Collection and analysis of Yukon River DNA baseline samples in Alaska, 2013

Yukon River Restoration and Enhancement Fund
Yukon River Panel Project CRE-78-13

By:

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Abstract

The purpose of this project is to continue to develop and refine genetic baselines for Yukon Chinook and chum salmon stocks through collection and genetic analysis of tissue samples from representative spawning populations in the Yukon River. Continued development of the genetic baselines is necessary to obtain the most accurate allocations in mixed stock analysis, a critical tool for both inseason management and postseason evaluation of Yukon River salmon runs. This project involved collection of baseline Chinook and chum salmon tissue samples in Alaska and Canada, and inclusion of those samples into existing ADF&G and DFO baselines. Samples were collected from live fish, preserved in ethyl alcohol, and shared among three genetics laboratories (DFO, ADF&G, USFWS) which conduct mixed stock analyses of Yukon River salmon runs. This report covers samples collected and included in baselines in Alaskan tributaries only; Canadian sampling and baseline inclusions are reported separately. In 2013, a total of 38 Chinook salmon tissue samples were collected from one tributary spawning population and no samples were collected from chum salmon spawning populations. Genotypes from these samples were analyzed and added to collections from the same locations from previous years. For Chinook salmon, the baseline estimate for one population was refined.

Introduction

Management of Chinook and chum salmon in the Yukon River requires differentiating between stocks originating from the various tributaries in both the US and Canada. Genetic stock identification is effectively used to distinguish country of origin and broad and fine scale stock groupings of Chinook salmon caught in the commercial and subsistence fisheries on the Yukon River (e.g. Decovich and Howard 2011). Chum salmon can be genetically differentiated into summer and fall runs, with broad scale stock groupings in each (Flannery et al. 2007). Fundamental to accurate genetic stock identification is the development of a comprehensive baseline genetic database which represents all spawning stocks that potentially contribute to the mixed stock run or fishery. Genetic baselines for Yukon salmon populations were originally constructed using allozyme markers starting in the late 1980s (e.g. Beacham et al. 1989). Single nucleotide polymorphisms (SNP) have been preferentially used as markers in the Chinook salmon baseline since 2004 (Smith et al. 2005), replacing the older allozyme database. At the beginning of the 2013 season, the Chinook baseline comprised 36 separate populations, and given adequate sample sizes, stocks can be identified to one of nine reporting groups (http://www.adfg.alaska.gov/index.cfm?adfg=fishinggeneconservationlab.yukonchinook_baseline). Similarly for chum salmon, a baseline using microsatellite markers was developed to replace the allozyme baseline around 2007 (Flannery et al. 2007). About 21 chum populations comprise the current chum baseline, from which stocks can be identified to one of two summer and two Alaskan and two Canadian fall chum reporting groups. Although not part of this project, a large number of Yukon chum salmon populations are also represented in the large Western Alaska Salmon Stock Identification Program (WASSIP) in the Coastal Western Alaska and Upper Yukon River reporting groups (DeCovich et al., 2013).

Sampling salmon populations within the Yukon drainage for genetic baselines is logistically difficult due to the large number of genetically discrete spawning populations distributed over a vast and remote region. Timing of spawning periods can be variable, and flooding and turbidity during the spawning period may preclude sampling at all. For these reasons, samples are collected somewhat opportunistically, depending on run timing and environmental conditions, based on a priority list. Several years ago, the genetics sub-committee of the Yukon River Joint Technical Committee developed this prioritized list for baseline collections, and it is updated annually and used as a guideline to direct sampling efforts each season (Appendices 1 and 2). High priority areas for sampling are those which could serve to further differentiate between genetically distinct groups and which contribute substantial numbers of spawners to Yukon Chinook and chum returns overall. The R&E genetics baseline sampling project, funded by the Yukon River Panel since 2007, has relied upon consultants, contractors, and local resource users to obtain samples from priority areas each year. Genetic baseline tissue samples have also been contributed by other projects and funding sources, and samples may be collected opportunistically when another project is operating in an area from which samples are needed. Sampling may extend over a number of years to achieve sample sizes needed to distinguish among stock groups within an acceptable level of precision. Adding to and improving the Yukon Chinook and chum baselines is an ongoing process which will ultimately result in more accurate and timely management decisions.

Objectives

1. Collect axillary fin tissues appropriate for genetic (DNA) analyses from Chinook and chum salmon (primarily fall run), representing spawning populations under-represented in current genetic baselines, and
2. Incorporate the sample genotypes into the agency baselines.

Methods

Alaska Department of Fish and Game (ADF&G) hired one local contractors to travel with ADF&G staff to collect Chinook salmon tissue samples for genetic analysis from a priority site on the Colleen River, a tributary of the Yukon River, in 201e. Live fish, or recently deceased fish with red gills, were sampled on or near the spawning grounds, and portions of the pelvic axillary processes of each fish were removed. The sample size goal for this tributary location was to provide for a minimum of 25 fish, which, when added to the existing collection of 24 fish was considered minimal for accurate identification in the baseline. In practice, due to sparseness of spawning salmon in most locations, samplers collected as many samples as possible. Tissue samples were stored in bulk vials partially filled with anhydrous ethyl alcohol; upon arrival at the ADF&G laboratory, the axillary processes were divided between paired vials to ensure that both labs, ADF&G and the Pacific Biological Station in Canada (DFO), received tissue samples from the same fish.. Samples were also shared with U.S. Fish and Wildlife Service Conservation Genetics Laboratory. The samples are currently being genotyped by ADF&G and data will be added to the existing baseline sample collections.

Results and Discussion

In 2013, a total of 37 Chinook salmon axillary process tissues samples were collected from one Alaskan tributary (Table 1). The size of collections from the Colleen River was small, primarily due to low numbers of spawners present. However, the total collection was sufficient to add the Colleen River population into the baseline.

Table 1. Location and numbers of adult Chinook salmon genetic baseline tissue samples collected from Alaska tributaries in 2013.

Tributary (main)	Branch tributary	Number of samples	
		2013	All years
Porcupine River			
	Colleen River	37	61

Overall, sample collections in 2013 fulfilled important needs in the Yukon Chinook and salmon genetic baseline. One new population was added to the Chinook baseline. Populations in the Black River will remain on the high priority sampling list (Appendix 1) and efforts will be made in the upcoming seasons to obtain enough samples to increase the total collections to over 50 fish. These additions and refinements to the Chinook baseline improve our ability to identify distinct stocks in mixed stock samples from Yukon River fisheries. Genetic differences for Yukon River chum salmon are less than for Yukon River Chinook salmon; the greatest difference in chum salmon is between the two seasonal races or runs, summer and fall (Flannery et al. 2007). However, making the distinction between summer and fall runs, and also distinguishing between US and Canadian stocks within the fall runs, is critical for management.

Acknowledgements

We wish to acknowledge ADF&G genetics laboratory staff for their time in organizing sampling materials and intaking, processing, and analyzing samples. We also thank our individual contractor, Paige Drobny of Spearfish Research, who assisted with sample collection in the field in 2013. Finally, acknowledgement is due to our Canadian counterparts at DFO and their contractors, who collected, processed, and analyzed samples from the Canadian Yukon tributaries.

References

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Appendix 1. Priorities for additional tissue sampling for adult Chinook baseline collections in US tributaries.

Tributary (main)	Branch tributary	Priority	Comments
Anvik River		2	Additional samples would be helpful
Archuelinguk River		3	Low priority, but current samples not useable
Nulato River		1	Currently unrepresented
Koyukuk River			
	Jim Creek	1	
	Kateel River	3	
	South Fork Koyukuk River	1	
	Clear/Hogatza	1	
Melozitna River		1	Current samples are of questionable value
Tanana River			
	Chatanika River	2	
	Goodpaster River	2	
Beaver Creek		3	
Porcupine River			
	Sheenjek River	3	Currently have enough samples
	Black	1	
Charley/Kandik/Nation		2	

Appendix 2. Priorities for additional tissue sampling for adult chum baseline collections in US tributaries.

Tributary (main)	Branch tributary/run	Priority	Comments
Archuelinguk		3	
Andreafsky			
	East Fork	3	
	West Fork	3	
Chulinak		3	
Innoko			
	California	3	
	Tolstoi	3	
Anvik			
	Beaver	3	
	Yellow	3	
	Swift	3	
	Otter	3	
	Canyon	3	
Kaltag		3	
Rodo		3	
Nulato		3	
Koyukuk			
	Gisasa	3	
	Dakli	2	
	Huslia	2	
	Clear	3	
	Henshaw	3	
	South Fork Late	1	
	South Fork Early	2	
	East Fork	2	
	Jim	1	
Melozitna		3	
Tozitna		3	
Tanana			
	Chena	2	
	Salcha	2	
	Toklat mainstream	3	
	Toklat - Sushana	3	
	Toklat - Geiger	3	
	Toklat - Downstream Geiger	3	
	Clearwater	3	
	Delta	3	
	Bluff	3	
Big Salt		1	
Chandalar		1	
Black		1	
Porcupine			
	Sheenjek	1	

Appendix 3. Financial summary.

Line Item	Allocation	Expenditures	Encumbrances	Credits	Obligated	Project Balance
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Line 100	$0.00	$0.00	$0.00	$0.00	$0.00	$0.00
Line 200	$0.00	$1,446.14	$0.00	$0.00	$1,446.14	($1,446.14)
Line 300	$30,701.75	$10,837.60	$0.00	$2,499.00	$8,338.60	$22,363.15
Line 400	$0.00	$2,112.38	$0.00	$0.00	$2,112.38	($2,112.38)
Line 500	$0.00	$0.00	$0.00	$0.00	$0.00	$0.00

Totals 200 - 500	$30,701.75	$14,396.12	$0.00	$2,499.00	$11,897.12	$18,804.63

Total All Lines	$30,701.75	$14,396.12	$0.00	$2,499.00	$11,897.12	$18,804.63

This is the current project balance as of (May 12, 2014), to be returned to PSC. The total to be returned to PSC will be $18,804.63.

Originally, all the funds for this project were allotted for contractual services. However, because Fish and Game staff were partly responsible for the collection of the genetic samples, some supplies/equipment (line 400) and travel expenses (line 200) were necessary for staff to conduct the fieldwork.