

Chum salmon bycatch in the Bering Sea pollock fishery

C. Kondzela*, S. Vulstek, J. Whittle, H. Nguyen, and J. Guyon

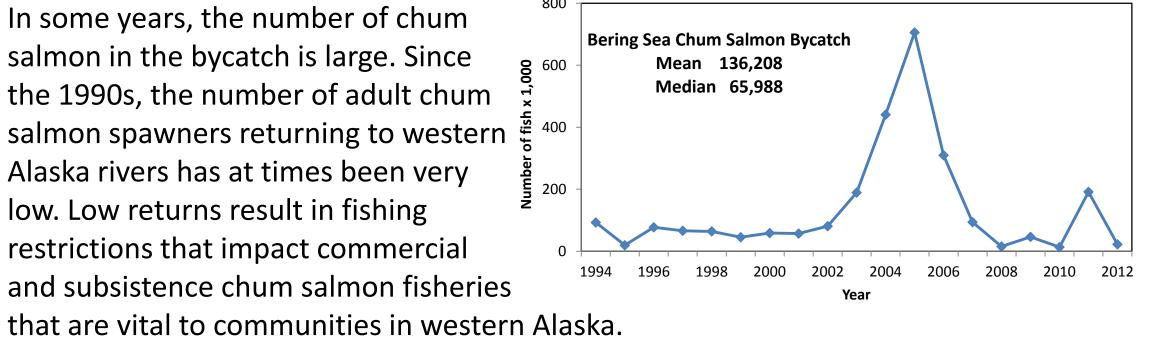
Auke Bay Fisheries Laboratory, Alaska Fisheries Science Center, National Marine Fisheries Service, NOAA, Juneau, Alaska

*chris.kondzela@noaa.gov

Issue Background

Chum salmon are one of the principal bycatch species in the Bering Sea walleye pollock trawl fishery, one of the world's largest single-species fisheries. The Bering Sea is an important habitat for chum salmon during their 2-5 year marine residency.

In some years, the number of chum salmon in the bycatch is large. Since the 1990s, the number of adult chum salmon spawners returning to western \(\frac{\varpsi}{2} \) 400 Alaska rivers has at times been very low. Low returns result in fishing restrictions that impact commercial and subsistence chum salmon fisheries



This situation leads naturally to the question: *How many chum salmon destined to* return to western Alaska rivers are intercepted in the pollock fishery?

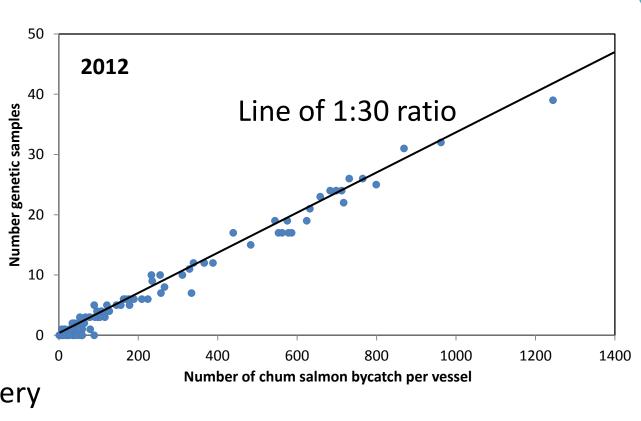
Management & Research

One of 8 regional U.S. fishery management councils, the North Pacific Fishery Management Council (NPFMC) developed the Fishery Management Plan for the pollock fishery in federal waters of the Bering Sea-Aleutian Island area. A variety of management measures over the last couple of decades seek to balance the pollock catch and salmon bycatch. Examples include: salmon bycatch limits, time and area closures, and incentive plan agreements such as the voluntary rolling hot -spot bycatch avoidance program.

The AFSC's Observer Program verifies at-sea catch and provides biological information and samples. Tissue samples from the chum salmon bycatch have been collected since 2005 for the Genetics Program at the AFSC's Auke Bay Laboratories to determine the freshwater origin of the samples. Although these collections provide insight into the stocks represented in the bycatch, the opportunistic nature of the sampling has resulted in bias of the genetic stock estimates to a greater or lesser extent from year-to-year.

Creative Solution

With support from management and research entities (NMFS's AFSC and Alaska Regional Office, NPFMC), and the fishing industry, advances in bycatch sampling have been made. Starting in 2011, the Observer Program counted all salmon bycatch in the Bering Sea pollock fishery and collected genetic samples from every 30th chum salmon caught.



Representative sampling now allows extrapolation of the genetic analyses of the samples to the entire bycatch with minimal bias. We can now 1) better quantify the impact of the pollock fishery on salmon stocks, 2) identify ocean migration patterns, and 3) examine the stability of spatial, seasonal, and yearly chum salmon stock distributions in the Bering Sea.

Salmon Excluder Device

Industry research on salmon bycatch reduction devices in recent years has provided genetic samples from individual trawl hauls. Samples from single hauls are useful for determining the extent of chum salmon stock mixing in the Bering Sea on very small spatial and temporal scales and can help answer the question: Are chum salmon stocks aggregated or randomly distributed in the Bering Sea?

2012 Bycatch

