

Project Number: RM-54-14

Project Title: Black River Fall Chum Salmon Genetic Sample Collections

Principal Investigator: Brian McKenna, Fisheries Biologist, Tanana Chiefs Conference
122 First Avenue, Suite 600, Fairbanks, Alaska 99701
Phone: (907) 452-8251 ext. 3318
Email: brian.mckenna@tananachiefs.org

Introduction:

The Yukon River flows for over 3,200 kilometers draining large portions of Canada and Alaska (Brabets et al. 2000). It provides essential habitat on both sides of the border necessary to sustaining the individual spawning stocks that contribute to the Yukon River mixed-stock and mixed-species fisheries. Among these species, two seasonally different races of chum salmon *Oncorhynchus keta* exist, exhibiting spatial and temporal differences that have led to genetic variation between the two races (Flannery et al 2007). Conservation of the Yukon River mixed-stock and mixed-species fisheries presents a daunting challenge to fisheries managers. Mixed Stock Analyses (MSA), through the development of a genetic stock identification (GSI) program (genetic baseline) has enabled fisheries managers and scientists to determine stock proportions, achieve escapement goals, and actively manage in-season runs (Flannery & Wenburg 2013). A genetic baseline has been, and continues to be developed for individual spawning stocks of fall chum salmon that are reproductively isolated from one another. To date, 15 individual spawning stocks of fall chum salmon have been identified, with 7 of those spawning stocks located in the middle and upper Yukon River within Alaska (Flannery et al 2007). The Black River is one of these stocks. Recommendations have been made by the U.S. Fish and Wildlife Service (USFWS), the Alaska Department of Fish and Game (ADF&G), and the Yukon River Panel (YRP) to improve the resolution of the genetic baseline for fall chum salmon in the Black River.

Improving the in-season and post-season resolution of genetic stock identification for fall chum salmon is a current management need, and the Black River has been identified by the YRP as having insufficient genetic resolution. In order to accomplish this management a sample size of 200 tissue samples is required by the ADF&G's Gene Conservation Laboratory (GCL). Sampling efforts in 1995 and 2001 have provided 112 genetic tissue samples for fall chum salmon on the Black River (Flannery et al 2007). This project enabled the collection of the remaining 88 genetic tissue samples to achieve the necessary sample size of 200 samples to improve the resolution of the genetic stock identification for the Black River fall chum salmon population. This genetic baseline data will be developed by the ADF&G – GCL, and used by Yukon River fisheries managers to help identify stock contribution from fall chum salmon caught in the lower Yukon River test fisheries and Pilot Station Sonar project, and to aid in the conservation of the Black River fall chum salmon population.

Project Objectives:

Objective 1: Collect 88 axillary process tissue samples from fall chum salmon in the Black River.

Objective 2: Deliver all collected tissue samples to the ADF&G - GCL for genetic analysis.

Study Area:

This study was conducted near Chalkyitsik, Alaska, located on the Black River within the Yukon Flats National Wildlife Refuge (YFNWR). Sampling occurred on village land, within 3 river miles above and below the Village of Chalkyitsik. Appendix 1 is a map of the Black River in relation to the Yukon Flats National Wildlife Refuge and Chalkyitsik Village lands.

Required Licenses and Permits: A fish resource permit was obtained from the Alaska Department of Fish and Game, Permit No. SF2014-180.

Methods:

The Tanana Chiefs Conference (TCC) collaborated with the Chalkyitsik Village Council, the U.S. Fish and Wildlife Service Subsistence Fisheries Branch, and the Yukon Flats National Wildlife Refuge for logistical and technical support. Additional collaboration was made with the ADF&G-GCL for technical support and genetic analyses. The TCC led the field sampling with assistance provided from Chalkyitsik Village Council's Natural Resources department and local fishers. A local boat driver and subsistence fisher from Chalkyitsik was hired to provide transportation between Chalkyitsik and the collection sites. Sampling occurred on village land, within the Yukon Flats National Wildlife Refuge.

Axillary process tissue samples (pelvic fin spine clips) were collected from the subsistence harvest of fishers from the Village of Chalkyitsik. To implement this the field crew sampled from the subsistence fishing grounds on the Black River above and below the village. All subsistence fishers supporting this project were compensated for the allowance of tissue samples to be collected from their harvest, and they were able to retain their harvest for subsistence use after the samples were collected. Tissue samples from subsistence caught fall chum salmon were purchased at a rate of \$5 per sample. All fish were sampled prior to cutting or processing.

Axillary process tissue samples (pelvic fin spine clips) were collected and stored following the Alaska Department of Fish and Game's Gene Conservation Laboratory's protocol (ADF&G 2014). Axillary process tissue samples were wiped dry to clean them of water and fish slime prior to being clipped and stored. Dog nail clippers were utilized to clip one piece (1/2" - 1") of the axillary process. The clipped pieces were stored in cryovials filled with Isopropanol/Methanol/Ethanol (ETOH) preservative. After the sampling event was finished, the preservative was refreshed by replacing the original preservative with entirely new preservative. For 200 axillary process samples, 250ml of preservative were used. This preservative allowed for DNA to be extracted at a later date without the need to freeze the samples. After the tissue samples were collected and properly stored, they were shipped to ADF&G's Gene Conservation Laboratory for analysis.

Results & Discussion:

Sampling occurred between September 25 and October 1, 2014. The TCC fisheries biologist, Brian McKenna, and the TCC fisheries technician, Nicole Farnham, traveled to Chalkyitsik from Fairbanks on September 25, 2014. A local fisherman, Jonas Carroll Sr., was contracted to provide transportation to the subsistence fishing grounds where the local fisherman had two gill nets set within 3 river miles of the village; one was 4-1/2" mesh and the other was 6" mesh. The nets were checked twice daily, once in the morning, and once in the evening, between September 25 and October 1, 2015. A total of 88 fall chum salmon were collected and sampled. An additional 8 Coho salmon *Oncorhynchus kisutch* were collected and sampled following the same protocol. Additionally, four northern pike *Esox lucius*, four whitefish *Coregonids*, and two sheefish *Stenodus nelma* were captured as bycatch during sampling, and were used by the local fishers for subsistence needs.

All tissue samples collected were shipped to the Alaska Department of Fish & Game's Gene Conservation Laboratory and will be added to the existing Single Nucleotide Polymorphism (SNP) genetic baseline data set. After the analyses are complete, tissue sub-samples will be shared with the USFWS' genetics lab and with the Department of Fisheries and Oceans Canada (DFO), and then will be permanently archived in the ADF&G Gene Conservation Laboratory. Resulting data from the analyses will be used to further develop the genetic baseline for the Black River fall chum salmon population. In turn, this baseline will be used to help identify stock contribution from salmon caught in the lower Yukon River test fisheries and Pilot Station Sonar project, and to better represent the Black River fall chum salmon population.

References:

- Brabets, T. P., B. Wang, and R. H. Meade. 2000. Environmental and hydrologic overview of the Yukon River Basin, Alaska and Canada. Water-Resources Investigations Report 99-4204, U.S. Geological Survey, Anchorage, Alaska.
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- Alaska Department of Fish and Game, Gene Conservation Laboratory. Anchorage, Alaska. 2014. Non-lethal Sampling Finfish Tissue for DNA Analysis. Available from: <http://www.adfg.alaska.gov/static/fishing/PDFs/research/geneconservation/Nonlethalsamplinginvials.pdf>

Appendices:

Appendix 1. – Land Status Near Chalkyitsik, Alaska.

