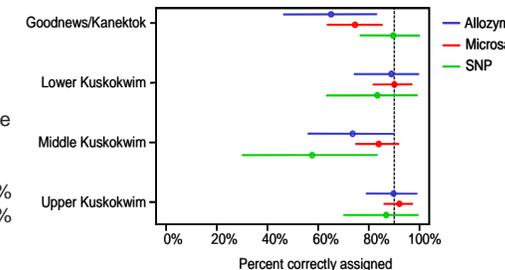
Goodnews/Kanektok Group

Stock Identification Results

The genetic information provided by this study can potentially be used to identify populations of Chinook salmon harvested in Kuskokwim River fisheries. By imitating a harvest that only has salmon from one of the four groups defined above and applying the genetic information from each type of marker, we can test how useful the data are for this purpose. Perfection is 100% correctly assigned to the contributing group; above 90% (the dotted line) is considered "Very Accurate." This test was repeated for each group using each of the genetic markers separately (**Top Graph**). The dot represents the best estimate and the line shows how confident we are; shorter lines show higher confidence. Microsatellites do the best overall, but SNPs help identify the Goodnews/Kanektok group.

Combining the microsatellite and SNP data improves our accuracy and confidence in identifying these groups (**Bottom Graph**).

Ricky Ciletti
Field Technician

— Allozyme
— Microsat
— SNP

Goodnews/Kanektok
Lower Kuskokwim
Middle Kuskokwim
Upper Kuskokwim

0% 20% 40% 60% 80% 100%
Percent correctly assigned

Group identification using each set of genetic markers

Goodnews/Kanektok
Lower Kuskokwim
Middle Kuskokwim
Upper Kuskokwim

0% 20% 40% 60% 80% 100%
Percent correctly assigned

Group identification using microsatellites and SNPs

Conclusions

- Allozyme, microsatellite and SNP markers all depict similar genetic structure of the Chinook salmon populations of the Kuskokwim Drainage.
- Four groups of populations were identified based on genetic and geographic factors.
- The microsatellite and SNP data show potential for identifying populations captured in Kuskokwim River salmon fisheries.
- Allozyme data wil be used in a larger baseline for trawl bycatch studies.

Acknowledgements

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