

Attachment 7

Initial Study Report Meetings

Action Item for Study 9.14

March 22, 2016



SUSITNA-WATANA HYDRO

Meeting Summary and Decision Points

Technical Meeting

Fish Genetics Study 9.14

April 12, 2016

- LOCATION:** Alaska Energy Authority
813 West Northern Lights Blvd.
Anchorage, AK 99503
- TIME:** 10:00 am – 12:00 pm
- SUBJECT:** Fish Genetics Study 9.14 - Data Analysis
- Goal:** To discuss with agencies the appropriate statistical analyses for Chinook Salmon data
- Attendees:** On location:
Betsy McGregor, Alaska Energy Authority
Betsy McCracken, United States Fish and Wildlife Service
Andy Barclay, Alaska Department of Fish and Game
Chris Habicht, Alaska Department of Fish and Game
- On teleconference:
MaryLouise Keefe, R2 Resource Consultants, Inc
Jeff Olsen, United States Fish and Wildlife Service
Jeff Guyon, National Marine Fisheries Service
Chuck Guthrie, National Marine Fisheries Service
Sean Eagan, National Marine Fisheries Service

Meeting Summary and **Decision Points (in bold)**

Reviewed population structure analyses on Chinook Salmon in Northern Cook Inlet (NCI).

- Populations: 32 in the Susitna River drainage and 9 from the west side Cook Inlet and Knik Arm.
- Only populations represented by at least 50 fish were included
- All populations below Devils Canyon were represented by spawning adults – 2 of the 3 populations from above Devils Canyon had some adult representation
- Markers: 36 SNPs with an average F_{ST} of 0.026
- Mean F_{IS} is distributed around zero with two collections showing relatively high values (Spink and Chunilna creeks)
- Overall high P-values for HWE except Oshetna River
- Genetic relationships based on F_{ST}
 - Oshetna River and Kosina Creek are the most divergent collections, but they likely do not represent independent samples. Lack of independence can upwardly bias F_{ST} .
 - Populations that spawn short distances from the ocean (Theodore, Sucker, Chuitna, Lewis), populations spawning short distances from the mainstem of Susitna River (Indian, Portage, Chunilna, Montana), and populations spawning short distances from the Knik River (Moose and Granite creeks), show little differentiation from each other.

- Populations that spawn farther away from the ocean or farther away from the mainstem of the Susitna River or Knik River seem to cluster by drainage: Talkeetna River (except Chuniilna Creek); Lower Susitna River (except Sucker and Montana creeks); Deshka River; Knik Arm except Moose and Granite creeks; upper Chulitna River)
- Yentna River fish cluster into two clusters with upstream collections showing the most divergence.
- Coal Creek and Bunco Creek are also basal.

Discussion about next steps; should we add another 47 SNP markers to the analysis?

- Pro: Would add certainty in the relationships among populations and add statistical power in testing for node support.
- Con: May not change relationships on a broad scale.
- **Decision Point: Screen and analyze data from additional 47 SNP markers. This full set of SNP markers will be adequate to examine relationships among populations in Upper Cook Inlet.**

Discussion about objective 4 and 5; should AEA file modifications?

- Objective 4: “Examine the genetic variation among Chinook Salmon populations from the Susitna River drainage, with emphasis on Middle and Upper River populations, for mixed-stock analyses (MSA).”
 - Population structure analysis indicates that it is unlikely that the Middle River collections below Devils Canyon (Indian River and Portage Creek) are differentiated enough from other tributaries draining into the Susitna River mainstem (Chuniilna and Montana creeks). In addition, “populations” above Devils Canyon may not have inter-annual stability in allele frequencies.
 - **Decision Point: Modification is premature because the population genetics component is not complete and we may still be able to test for MSA performance for at least the populations in the Middle River below Devils Canyon.**
- Objective 5: “If sufficient genetic variation is found for MSA, estimate the annual percent of juvenile Chinook Salmon in selected Lower River habitats that originated in the Middle and Upper Susitna River in 2013 and 2014 (Figure 2-1).”
 - After concerted sampling effort, only 8 juvenile Chinook Salmon were sampled from the Lower River. All of these were sampled from a single habitat type. Even if MSA is possible, no samples are available for analysis.
 - **Decision Point: Modification to remove this objective from the FERC-approved Study Plan is appropriate at this time and should be filed with FERC as a proposed modification to the Study Plan.**

Reviewed fine-scale relationships among Chinook Salmon collections in the Middle and Upper Susitna River.

- Markers: A subset of samples successfully screened for 36 SNPs. Most samples successfully screened for 12 uSATs. Statistical analysis based on uSATs.
- Low DNA volumes and concentrations resulted in lack of SNP data for some juvenile collections. Additional focused laboratory analyses were not successful in SNP genotyping.

- Good representation (spawning adults) from the two largest spawning areas in the Middle Susitna River below Devils Canyon (Indian River and Portage Creek).
- More than 50 adults collected from one spawning location within Devils Canyon (Cheechako Creek, n=67) and only a handful of adult samples from spawning areas above Devils Canyon.
- At least 50 juvenile samples passed QC tests from two spawning areas above Devils Canyon (Black/Oshetna River, n = 57; Kosina Creek, n=137) and from two sampling locations within Devils Canyon (Chinook Creek, n= 55 and Cheechako Creek, n= 68) and handfuls of samples from other locations within and above Devils Canyon.
- Juvenile samples from within and above Devils Canyon locations are confounded by year and location (most samples from each location are only available from one year)
- Three clusters jump out from the PCA analysis: Kosina Creek, Black/Oshetna rivers, and all others. This result is concordant with the F_{ST} tree from the NCI analysis.
- New preliminary analyses on relatedness among juvenile samples taken above Devils Canyon showed high levels of related individuals (sharing parents) within geographic areas and years.

Discussion on whether AEA should file a modification as a result of failure to screen 190 SNP markers.

- Previous consultation with the Services resulted in a modification to increase the number of markers screened for Chinook Salmon in the Middle and Upper River to 13 uSATs and 190 SNP markers.
- Low quality and quantity of DNA yields from some juvenile collections within and above Devils Canyon resulted in high failure rates for SNP genotyping and a null allele in one uSAT locus resulted in excluding this locus from statistical analyses.
- **Decision Point: No modification will be filed. The plan to screen markers remains the same. If additional samples become available, AEA would screen for the full set of markers.**

Consulted on analysis roadmap for testing the hypothesis that Chinook Salmon captured within and above Devils Canyon represent one or more self-sustaining populations.

- **Decision Points:**
 - **Results of relatedness among juveniles should be taken into account in the interpretation of results.**
 - **Pedigree analyses are appropriate to reconstruct parental genotypes.**
 - **Collections within and above Devils Canyon should only be included in the population structure analyses if adequate numbers of adults and reconstructed parents are available.**
 - **A battery of tests should be used to develop multiple lines of evidence supporting or debunking the hypothesis. Tests discussed as appropriate included:**
 - **Allele richness (compare populations below and above Devils Canyon)**
 - **Linkage Disequilibrium (signals of multiple contributing populations)**
 - **Assignment (include potentially contributing populations from below Devils Canyon)**
 - **Garza's M (signal of genetically bottlenecked population(s))**
 - **Homogeneity between collections above and below Devils Canyon**
 - **The available data may provide insights but may not be adequate to conclusively accept or reject the hypothesis.**