

3-1. Migration and Distribution of Salmon (Poster-12)

High-Resolution Stock Identification for Migratory Studies of Chinook Salmon

William D. Templin*¹, Lisa W. Seeb², James Murphy³, and James E. Seeb²

¹ *Gene Conservation Laboratory, Division of Commercial Fisheries, Alaska Department of Fish and Game, 333 Raspberry Road, Anchorage, Alaska 99518, USA; E-mail, bill.templin@alaska.gov*

² *University of Washington, School of Aquatic and Fishery Sciences, Box 355020, Seattle, WA 98195, USA*

³ *Ted Stevens Marine Research Institute, Alaska Fisheries Science Center, NOAA Fisheries, 17109 Point Lena Loop Road, Juneau, AK 99801, USA*

While the life history and ecology of Chinook salmon in freshwater is well known, less is known of the oceanic migration patterns and relative survival of individual stocks in the marine environment. 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. The Alaska Department of Fish and Game has developed a baseline of 53 markers based on single nucleotide polymorphisms (SNPs) surveyed in 175 populations across the species range in the North Pacific. This baseline provides the foundation for the application of genetic stock identification to the high-resolution exploration of the distribution of Chinook salmon in marine waters. We compare this method to the resolution possible from previous methods to demonstrate its utility for mixed stock analysis of high seas samples. Our results show that this baseline provides a rapid and cost effective approach to analysis of samples from complex mixtures encountered in multi-national research and fishery monitoring efforts.