



George River Weir

Allozymes, Microsatellites and SNPs Concur on Population Structure of Chinook Salmon in the Kuskokwim River



William Templin and Lisa Seeb
Division of Commercial Fisheries, Alaska Department of Fish and Game



Introduction

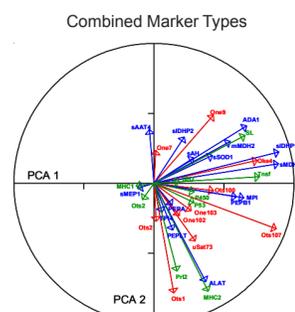
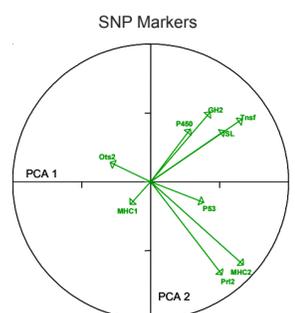
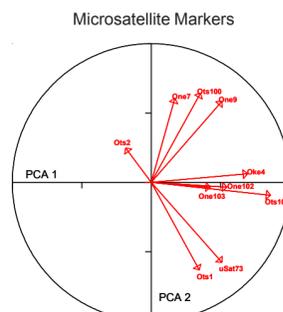
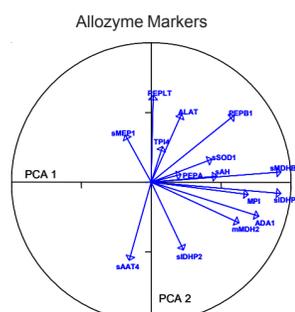
The subsistence fishery for Chinook salmon in the Kuskokwim River region is one of the largest and most significant in Alaska. The average annual subsistence harvest between 1991 and 2000 was approximately 85,000 Chinook salmon. Low returns in recent years have yielded shortfalls in escapements basin-wide 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 population structure of Chinook salmon from the Kuskokwim River using three different types of genetic markers: allozymes, microsatellites and single nucleotide polymorphisms (SNPs). A baseline was developed 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.



Correlation of Genetic Markers

Explanation of Method

Concurrence of the information provided by individual markers can be examined by plotting the correlation between inter-population genetic distances calculated from each marker and the first two principal components. These correlations can be plotted on a unit circle (radius = 1) with axes representing the first and second principal components (PCA 1 and PCA 2). On such a circle, markers which provide similar information on population structure will cluster together. Orthogonal vectors on this circle represent markers which provide complementary information on population structure.

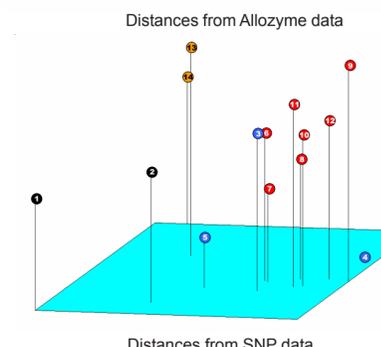
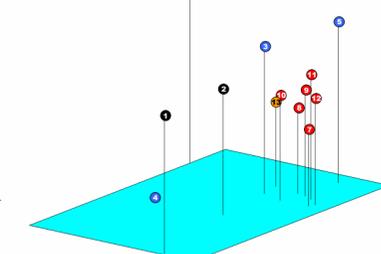
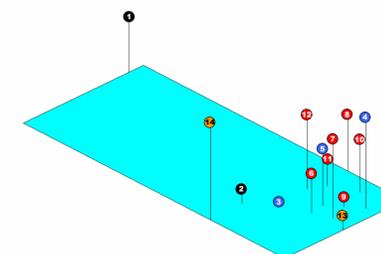


Marker Type Agreement

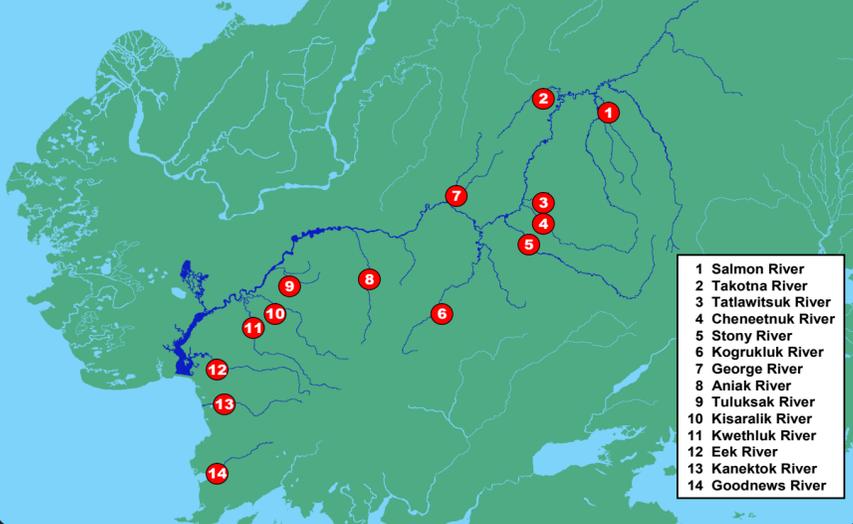
All three types of markers generally form two or three groups on the unit circle, falling in the first and fourth quadrants as well as along the axis of PCA 1. Vectors falling near PCA 1 indicate markers providing the major distinction between populations. Those in the first and fourth quadrants indicate markers providing additional levels of distinction. A similar pattern is shown when all markers are used in a combined analysis. This indicates agreement both within and between marker types on the population structure of Kuskokwim River Chinook salmon. Additional support for marker concordance is provided by Mantel correlations between genetic distances calculated from each marker type: allozyme/microsatellite (72%), allozyme/SNP (62%), and microsatellite/SNP (73%).

Population Structure

Chord distances were calculated between populations using each of the three types of genetic marker and these distances were plotted in three dimensions (multidimensional scaling analysis) to display relationships between populations. (The dots and numbers match the populations on the map.) Markers agreed that populations could be 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.



Kuskokwim River Chinook Sampling Sites



- 1 Salmon River
- 2 Takotna River
- 3 Tatlawitsuk River
- 4 Cheneetnu 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



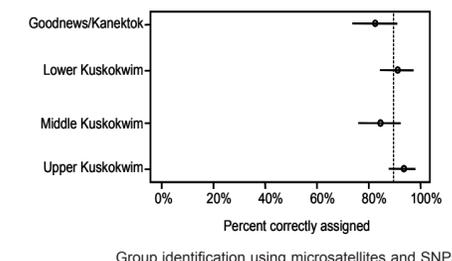
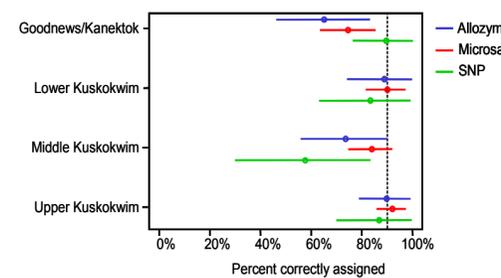
Sampling cheek muscle



Laboratory analysis

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 (**Left 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 (**Right Graph**).



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 can be used to identify populations captured in Kuskokwim River salmon fisheries.

Acknowledgements

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