Stock identification of Yukon River Chum Salmon using Microsatellite DNA Loci

Report to Yukon River Panel : Project CRE 79-02

March 15, 2003

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Abstract

Population structure and the application to genetic stock identification for chum salmon (Oncorhynchus keta) in the Yukon River was examined using microsatellite markers. Variation at 15 microsatellite loci (*Ots3, Ots103*, *Oke3, Oki2, Oki100*, *One101, One102, One104, One106, One108, One109, One111, One114*, Ssa419, and OtsG68) was surveyed for approximately 1,500 chum salmon from 11 sites in the Yukon River drainage. Differentiation between the Fishing Branch River and Kluane River populations accounted for about 2.5 times the variation observed among years within populations, indicative of relative stability of allele frequencies.

Applications to mixed-stock analysis were evaluated with simulated fishery samples. Simulated mixtures containing White River drainage populations were estimated with a high degree of accuracy, and single populations in the Chandindu and Teslin rivers were estimated with an acceptable degree of accuracy, with mean estimated stock compositions in excess of 90%. The results of the simulations suggest that microsatellite variation has the potential to provide reliable estimates of stock composition for regional groups of Yukon River chum salmon.

Introduction

Chum salmon (*Oncorhynchus keta)* are widely distributed within the Yukon River drainage, spawning in tributaries ranging from the headwaters to near the mouth of the river. Management for conservation of biodiversity within the drainage requires knowledge of genetic variation among populations as well as population-specific information from fisheries. Effective management of fisheries within major drainages like the Yukon River generally requires that information on the harvesting and timing of specific populations be known, should managers wish to change exploitation rates on specific populations for conservation purposes. For example, the Canada/U.S. Yukon River Salmon Agreement established specific escapement targets and harvest sharing provisions for Canadian-origin chum salmon stocks. It is therefore important to develop a management system that allows managers to assess accurately the status of these stocks in fisheries throughout the drainage during the season so that Treaty obligations can be actively managed for. Accurate post-season run reconstructions are essential in evaluating whether management actions were consistent with meeting overall objectives and Treaty obligations. Run reconstructions are also important in monitoring the productivity of stocks and assessing the adequacy of current escapement targets and both pre-season and in-season run forecasting techniques. A suitable technique for identifying Canadian-origin chum salmon in lower river catches has not yet been found either for post-season analysis or for in-season use in fisheries management. Consequently, this makes managing to achieve Treaty obligations very difficult and it

severely limits the assessment of factors influencing stock productivity, which appears to have fluctuated widely in recent years.

Stock identification of chum salmon migrating through the lower river is a continuing issue of management concern, and there is no effective way to provide estimates of stock composition in the detail required by fishery managers. Although allozyme-based methods of stock identication have proven useful in estimation of chum salmon stock composition in mixed-stock fisheries (Shaklee et al. 1999), and differentiation at allozyme loci occurs among Yukon River chum salmon (Beacham et al. 1988; Wilmot et al. 1994), the level of population discrimination available in the Yukon River is not yet sufficient for population-specific applications. Variation in microsatellite loci has been applied in other species requiring discrimination among salmonid populations within watersheds (Small et al. 1998; Beacham and Wood 1999; Beacham et al. 2001), and has been shown to be useful in stock discrimination in chinook salmon (Banks et al. 2000). Variation at microsatellite loci has been particularly useful for population-specific estimates of stock composition of Fraser River chinook salmon (Beacham et al. 2003), and would likely work equally well for both the summer and fall runs of Yukon River chum salmon.

In the present study, we survey variation at 15 microsatellite loci, provide information on allele size ranges and heterozygosity of the loci, and evaluate the utility of using microsatellite variation for stock identification of Yukon River chum salmon. This is accomplished by analysis of simulated mixtures containing simulated chum salmon from only a single population.

Methods

Collection of DNA samples and laboratory analysis

Tissue samples were collected from adult fish in chum salmon populations in the Yukon River drainage (Figure 1), and DNA extracted from the samples as described by Withler et al. (2000). For the survey of baseline populations, PCR products at 15 microsatellite loci: *Ots3* (Banks et al. 1999), *Ots103* (Small et al. 1998), *Oke3* (Buchholz et al. 1998), *Oki2* (Smith et al. 1998), *Oki100* (Miller et al. unpub), *One101, One102, One104, One106, One108, One109, One111,* and *One114* (Olsen et al. 2000), Ssa419 (Cairney et al. 2000), and OtsG68 (Morris et al. 1996) were size fractionated on denaturing polyacrylamide gels with the ABI 377 automated DNA sequencer. Allele sizes were determined with Genescan 3.1 and Genotyper 2.5 software (PE Biosystems, Foster City, CA). Allele frequency differences among populations were then compared.

Baseline populations

The baseline survey consisted of analysis of approximately 1500 chum salmon from nine Yukon and two Alaskan sampling sites or populations in the Yukon River drainage (Table 1). Each population at each locus was tested for departure from Hardy-Weinberg equilibrium (HWE) using GDA (Lewis and Zaykin 2001). Annual samples within populations were tested separately, with 15 tests conducted at each locus (Table 1. Critical significance levels for simultaneous tests were evaluated using sequential Bonferroni adjustment (Rice, 1989). F_{ST} estimates for each locus were calculated with FSTAT (Goudet, 1995), and the standard deviation of the estimate for an individual locus was determined by jackknifing over populations and for all loci combined by

bootstrapping over loci. Estimation of variance components of annual variation within populations was determined with GDA, with only those populations (Fishing Branch, Kluane) included in the analysis for which two or more years of sampling were available. All annual samples available for a location were combined to estimate population allele frequencies, as was recommended by Waples (1989).

Estimation of stock composition

Genotypic frequencies were determined at each locus in each population and a statistical package similar to the analysis of mixtures software program (SPAM) (Debevec et al. 2000) was used to estimate stock composition of each simulated mixture. The difference to SPAM was that a correction to population allele frequencies for small sample sizes was included (S. Kalinowski, pers. comm.). Each locus was assumed to be in HWE, and expected genotypic frequencies were determined from the observed allele frequencies and used as model inputs.

Each baseline population was resampled with replacement in order to simulate random variation involved in the collection of the baseline samples before the estimation of stock composition of each simulated mixture. Simulated mixtures composed of chum salmon from different populations were examined in order to evaluate accuracy and precision of the estimated stock compositions. Simulated fishery samples comprising only a single population of 150 fish were generated by randomly resampling with replacement the baseline populations in each drainage. Estimated stock composition of a simulated mixture was then determined, and the whole process was repeated 100

times to estimate the mean and standard deviation of the individual stock composition estimates.

Results and Discussion

Variation within populations

All loci surveyed were polymorphic in all populations sampled. The number of observed alleles at each locus ranged from 7 to 77, with lower heterozygosity observed at those loci with fewer alleles (eg. *Oke3*) (Table 2). Heterozygosity varied both among loci and among the populations surveyed. Genotypic frequencies at each locus within sampling location and year generally conformed to those expected under Hardy-Weinberg equilibrium, except for *One108* and *One109* (Table 2). In order for a genetic based method of stock identification to be applied successfully, there must be significant genetic differences among the populations that fishery mangers wish to separate. Significant genetic differentiation at the microsatellite loci was observed among the 11 chum salmon populations surveyed to date from the Yukon River drainage. The average Fst value over all loci was 0.021, indicative of only moderate differentiation among populations (Table 2).

Distribution of genetic variation

Gene diversity analysis of the 15 loci surveyed was used to determine the magnitude of annual variation within populations and of variation among two salmon populations, with only populations having two or more years of sampling included in the analysis (Kluane River, Fishing Branch River). The amount of variation contained within

populations ranged from 93.3% (*Oke3*) to 99.2% (*Ssa419*), with the average for microsatellite loci 97.2% (Table 3). The maximum range of sampling times was approximately 10 years for the Fishing Branch River population, and 14 years for the Kluane River population. Genetic differentiation between these two populations was, on average, 2.5 times greater than annual variation within these populations. This stability of allele frequencies relative to population differentiation is a key characteristic of microsatellite loci (Beacham and Wood 1999; Tessier and Bernatchez 1999), and is in sharp contrast to other techniques such as scale pattern analysis, where annual variability in the scale patterns used in stock identification requires annual sampling of the baseline. Owing to the relative stability of the microsatellite allele frequencies, baseline samples collected in one year can be used to estimate stock compositions of samples collected in following years, or indeed in years previous to collection of the baseline samples. Annual stability of the characters used to discriminate among stocks is a key attribute of any technique used in stock identification, particularly if the baseline populations cover a wide geographic area.

Population structure

Regional structuring of population samples was observed in the survey. Two populations in the White River drainge, Kluane River and Donjek River, were most similar to each other and clustered together in the dendrogram analysis (Figure 2). The two samples from Alaska (Sheenjek River and Andreafsky River) were most similar to each other, and the Sheenjek River population was distinct from the Fishing Branch River population, even though both are located in the Porcupine River drainage.

Samples from spawning areas in the mainstem Yukon River tended to cluster together, and were differentiated from population samples in the Teslin River and Chandindu River drainages.

Applications to stock identification

Based upon analysis of the genetic differences between specific populations, the following reporting groups or stocks may be possible for Canadian populations in estimation of stock composition in mixed-stock fishery samples:

Fishing Branch, Chandindu, Teslin, Kluane/Donjek, Mainstem Yukon River

At a minimum, both populations surveyed from Alaska (Sheenjek fall run, Andreafsky summer run) would likely be reporting groups in mixed stock analysis.

Simulated mixed-fishery samples

Reporting units were judged acceptable for mixture analysis if approximately 90% of the mixture on average was allocated to the correct regional group of populations, with five regional groups investigated for Canadian populations and one regional group for Alaskan populations. Simulated mixtures containing White River drainage populations (Kluane, Donjek) were estimated with a high degree of accuracy (Table 4), given the distinctive differentiation of populations in this drainage. Single populations in the Chandindu and Teslin rivers were estimated with an acceptable degree of accuracy, with mean estimated stock compositions in excess of 90% (Table 4). The Fishing

Branch population was well estimated, but the lower accuracy of estimation of the Sheenjek River sample (about 90%) may reflect the smaller sample size for that population. Generally, the results of the simulations suggest that microsatellite variation has the potential to provide reliable estimates of stock composition for regional groups of Yukon River chum salmon.

The number of populations included in this initial survey of microsatellite variation in Yukon River chum salmon was limited. Although preliminary simulations indicate that differentiation between Alaskan and Canadian populations is possible, a more extended survey of variation in Alaskan populations is required before firm conclusions can be drawn concerning the utility of microsatellites for stock identification of Yukon River chum salmon.

Acknowledgments

I acknowledge the able assistance of Department of Fisheries and Oceans and Alaska Department of Fish & Game staff who coordinated the collection of the spawning ground samples. Financial support for the project was provided by the Yukon River Restoration and Enhancement Fund as well as the Department of Fisheries and Oceans.

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Table 1. Chum salmon samples collected and analyzed from 11 populations in the Yukon River drainage. Sample sizes (N) are for years sampled.

Population	Years sampled	N	Total N
Canadian populations			
Fishing Branch	1987, 1994, 1997	95, 75, 161	331
Chandindu	1998	35	35
Kluane	1987, 1992, 2001	41, 100, 358	462
Donjek	1994	72	72
Teslin	1992	100	100
Mainstem@Pelly	1993	84	84
Mainstem@Big_Creek	1995	100	100
Mainstem@Minto	1989	100	100
Mainstem@Tatchun	1987	75	75
American populations			
Sheenjek	1987	108	108
Andreafsky	1987	61	61

Table 2. Number of alleles observed, expected heterozygosity (H_e), observed heterozygosity (H_o), number of significant Hardy-Weinberg equilibrium tests (HWE, N=15 tests), and F_{ST} among 11 chum salmon populations for 15 microsatellite loci. Standard deviations are in parentheses.

Locus	Alleles	H_e	H_o	HWE	F_{ST}
Oki2	19	0.73	0.74	0	0.028 (0.016)
Oke3	7	0.62	0.61	0	0.031 (0.020)
One104	23	0.90	0.89	1	0.023 (0.006)
Oki100	22	0.81	0.83	0	0.023 (0.011)
Ots3	19	0.71	0.69	2	0.016 (0.004)
Otsg68	37	0.90	0.93	0	0.021 (0.010)
Ots103	35	0.84	0.88	0	0.028 (0.013)
Ssa419	13	0.84	0.89	1	0.006 (0.002)
One101	39	0.84	0.81	1	0.033 (0.014)
One102	36	0.89	0.81	3	0.016 (0.004)
One106	45	0.95	0.91	2	0.009 (0.003)
One108	49	0.94	0.83	6	0.011 (0.003)
One109	26	0.83	0.69	7	0.022 (0.010)
One111	77	0.77	0.77	2	0.039 (0.018)
One114	34	0.88	0.92	0	0.018 (0.010)
All loci					0.021 (0.002)

Table 3. Hierarchical gene-diversity analysis of Kluane River and Fishing Branch chum salmon for 15 microsatellite. Populations and years within populations were outlined in Table 1.

Locus	Within Populations	Among years within populations	Among populations
Oki2	0.9701	0.0299	0.0000
Oke3	0.9330	0.0195	0.0475
One104	0.9677	0.0041	0.0282
Oki100	0.9671	0.0093	0.0236
Ots3	0.9772	0.0123	0.0105
Otsg68	0.9754	0.0026	0.0220
Ots103	0.9588	0.0035	0.0377
Ssa419	0.9915	0.0024	0.0061
One101	0.9483	0.0124	0.0393
One102	0.9847	0.0030	0.0123
One106	0.9901	0.0014	0.0085
One108	0.9884	0.0021	0.0095
One109	0.9887	0.0016	0.0097
One111	0.9447	0.0254	0.0299
One114	0.9749	0.0000	0.0251
All loci	0.9724	0.0078	0.0198

Table 4.- Simulations (values for True, estimated, and standard deviations) for 100% by population for Yukon River chum salmon for simulated mixtures of 150 chum salmon from each population using Rannala and Mountain correction for small sample size.

	TRUE	Est	SD	T	Est	SD	T	Est	SD	T	Est	SD	T	Est	SD	T	Est	SD
Tatchun	100	81.3	(5.3)	0	0.0	(0.1)	0	0.2	(0.4)	0	0.3	(0.5)	0	0.3	(0.5)	0	0.0	(0.1)
Kluane	0	0.2	(0.4)	100	99.4	(0.7)	0	0.1	(0.2)	0	0.0	(0.1)	0	0.1	(0.3)	0	0.3	(0.5)
Andreafsky	0	0.1	(0.2)	0	0.0	(0.0)	100	97.8	(1.3)	0	0.1	(0.2)	0	0.0	(0.1)	0	0.0	(0.1)
Sheenjek	0	0.6	(0.7)	0	0.0	(0.1)	0	0.4	(0.5)	100	90.6	(3.4)	0	0.4	(0.5)	0	0.1	(0.1)
Fishing_Br	0	8.9	(3.6)	0	0.1	(0.2)	0	0.9	(0.8)	0	7.8	(3.1)	100	97.6	(1.4)	0	0.8	(0.9)
Pelly	0	0.0	(0.1)	0	0.0	(0.1)	0	0.0	(0.1)	0	0.0	(0.1)	0	0.0	(0.1)	100	98.6	(1.2)
Donjek	0	0.1	(0.2)	0	0.4	(0.6)	0	0.0	(0.0)	0	0.0	(0.1)	0	0.0	(0.1)	0	0.0	(0.1)
Big_Creek	0	3.4	(2.3)	0	0.1	(0.1)	0	0.3	(0.4)	0	0.8	(0.9)	0	0.7	(0.8)	0	0.1	(0.2)
Teslin	0	0.3	(0.4)	0	0.0	(0.0)	0	0.0	(0.1)	0	0.0	(0.1)	0	0.1	(0.2)	0	0.0	(0.0)
Minto	0	5.1	(2.5)	0	0.0	(0.1)	0	0.3	(0.5)	0	0.3	(0.5)	0	0.7	(0.8)	0	0.1	(0.2)
Chandindu	0	0.0	(0.1)	0	0.0	(0.0)	0	0.0	(0.1)	0	0.0	(0.1)	0	0.0	(0.1)	0	0.0	(0.0)
Yukon(mainstem)	100	90.0	(0.9)	0	0.1	(0.3)	0	0.8	(1.2)	0	1.4	(3.3)	0	1.7	(0.6)	100	98.8	(0.5)
Fishing Branch	0	8.9	(3.6)	0	0.1	(0.2)	0	0.9	(0.8)	0	7.8	(3.1)	100	97.6	(1.4)	0	0.8	(0.9)
White River	0	0.3	(0.4)	100	99.8	(0.3)	0	0.1	(0.2)	0	0.1	(0.1)	0	0.1	(0.3)	0	0.4	(0.5)
Yukon(US)	0	0.7	(0.8)	0	0.0	(0.1)	100	98.2	(1.2)	100	90.7	(3.3)	0	0.5	(0.5)	0	0.1	(0.2)
Teslin	0	0.3	(0.4)	0	0.0	(0.0)	0	0.0	(0.1)	0	0.0	(0.1)	0	0.1	(0.2)	0	0.0	(0.0)

Table 4. continued

	T	Est	SD	T	Est	SD	T	Est	SD	T	Est	SD	T	Est	SD
Tatchun	0	0.1	(0.2)	0	1.4	(1.2)	0	0.4	(0.5)	0	2.1	(1.5)	0	0.2	(0.3)
Kluane	0	17.5	(5.6)	0	0.3	(0.4)	0	0.0	(0.0)	0	0.1	(0.2)	0	0.0	(0.1)
Andreafsky	0	0.0	(0.0)	0	0.0	(0.1)	0	0.0	(0.1)	0	0.1	(0.2)	0	0.1	(0.1)
Sheenjek	0	0.0	(0.1)	0	0.6	(0.7)	0	0.1	(0.2)	0	0.2	(0.4)	0	0.2	(0.4)
Fishing_Br	0	0.2	(0.3)	0	10.3	(3.5)	0	0.5	(0.7)	0	7.2	(3.0)	0	3.2	(2.1)
Pelly	0	0.0	(0.0)	0	0.0	(0.1)	0	0.0	(0.0)	0	0.0	(0.1)	0	0.0	(0.0)
Donjek	100	82.2	(5.6)	0	0.1	(0.1)	0	0.0	(0.0)	0	0.0	(0.1)	0	0.0	(0.0)
Big_Creek	0	0.1	(0.2)	100	80.9	(4.7)	0	0.6	(0.8)	0	6.3	(3.0)	0	0.5	(0.8)
Teslin	0	0.0	(0.1)	0	0.3	(0.4)	100	97.3	(1.6)	0	0.4	(0.5)	0	0.1	(0.2)
Minto	0	0.0	(0.1)	0	6.3	(2.9)	0	1.1	(1.0)	100	83.6	(4.7)	0	1.0	(1.0)
Chandindu	0	0.0	(0.0)	0	0.0	(0.1)	0	0.0	(0.1)	0	0.0	(0.1)	100	94.7	(2.8)
Yukon(mainstem)	0	0.1	(0.2)	100	88.5	(0.9)	0	2.2	(1.6)	100	92.0	(0.7)	100	96.4	(0.5)
Fishing Branch	0	0.2	(0.3)	0	10.3	(3.5)		0.5	(0.2)	0	7.2	(3.0)	0	3.2	(2.1)
White River	100	99.7	(0.4)	0	0.3	(0.4)	0	0.0	(0.1)	0	0.1	(0.3)	0	0.0	(0.1)
Yukon(US)	0	0.0	(0.1)	0	0.6	(0.7)	0	0.1	(0.2)	0	0.3	(0.4)	0	0.3	(0.4)
Teslin	0	0.0	(0.1)	0	0.3	(0.4)	100	97.3	(1.6)	0	0.4	(0.5)	0	0.1	(0.2)

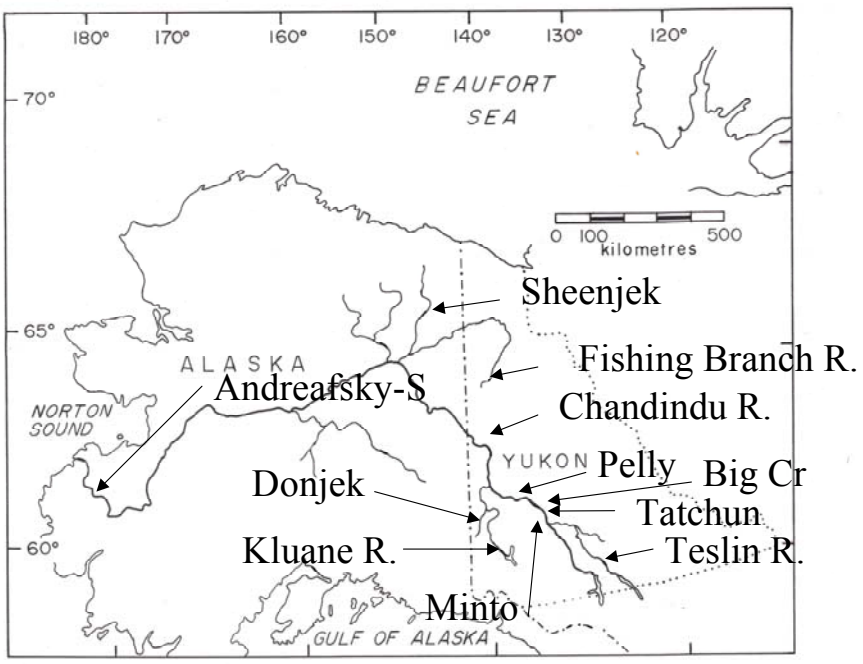

Figure 1. Locations of chum salmon populations sampled in the Yukon River drainage. Numbers and locations are indicated in Table 1.

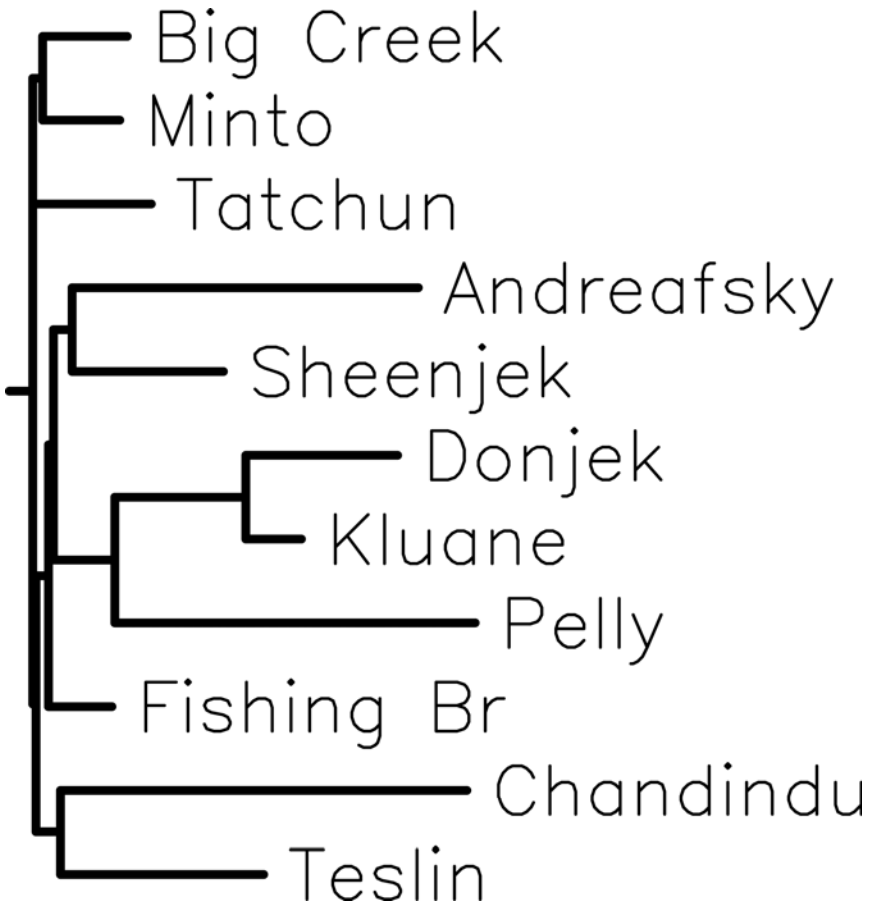

Figure 2. Neighbor-joining dendrogram based on Cavalli-Sforza and Edward's (1967) chord distance for 11 Yukon River chum salmon populations.