

# **The Origin of Marked-Untagged Chinook Found on the Skagit River Spawning Grounds**

Developed for  
PSC Southern Boundary Restoration and Enhancement Fund

Developed by  
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## **Abstract**

All hatchery Chinook released in the Skagit Basin are used as indicator stocks and are 100% coded-wire tagged (CWT). However, in recent years a significant number of adipose-clipped and untagged (ACU) Chinook have been recovered on spawning grounds and river traps in the Skagit River. These ACU fish are either mass-marked strays from other systems or they are Skagit indicator stock releases that lost their tags. This project used mixed stock analysis (MSA) and GAPS standardized microsatellite data to identify the stock-of-origin for a mixture collection of N=45 ACU Chinook sampled during the 2007 fall spawning ground surveys and N=12 ACU Chinook sampled during the 2009 summer spawning ground surveys. The reference genetic baseline itself was analyzed initially to determine its power to correctly assign ACU Chinook from the Skagit River Basin. Misassignments between certain reference collections required adjustments to the subsequent stock composition observed for the ACU Chinook. The fall survey ACU fish were estimated using genetic methods to be composed of 58% Skagit Basin fish and 42% out of basin fish. Coded-wire tag recoveries in 2007 suggested hatchery fish on the spawning grounds were composed of 87% Skagit Basin fish. Additionally, CWT recoveries from 2003 – 2007 suggest that 93% of hatchery fish on the spawning grounds were from Skagit Basin. The summer survey ACU fish were estimated using genetic methods to be composed of 30% Skagit Basin fish and 70% out of basin fish. Yet, CWT recover information from 2003 – 2007 suggested 99% of hatchery fish on the spawning grounds during the summer surveys should be of Skagit origin. These observations suggested substantial tag loss was possible for Skagit Basin indicator releases. Yet, tag loss did not account for all ACU Chinook. The genetic estimates showed non Skagit Basin fish in the ACU sample were present at higher numbers than would be expected given CWT recovery information, suggesting straying of non-local hatchery stocks to the Skagit spawning grounds is much higher than previously estimated.

## Introduction

All hatchery Chinook released in the Skagit Basin are used as indicator stocks and are 100% coded-wire tagged (CWT). However, in recent years a significant number of adipose-clipped and untagged (ACU) Chinook have been recovered on spawning grounds and river traps in the Skagit River. In 2005, the most recent year for which data have been summarized, there were 35 observed recoveries of CWT Skagit summer Chinook from the spawning grounds, which expand to 628 estimated CWT returns, and 13 recoveries of ACU Chinook during spawning ground surveys, which expand to 283 estimated ACU Chinook in Skagit summer Chinook spawning reaches. Sampling crews also recovered 186 CWT Skagit fall Chinook, and 55 ACU Chinook in Skagit fall Chinook spawning areas. These ACU fish are either 1) mass-marked strays from other systems (in which case, straying of non-local hatchery stocks to the Skagit spawning grounds is much higher than had previously been estimated from the few non-local CWT recoveries that have been observed); or 2) they are Skagit indicator stock releases that lost their tags (in which case, the survival of the indicator stock releases is considerably higher than currently estimated, and there is a problem with tag retention). It is also possible that a combination of both explanations for the untagged fish is occurring.

The purpose of this project was to use mixed stock analysis (MSA) techniques to identify the stock-of-origin for each of the ACU fish. These results will then be expanded to re-evaluate the total number of hatchery strays into the Skagit system and the tag-lost percentage for Skagit River fish. The MSA method employed was an extension of a procedure using the Rannala and Mountain (1997) algorithm, which computes the probability that the source of a multilocus genotype (i.e., a genetic fingerprint from an individual fish) is an individual stock in the reference genetic baseline (one probability for each stock in the baseline). Others have used the basic methods developed by Rannala and Mountain (1997) to provide population-of-origin assignments of unknown individuals (Hauser et al. 2006, Taylor and Costello 2006, and Waples and Gaggiotti 2006). The reference genetic baseline used was a subset of the Chinook coastwide microsatellite DNA baseline developed by the Genetic Analysis of Pacific Salmonids (GAPS) consortium. This consortium was established to standardize protocols for the collection and reporting of microsatellite data, and the GAPS dataset consists of 13 microsatellite loci for 165

Chinook stocks, categorized into 44 regional reporting units (Seeb et al. 2007). As the ACU Chinook in the present study were of hatchery origin, the hatchery collections from the GAPS dataset (see Table 1) were used to investigate the population-of-origin for each adult ACU Chinook analyzed from the Skagit River.

## Methods

### *Sampling*

Adipose fin absent, non coded-wire tagged (ACU) Chinook were collected during Skagit River spawning ground surveys in 2007 and 2009. In 2007, a mixture collection of N=45 ACU Chinook were sampled during fall spawning ground surveys and in 2009 during the summer spawning ground surveys N=12 ACU Chinook were sampled. Genomic DNA was extracted for all samples by digesting a small piece of fin tissue using silica membrane based kits obtained from Macherey-Nagel (Bethlehem, PA, USA) following the manufacturers recommendations.

### *Laboratory Analysis*

We performed polymerase chain reaction (PCR) amplification using the 13 fluorescently end-labeled microsatellite marker loci standardized as part of the Genetic Analysis of Pacific Salmonids (GAPS) project (Seeb et al. 2007). GAPS genetic loci are: *Ogo2*, *Ogo4* (Olsen et al. 1998); *Oki100* (unpublished); *Omm1080* (Rexroad et al. 2001); *Ots201b* (unpublished); *Ots208b*, *Ots211*, *Ots212*, and *Ots213* (Grieg et al. 2003); *Ots3M*, *Ots9* (Banks et al. 1999); *OtsG474* (Williamson et al. 2002); *Ssa408* (Cairney et al. 2000). PCR reaction volumes were 10  $\mu$ L, and contained 2  $\mu$ L 5x PCR buffer (Promega), 0.6  $\mu$ L MgCl<sub>2</sub> (1.5 mM final) (Promega), 1.0  $\mu$ L dNTP mix (0.2 mM final) (Promega), and 0.1  $\mu$ L (5 units/mL) GoTaq DNA polymerase (Promega). Loci were amplified as part of multiplexed sets, so primer molarities and annealing temperatures varied. Multiplex One had an annealing temperature of 50°C, and used 0.37 Molar (M) *Oki100*, 0.35 M *Ots201b*, and 0.20 M *Ots208b*, and 0.20 M *Ssa408*. Multiplex Two had an annealing temperature of 60°C, and used 0.10 M *Ogo2*, and 0.25 M of the non-GAPS locus *Ssa197* (O'Reilly et al. 1996). Multiplex Three had an annealing temperature of 56°C, and used 0.18 M *Ogo4*, 0.18 M *Ots213*, and 0.16 M *OtsG474*. Multiplex Four had an annealing

temperature of 53°C, and used 0.26 M *Omm1080*, and 0.12 M *Ots3M*. Multiplex Five had an annealing temperature of 60°C, and used 0.30 M *Ots212*, 0.20 M *Ots211*, and 0.10 M *Ots9*. All thermal cycling was conducted on either a PTC200 thermal cycler (MJ Research) or 9700 (Applied Biosystems) as follows: 94°C (2 min); 39 cycles of 94°C for 10 sec., 30 sec. annealing, and 72°C for 1 min.; a final 72°C extension and then a 10°C hold.

All PCR products were visualized by electrophoresis on an ABI 3730 automated capillary sequencer (Applied Biosystems). Fragment analysis was completed using GeneMapper 3.7 (Applied Biosystems). Standardization of genetic data to GAPS allele standards was conducted following Seeb et al. (2007).

### *Mixed Stock Analysis*

Population composition of mixture collections (i.e., captured juveniles) were estimated by using a partial Bayesian procedure based on the likelihood of unknown-origin genotypes being derived from genetic baseline reference stocks/populations (see Table 1 for baseline), given the allele frequencies for baseline stocks/populations. In brief, the mixed stock analysis (MSA) procedure is as follows. Within a mixture, we first generated the conditional probability of each genotype occurring in each reference population, based on the allele frequencies in each reference populations, using equation 10 of Rannala and Mountain (1997) (i.e., probability of the genotype, conditioned on the allele frequencies for each reference population). For each genotype in the mixture, we then calculated the probability (i.e., posterior probability) that the sample was from each reference population by taking the Rannala and Mountain (1997) conditional probability and multiplying it by a prior, and then dividing by a normalizing constant. Initially, the prior was uniform,  $1/N$ , where  $N$  was the number of populations used from the reference baseline (see Table 1). The initial probability matrix provided information about the likely source population for each unknown individual, but more importantly, provided an estimate of which reference populations were contributing to the unknown mixture. Since the reference populations did not contribute equally to the mixture, the initial use of a uniform prior can be improved. The mean probability for a reference baseline population in the mixture analyzed (i.e., mean posterior probability over all unknown individuals) is the estimated contribution of that reference population to the mixture. Therefore, the population composition

of the mixture was represented by the mean posterior probabilities of all reference collections from the initial matrix. This newly gained information about the population composition of the mixture replaced the uniform prior during an additional round of probability estimation to generate a second probability matrix. Once again, the mean posterior probabilities that represent estimates of baseline population contributions to the mixture were used as new priors. This iterative refinement of the probability matrix continued until the mean posterior probabilities change less than a predefined threshold from round to round. This procedure results in the maximum likelihood solution for stock composition (Millar 1985), and the final posterior probabilities of each individual for each reference population were reported. The MSA procedure was implemented using a program written by K.I. Warheit in MatLab (Mathworks 2009). Population assignments for each Skagit River ACU Chinook were reported by reference collection to which they assigned.

Assignment error (i.e., variance around composition point estimates) can be quantified by various means, and the error itself is influenced by several factors, from power and completeness of the reference baseline to composition of the mixture analyzed. Regarding the reference baseline, some quantitative measures of assignment accuracy are 1) quantifying where individuals from a source collection are assigned assuming the collection source is the truth, or 2) given the assignments to reference collections, determine the quantity of those assignments that were to the correct reference source collection. A quantitative measure for assignment “quality” is the posterior probability of each assignment, which is the proportion of the total likelihood attributed to each baseline reporting group. For example, if an individual was assigned to fall run with a probability 0.90, then 90% of the total probability for that individual was attributed to fall run and 10% was attributed to the other reference baseline group(s). While a higher posterior probability may denote higher “quality”, currently there is no agreed upon absolute probability threshold of “correct” assignment. Rather, a tolerated error for a given application is generally determined. For this report, an absolute assignment threshold criterion was not used. Rather, a bootstrap resampling procedure was employed to determine whether a particular assignment was statistically significant. For individual assignments within the bootstrap procedure, the ratio of “most likely” population assignments over any other secondary

population assignments quantified statistical significance, irrespective of the initial assignment posterior probability.

## **Results/Discussions**

Assessing the power of the reference genetic baseline is an important first step for mixed stock analysis procedures. Of the assignment accuracy metrics that focus on the baseline itself, 1) assuming the source collection is the truth and quantifying where individuals from that collection are assigned, or 2) given the assignments to reference collections, determining the quantity of those assignments that were to the correct reference source collection, the latter measure may be a more informative quantity, as by definition the source populations are not known when assigning mixture samples. Figure 1 shows an analysis of the reference baseline collections, with the probability that an individual assigned to a reference collection was actually from that source. Assignment accuracy was below 90% for nine baseline collections, and notably for this report (see below); L\_Skagit\_R\_Fa and NF\_Stilly were included in those nine. In general, the spring/summer collections tended to assign with more accuracy than the fall collections from Puget Sound.

Regarding assignments to the L\_Skagit\_R\_Fa reference collection, Figure 2 shows that Marblemount\_H\_su and Samish\_H reference collections misassigned to L\_Skagit\_R\_Fa. Additionally, L\_Skagit\_R\_Fa individuals misassigned to NF\_Stilly and other fall-run collections from Puget Sound (Figure 3). Evaluating the assignments of NF\_Stilly reference individuals, Marblemount\_H\_su individuals falsely assigned to NF\_Stilly (Figure 2). Yet, in contrast to L\_Skagit\_R\_Fa, the NF\_Stilly source population assigned with over 90% probability, having only slight misassignments to L\_Skagit\_R\_Fa, Marblemount\_H\_su, and Wallace\_H (Figure 3). Given the observed assignment accuracy of the reference individuals, the composition of unknown ACU Chinook was adjusted to account for the false exclusion of true source individuals (e.g., L\_Skagit\_R\_Fa), and the false inclusion of non-source individuals (e.g., Marblemount\_H\_su).

Table 1. Reference genetic collections used for mixed stock analysis.

Region	Hatchery	Region	Hatchery
<b>Alaska</b>		<b>Columbia/Snake River</b>	
NSE_Alaska_Chilkat_R	Tahini_MacH	L_Columbia_R_fa	Abernathy_NFH_Fa
SSE_Alaska	Chickamin_H	L_Columbia_R_fa	Cowlitz_H_fa
SSE_Alaska_Stikine_R	Andrew_CryH	L_Columbia_R_fa	Spring_Cr_H
SSE_Alaska_Stikine_R	Andrew_MacH	L_Columbia_R_sp	Cowlitz_H_sp
SSE_Alaska_Stikine_R	Andrew_MedH	L_Columbia_R_sp	Kalama_H_sp
		L_Columbia_R_sp	Lewis_H_sp
		Willamette_R	McKenzie_H
<b>British Columbia</b>		Willamette_R	N_Santiam_H
U_Skeena_R	Babine_H	Mid/Upper_Columbia_R_sp	Carson_H
Central_BC_Coast	Atnarko_H	Mid/Upper_Columbia_R_sp	Entiat_H
Central_BC_Coast	Kitimat_H	Mid/Upper_Columbia_R_sp	Klickitat_H
Central_BC_Coast	Wannock_H	Mid/Upper_Columbia_R_sp	L_Wh_Sal_H_sp
S_BC_Mainland	Porteau_Cove_H	Mid/Upper_Columbia_R_sp	Shitike_H
L_Fraser_R	Birkenhead_H	Mid/Upper_Columbia_R_sp	U_Yakima_H
L_Fraser_R	W_Chilliwack_H	Mid/Upper_Columbia_R_sp	Warm_Springs_H
L_Thompson_R	Nicola_H	Mid/Upper_Columbia_R_sp	Wenatchee_H_sp
L_Thompson_R	Spius_H	U_Columbia_R_su/fa	L_Wh_Sal_H_s/f
N_Thompson_R	Deadman_H	U_Columbia_R_su/fa	Priest_Rapid_H
S_Thompson_R	L_Adams_H	U_Columbia_R_su/fa	Umatilla_H
S_Thompson_R	M_Shuswap_H	U_Columbia_R_su/fa	Wells_H
E_Vancouver_Is	Big_Qual_H	Snake_R_fa	Lyons_Ferry_H
E_Vancouver_Is	Cowichan_H	Snake_R_fa	Nez_PerceT_H
E_Vancouver_Is	Nanaimo_H_f	Snake_R_sp/su	Dworshak_H
E_Vancouver_Is	Puntledge_H_f	Snake_R_sp/su	Johnson_H
E_Vancouver_Is	Quinsam_H	Snake_R_sp/su	LookingGlass_H
W_Vancouver_Is	Conuma_H	Snake_R_sp/su	Rapid_R_H
W_Vancouver_Is	Marble_H	Snake_R_sp/su	Sawtooth_H
W_Vancouver_Is	Nitinat_H	Snake_R_sp/su	Tucannon_H
W_Vancouver_Is	Robertson_H		
W_Vancouver_Is	Sarita_H		
		<b>Oregon</b>	
<b>Puget Sound</b>		N_Oregon_Coast	Necanicum_H
Hood_Canal	George_Adams_H	N_Oregon_Coast	Nestucca_H
Juan_de_Fuca	Elwha_H	Mid_Oregon_Coast	Coos_H
Skagit_Basin	L_Skagit_R_Fa	Mid_Oregon_Coast	Elk_H
Skagit_Basin	Marblemount_H_sp	Mid_Oregon_Coast	S_Coos_H
Skagit_Basin	Marblemount_H_su	Mid_Oregon_Coast	S_Umpqua_H
N_Puget_Sound	NF_Nooksack_H	Mid_Oregon_Coast	Umpqua_H
N_Puget_Sound	Samish_H	Rogue_R	Cole_Rivers_H
N_Puget_Sound	NF_Stilly		
N_Puget_Sound	Wallace_H	<b>California</b>	
S_Puget_Sound	Clear_Cr_H	Klamath_R	Trinity_H_f
S_Puget_Sound	Grovers_Cr_H	Klamath_R	Trinity_H_sp
S_Puget_Sound	Hupp_Sp_H	Central_Valley_fa	Feather_H_fa
S_Puget_Sound	Soos_H	Central_Valley_sp	Feather_H_sp
S_Puget_Sound	UW_H_SuFa	Central_Valley_wi	Sacramento_H
S_Puget_Sound	Voights_H		
S_Puget_Sound	White_H		



Table 1. Continued

Region	Hatchery	Region	Hatchery
<b>Washington</b>		<b>Washington</b>	
Washington_Coast	Forks_Cr_H	Washington_Coast	Makah_H
Washington_Coast	Hoko_H_Fa	Washington_Coast	Quinalt_NFH_Fa
Washington_Coast	Humptulips_H	Washington_Coast	Sol_Duc_H

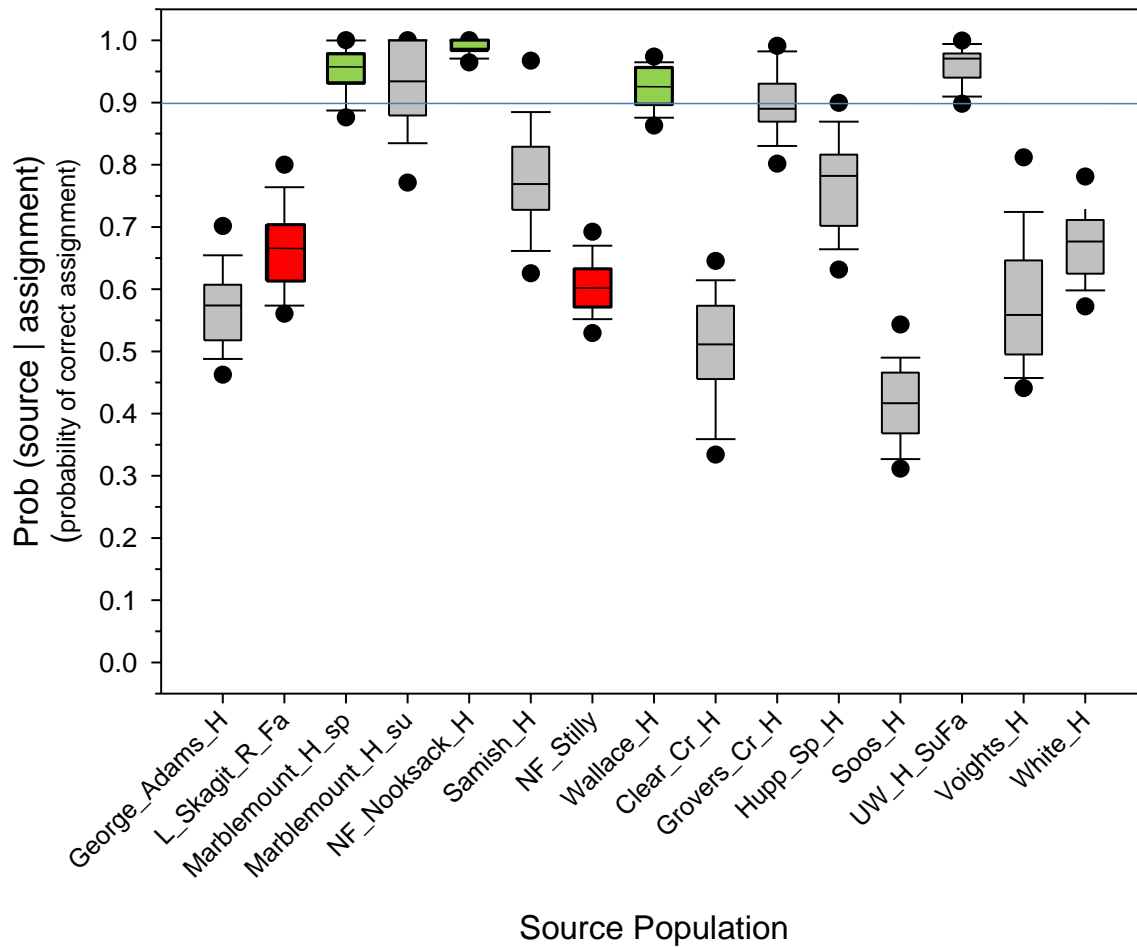


Figure 1. Assignment accuracy of the reference baseline. The chart shows the probability that an individual assigned to a source collection actually originated from that source collection. Individuals from L\_Skagit\_R\_Fa and NF\_Silly (red boxes) were commonly observed in the fall ACU mixture, but these reference collections had assignment probabilities under 90% correct.

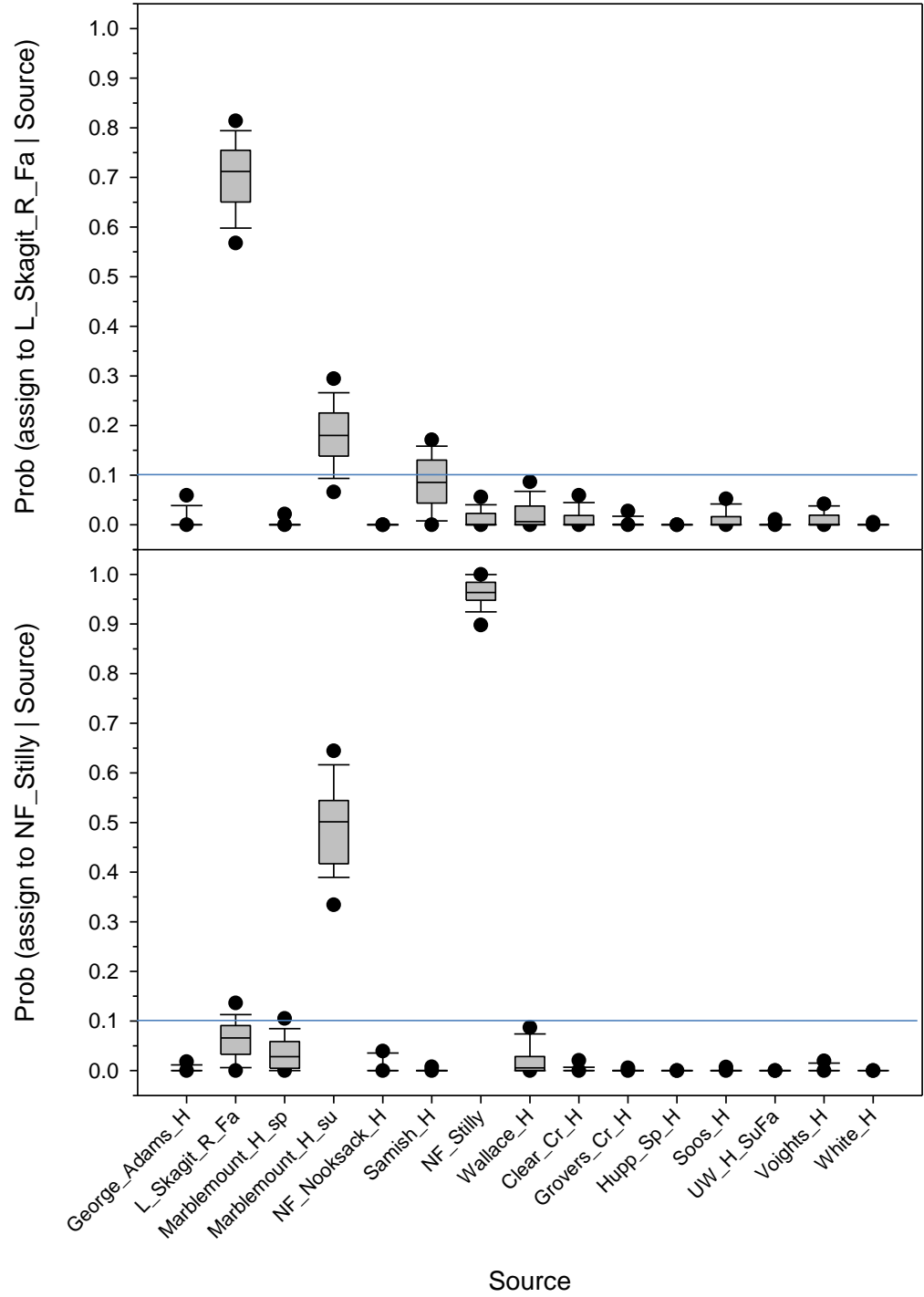


Figure 2. The chart shows the probability that individuals from each source population assign to L\_Skagit\_R\_Fa (top panel) or NF\_Silly (bottom panel).

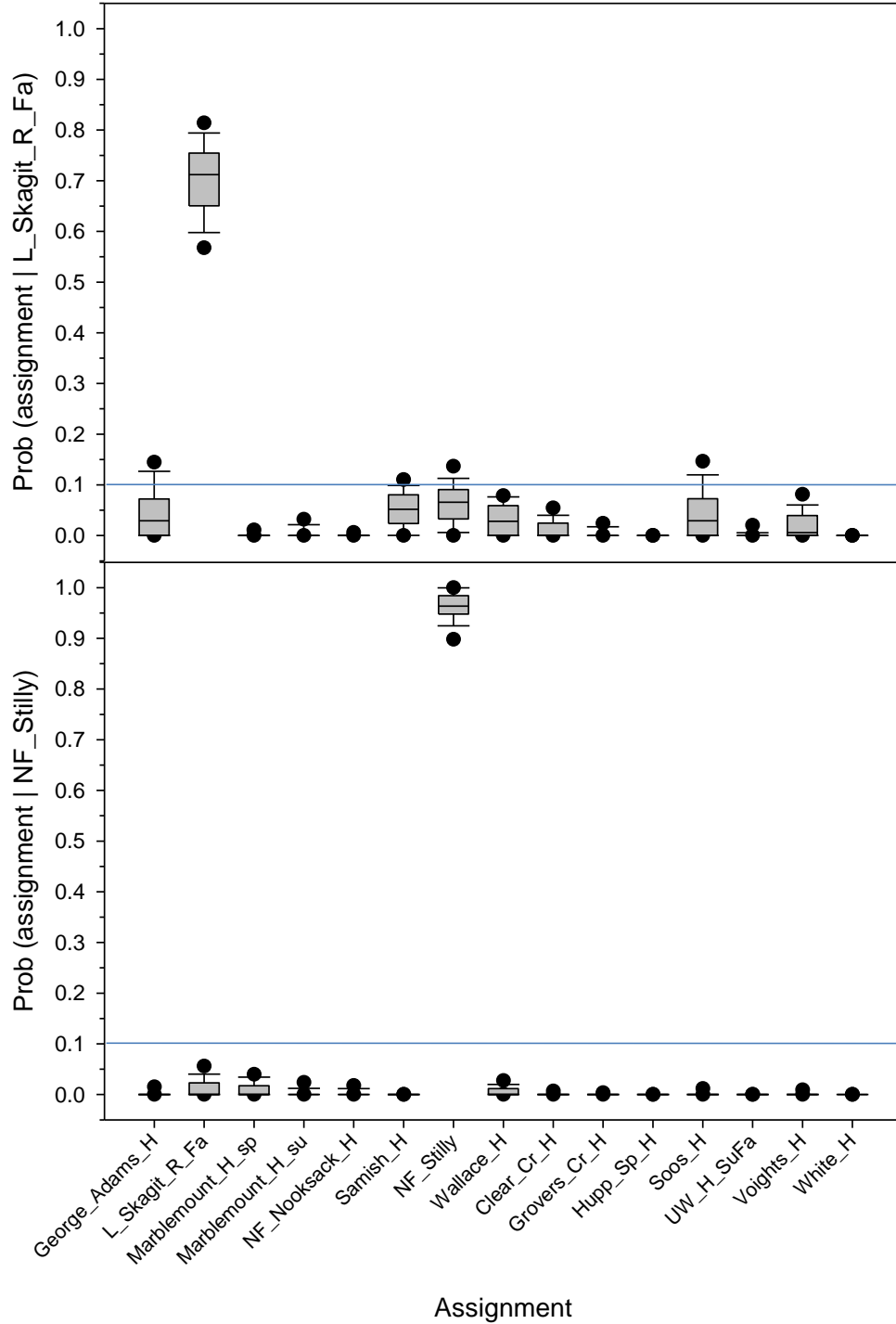


Figure 3. The chart shows the probability that individuals from the L\_Skagit\_R\_Fa source collection (top panel) or NF\_Silly source population (bottom panel) assign to each source population.

Following the assessment of the reference genetic baseline, the stock-of-origin was estimated for N=45 ACU Chinook collected during the 2007 fall spawning ground surveys. Sixteen individuals were assigned to Skagit Basin collections, fifteen individuals were assigned to Puget Sound collections, one individual each was assigned to Lower Fraser River, Oregon Coast, and Willamette River collections, respectively, and eleven individuals were not assigned conclusively to a stock (Table 2). Please see Appendix 1 for individual assignment details. The composition was adjusted for observed misassignment rates within the reference baseline, causing the number of L\_Skagit\_R\_Fa, NF\_Stilly, and George\_Adams\_H individuals to decrease and the number of Marblemount\_H\_su and Samish\_H individuals in the mixture to increase (Table 2). The aggregate assignment of ACU fall Chinook to inside and outside Skagit Basin was 0.58 and 0.42, respectively.

Regarding the N=12 ACU fish collected during the 2009 summer spawning ground surveys, a similar procedure was employed to estimate the population-of-origin of each fish and subsequent composition of the mixture (Table 2). Overall composition was adjusted due to misassignment rates observed for reference baseline, but the only change that occurred was the removal of a single assignment to Soos\_H (Table 2). The aggregate assignment of ACU spring Chinook to inside and outside Skagit Basin was 0.30 and 0.70, respectively.

## **Conclusions**

The objective of this study was to determine whether ACU fish observed on Skagit River spawning grounds were either mass-marked strays from other systems or Skagit indicator stock releases that lost their tags. The fall survey ACU fish were estimated using genetic methods to be composed of 58% Skagit Basin fish and 42% out of basin fish. This observation suggested that a large number of indicator stock releases lose their tags. Yet, tag loss did not account for all the ACU fish. Coded-wire tag recoveries in 2007 suggested hatchery fish on the spawning grounds were composed of 87% Skagit Basin fish (Table 3). Additionally, CWT recoveries from 2003 – 2007 suggest that 93% of hatchery fish on the spawning grounds were from Skagit Basin. The results regarding ACU Chinook suggest that fewer fish than expected were of Skagit origin. Straying of non-local hatchery stocks to the Skagit spawning grounds appears higher than had previously been estimated from CWT recoveries. Similar observations were made regarding

summer ACU Chinook. The summer survey ACU fish were estimated using genetic methods to be composed of 30% Skagit Basin fish and 70% out of basin fish. This observation suggested significant tag loss was possible. Yet, CWT recover information from 2003 – 2007 suggested 99% of hatchery fish on the spawning ground during summer surveys should be of Skagit origin. The genetic estimate of 70% non Skagit Basin fish in the ACU sample differs from CWT recovery information, suggesting straying of non-local hatchery stocks to the Skagit spawning grounds may be higher than previously estimated.

Table 2. Summary of individual assignments for ACU Chinook. Fall Analysis pertains to 2007 fall surveys and Spring Analysis pertains to 2009 summer surveys. See text for explanation of unadjusted and adjusted composition.

Source Region / Hatchery	Fall Analysis		Spring Analysis	
	unadjusted	adjusted	unadjusted	adjusted
<b>Skagit Basin</b>				
L_Skagit_R_Fa	16	12	-	-
Marblemount_H_su	-	7	-	-
Marblemount_H_sp	-	-	3	3
<i>Total</i>	<i>16</i>	<i>19</i>	<i>3</i>	<i>3</i>
<b>Puget Sound</b>				
NF_Nooksack_H	-	-	4	4
NF_Stilly	11	7	-	-
Samish_H	-	1	-	-
Soos_H	-	-	1	0
Wallace_H	-	-	3	3
Grovers_Cr_H	1	1	-	-
George_Adams_H	3	2	-	-
<i>Total</i>	<i>15</i>	<i>11</i>	<i>8</i>	<i>7</i>
<b>Lower Fraser River</b>				
W_Chilliwack_H	1	1	-	-
<b>Oregon Coast</b>				
S_Umpqua_H	1	1	-	-
<b>Willamette River</b>				
McKenzie_H	1	1	-	-
<b>No assignment</b>	11	12	1	2
<b>Summary</b>				
In-Skagit Basin	0.47	0.58	0.27	0.30
Out-Skagit Basin	0.53	0.42	0.73	0.70

Table 3. Summary of coded-wire tag recoveries from Skagit Basin.

Source Region / Hatchery	Fall 2007		Fall 2003-2007		Spring 2003-2007	
	Stream	Marblemount	Stream	Marblemount	Stream	Marblemount
<b>Skagit</b>						
Marblemount	110	43	436	469	720	9504
County Line Ponds	60	8	228	23	3	4
<i>Total</i>	<i>170</i>	<i>51</i>	<i>664</i>	<i>492</i>	<i>723</i>	<i>9508</i>
<b>Puget Sound</b>						
NF_Nooksack_H (Kendall Cr)	-	-	5	3	7	5
NF_Stilly (Whitehorse Pond)	6	1	16	1	3	1
Samish_H	17	-	18	-	1	-
Wallace_H	1	-	1	-	-	-
Elliott Bay Tribal Net Pens	-	-	-	-	-	1
Grovers_Cr_H	-	-	5	-	-	1
Tulalip (Bernie Gobin)	-	-	1	-	-	-
Lummi Sea Ponds	-	-	-	1	-	-
<i>Total</i>	<i>24</i>	<i>1</i>	<i>46</i>	<i>5</i>	<i>11</i>	<i>8</i>
<b>Strait of Juan de Fuca</b>						
Dungeness	-	-	-	1	-	-
<b>Lower Columbia River</b>						
Kalama (Fallert Creek)	-	-	-	-	-	1
<b>Vancouver Island</b>						
Chemainus Hatchery	-	-	1	-	-	-
Cowichan Hatchery	1	-	1	-	-	-
Robertson Creek	-	-	3	-	-	-
<i>Total</i>	<i>1</i>	<i>0</i>	<i>5</i>	<i>0</i>	<i>0</i>	<i>0</i>
<b>Summary</b>						
In-Skagit Basin	0.87	0.98	0.93	0.99	0.99	1.00
Out-Skagit Basin	0.13	0.02	0.07	0.01	0.01	0.00

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APPENDIX 1. Detailed individual assignment metrics for each ACU Chinook. Posterior denotes the individual assignment posterior probabilities derived from the MSA procedure. The Resample probabilities were from the bootstrap procedure, with a low probability meaning a secondary assignment was unlikely to be correct.

Individual	Collection Date	Population Assignment	Analysis	Probability	
				Posterior	Resample
07LL0011	15-Aug-07	NF_Stilly	Fall	0.42	0.00
07LL0001	29-Aug-07	no assignment	Fall	na	na
07LL0002	7-Sep-07	L_Skagit_R_Fa	Fall	0.92	0.00
07LL0004	18-Sep-07	L_Skagit_R_Fa	Fall	0.85	0.00
07LL0014	20-Sep-07	L_Skagit_R_Fa	Fall	0.46	0.00
07LL0013	20-Sep-07	L_Skagit_R_Fa	Fall	0.85	0.00
07LL0015	20-Sep-07	NF_Stilly	Fall	0.86	0.00
07LL0018	21-Sep-07	L_Skagit_R_Fa	Fall	1.00	0.00
07LL0019	21-Sep-07	L_Skagit_R_Fa	Fall	0.91	0.00
07LL0020	21-Sep-07	no assignment	Fall	na	na
07LL0016	21-Sep-07	S_Umpqua_H	Fall	0.99	0.00
07LL0021	23-Sep-07	L_Skagit_R_Fa	Fall	0.98	0.00
07LL0022	23-Sep-07	no assignment	Fall	na	na
07LL0005	24-Sep-07	L_Skagit_R_Fa	Fall	0.99	0.00
07LL0024	26-Sep-07	L_Skagit_R_Fa	Fall	0.93	0.00
07LL0008	26-Sep-07	NF_Stilly	Fall	0.99	0.00
07LL0023	26-Sep-07	NF_Stilly	Fall	0.91	0.00
07LL0028	28-Sep-07	L_Skagit_R_Fa	Fall	0.99	0.00
07LL0029	28-Sep-07	L_Skagit_R_Fa	Fall	1.00	0.00
07LL0027	28-Sep-07	NF_Stilly	Fall	0.95	0.00
07LL0030	28-Sep-07	no assignment	Fall	na	na
07LL0033	30-Sep-07	George_Adams_H	Fall	0.80	0.00
07LL0037	30-Sep-07	L_Skagit_R_Fa	Fall	0.68	0.00
07LL0038	30-Sep-07	L_Skagit_R_Fa	Fall	0.99	0.00
07LL0039	30-Sep-07	L_Skagit_R_Fa	Fall	1.00	0.00
07LL0035	30-Sep-07	NF_Stilly	Fall	0.68	0.00
07LL0031	30-Sep-07	no assignment	Fall	na	na
07LL0034	30-Sep-07	no assignment	Fall	na	na
07LL0032	30-Sep-07	W_Chilliwack_H	Fall	0.91	0.00
07LL0042	2-Oct-07	L_Skagit_R_Fa	Fall	1.00	0.00
07LL0041	2-Oct-07	NF_Stilly	Fall	0.81	0.00
07LL0046	3-Oct-07	George_Adams_H	Fall	0.88	0.00
07LL0045	3-Oct-07	L_Skagit_R_Fa	Fall	0.79	0.00

07LL0044	3-Oct-07	no assignment	Fall	na	na
07LL0043	3-Oct-07	no assignment	Fall	na	na
07LL0048	5-Oct-07	George_Adams_H	Fall	0.95	0.00
07LL0047	5-Oct-07	no assignment	Fall	na	na
07LL0049	10-Oct-07	McKenzie_H	Fall	0.52	0.00
07LL0009	10-Oct-07	NF_Stilly	Fall	0.93	0.00
07LL0050	11-Oct-07	Grovers_Cr_H	Fall	0.93	0.00
07LL0051	13-Oct-07	NF_Stilly	Fall	0.99	0.00
07LL0052	13-Oct-07	NF_Stilly	Fall	0.70	0.00
07LL0012	16-Nov-07	NF_Stilly	Fall	0.98	0.00
09FT0072	22-Sep-09	no assignment	Fall	na	na
07LL0010	no data	no assignment	Fall	na	na
09FT0061	14-May-09	NF_Nooksack_H	Spring	1.00	0.00
09FT0062	14-May-09	Wallace_H	Spring	0.86	0.00
09FT0063	14-May-09	NF_Nooksack_H	Spring	1.00	0.00
09FT0064	21-May-09	Soos_H	Spring	0.52	0.01
09FT0065	21-May-09	Marblemount_H_sp	Spring	1.00	0.00
09FT0066	21-May-09	Marblemount_H_sp	Spring	1.00	0.00
09FT0069	21-May-09	Marblemount_H_sp	Spring	1.00	0.00
09FT0070	7-Jul-09	Wallace_H	Spring	1.00	0.00
09FT0071	14-Jul-09	Wallace_H	Spring	1.00	0.00
09FT0002	29-Jul-09	NF_Nooksack_H	Spring	1.00	0.00
09FT0003	4-Aug-09	NF_Nooksack_H	Spring	1.00	0.00
09FT0006	9-Sep-09	no assignment	Spring	na	na

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**The Origin of Marked-Untagged Chinook Found on the Skagit River Spawning Grounds**  
WDFW CAPS # CAPS 08-1246  
Pacific Salmon Commission # SF-2008-I-8

	Hours	rate per Hour	Actual Expenditures	
			Federal	In-kind
<b>Wages &amp; Salaries (A)</b>				
Lab Director	80	\$39.11	\$3,129	
Lab Operations Manager	24	\$29.81	\$715	
Lead Technician	8	\$25.09	\$201	
Lab Technician	60	\$22.70	\$1,362	
Biologist 3	24	\$29.81	\$715	
DivisionSupport	8	\$38.85		\$310.80
<b>Labour - Employer Costs (percent of wages)</b>			\$1,591.82	\$80.81
<b>Total Labour Costs</b>			<b>\$7,714</b>	<b>\$391.61</b>
<b>Site / Project Costs</b>				
Chemicals and consumables			\$748	
Instrument Maintenance contract				\$1,960
Equipment				
Other				
Travel (do not include to & from work)				
<b>Total Site / Project Costs</b>			<b>\$748</b>	<b>\$1,960</b>
<b>Total Indirect Costs</b>			<b>\$2,430</b>	
<b>Total Project Costs</b>			<b>\$10,892</b>	<b>\$2,352</b>



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