

3-1. Migration and Distribution of Salmon (Oral-5)

Stock-Structured Distribution and Abundance of Western Alaska Juvenile Chinook Salmon Populations in the Eastern Bering Sea, 2002-2007

James M. Murphy*¹, William D. Templin², Edward V. Farley, Jr.¹, and James E. Seeb³

¹ *Ted Stevens Marine Research Institute, Alaska Fisheries Science Center, NOAA Fisheries, 17109 Point Lena Loop Road, Juneau, AK 99801, USA; E-mail, Jim.Murphy@noaa.gov*

² *Gene Conservation Laboratory, Division of Commercial Fisheries, Alaska Department of Fish and Game, 333 Raspberry Road, Anchorage, Alaska 99518, USA*

³ *University of Washington, School of Aquatic and Fishery Sciences, Box 355020, Seattle, WA 98195, USA*

Stock-structured distribution and abundance estimates from United States BASIS surveys in the eastern Bering Sea during 2002-2007 are used to provide insight into the migratory behavior and processes impacting the production of Western Alaska Chinook salmon. Origin of juvenile Chinook is evaluated using a single nucleotide polymorphism (SNP) baseline developed and refined for Western Alaska Chinook populations by the Gene Conservation Laboratory at the Alaska Department of Fish and Game. Stock information is integrated into abundance estimates using spatial models of distribution and abundance and from expansions of average catch rate within spatial strata optimized to the estimated migration corridors of juvenile Chinook salmon. Abundance estimates are compared with escapement levels and subsequent adult returns and evaluated in terms of the production and survival of Western Alaska Chinook populations.