DNA Analysis of the Origins of Chinook Salmon Bycatch in Alaska Trawl Fisheries

Determining the natal origin of chinook salmon

Salmon bycatch, by the Bering Sea trawl fishery in the Gulf of Alaska and Bering Sea, poses problems for both pollock fishermen and for Western Alaska subsistence and commercial fishermen dependent on healthy stocks. Genetic analysis offers researchers the opportunity to determine the origins of salmon bycatch in the trawl fleet. A better understanding of the origins of bycatch salmon is critical to effective management of pollock and salmon.

Why is PCCRC interested?

The commercial trawl fleet would like to limit their bycatch of salmon stocks deemed important to commercial and subsistence fisheries in Western Alaska. Research to determine where these salmon stocks come from is valuable to fishery managers, salmon fishermen, and the trawl fleet.

What Scientists Did

Researchers obtained samples from 20 chinook salmon populations: six populations from the Kamchatka region of the Russian Far East, and populations ranging from central California to the Yukon River. They examined the genetic divergence between Russian populations and North American chinook salmon lineages, and quantified genetic variation using both microsatellite and mtDNA to determine if there are markers that could assist in separating Russian salmon from North American fish in groundfish bycatch.

Objectives

Quantify genetic variation using both microsatellites and mtDNA to determine if there are markers that would assist in separating Russian salmon from North American fish in groundfish bycatch.

Use the data to examine the recent evolutionary history of chinook salmon.

Bottom Line

Results show a genetic basis for resolving stock mixtures, including estimating the contribution of Asian chinook salmon to groundfish bycatch.
What Scientists Learned
Analysis of mtDNA shows that chinook salmon have a much deeper “haplotype tree” than other species of Pacific salmon. The southeastern populations from Yakutat to California exhibit substantial divergence, which indicates that they have been isolated for a long time and little gene flow connects them.

These populations are generally distinct from Western Alaska and Asian populations. It appears that the two Asian populations emerged much more recently than the southern North American populations and may be related to Western Alaska populations.

Further Study
The development of chinook salmon microsatellite baseline information by Alaska Department of Fish and Game, U.S. Fish and Wildlife Service, National Marine Fisheries Service, and Department of Fisheries and Oceans Canada, will provide the baseline for addressing the issue.