High-Resolution Stock Identification for Migratory Studies of Chinook Salmon

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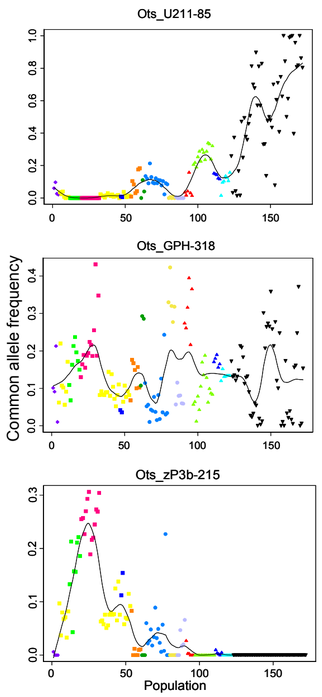
Introduction

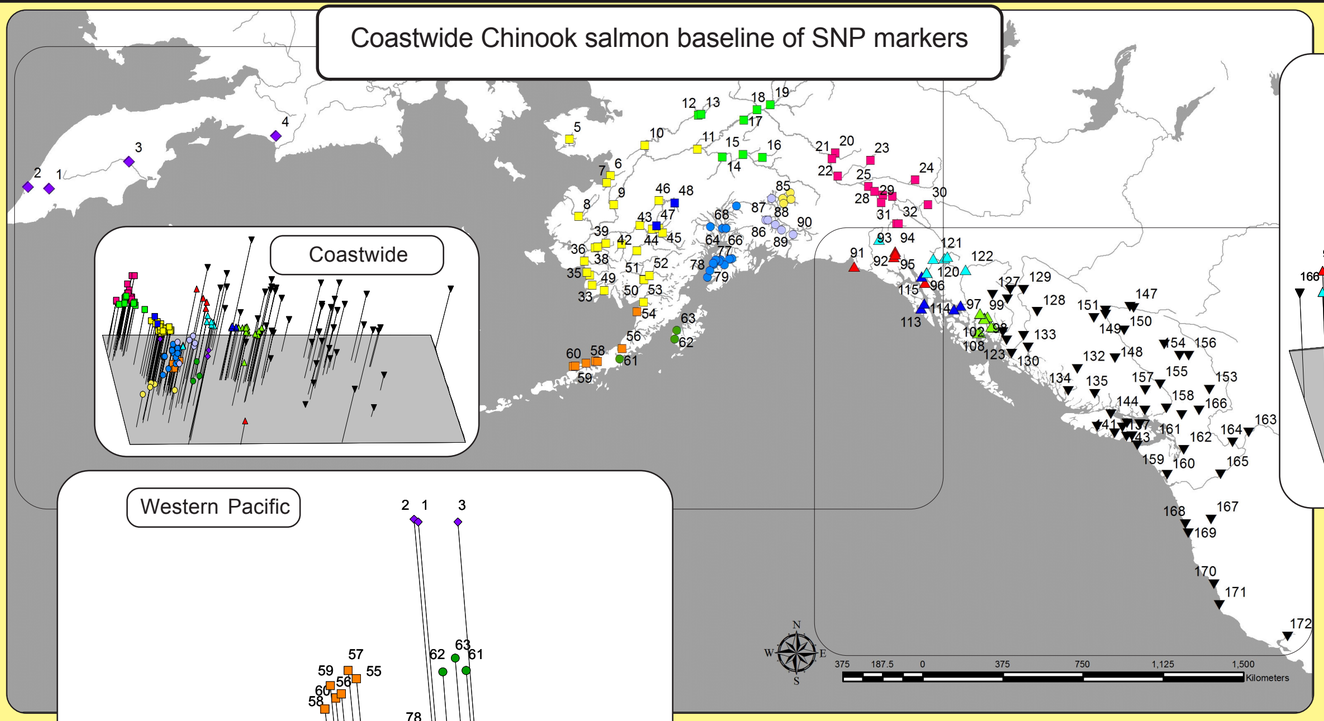
Little is known of the oceanic migration patterns and relative survival of individual stocks of Chinook salmon. Until recently, investigation of the effects of fluctuating marine conditions on the abundance and distribution of Chinook salmon has only been approachable through the sporadic collection of tagged individuals and analysis of scale patterns. Here we present a baseline of genetic markers based on 45 single nucleotide polymorphisms (SNPs) surveyed in 172 populations across the species range in the North Pacific. This baseline provides the foundation for the application of genetic stock identification for high-resolution exploration of the distribution of Chinook salmon in marine waters. Initial results indicate that 15 broad-scale groups can be identified in mixed stock analysis of high seas samples, an increase in the available resolution.

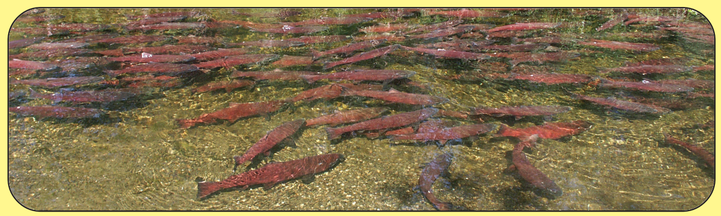
Measuring Genetic Variation

Genetic variation is measured by identifying locations along the genome (markers) where differences exist. Variant forms of these markers are called alleles. Single nucleotide polymorphisms (SNPs) are markers where two different nucleotides (alleles) have been found at the same location. The frequency of alleles at each SNP can vary widely between populations and population groups. The frequency variations at many SNPs can be used to distinguish populations and groups of populations in mixtures (e.g. juvenile samples, bycatch, or commercial harvest).



Coastwide Chinook salmon baseline of SNP markers





Reporting Groups

- Russia
- Coastal Western Alaska
- Middle Yukon River
- Upper Yukon River
- Upper Kuskokwim River
- North Alaska Peninsula
- South Alaska Peninsula
- Cook Inlet
- Upper Copper River
- Lower Copper River
- Northern SE Alaska
- Coastal SE Alaska
- Andrew Creek
- Transboundary Taku
- BC/WA/OR/CA

Estimated population contributions to mixtures of salmon were combined into broad-scale reporting groups. Reporting groups in this study were defined based on genetic similarity, geographic proximity, and management needs. Geographic organization can be seen on the maps and genetic organization can be seen using multidimensional scaling to represent genetic distances among populations in three dimensions. Clusters of populations in these plots indicate genetic similarities between the component populations. By comparing these plots with the maps potential reporting groups can be identified.

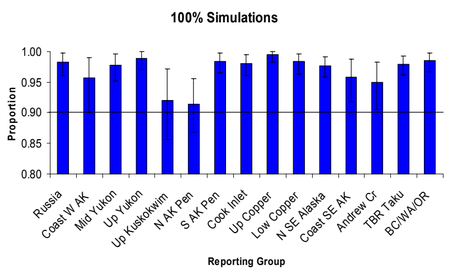
Coastwide
Three major groups of populations were identified: two within the Eastern Pacific populations (including Southeast Alaska) and a Western group (including Russia, Yukon River, and coastal Alaska to Copper River).

Eastern Pacific
British Columbia, Washington, Oregon, Idaho, and California populations are combined into a single genetically diverse reporting group because current representation is insufficient to allow further subdivision. Southeast Alaska and transboundary populations cluster into four groups.

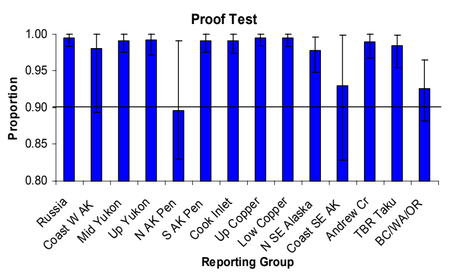
Western Pacific
Populations within this major group exhibit strong geographic and genetic clustering with the exception of the Coastal Western Alaska group, where populations are geographically dispersed, but genetically similar.

Testing the Baseline

100% Simulations
The first step to investigate the precision and accuracy possible for mixed stock analysis using this baseline involves simulated mixtures of hypothetical salmon in which all the individuals belong to a single reporting group. These 100% simulations are repeated 1,000 times. If the mixed stock analysis works perfectly then 100% of mixture would be attributed to the correct reporting group and any deviation would indicate error in the estimation process. Generally, 90% mean correct assignment indicates a high degree of genetic identifiability. All 15 reporting groups show correct allocations above the 90% thresh hold.



Known Sample Tests
The second step to investigate the precision and accuracy possible involves removing individual salmon from the baseline and using them to create a mixture of real salmon. This is a more stringent test than the simulations because the information in the baseline is reduced and real (not hypothetical) genotypes are used. As previously, these mixtures were composed entirely of individuals from the same reporting group. The results indicate that all groups are identifiable at or above the 90% thresh hold. Insufficient individuals were available from the Upper Kuskokwim reporting group to allow for inclusion in this test.



Conclusions

- The baseline of SNP markers demonstrates significant genetic variation among Chinook salmon populations.
- Genetic variation in Chinook salmon on a coastwide scale is closely associated with geographic features.
- Mixed stock analysis using genetic markers can identify 15 reporting groups on a coastwide basis.

Acknowledgements

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