What are the origins of the chum salmon in the North Pacific?

Chum salmon returns to Western Alaska river systems, such as the Yukon and Kuskokwim, are critical to the livelihood and culture of rural Alaskans. Chum salmon bycatch in the Gulf of Alaska and Bering Sea has created problems for Bering Sea pollock trawl fisheries, as well as rural Alaskans who rely on chum salmon. In addition, chum salmon are the focus of international treaties between the United States and Canada. To reduce bycatch and improve Western Alaska chum fisheries, scientists need better information on just where these salmon come from and where they are headed.

Why Is PCCRC Interested?

Knowing where bycaught chum salmon come from is valuable to fishery managers, salmon fishermen, and the pollock trawl fleet, who would like to further reduce the incidental catch of salmon.

What Scientists Did

Substantial effort has been devoted to using genetics to trace the origins of North American chum salmon stocks to their natal rivers or streams. An extensive allozyme baseline exists to help in this regard. Unfortunately, because of the logistics and increased costs of storing and processing the samples, most labs have ceased their allozyme operations. In addition, allozymes may not provide the fine-scale resolution needed to address some chum salmon questions.

An alternative approach is to use DNA variation. However, there are no baselines for DNA markers. In this project, researchers sought to develop DNA markers, particularly single nucleotide polymorphism...
(SNP) markers, for application to trawl fishery chum salmon bycatch. The challenge has been to discover the variation, design the specific molecular tool, and verify its utility in separating stocks. In the first phase of the project, researchers developed markers. In future efforts, researchers plan to survey the variability in much of the geographic range of chum salmon and evaluate the success that the markers can be expected to have in resolving populations in mixtures, for example, between or within the Yukon and Kuskokwim drainages.

**What Scientists Learned**

Researchers modified a genetic sequencing technique called ecotilling to rapidly screen DNA fragments for variation at the single nucleotide level, and detect natural polymorphisms in chum salmon DNA. Such polymorphisms can be used as markers to determine the natal origin of salmon.

The investigators also modified a method that is a variation on ecotilling. This method allows researchers to detect simple mutations and polymorphisms in large genomic regions without using a sequencer and expensive labeled primers. The researchers call the method decotilling (double strand cleavage ecotilling). The advantage of the method is that it allows the user to look for genetic variation in numerous genes both cheaply and rapidly.

**Further Study**

Researchers plan to demonstrate their genetic methods on a sample of chum salmon bycatch.