



Results of Fish Assemblages and Genetic Stock Determination of Salmon in Bering Land Bridge National Preserve, 2021–2023

The National Park Service and Alaska Department of Fish and Game partnered to establish a baseline inventory of subsistence fish assemblages and salmon population genetic structure in major rivers flowing through Bering Land Bridge National Preserve, focusing on Serpentine, Nuluk, Arctic, and Nugnugaluktuk Rivers. This project, funded by the Office of Subsistence Management Fisheries Resource Monitoring Program, sampled a total of 96 sites during the 2021–2023 field seasons (June–October), and 20 species (including 10 anadromous) were inventoried.

A total of 718 genetic tissues samples from chum salmon were collected across 7 rivers, and 7 new chum salmon populations were defined and added to the coastwide chum salmon genetic baseline. A total of 1,287 genetic tissues samples (odd-year: $n = 917$, even-year: $n = 370$) were collected from pink salmon across 10 rivers, and 12 new pink salmon populations (odd-year: $n = 8$, even-year: $n = 4$) were defined and added to the coastwide pink salmon genetic baseline. A total of 81 genetic tissue samples were collected from coho salmon across 2 rivers, and 1 new coho salmon population was defined and added to the western Alaska coho salmon genetic baseline.

OBJECTIVES

The overarching goal of this project was to create a baseline inventory of subsistence fish assemblages and salmon population genetic structure in major rivers flowing through BELA, focusing on Serpentine, Nuluk, Arctic, and Nugnugaluktuk Rivers:

1. Document fish species assemblages with an emphasis on Pacific salmon,
2. Evaluate genetic variation within salmon species and potential for mixed stock analysis,
3. Collect age, sex, and length (ASL) on chum salmon sampled for genetics.

FISH ASSEMBLAGE RESULTS

A total of 63 nominations were submitted to the Anadromous Waters Catalog and included documented spawning by all 5 species of Pacific salmon *Oncorhynchus* spp.; juvenile rearing of coho salmon *O. kisutch*, and Dolly Varden *Salvelinus malma*; and presence of pond smelt *Hypomesus olidus*, rainbow smelt, Bering cisco *Coregonus laurettae*, and humpback whitefish *Coregonus pidschian*.

GENETIC RESULTS

Chum Salmon: This project successfully described the genetic composition of 7 new chum salmon populations from the BELA area, and these new populations were added to the ADF&G chum salmon genetic baseline. The 7 new populations from the BELA area had more genetic variation than Norton Sound populations. The 7 new BELA area populations were not genetically distinct enough from the other populations to be separated out into a new baseline reporting group for Mixed Stocked Analysis (MSA). However, the 7 new BELA area populations were genetically similar to the Kotzebue Sound populations.

Pink Salmon: This project successfully described the genetic composition of 12 new pink salmon populations (odd-year: $n = 8$, even-year: $n = 4$) from the BELA area, and these new populations were added to the ADF&G pink salmon genetic baseline.

Coho Salmon: This project successfully described the genetic composition of 1 new coho salmon population from the BELA area (South Fork Serpentine River), and this new population was added to the ADF&G coho salmon genetic baseline.

Sockeye Salmon: There were 5 sockeye salmon genetic tissue samples collected and archived during this project. The sample size was too small to assess genetic population structure and MSA potential.

AGE-SEX-LENGTH (ASL) RESULTS

Only chum salmon were sampled for age, sex, and length during this project. A total of 285 chum salmon were sampled from 6 rivers: Arctic River ($n = 74$), Goodhope River ($n = 13$), Nugnugaluktuk River ($n = 74$), Nuluk River ($n = 40$), Pinguk River ($n = 40$), and Serpentine River ($n = 44$). A total of 91 chum salmon were successfully aged, and the predominant age class was age-0.3 (4-year-old) salmon.

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