

Collection and analysis of Yukon River DNA baseline samples in Alaska, 2011

Yukon River Restoration and Enhancement Fund
Yukon River Panel Project CRE-78-11

By:

Jan Conitz, Nick Decovich, and Dr. Kathrine Howard

Alaska Department of Fish and Game
Commercial Fisheries Division
333 Raspberry Road
Anchorage, AK 99518
Phone 907 267 2135
E-mail jan.conitz@alaska.gov

Contents

List of Tables 2
Abstract 3
Introduction 3
Objectives 4
Methods 4
Results and Discussion 5
Acknowledgements 6

List of Tables

Table 1. Location and numbers of adult Chinook salmon genetic baseline tissue samples collected from Alaska tributaries in 2011 5
Table 2. Location and numbers of adult chum salmon genetic baseline tissue samples collected from Alaska tributaries in 2011 5

List of Appendices

Appendix 1. Priorities for additional tissue collections of adult Chinook baseline in US tributaries 8
Appendix 2. Priorities for additional tissue collections of adult chum baseline in US tributaries 9

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 2011, a total of 112 Chinook salmon tissue samples was collected from 5 tributary spawning populations, and a total of 181 chum salmon tissue samples was collected from 8 Alaskan tributary spawning populations. Genotypes from these samples were analyzed and added to collections from the same locations from previous years. For Chinook salmon, one new population was added to the baseline, the baseline estimate for one population was refined, and collection from a previously unrepresented population was initiated. For chum salmon, new collections were initiated for several populations, and samples from other populations will be used to update baselines.

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 2011 season, the Chinook baseline comprised 31 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., *in prep*).

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 three local contractors to collect Chinook and chum salmon tissue samples for genetic analysis from priority sites on Yukon River tributaries in 2011. Live fish, or recently deceased fish with red gills, were sampled on or near the spawning grounds, and portions of both pelvic axillary processes of each fish were removed. The sample size goal for each species and tributary location was to provide for a minimum of 50 fish, but 200 fish was considered optimal 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 paired bulk vials partially filled with anhydrous ethyl alcohol; paired axillary processes were divided between paired vials to ensure that both labs received tissue samples from the same fish. One vial from each pair was shipped to the Pacific

Biological Station in Canada, and the other vial was shipped to the Alaska Department of Fish and Game Gene Conservation Laboratory. Samples were also shared with U.S. Fish and Wildlife Service Conservation Genetics Laboratory. The samples were genotyped by these laboratories and the genotypes were added to or included in existing baseline sample collections.

Results and Discussion

In 2011, a total of 112 Chinook salmon tissue samples was collected from 5 Alaskan tributaries (Table 1). The size of collections from individual tributaries was very small, primarily due to low numbers of spawners present. The samples sizes from the two Koyukuk River tributaries remained too small (<50 fish) to add these populations to the baseline. However, the samples collected from the Goodpaster River in 2011 increased the total collection sufficiently to add this Tanana tributary population into the Chinook baseline. The Sheenjek River population was already in the baseline but the 2011 samples served to refine estimates of allele frequencies that determine this population's position within the overall stock structure. Samples from the Colleen River were collected for the first time in 2011, but this collection was still insufficient to include this tributary population in the baseline.

Table 1. Location and numbers of adult Chinook salmon genetic baseline tissue samples collected from Alaska tributaries in 2011.

Tributary (main)	Branch tributary	Number of samples	
		2011	All years
Koyukuk River			
	Middle Fork Koyukuk	13	23
	Jim River	4	9
Tanana River			
	Goodpaster River	49	81
Sheenjek River		21 ¹	72
Colleen River		25	25
Totals		112	210

¹Samples from the Sheenjek River were collected in 2011 outside of of this R&E project and funding.

A total of 181 chum salmon tissue samples were collected from 8 Alaskan tributary locations in 2011 (Table 2). Fish from tributaries in the Koyukuk River comprised only summer chum salmon. Fish sampled in tributaries of the Tanana River were a mix of summer and fall chum salmon, and fish sampled from the Chandalar and Sheenjek Rivers were all fall chum salmon. The Middle Fork Koyukuk samples and the samples from the Goodpaster and Bear Creek tributaries of the Tanana River were the first collections from these locations, but sample sizes were insufficient to include these populations in the baseline. Samples collected on the Jim, Salcha, Chandalar, and Sheenjek Rivers updated older baseline sample collections, some having samples dating back as far as 1987. Genetic analysis of these chum salmon samples had not been completed as of May 2012.

Table 2. Location and numbers of adult chum salmon genetic baseline tissue samples collected from Alaska tributaries in 2011.

Tributary (main)	Branch tributary	Run	Number of samples	
			2011	All years
Koyukuk	Middle Fk, Wiseman	summer	21	21
	Middle Fk, Slate Creek Mouth	summer	12	12
	Jim	summer	33	305
Tanana	Salcha	summer, fall	53	400
	Goodpaster	summer	4	4
	Bear Creek	summer	28	28
Chandalar		fall	63	474
Porcupine	Sheenjek	fall	175	604
Totals			181	1,848

Overall, sample collections in 2011 fulfilled important needs in the Yukon Chinook and chum salmon genetic baselines. One new population was added to the Chinook baseline, and collections were initiated and samples were added to existing collections from other high priority populations. Populations in the Koyukuk River tributaries and the Coleen 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. Samples collected in 2011 will serve to update the genetic database, and provide a start on adding new populations that could improve our understanding of Yukon chum genetic structure. These samples will also contribute to stock structure analyses through WASSIP. Priority areas for chum salmon sampling in Alaska continue to be certain tributaries in the Koyukuk River and upper river (U.S.) tributaries above the Tanana River (Appendix 2).

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 and agency contractors who collected samples in the field in 2011: Jack Reakoff, Chris Stark (Bering Sea Fishermen's Association), and Paige Drobny (Tanana Chiefs Council). 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

- Beacham, T.D., C.B. Murray, and R.E. Withler. 1989. Age, morphology, and biochemical genetic variation of Yukon River Chinook salmon. *Transactions of the American Fisheries Society*, 118:1, 46-63.
- DeCovich, N.A., and K.G. Howard. 2011. Genetic stock identification of Chinook salmon harvest on the Yukon River 2010. Alaska Department of Fish and Game, Fishery Data Series No. 11-65, Anchorage.
- DeCovich, N., T. Dann, S. Rogers, H. Liller, L. Fox, J. Jasper, C. Habicht, W. Templin. *In prep.* Chum salmon baseline based upon 96 SNPs. Alaska Department of Fish and Game, Regional Information Report series.
- Flannery, B.G., T.D. Beacham, R.R. Holder, E.J. Kretschmer, and J.K. Wenburg. 2007. Stock structure and mixed stock analysis of Yukon River chum salmon. U.S. Fish and Wildlife Service, Alaska Fisheries Technical Report 97.
- Smith, C.T., W.D. Templin, J.E. Seeb, and L.W. Seeb. 2005. Single nucleotide polymorphisms provide rapid and accurate estimates of the proportions of U.S. and Canadian Chinook salmon caught in Yukon River fisheries. *North American Journal of Fisheries Management*, 25:3, 944-953.

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

Tributary (main)	Branch tributary	Priority	Cumulative sample size	Comments
Anvik River		2	246	Additional samples would be helpful
Archuelinguk River		3	78	Low priority, but current samples not useable
Nulato River		1	0	Currently unrepresented
Koyukuk River	Jim Creek	1	9	
	Kateel River	1	23	
	South Fork Koyukuk River	1	68	
	Clear/Hogatza	1	0	
Melozitna River		1	87	Current samples are of questionable value
Tanana River	Chatanika River	2	50	
	Goodpaster River	2	81	
Beaver Creek		3	100	
Porcupine River	Sheenjok River	1	72	
	Colleen River	1	25	
	Black	1	0	
Charley/Kandik/Nation		2	54	

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

Tributary (main)	Branch tributary/run	Priority	Cumulative sample size	Comments
Archuelinguk		3	100	
Andreafsky				
	East Fork	3	304	
	West Fork	3	100	
Chulinak		3	100	
Innoko				
	California	3	200	
	Tolstoi	3	200	
Anvik				
	Beaver	3	200	
	Yellow	3	100	
	Swift	3	200	
	Otter	3	100	
	Canyon	3	50	
Kaltag		3	100	
Rodo		3	78	
Nulato		3	296	
Koyukuk				
	Gisasa	3	100	
	Dakli	2	100	
	Huslia	2	100	
	Clear	3	304	
	Henshaw	3	462	
	South Fork Late	1	100	
	South Fork Early	2	200	
	East Fork	2	100	
	Jim	1	304	
Melozitna		3	246	
Tozitna		3	321	
Tanana				
	Chena	2	286	

	Salcha	2	400
	Toklat mainstream	3	315
	Toklat - Sushana	3	300
	Toklat - Geiger	3	100
	Toklat - Downstream Geiger	3	100
	Clearwater	3	80
	Delta	3	300
	Bluff	3	100
Big Salt		1	71
Chandalar		1	474
Black		1	112
Porcupine			
	Sheenjek	1	602