Shared Chum Salmon Baseline Development

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Abstract:

There is a pressing need to improve and enhance the Bering Sea/ N. Pacific chum salmon baseline of genetic markers to provide greater resolution in mixed stock genetic analysis. Existing genetic baselines do not include sufficient markers to resolve some important stock groups. In this collaborative project between genetics labs within National Marine Fisheries Service (NMFS), Alaska Department of Fish and Game (ADF&G), and the University of Alaska Fairbanks (UAF) we will (1) conduct a gap analysis to identify deficiencies in the genetic sample locations, sample sizes, and sample quality for Bering Sea/ N. Pacific chum salmon populations and identify specific populations that will be used in a SNP discovery panel; (2) conduct a comprehensive gap analysis of deficiencies in genetic samples for Bering Sea/ N.

Pacific chum salmon populations and (2) develop new single nucleotide polymorphism (SNP) markers that focus specifically on delineation of western Alaskan (including Norton Sound, lower Yukon and Kuskokwim) populations; and (3) identify approximately 50 critical populations for which data are missing or inadequate for the baseline. In this project, we will add SNP and microsatellite data for about 10 to 12 populations. By improving the chum salmon baseline, this research will assist both NMFS and ADF&G to better address western Alaska chum salmon management challenges.

Project Objectives:

Objective 1: Conduct a collaborative (ADF&G, NMFS, UAF) effort to produce and improve the chum salmon baseline for SNP and microsatellite data for applications to Alaskan MSAs. This will include conducting a gap analysis to identify deficiencies in the genetic sample locations, sample sizes, and sample quality for Bering Sea/ N. Pacific chum salmon populations. It will also include identifying the specific populations that will be used in our SNP discovery panel

Objective 2: Develop new informative SNP markers to improve delineation of coastal western Alaskan chum salmon populations, including lower Yukon River, Kuskokwim River, and Norton Sound populations. Work on this objective will begin under the initial phase of the project described herein. Completion of this objective would proceed with funding for the latter phase of this project which has been requested from the AKSSF program.

Objective 3: Based on consensus reached under Objective A and over the course of the combined AKSSF and AYKSSI project, in which we conducted a gap analysis, we will identify approximately 50 critical populations for which data are missing or inadequate. We will add SNP and microsatellite data for key populations not in the baseline or fill in missing data types (SNP or microsatellite) in order to strengthen the coastwide baseline for chum salmon. About 10 to 12 populations will be the focus of this project, and we plan to complete the other loci in the AKSSF

project for which we have applied. Much of the work of this objective can be done at the same time that the SNP discovery is being carried out.