

3-1. Migration and Distribution of Salmon (Oral-4)

The Use of Genetic Stock Identification to Determine the Distribution, Migration, Early Marine Survival, and Relative Stock Abundance of Sockeye, Chum and Chinook Salmon in the Bering Sea

J. E. Seeb*¹, S. Abe², S. Sato³, S. Urawa^{3,4}, N. Varnavskaya⁵, N. Klovatch⁶, E.V Farley⁷, C. Guthrie⁸, B. Templin⁸, C. Habicht⁸, J.M. Murphy⁷, and L.W. Seeb¹

¹ *School of Aquatic and Fishery Sciences, University of Washington, 1122 NE Boat Street, Box 355020, Seattle, WA 98105-5020, USA; E-mail, jseeb@u.washington.edu*

² *Graduate School of Fisheries Science, Hokkaido University, 3-1-1 Minato, Hakodate 941-8611, Japan*

³ *National Salmon Resources Center, Fisheries Research Agency, 2-2 Nakanoshima, Toyohira-ku, Sapporo 062-0922, Japan*

⁴ *Present address: North Pacific Anadromous Fish Commission, 502-889 West Pender Street, Vancouver, BC, V6C 3B2, Canada*

⁵ *Kamchatka Fishery and Oceanography Research Institute, KamchatNIRO, 18, Naberezhnaya Street, Petropavlovsk-Kamchatsky 683000, Russia*

⁶ *Russian Federal Research Institute of Fisheries & Oceanography (VNIRO), 17, V. Krasnoselskaya, Moscow 107140, Russia*

⁷ *National Marine Fisheries Service, Auke Bay Laboratories, Ted Stevens Marine Research Institute, 17109 Point Lena Loop Rd, Juneau, AK 99801, USA*

⁸ *Gene Conservation Laboratory, Division of Commercial Fisheries, Alaska Department of Fish and Game, 333 Raspberry Road, Anchorage, Alaska 99518, USA*

We report the stock composition and seasonal distribution of Asian and North American salmon collected in the Bering Sea during 2002-2006 using genetic markers. This collaboration stems from seed monies from the North Pacific Research Board and extensive funding from the host agencies. We detail the BASIS stock composition research that progressively improved through genetic markers including allozymes, microsatellites, and finally single nucleotide polymorphisms (SNPs). Improvements in DNA techniques during this project were so profound that continuation support was provided for the additional development of public SNP data bases for use by NPAFC and other agencies. We report rapid advances in DNA technology for chum salmon studies using highly parallel DNA sequencing for SNP discovery. Here we focus upon the SNP database for chum salmon and provide examples for resolving proportional and individual assignment of migrating fish in Bering Sea mixtures.