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Special Publication No. 12-12

Sockeye Salmon Baseline for the Western Alaska Salmon Stock Identification Project

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Sockey e salmon (Oucar/nuclus neeka) are Alaska's most comm the majority originate from and are harvested in Western Alaska Hugaev et al. 2003). The combination of sockeye satmon life his the geography of Western Maska create the potential for the harvest they return to hatal streams. While a majority of the harvest al 2009), the nurvers of nonlocal populations does occar and mock productivity. The relative hapact of this birs depends to the impetus for the Western Alaska Salmon Stock Identification Project (WASSIP), W bns a consensus-driven project with 11 signatories representing fishing. Alaska Nurive, William D. Templin and Advisory Panel (AP), a 1-miniform William D. Templin and the Panel (AP), a 1-miniform Panel (AP), (TC), and is governed by a Memorandum of Understanding. WASSIP was designed to use sensitic data in mixed stock analysis (MSA) to try to reduce this uncertainty

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Uncertainty about the magnitude, frequency, location, and tin salmon in Western Alaska fisheries was the impetus for the V (WASSIP). The project was designed to use genetic data in mix A baseline of allele frequencies is required for use in mixed

harvested fish. This report describes the methodology we used to understand the population genetic structure and build a baseline for use in MSA, describes the performance of the baseline for MSA, and provides guidance on how to interpret biases documented in the MSA tests when evaluating future stock composition estimates of WASSIP mixtures. Of the 42,636 individuals from 485 collections selected to be genotyped, the final baseline was composed of 39,205 individuals from 450 collections representing 294 populations. Average population sample size was 133 individuals. We used 2 types of tests to measure the baseline's ability to correctly allocate to reporting groups: proof tests and escapement samples. Correct allocations for proof tests averaged 0.96, ranged from 0.81 to 0.99, and 21 of the 24 proof tests met our goal of 90% correct allocation. Correct allocations for escapement tests averaged 0.93, ranged from 0.49 to 0.99, and 28 of the 32 escapement tests met our goal of 90% correct allocation. The baseline tests provide bias information for interpreting stock composition estimates of WASSIP fisheries, especially for areas where sea/river ecotype sockeye are present. We believe this baseline will provide accurate and precise estimates of stock composition in Western Alaska sockeye salmon fisheries.

Key words Western Alaska Salmon Stock Identification Project, WASSIP, sockeye salmon, Oncorhynchus nerka, mixed stock analysis, genetic baseline

INTRODUCTION

Sockeye salmon (*Oncorhynchus nerka*) are Alaska's most commercially valuable salmonid, and the majority originate from and are harvested in Western Alaska (Eggers and Carroll 2011; Bugaev et al. 2008). The combination of sockeye salmon life history, migratory pathways and the geography of Western Alaska create the potential for the harvest of nonlocal populations as they return to natal streams. While a majority of the harvest of sockeye salmon in Western Alaska occurs in terminal fisheries, where nonlocal harvest is minimal (e.g., Bristol Bay; Dann et al. 2009), the harvest of nonlocal populations does occur and can bias estimates of total run and stock productivity. The relative impact of this bias depends on population size: less abundant populations are more affected by their nonlocal harvest than very abundant populations. Uncertainty about the magnitude, frequency, location, and timing of this nonlocal harvest was the impetus for the Western Alaska Salmon Stock Identification Project (WASSIP). WASSIP is a consensus-driven project with 11 signatories representing fishing, Alaska Native, and government interests who serve as the Advisory Panel (AP), a 4-member Technical Committee (TC), and is governed by a Memorandum of Understanding¹. WASSIP was designed to use genetic data in mixed stock analysis (MSA) to try to reduce this uncertainty.

MSA has been used effectively for Pacific salmon and specifically for sockeye salmon for estimating stock compositions of mixtures of fish of unknown origin. The earliest work was based on allozymes and covered more restricted geographic ranges, while more recent work is based on microsatellites and/or single nucleotide polymorphisms (SNPs) and covers broader geographic ranges. Population structure and/or MSA has been investigated in sockeye within Bristol Bay (Habicht et al. 2007, Dann et al. 2009), within Cook Inlet (Grant et al. 1980, Seeb et al. 2000, Barclay et al. 2010), within Kuskokwim River (McPhee et al. 2009), within British

¹ Western Alaska Salmon Stock Identification Program Memorandum of Understanding. Signed May 5, 2006 and revised March 24, 2008 by the following signatories: Alaska Department of Fish and Game, Aleut Corporation, Aleutians East Borough, Association of Village Council and Peninsula Borough, Tanana Chiefs Conference, and Yukon Drainage Fisheries Association.