Genetic Analysis of Chum Salmon Bycatch Samples from the Bering Sea Groundfish Fisheries

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Introduction

Protection of western Alaska chum salmon populations are of primary concern for salmon bycatch managers in the Bearing Sea groundfish fisheries because this area is a known feeding habitat for multiple brood years of chum salmon (*Oncorhynchus keta*) from many different localities in North America and Asia. With the past increases of chum bycatch in the Bering Sea pollock fisheries, it is important to determine the geographic origin of salmon caught in the federally managed fisheries which is essential to understanding whether management of federal fisheries could address conservation concerns.

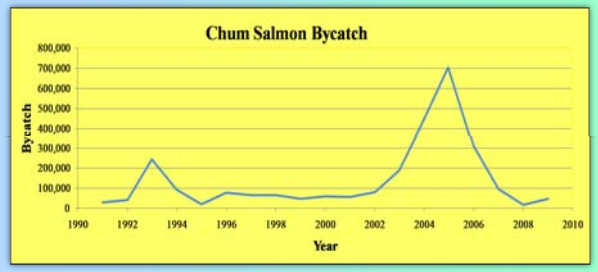


Figure 1. Yearly estimates for the non-Chinook salmon (>98% are chum salmon) bycatch from the Bering Sea pollock trawl fishery (NMFS, 2010).

Our Approach

1. Chum salmon caught in the Bering Sea pollock fisheries were sampled during the 2005-2009 pollock A&B seasons by NMFS observers.
2. We compared genetic information (11 microsatellites) from chum salmon bycatch sample sets collected in 2005-2009 to the Fisheries and Oceans Canada (DFO) chum salmon microsatellite baseline (381 populations) to identify their origin. 1994-95 sample sets were analyzed using allozymes with a different but overlapping genetic baseline.
3. Temporal stratification of the bycatch samples were compared across years (2005-2009).
4. Potential sample bias was evaluated by comparing the chum salmon bycatch with the bycatch samples by statistical area over time.

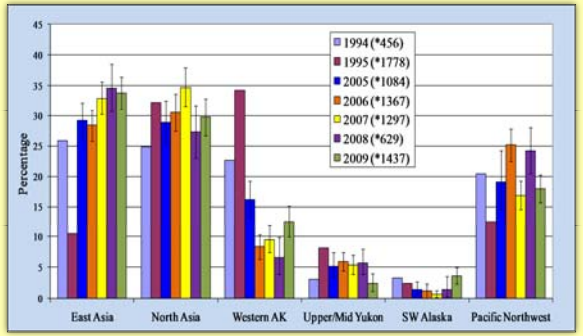


Figure 2. Origin of chum salmon genetic samples from the Bering Sea chum salmon bycatch. *Sample size.

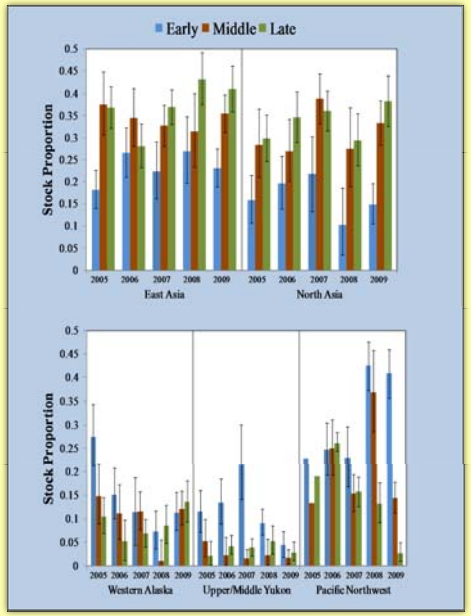
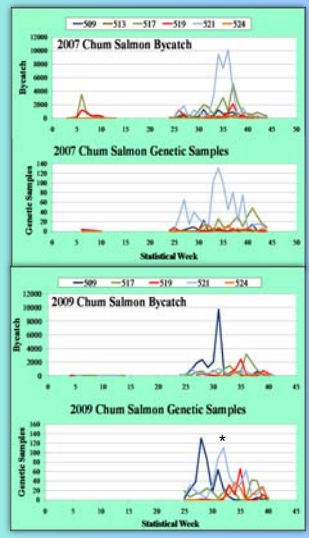


Figure 3. Temporal comparison of 2005-2009 stock composition estimates of chum bycatch genetic samples from the early, middle, and late stratum of the Bering Sea pollock fisheries "B" season (June-October).

Figure 4. Statistical areas associated with the Bering Sea-Aleutian Island groundfish fishery.

Figure 5. Examples of sample bias. Sample and bycatch distribution by area were very similar in 2007, although other years showed apparent biases for particular areas. For example in 2009 spatial bias is seen with the overrepresentation of genetic samples in area 521*.



Summary

Overall, genetic samples collected from the chum salmon bycatch were predominantly from Asian stocks although substantial contributions were also from the Pacific Northwest (Prince William Sound to Washington) followed by western Alaska and the upper and middle Yukon. Also observed is the tendency of North American stocks to decrease and Asian stocks to increase in the bycatch samples of the Bering Sea pollock fisheries during the "B" season, a time when the majority of the chum salmon are caught in the bycatch. While temporal and spatial bias exists in the bycatch sample sets and this limits their application as stock composition estimates for the entire chum bycatch, this analysis provides a rough measure of stock distribution, and at a minimum, provides an indication of the presence and/or absence of specific stocks within the bycatch. NMFS recently implemented Amendment 91 to the Fishery Management Plan for Groundfish of the Bering Sea and Aleutian Islands Management Area which will help alleviate sample bias starting in 2011.

References

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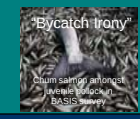
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