Report on survey of microsatellite variation in southern British Columbia Chinook salmon

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September 2007

A project funded by the Southern Boundary Restoration and Enhancement Fund 2005-2007.

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Abstract

Approximately 9,000 Chinook salmon from 73 populations in southern British Columbia were surveyed for variation at 13 microsatellite loci that comprised the suite incorporated in the Genetic Analysis of Pacific Salmon (GAPS) shared database. The multi-locus genotypes of all fish surveyed were provided to Dr. P. Moran of the National Marine Fisheries Service Montlake Laboratory for incorporation into the GAPS database. The number of alleles observed at a locus varied from 11 (Ots9) to 71 (Omm1070), with all loci in Hardy-Weinberg equilibrium (Table 2). The average F_{ST} value was 0.063, with individual locus values ranging from 0.027 (Omm1080) to 0.161 (OtsG474). A regional population structure was observed, with populations clustering into 10 geographic regions.

Introduction

Conservation of Chinook salmon genetic diversity around the Pacific Rim requires an understanding of their origins and the evolutionary processes promoting and maintaining their differentiation, and delineation of phylogenetically and adaptively distinct groups in the distribution. Genetic variation can be employed as a very effective tool to evaluate the population structure of salmonids, is a key component in the elucidation of management units or conservation units in a species, and can be applied to manage fisheries exploiting specific stocks of salmon. For Chinook salmon, variation at allozymes was the initial principal genetic technology employed in evaluation of population structure, ranging from the Yukon River (Beacham et al. 1989), Alaska (Gharrett et al. 1987), Southeast Alaska and northern British Columbia (Guthrie and Wilmot 2004), British Columbia (Teel et al. 2000), to the Pacific northwest (Winans 1989; Utter et al. 1989, 1995; Shaklee et al. 1999). Increased resolution among populations relative to that detected with allozymes became possible with the advent of DNA-level assays. Initial surveys employed variation at mitochondrial DNA (Wilson et al. 1987; Cronin et al. 1993) and minisatellites (Beacham et al. 1996), but these techniques were soon replaced by surveys of microsatellite variation (Banks et al. 2000; Nelson et al. 2001; Beacham et al. 2003). Microsatellites have been recognized as providing the ability to evaluate fine-scale population structure in salmonids (Banks et al. 2000), as well as the capability to investigate population structure on a Pacific Rim basis (Beacham et al. 2006a).

This report outlines the contributions made to a shared microsatellite baseline for Chinook salmon that is commonly known at the Genetic Analysis of Pacific Salmon (GAPS) microsatellite baseline. This baseline is shared by management and assessment agencies from Alaska through California.

Methods and Materials

Collection of DNA samples

Genomic DNA was extracted from either liver, scales, operculum punches or fin clips from Chinook salmon sampled initially using the phenol-chloroform protocol of Miller et al. (1996) and later a chelex resin protocol (Withler et al. 2000). Samples were derived from adults in all areas except for some locations, where due to the difficulty of obtaining adults, juveniles were sampled. Adults could have been sampled and released, freshly killed and sampled, or samples could have been obtained from carcasses on the spawning grounds.

Template DNA was amplified via the polymerase chain reaction (PCR) at a total of 13 microsatellite loci (Table 1) including nine tetranucleotide microsatellite loci, Oki100 (K. Miller, unpub. data), OMM1080 (Rexroad et al. 2001), Ots211, Ots212, Ots213, Ots201b, Ots208b (Grieg et al. 2003), OtsG474 (Williamson et al. 2002), Ssa408 (Cairney et al. 2000) and four dinucleotide loci, Ogo2, Ogo4 (Olsen et al. 1998), Ots3, Ots9 (Banks et al. 1999). All multi-locus genotypes were provided to Dr. P. Moran of the National Marine Fisheries Service Montlake Laboratory for incorporation into the Genetic Analysis of Pacific Salmon (GAPS) database for Chinook salmon. These data can be accessed at http://webapps.nwfsc.noaa.gov/gaps.

Data Analysis

All annual samples available for a location were combined to estimate population allele frequencies, as was recommended by Waples (1990). Weir and Cockerham's (1984) F_{ST} estimates for each locus over all populations were calculated with FSTAT

version 2.9.3.2 (Goudet 1995). Cavalli-Sforza and Edwards (CSE) (1967) chord distance was used to estimate genetic distances among all populations. An unrooted neighbor-joining tree based upon CSE was generated using NJPLOT (Perriere and Gouy 1996). Computation of the number of alleles observed per locus was carried out with GDA (Lewis and Zaykin 2001).

Results and Discussion

During the study, approximately 9,000 fish from 73 populations in southern British Columbia were surveyed at 13 microsatellite loci that comprised the Genetic Analysis of Pacific Salmon suite (Table1). The number of alleles observed at a locus varied from 11 (Ots9) to 71 (Omm1070), with all loci in Hardy-Weinberg equilibrium (Table 2). The average F_{ST} value was 0.063, with individual locus values ranging from 0.027 (Omm1080) to 0.161 (OtsG474).

Analysis of genetic relatedness among populations indicated that there was a regional population structure. Populations clustered into the following regions: west coast Vancouver Island, east coast Vancouver Island, southern British Columbia mainland, upper Fraser River, middle Fraser River, lower Fraser River, South Thompson River, North Thompson River, lower Thompson River, and Boundary Bay (Figure 2).

Funding was originally provided to survey variation in approximately 5,000 individual Chinook salmon. However, during the course of the survey, the Molecular Genetics Laboratory was able to upgrade the automated DNA sequencers in the laboratory, reducing the cost of analysis of individual fish. These cost savings were incorporated in the survey of Chinook salmon microsatellite variation, with approximately 9,000 individuals surveyed instead of the proposed 5,000 individuals.

The multi-locus genotypes of all individuals surveyed in the study have been provided to Dr. P. Moran (NMFS, Seattle) for incorporation into the GAPS database. A

number of publications are anticipated from the analysis of these data, and some are currently under scientific review.

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Table 1. Summary of population surveyed, region, and number of fish analyzed for variation at 13 microsatellite loci in the study. Regions are: ECVI (East Coast Vancouver Island), LwFR (Lower Fraser River, F-fall, Sp-spring, Su-summer), LWTH (Lower Thompson), MUFR (Middle Fraser), NOTH (North Thompson), Boundary (Boundary Bay), SOMN (Southern BC Mainland), SOTH (South Thompson), Up Col (Upper Columbia), UPFR (Upper Fraser), WCVI (West Coast Vancouver Island).

Population	Region	Number
Big Qualicum	ECVI	98
Chemainus	ECVI	213
Cowichan	ECVI	252
L. Qualicum	ECVI	187
Nanaimo F	ECVI	480
Nanaimo SP	ECVI	95
Nanaimo SU	ECVI	208
NanaimoUpper	ECVI	117
Nimpkish	ECVI	70
Puntledge SU	ECVI	265
Puntledge F	ECVI	326
Woss Lake	ECVI	21
Chilliwack@Stave	LWFR-F	40
Harrison	LWFR-F	239
White Chilliwack	LWFR-F	264
Big Silver	LWFR-Sp	52
Birkenhead	LWFR-Sp	45

BlueCr(UpPitt)	LWFR-Sp	20
Sloquet Creek	LWFR-Sp	23
Upper Pitt	LWFR-Sp	38
Maria Slough	LWFR-Su	326
Deadman	LWTH	171
Louis	LWTH	20
Nicola	LWTH	86
U. Coldwater	LWTH	71
Bridge	MUFR	88
Chilako	MUFR	32
Cottonwood	MUFR	44
Elkin	MUFR	186
L. Chilcotin	MUFR	180
Nazko	MUFR	177
Portage	MUFR	120
Taseko	MUFR	140
U. Cariboo	MUFR	169
U. Chilcotin	MUFR	209
Westroad	MUFR	31
Blue River	NOTH	46
Finn	NOTH	152
Lemieux Creek	NOTH	73
Raft	NOTH	89
Little Campbell	Boundary	29
Serpentine	Boundary	23

Capilano	SOMN	80
Devereux	SOMN	175
Klinaklini	SOMN	61
Phillips	SOMN	204
Porteau Cove	SOMN	38
Bessette	SOTH	63
Eagle	SOTH	82
M. Shuswap	SOTH	26
Salmon@SA	SOTH	139
Okanagan River	Up Col-Su/F	48
Bowron	UPFR	100
Goat	UPFR	42
Holmes	UPFR	123
Kenneth Creek	UPFR	35
R_Chehalis	UPFR	48
Slim	UPFR	129
Tete Jaune	UPFR	193
Willow	UPFR	35
Burman	WCVI	245
Gold	WCVI	345
Kennedy	WCVI	190
Nahmint	WCVI	50
San Juan	WCVI	188
Sarita	WCVI	3
Sooke	WCVI	37

Tahsis	WCVI	200
Thornton	WCVI	172
Tlupana	WCVI	60
Toquart	WCVI	74
Tranquil	WCVI	246
Zeballos	WCVI	50

Table 2. Number of alleles, expected heterozygosity (H_E), observed heterozygosity (H_O), and genetic differentiation (F_{ST}) for 13 microsatellites examined in 73 collections of Chinook salmon.

Locus	Number of alleles	H_E	H_O	F_{ST}
Ogo2	26	0.73	0.72	0.073
Ogo4	20	0.78	0.79	0.107
Oki100	42	0.93	0.92	0.033
Omm1080	71	0.94	0.94	0.027
Ots201b	54	0.90	0.90	0.051
Ots208b	60	0.92	0.92	0.035
Ots211	40	0.92	0.92	0.044
Ots212	35	0.87	0.87	0.054
Ots213	54	0.92	0.92	0.040
Ots3M	15	0.67	0.67	0.127
Ots9	11	0.56	0.55	0.075
OtsG474	17	0.48	0.49	0.161
Ssa408	31	0.88	0.86	0.053
Overall				0.063

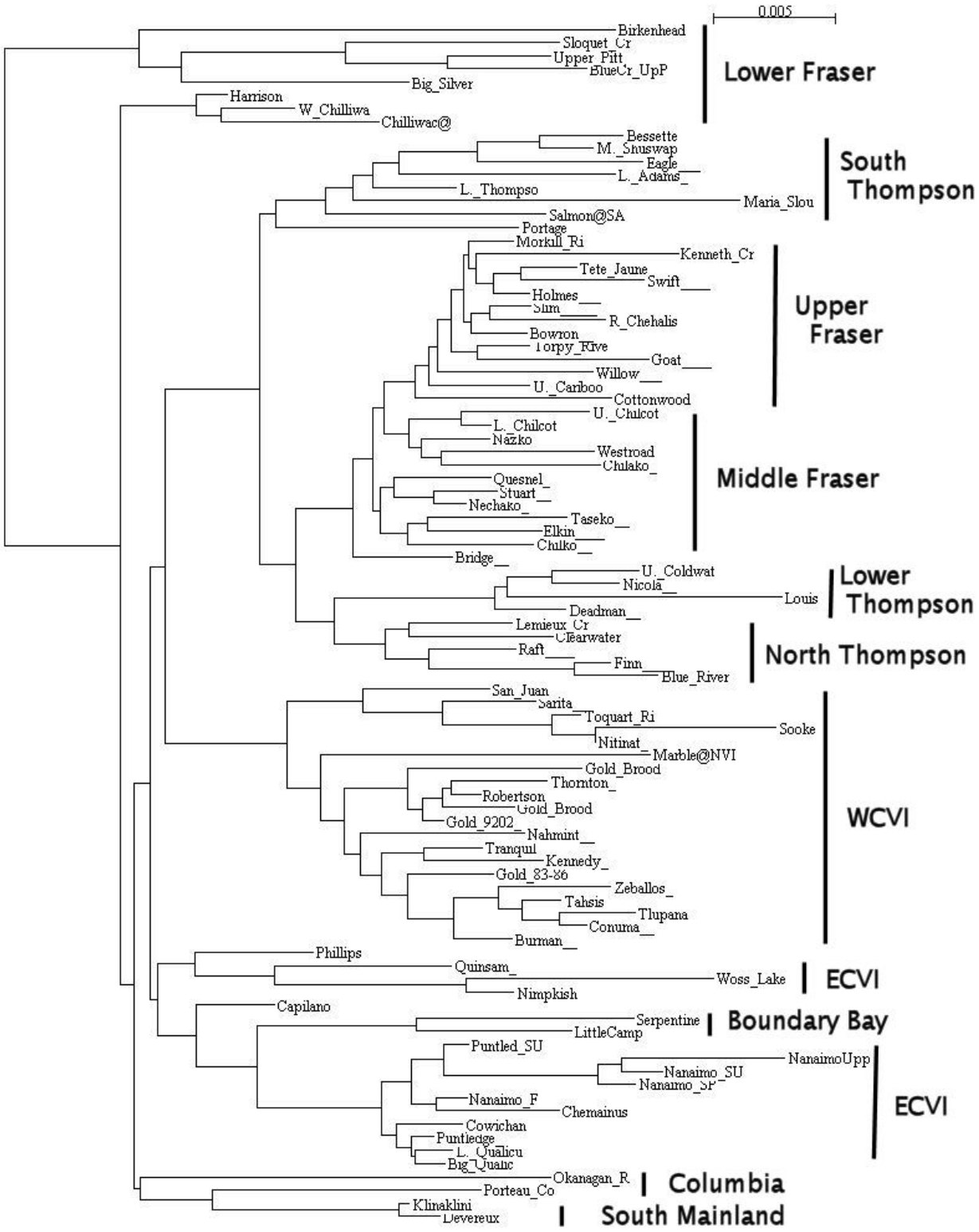

Figure 1. Neighbour-joining dendrogram of Cavalli-Sforza and Edwards (1967) chord distance for southern British Columbia populations of Chinook salmon surveyed at 13 microsatellite loci.