

# **Black River Fall Chum Salmon Genetic Sample Collections**

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By

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**Project Title:** Black River Fall Chum Salmon Genetic Sample Collections

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### **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 seven of those spawning stocks located in the middle and upper Yukon River Basin within Alaska (Flannery et al 2007).

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, Porcupine River Sub-Basin, has been identified by the Yukon River Panel as having insufficient genetic resolution. In order to gain sufficient genetic resolution to determine population structure, a sample size of 200 tissue samples is required by the Alaska Department of Fish and Game's (ADF&G) 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 required 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:** During the fall of 2014, the Tanana Chiefs Conference staff will collect 88, at minimum, axillary process tissue samples from Fall Chum Salmon in the Black River.

**Objective 2:** During the fall of 2014, the Tanana Chiefs Conference staff will deliver all collected Fall Chum Salmon genetic samples to the ADF&G - GCL to be added to the existing Single Nucleotide Polymorphism (SNP) genetic baseline data set.

**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 three river miles above and below the Village of Chalkyitsik. Appendix 1 is a map of the Black River in relation to the YFNWR 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. Samples were collected from subsistence harvested fish 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 ADF&G GCL's protocol (ADF&G 2014). Axillary process tissue samples were wiped dry to clean them of water and fish mucous 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 250ml of Isopropanol/Methanol/Ethanol (ETOH) preservative. This preservative allowed for DNA to be extracted at a later date without the need to freeze the samples. After the sampling event was finished, the preservative was refreshed by replacing the original preservative with entirely new preservative. 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. Jonas Carroll Sr. (a local fisherman), was contracted to provide transportation and access to fish for sampling. The crew traveled to the subsistence fishing grounds, N66.65012, W143.711120, and N66.67222, W143.70941. Mr. Carroll Sr. utilized two gill nets to capture fish; 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 eight 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 ADF&G's GCL and will be added to the existing SNP genetic baseline data set. After the analyses are complete, tissue sub-samples will be shared with the USFWS's Conservation Genetics Laboratory and with the Department of Fisheries and Oceans Canada (DFO). Samples will also be permanently archived in the ADF&G GCL. Information derived from the analyses will be used to further develop the genetic baseline for the Black River fall chum salmon population.

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**Appendices:**

Appendix 1. – Map illustrating 2014 Fall Chum Salmon genetic sampling area near Chalkyitsik, Alaska. The red circle denotes the sampling area.

