Run composition of Chinook salmon at Red Bluff Diversion Dam during gates-in operations: A comparison of phenotypic and genetic assignment to run type

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INTRODUCTION

The Red Bluff Diversion Dam (RBDD) is located in Red Bluff, California, on the Sacramento River (RKM 391; Figure 1). The RBDD was constructed in 1964, and is a significant component of the Central Valley Project (CVP). The purpose of the RBDD is to allow gravity diversion of Sacramento River water into the Tehama-Colusa Canal, which is also a component of the CVP (USFWS and USBOR, 1998). The operation of the RBDD involves lowering its 11 gates to impound the Sacramento River. When the RBDD gates are lowered ("gates-in"), upstream fish passage of adult salmonids occurs through the two permanent fish ladders, the East Fish Ladder, the West Fish Ladder, and a temporary Center Fish Ladder (CFL). The East Fish Ladder and West Fish Ladder are concrete "weir and pool" type ladders that are situated on either side of the RBDD. The CFL is a wooden fish ladder that is manually assembled and installed annually, during the "gates-in" operations of the RBDD. Prior to 1993, the RBDD gates were in operation year-round. Since 1993, the RBDD gates are lowered ("gates-in" condition) on May 15, and remain down through September 15, annually. During this time period, the RBDD impounds the Sacramento River and forms Lake Red Bluff.

The current gates-in period of operation was chosen in order to minimize impacts on Endangered Species Act (ESA) listed winter run Chinook salmon (*Oncorhynchus tshawytscha*). In addition to the winter run Chinook salmon, the Sacramento River also supports fall, late-fall, and spring runs. The spring run of Chinook salmon in the Sacramento River was federally listed as a threatened species in 1994. The operation of the RBDD in the "gates-in" period is known to cause delays in upstream passage of adult anadromous salmonids. Recognizing that RBDD operations may impact upstream fish migration, the Bureau of Reclamation and the United States Fish and Wildlife Service Red Bluff Fish and Wildlife Office (RBFWO) sought information on which Chinook runs were encountering the RBDD during the "gates-in" time period. The RBFWO collaborated with the Service's Abernathy Fish Technology Center (AFTC) to understand the genetic composition of Chinook salmon runs during this time period.

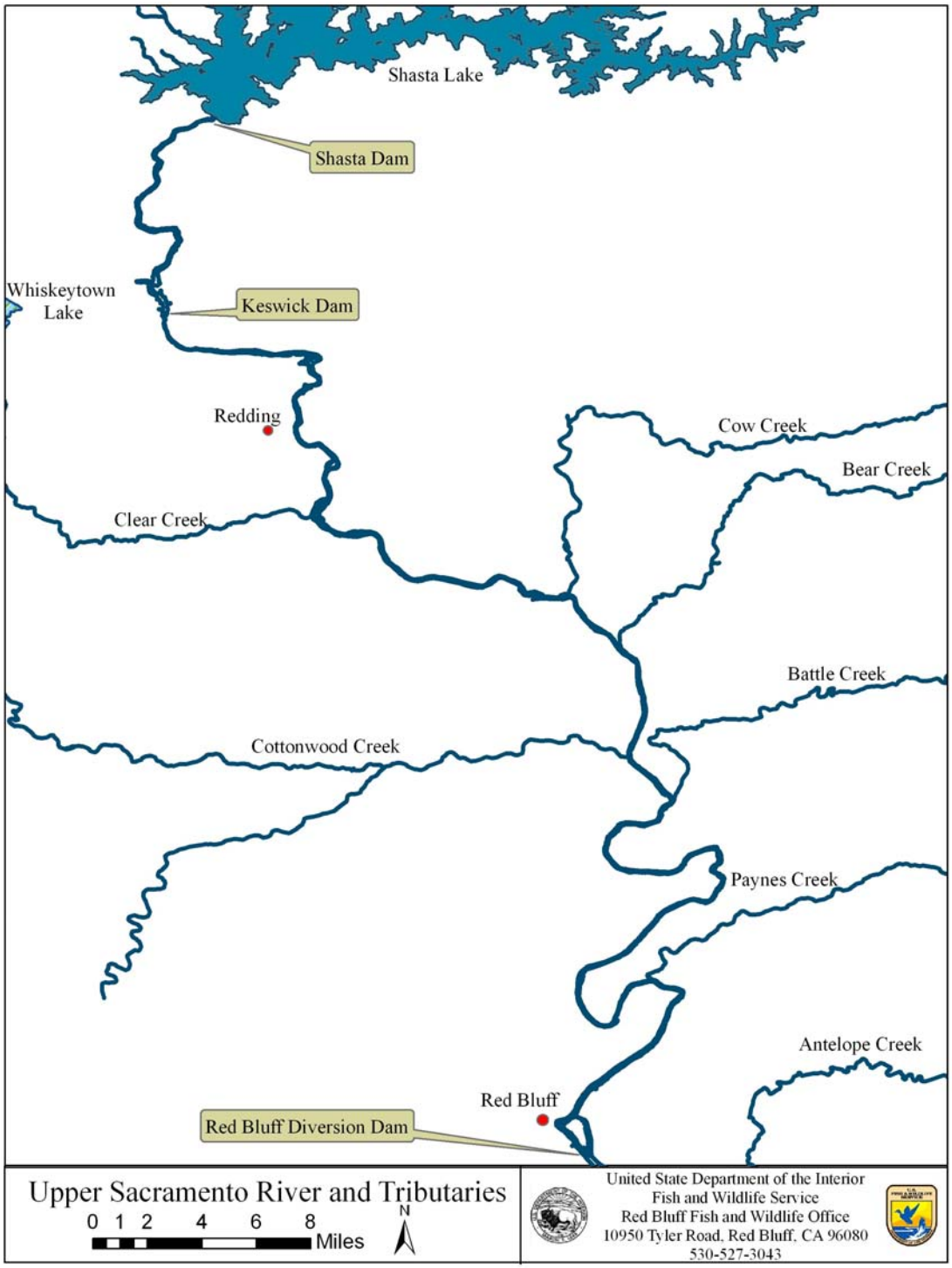


Figure 1. Map of the upper Sacramento River showing the location of Red Bluff Diversion Dam and several tributaries.

During the RBDD "gates-in" time period, the California Department of Fish and Game (CDFG) conducts fish sampling operations at the East Fish Ladder, which has a fish trapping facility. Adult salmonids are shunted from the ladder fishway into a sampling area, where the fish are examined and identified as to respective run-type, by phenotypic assignment. These phenotypic assignments and historic run-timing information are currently the only means employed to infer the run composition of adult salmon ascending the RBDD fish ladders. There are differences in opinion amongst local agency biologists as to the actual existence of spring run Chinook population(s) in the upper Sacramento River, upstream of the RBDD. Although local streams (such as Battle Creek, Clear Creek, Beegum Creek within the Cottonwood Creek drainage, etc.) have small runs of Chinook salmon which appear during the traditional spring run timing period, the true origin of these individuals remains unclear.

Spring-run Chinook salmon in the Sacramento-San Joaquin River system was historically one of the largest runs of salmon in the Pacific coast (Moyle 2002). Prior to the construction of Red Bluff Diversion Dam, Keswick and Shasta dams, spring-run Chinook ascended the Sacramento River to its headwater tributaries. Spring-run spawned in the Upper (Little) Sacramento River, McCloud River, and the Pit River (CDFG 1998). Spring-run Chinook were also known or believed to migrate into Cottonwood Creek, Clear Creek, Battle Creek, Antelope Creek, Mill Creek, Deer Creek, Stony Creek, Big Chico Creek, Butte Creek, Feather River, and the American River (CDFG 1998). The historical range and distribution of spring-run Chinook within the San Joaquin River basin is also detailed in CDFG 1998.

Presently, the mainstem Sacramento River supports some putative spring-run Chinook salmon (Moyle 2002). Because Keswick and Shasta dams now block spring-run Chinook from accessing historic headwater spawning habitats, spring-run Chinook in the mainstem Sacramento River are no longer spatially segregated from the later-running fall-run Chinook and hybridization likely occurs. For the Sacramento River tributary streams upstream of the RBDD, spring-run Chinook are known to occur in Battle Creek, Antelope Creek, and Beegum Creek, a tributary to Cottonwood Creek (CDFG 1998).

Spring-run Chinook juveniles from Feather River Hatchery were planted into Clear Creek during the early 1990's in an effort to help re-establish a spring-run population (Newton and Brown 2004).

Genetic markers provide an additional means of identifying run type of individual Chinook salmon (e.g. Banks et al. 2000; Hedgecock et al. 2001). At the outset of this study published (Banks et al. 2000) and newer unpublished (Michael Banks, presentation at Pacific Salmon Commission meeting, October 2004) baselines were available to identify run type of Central Valley Chinook salmon. Both baselines were created with microsatellite DNA markers, and simulations indicated that the newer baseline provided improved resolution among Central Valley run types. Descriptions of two additional microsatellite baselines have been published in the past year (Garza et al. 2007; Seeb et al. 2007) and construction of another baseline using single nucleotide polymorphism (SNP) markers is presently underway (Carlos Garza, personal communication, December 2007). Available genetic markers and baselines allow researchers to assign Chinook salmon to one of four run-types (spring run, winter run, fall run and late-fall run). Comparison of phenotypic and genetic run assignments could provide insight into the accuracy of the phenotypic methods presently used.

The objectives of this study were to 1) compare phenotypic and genetic assignments of Chinook salmon encountered at RBDD during the gates-in time period and 2) to evaluate run-composition of Chinook salmon encountering RBDD during the same period.

METHODS AND MATERIALS

Tissue sampling

Tissue samples were collected by RBFWO personnel, in collaboration with State of California Department of Fish and Game, at the fish trapping facility of the East Fish Ladder of RBDD. Tissue sampling was done daily on a week-day (Mon thru Fri) basis, during the "gates-in" period. The fish trap was checked on an hourly basis, from 0600 hrs through 1400 hrs. All Chinook salmon captured in the trap were sampled, unless the

catch numbers exceeded the ability of the field personnel to process them (i.e. if a single catch sample exceeded 30 fish). In 2007 the fish trap at RBDD was operated from May 7 through May 8 and from May 16 through September 12.

Chinook salmon were measured for fork length, identified to gender, noted for fin-clips, and assigned to run type based on phenotypic characteristics (for a description see Killam 2007). A small piece of caudal fin tissue (approximately 0.5 cm^2) was excised from each individual and placed into a vial filled with 95% ethanol.

Genetic analysis

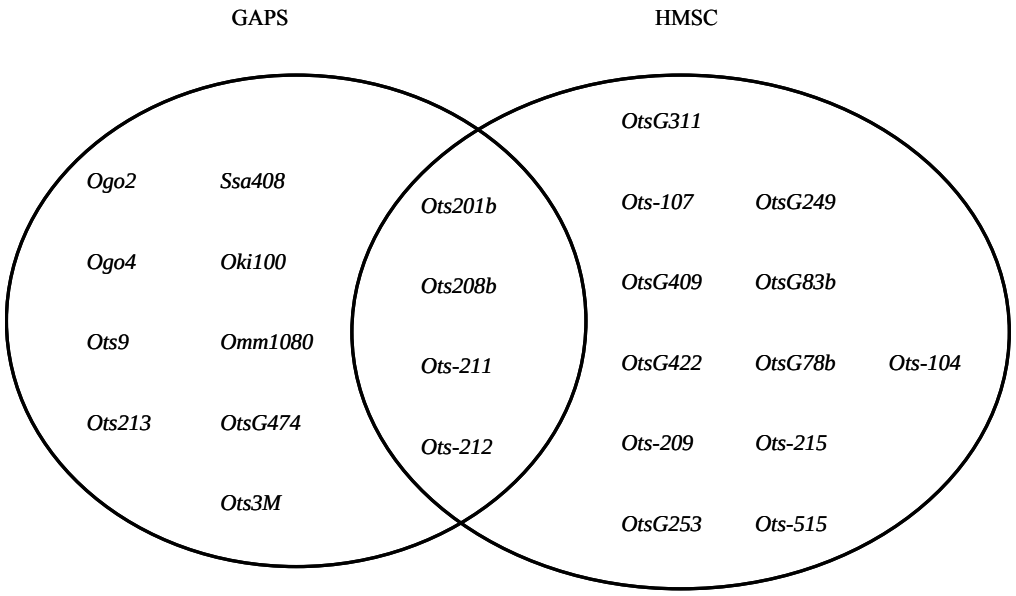
The microsatellite baseline presented by Michael Banks in 2004, hereafter referred to as the HMSC (Hatfield Marine Science Center) baseline, was chosen for this work based on simulations that demonstrated its enhanced performance relative to the existing published baseline (Banks et al. 2000). During the course of this study, AFTC began using the newer standardized microsatellite baseline also (the Genetic Analysis of Pacific Salmon [GAPS] Consortium baseline; Seeb et al. 2007). In an effort to ensure that the best available markers were used for the present work we chose to analyze both the GAPS and HMSC markers (Table 1; Figure 2).

DNA was extracted by boiling the tissue samples in a resin solution (Chelex 100, Sigma Chemical Co.). The polymerase chain reaction (PCR) was used to amplify 25 microsatellite loci (16 HMSC loci plus 13 GAPS loci with 4 loci overlapping; Figure 2) from each DNA sample. Loci were amplified in 10µl reaction volumes consisting of 5.0µl 2x QIAGEN Multiplex PCR Master Mix (final concentration of 3 mM $MgCl_2$), and 0.2µl oligonucleotide PCR primer mix. Primer mix compositions and thermal cycling profiles are listed in Appendix 1. Liquid handling was performed using a JANUS Automated Workstation (PerkinElmer). PCR products were size fractionated using an AB3130 DNA Sequencer (Applied Biosystems), and raw microsatellite data (electropherograms) were analyzed using GENEMAPPER 4.0. All genotypes were scored by two independent readers (double-scoring).

Table 1. Microsatellite loci used to assign Chinook salmon to run type. The numbers of alleles observed in the fish sampled at Red Bluff Diversion Dam are listed for each locus.

Baseline	Locus	Number of Alleles	Citation
GAPS			
	Ogo2	15	Olsen et al. 1998
	Ogo4	10	Olsen et al. 1998
	Oki100	35	CDFO unpublished
	Omm1080	42	Rexroad et al. 2001
	Ots201b	29	Grieg et al. 2003
	Ots208b	48	Grieg et al. 2003
	Ots211	27	Grieg et al. 2003
	Ots212	28	Grieg et al. 2003
	Ots213	31	Grieg et al. 2003
	Ots3M	11	Grieg and Banks 1999
	Ots9	4	Banks et al. 1999
	OtsG474	14	Williamson et al. 2002
	Ssa408	21	Cairney et al. 2000
		315	
HMSC			
	OtsG311	48	Williamson et al. 2002
	Ots-107	33	Nelsen & Beacham 1999
	OtsG409	33	Williamson et al. 2002
	OtsG422	43	Williamson et al. 2002
	Ots-209	27	Greig et al. 2003
	OtsG253	36	Williamson et al. 2002
	Ots-212	38	Greig et al. 2003
	Ots-104	36	Nelsen & Beacham 1999
	OtsG249	27	Williamson et al. 2002
	Ots-211	39	Greig et al. 2003
	OtsG83b	35	Williamson et al. 2002
	Ots-515	46	Naish & Park 2002
	Ots-201	41	Greig et al. 2003
	Ots-215	28	Greig et al. 2003
	OtsG78b	16	Williamson et al. 2002
	Ots-208	48	Greig et al. 2003
		526	

Figure 2. Distribution of 25 microsatellite markers among the GAPS and HMSC baselines.



Following completion of the data collection, 95 individuals were re-analyzed as part of AFTC's standard QA/QC protocol. The Microsoft Excel add in Microsatellite Toolkit (Park 2001) was used to scan the dataset for individuals with identical genotypes.

Standardization of HMSC baseline allele nomenclature

Analysis of both GAPS and HMSC microsatellite loci on the RBDD samples was conducted at AFTC. In order for fish analyzed at AFTC to be assigned to run type using the HMSC baseline (which was run at Oregon State University; OSU), standardization of allele nomenclature between AFTC and OSU was required. Standardization was accomplished and evaluated as follows:

1) **Bin definition plate 1:** OSU provided a plate of 96 DNA samples, along with genotype data, to AFTC. AFTC analyzed these samples and defined allele bins in their analysis software based on results from those samples.
2) **Test plate 1 / bin definition plate 2:** OSU provided a second plate of 96 DNA samples to AFTC, but no genotype data. AFTC analyzed these samples, creating new allele bins by interpolation where necessary, and reported genotypes back to OSU. Standardization was assessed at this point by comparing genotypes called by the two laboratories.
3) **Test plate 2 / bin definition plate 3:** OSU provided a third plate of 96 DNA samples to AFTC, but no genotype data. AFTC analyzed these samples, creating new allele bins by interpolation where necessary, and reported genotypes back to OSU. Standardization was assessed at this point by comparing genotypes called by the two laboratories.

Assessment of the degree to which standardization of the HMSC markers between OSU and AFTC was successful was performed using the criteria used by the GAPS Consortium (i.e. goal of 95% across loci, with no locus below 90%).

Genetic assignment

Genetic assignments were required for two purposes in the present study: 1) to compare phenotypic run assignment to genetic run assignment, and 2) to evaluate run composition of fish encountered at RBDD during the gates-in period. To address the first question we used individual assignment and to address the second question we used proportional assignment.

The accuracies of the baselines for assigning individuals to run type were assessed using "leave-one-out" simulations. Briefly, fish were sequentially removed from the baseline, the baseline allele frequencies were re-calculated and the fish in question was assigned to run type using the new baseline. Individual assignment was performed using the Bayesian method of Rannala and Mountain (1997) as implemented in the program ONCOR (Steven Kalinowski 2008; available at:

http://www.montana.edu/kalinowski/ONCOR.htm). The probability that each individual belonged in each baseline collection was calculated, these probabilities were summed for each run type and the individual was assigned to the run type for which it had the highest probability. We used an assignment cut-off value of 90%, meaning that if the highest probability was <90% the fish was not assigned. This is expected to increase accuracy, but leave some proportion of fish unassigned. Individual assignment of fish sampled at RBDD was done similarly: the probability of each fish belonging to each baseline collection was calculated, probabilities were summed for collections within each run type, and if the probability of the fish belonging to any run type was >90%, the fish was assigned to that run type.

The accuracies of the baselines for performing proportional assignment were assessed using 100% simulations. Mixtures of 400 individuals, all from a single run type, were simulated and fractionally allocated to the baseline using the methods of Anderson et al. (*in press*) in the program ONCOR. One thousand bootstrap replicates of this process were used to generate mean accuracies and 95% confidence intervals for each baseline to assign to each run type. Prior to performing proportional assignment on fish sampled at RBDD, individual fish were divided among three groups based on collection month: 1) May-June, 2) July and 3) August-September. The samples in these three periods were then fractionally allocated among three (GAPS baseline) or four (HMSC baseline) run types using the conditional maximum likelihood (Millar 1987) as implemented in ONCOR.

RESULTS

Sample Collection

Genetic samples were collected from 400 Chinook salmon. Field data for two individuals (1059-098 and 980-038) were missing, leaving 398 potential comparisons between genetic and phenotypic run assignments.

Genotyping

A total of 400 Chinook salmon were genotyped (the two samples without field data were processed so that they could be used in proportional assignment). The genotyping failure rate was 2.8% for the GAPS markers and 6.1% for the HMSC markers. The HMSC genotyping failure rate was higher because it included individuals for which amplification products fell outside standardized allele bins. Of 1,235 genotypes (95 fish x 13 loci) compared in the QA/QC of the GAPS data, 0 conflicts were observed, suggesting an error rate ~0.0%. Of 1,520 genotypes (95 fish x 16 loci) compared in the QA/QC of the HMSC data, 5 conflicts were observed, suggesting an error rate ~0.3%.

Both GAPS and HMSC markers revealed three pairs of individuals that had identical genotypes (1038-025=980-053, 1059-003=981-019, 1038-081=980-041). One of these individuals was phenotypically assigned to spring run (980-053), and the other five were phenotypically assigned to fall run. One individual from each of these three pairs was removed prior to proportional assignment (i.e.:1038-025, 1059-003 and 1038-081 were removed).

Standardization of HMSC baseline allele nomenclature

The results from the first test plate indicated that, at the time that plate was run, AFTC and OSU were calling alleles 97% identical (Table 2). The only locus that did not meet our target criteria (average 95% identity, with no locus below 90% identity) at that time was *Ots208b*. By the time the second plate was run AFTC and OSU allele calls were 98% identical, however, *Ots208b* remained below our target at 88% identity. Because we were not able to meet our 90% identity target in calling HMSC alleles for Ots208b, this locus was excluded from subsequent analyses. Excluding *Ots208b*, concordance between the two laboratories was 99%.

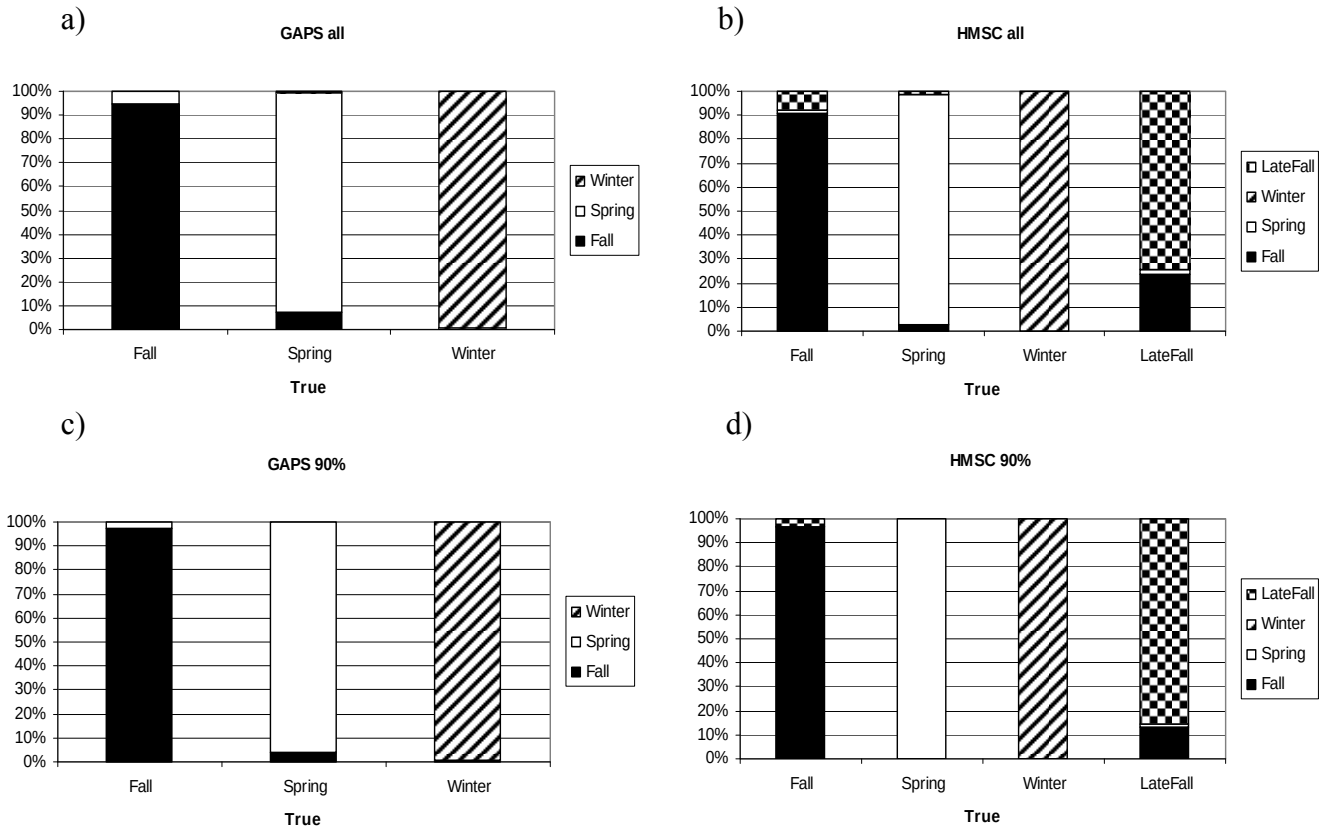
Table 2. Results from tests of concordance in allele calling between AFTC and OSU for the HMSC baseline loci. Values listed for each locus indicate percent identity between the two laboratories for Test 1 and Test 2. The target for standardization between the two laboratories was an average of ≥95% with no locus below 90%.

Locus	Test 1	Test 2
Ots104	0.959	0.994
Ots107	1.000	0.988
Ots201b	0.988	0.994
Ots208b	0.883	0.877
Ots209	0.977	0.971
Ots211	0.960	1.000
Ots212	0.994	0.989
Ots215	1.000	1.000
Ots249	0.994	0.978
Ots253b	0.925	0.989
Ots515	0.923	0.948
OtsG311	0.992	0.993
OtsG409	0.949	0.994
OtsG422	1.000	1.000
OtsG78b	0.944	1.000
OtsG83b	1.000	0.994
Average	0.968	0.982

Individual Assignment

Leave-one-out simulations suggested that both the GAPS and HMSC baselines assign individuals to run type with ~95% accuracy for winter run, spring run and fall run (Figure 3). Application of a 90% likelihood filter to the assignments resulted in small (1-3%) improvements, and resulted in 9% of fish unassigned for the GAPS baseline and 11% unassigned for the HMSC baseline. The greatest improvement was in assignment of late-fall run, which improved ~10% with application of the filter. Overall these simulations suggested that both baselines could assign individuals to winter run, spring run and fall

Figure 3. Accuracy of GAPS and HMSC baselines for assigning individual Chinook salmon to run type as indicated by leave-one-out simulations. Figures a and b indicate accuracies when all fish were assigned to most probable run type. Figures c and d indicate accuracies when fish for which the most likely run was assigned with less than 90% probability were discarded.



run with ≥95% accuracy and the HMSC baseline could also assign individuals to late-fall run with ~85% accuracy (with the greatest mis-allocation being from fall to late-fall).

Analysis of one sample (1038-045) failed to amplify for every marker, and was therefore excluded from further comparisons. The three duplicate samples were included for the purpose of comparing phenotypic to genetic run assignments, but were excluded from proportional analysis.

Individual assignment of fish sampled at RBDD was performed with ninety percent or greater probability for 91.5% of the samples using the GAPS baseline and 91.0% of the samples using the HMSC baseline. Concordance between genetic and phenotypic run assignments was greatest (~90%) for fall run, moderate for spring run (~40%) and lowest for winter run (~20%; Table 3). Concordance between phenotypic and GAPS assignments was slightly (~1-3%) higher than between phenotypic and HMSC, but the difference was not statistically significant (lower 95% CI of difference < 0 for every run. Concordance between the two genetic baselines was higher than concordance between either with the phenotypic assignments (Table 4). Individuals that were phenotypically assigned to winter run were often (77-79% of the time) genetically assigned to spring or fall run (Table 3). It was noted, however, that individuals genetically assigned as winter run were phenotypically assigned to winter run most of the time (90%). In general, a large proportion of genetic spring run fish were assigned phenotypically to winter run. Individuals phenotypically assigned to spring run appeared to be nearly evenly divided between genetic spring run and genetic fall run, regardless of which baseline was used (Table 3).

Table 3. Comparison of run assignments based on phenotypic (rows) and genetic (columns) data. Genetic assignments were made using GAPS (a) and HMSC (b) microsatellite baselines. A cut-off assignment score of 90% was used for both baselines, and the total number of samples in each table is the number that the corresponding baseline identified with this level of confidence. The "Match" column lists the proportion of individuals assigned to each run based on phenotype that were assigned to that same run based on genetics.

a)

Phenotypic Assignment	Genetic Assignment (GAPS baseline)				Match
	Spring	Fall	Late-fall	Winter	
Spring	11	14		0	0.440
Fall	19	279		1	0.933
Winter	13	17		9	0.231

b)

Phenotypic Assignment	Genetic Assignment (HMSC baseline)				Match
	Spring	Fall	Late-fall	Winter	
Spring	10	14	0	0	0.417
Fall	28	266	0	1	0.902
Winter	15	18	0	9	0.214

Table 4. Comparison of individual assignment to run based on GAPS and HMSC microsatellite baselines. Percent identity is the number of fish assigned to a run by both markers divided by the sum of fish assigned to that same run based on either baseline.

GAPS baseline	HMSC baseline				Percent Identity
	Spring	Fall	Late-fall	Winter	
Spring	32	3	0	0	0.681
Fall	12	274	0	0	0.948
Winter	0	0	0	10	1.000

Proportional Assignment

The 100% simulations did not suggest substantial differences in the accuracies of the two baselines used here for assigning to spring run or winter run (Figure 4). Mis-allocation between fall and late-fall in the HMSC baseline gave that baseline a lower mean accuracy to fall run, but the difference was not significant (95% CIs for the two baselines overlap).

Proportional assignment of the fish sampled at RBDD suggested that the large majority of fish sampled in all three time periods were fall run (Figure 5). Spring run fish were most common early in the season, but were still present at detectable levels in the August-September sample. Winter run fish were also most common early in the season, but proportions of winter run were not significant (90% bootstrap confidence intervals included 0%) by the July sample. Proportions of late-fall were not significantly greater than zero in any period. No significant differences between estimates provided by the two baselines (GAPS and HMSC) were observed.

Figure 4. Accuracy of GAPS and HMSC baseline for performing proportional assignment as indicated by 100% simulations. Mean correct allocation to each run type is shown. Error bars indicate 95% bootstrap confidence intervals.

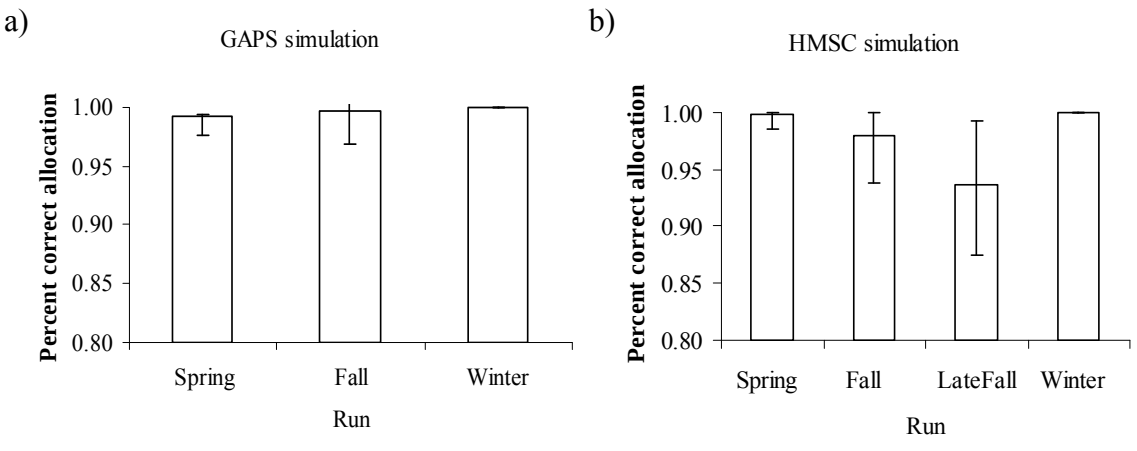
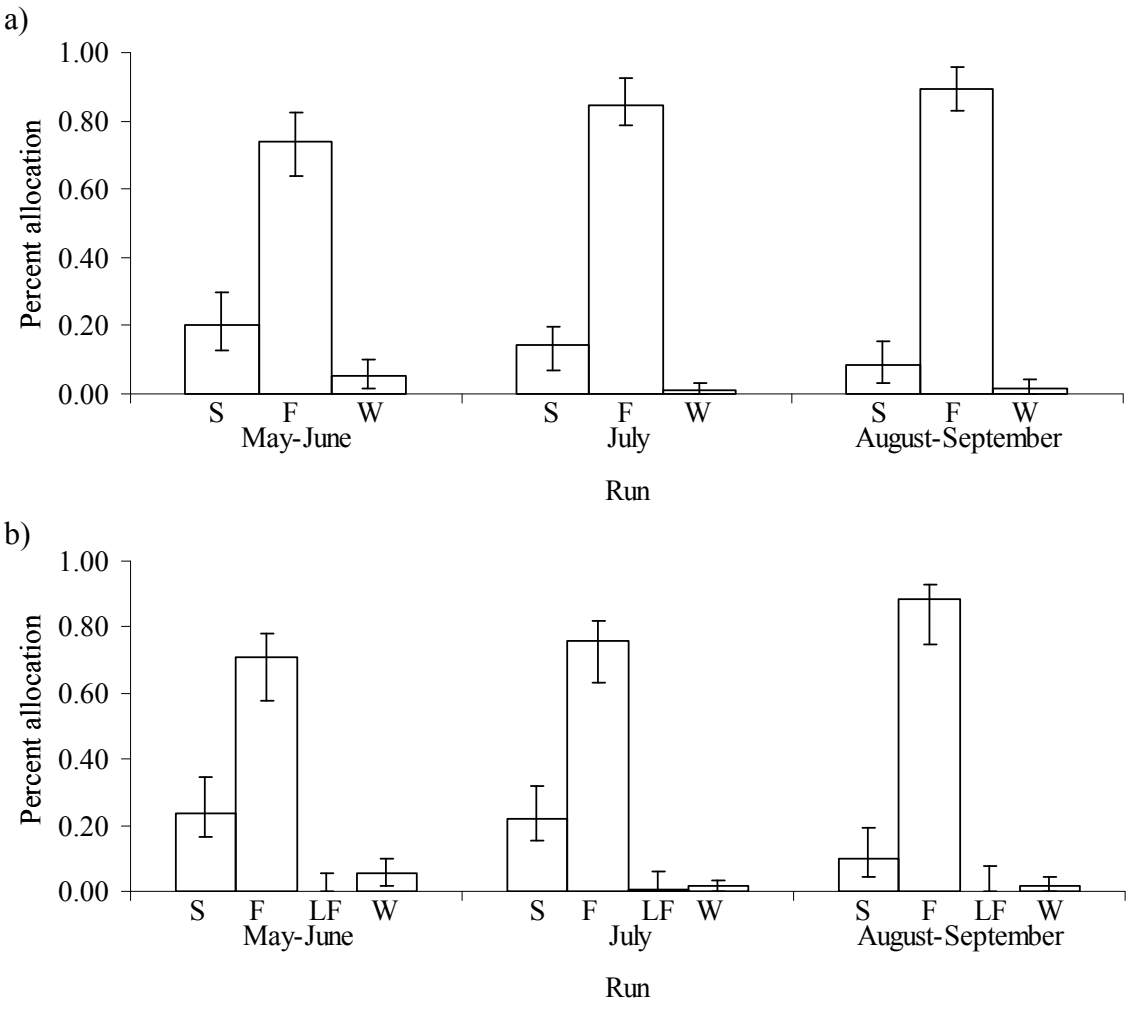


Figure 5. Proportional allocation (PA) of Chinook salmon sampled at RBDD using (a) the GAPS baseline and (b) the HMSC baseline. The sample collected in 2007 was divided among three time periods along the x-axis (May-June n=109, July n=170, August-September n=117). Mixture proportions were estimated for spring run (S), fall run (F), and winter run (W) using both baselines. Late-fall run (LF) was also estimated using the HMSC baseline. Ninety-five percent bootstrap confidence intervals around each proportional estimate are shown.



DISCUSSION

Discrepancies between phenotypic and genetic assignments appeared to be substantial in the set of samples examined here. Because both genetic and phenotypic assignments are expected to have some error, and the true origins of the fish examined here are not known, it is not possible to quantify the error associated with either method. Since the two genetic baselines are based on different sets of samples and different (albeit overlapping) markers, the high degree of concordance between the marker sets does lend a qualitative measure of confidence to the genetic assignments. Assuming the genetic assignments are generally correct, our results suggest that the number of spring run individuals encountered at RBDD is more than double the estimate based on phenotypic assignments. Conversely, our results suggest that the number of winter run encountered at RBDD is around a quarter of the estimate based on phenotypic assignments.

Proportional allocation of the majority of fish sampled in each time period to fall run was not surprising, and was concordant with patterns documented by California Department of Fish and Game (e.g. Killam 2007). Similarly, allocation of fish to winter run during the first time period but not in the second two time periods reflects the expected pattern. A result that was less expected was the significant (Lower 95% CI >0) fraction of fish from each time period that was assigned to spring run. This result could reflect limitations of the baselines used here (in discriminating fall run from spring run) or the limitation of examining only a single sample of ~100 fish to represent the August-September time period. Alternatively, it could represent a late-migrating component of the spring run lineage. Ongoing research characterizing additional samples, along with power analyses of the genetic markers (including analysis of known spring run from this region) will likely provide additional insight regarding this result.

The two genetic baselines used for this work provided highly concordant results. Accuracy and precision of each baseline for assigning Chinook salmon was influenced by the samples and microsatellites contained in each. A thorough comparison of the resolution provided by these baselines would require a common set of baseline samples be genotyped using all marker sets, and a variety of samples of known origin be assigned

using each. Such an analysis could provide insight into the relative power of these baselines for a broad range of issues in the Sacramento River, but was not possible under the present study. Nevertheless, concordant levels of resolution indicated by our simulations, and concordant allocation of the samples collected at RBDD suggest similar utility of these baselines in the present context. Specifically, resolution of fall run, winter run and spring run provided by the two baselines appears to have been very similar. The limited occurrence of late-fall run, as indicated by the HMSC baseline, suggests that the presence of this run in only one of the baselines did not substantially change the results of the present study. Concordance between results based on the two baselines provides additional confidence in the genetic assignments presented here and thus in our findings regarding phenotypic versus genetic identification at RBDD.

In conclusion, our results revealed large discrepancies between phenotypic and genetic run assignments of Chinook salmon collected at RBDD. If one assumes that the samples examined here are representative and the genetic assignments are correct, then it appears that phenotype-based estimates of the numbers of threatened spring run Chinook salmon encountered at RBDD are approximately half the true numbers. It also appears that phenotype-based estimates of the numbers of endangered winter run Chinook encountered at RBDD may be several times the true numbers.

FUTURE RECCOMENDATIONS

- In order to understand year-to-year variability we recommend analysis of at least three more years worth of samples.
- If finer within-year temporal run composition estimates are needed (i.e. composition by month or by week), then we recommend analysis of sufficient samples to keep the number of samples per mixture at $\geq$100 individuals.
- In order to ensure that the best available technology is used for this work, we recommend evaluation of new genetic baselines and markers as they become available.

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Appendix 1. Oligonucleotide PCR primer mixes and thermal cycling conditions for microsatellite markers.

A. GAPS primer mixes

MSA		MSB		MSC	
Ots3M (6FAM)	5.0	*Ots213* (NED)	20.0	*Ots208b* (NED)	30.0
Ots211 (VIC)	10.0	*Ots212* (VIC)	4.0	*Omm1080* (VIC)	15.0
Ogo4 (PET)	6.0	*OtsG474* (PET)	30.0	*Oki100* (6FAM)	40.0
Ssa408 (PET)	30.0	*Ots9* (6FAM)	4.0		
Ots201b (NED)	8.0	*Ogo2* (6FAM)	8.0		
dH2O	41.0	dH2O	34.0	dH2O	15.0
Total	100.0	Total	100.0	Total	100.0

B. GAPS thermal cycler profiles

MSA and MSB (°C/min.)	MSC (°C/min.)	
95.0/15:00	95.0/15:00	
95.0/0:30	95.0/0:30	} 29 cycles
59.0/1:30	54.0/1:30	
72.0/1:00	72.0/1:00	
60.0/20:00	60.0/20:00	

C. HMSC primer mixes

Label	MSA	µL	MSB	µL	MSC	µL	MSD	µL	MSE	µL
6FAM	*Ots104*	30.0					*OtsG422*	10.0	*Ots211*	6.0
VIC	*Ots107*	15.0	*OtsG409*	20.0	*OtsG253*	20.0	*OtsG78b*	15.0	*Ots212*	4.0
NED	*Ots208b*	20.0	*OtsG83b*	20.0	*Ots209*	20.0	*Ots215*	20.0	*Ots201b*	8.0
PET			*Ots515*	30.0	*OtsG249*	30.0	*OtsG311*	30.0		
	dH2O	35.0	dH2O	30.0	dH2O	30.0	dH2O	25.0	dH2O	82.0
	Total	100.0	Total	100.0	Total	100.0	Total	100.0	Total	100.0

D. HMSC thermal cycler profiles

MSA (°C/min.)	MSB (°C/min.)	MSC and MSD (°C/min.)	MSE (°C/min.)	
95.0/15:00	95.0/15:00	95.0/15:00	95.0/15:00	
95.0/0:30	95.0/0:30	95.0/0:30	95.0/0:30	} 29 cycles
56.0/1:30	61.0/1:30	62.0/1:30	59.0/1:30	
72.0/1:00	72.0/1:00	72.0/1:00	72.0/1:00	
60.0/20:00	60.0/20:00	60.0/20:00	60.0/20:00	

Appendix 1. Phenotypic assignments and genetic assignments based on the GAPS and HMSC baselines. Numbers indicate probability for assignment to the corresponding run type.

Year	Sample ID	Phenotype	GAPS	P	HMSC	P
2007	1038-001	fa	fa	1.000	fa	0.988
2007	1038-002	wi	sp	0.977	sp	1.000
2007	1038-003	fa	fa	1.000	fa	1.000
2007	1038-004	fa	fa	0.999	fa	1.000
2007	1038-005	fa	fa	1.000	fa	0.920
2007	1038-006	fa	fa	0.945	fa	1.000
2007	1038-007	fa	fa	0.996	fa	0.802
2007	1038-008	fa	fa	0.998	sp	0.992
2007	1038-009	fa	sp	0.904	fa	0.823
2007	1038-010	fa	fa	1.000	fa	0.933
2007	1038-011	fa	fa	0.631	fa	1.000
2007	1038-012	sp	sp	1.000	sp	0.995
2007	1038-013	fa	fa	0.962	fa	0.840
2007	1038-014	fa	fa	1.000	fa	1.000
2007	1038-015	fa	fa	1.000	sp	0.825
2007	1038-016	fa	fa	0.982	fa	1.000
2007	1038-017	fa	fa	0.864	sp	1.000
2007	1038-018	fa	fa	0.997	fa	0.988
2007	1038-019	fa	sp	0.803	sp	0.974
2007	1038-020	fa	fa	1.000	fa	1.000
2007	1038-021	fa	fa	1.000	fa	1.000
2007	1038-022	fa	fa	1.000	sp	0.999
2007	1038-023	fa	fa	1.000	fa	1.000
2007	1038-024	fa	fa	0.999	fa	1.000
2007	1038-025	fa	fa	0.900	fa	1.000
2007	1038-026	fa	sp	1.000	sp	0.891
2007	1038-027	fa	fa	1.000	fa	1.000
2007	1038-028	fa	fa	1.000	fa	0.926
2007	1038-029	fa	fa	0.799	fa	1.000
2007	1038-030	fa	fa	1.000	fa	1.000
2007	1038-031	fa	fa	0.839	fa	1.000
2007	1038-032	fa	fa	1.000	fa	1.000
2007	1038-033	fa	fa	0.998	fa	0.937
2007	1038-034	fa	sp	0.751	sp	0.561
2007	1038-035	fa	fa	1.000	fa	1.000
2007	1038-036	fa	fa	0.996	fa	0.840
2007	1038-037	fa	fa	1.000	fa	1.000
2007	1038-038	fa	fa	1.000	fa	0.843
2007	1038-039	fa	fa	1.000	fa	0.955
2007	1038-040	fa	fa	1.000	fa	1.000

Year	Sample ID	Phenotype	GAPS	P	HMSC	P
2007	1038-041	fa	fa	1.000	fa	1.000
2007	1038-042	fa	fa	0.991	fa	0.630
2007	1038-043	fa	fa	0.997	fa	0.999
2007	1038-044	fa	fa	1.000	sp	0.946
2007	1038-045	fa	fa	0.827	fa	0.796
2007	1038-046	fa	fa	0.924	sp	0.983
2007	1038-047	fa	fa	0.992	fa	1.000
2007	1038-048	fa	fa	1.000	fa	1.000
2007	1038-049	fa	fa	1.000	fa	1.000
2007	1038-050	fa	sp	0.958	fa	0.865
2007	1038-051	fa	fa	1.000	fa	0.999
2007	1038-052	fa	fa	1.000	fa	1.000
2007	1038-053	fa	sp	0.947	sp	1.000
2007	1038-054	fa	fa	1.000	fa	1.000
2007	1038-055	fa	fa	1.000	fa	1.000
2007	1038-056	fa	fa	1.000	fa	0.988
2007	1038-057	fa	fa	1.000	fa	1.000
2007	1038-058	fa	fa	1.000	fa	1.000
2007	1038-059	fa	fa	1.000	fa	0.999
2007	1038-060	fa	fa	0.651	fa	0.998
2007	1038-061	fa	fa	1.000	fa	1.000
2007	1038-062	fa	fa	0.999	fa	0.997
2007	1038-063	fa	fa	1.000	fa	1.000
2007	1038-064	fa	sp	0.973	sp	0.832
2007	1038-065	fa	fa	1.000	fa	1.000
2007	1038-066	fa	fa	1.000	fa	1.000
2007	1038-067	fa	fa	1.000	fa	1.000
2007	1038-068	fa	fa	1.000	fa	1.000
2007	1038-069	fa	fa	1.000	fa	1.000
2007	1038-070	fa	fa	1.000	wi	0.601
2007	1038-071	fa	fa	1.000	fa	1.000
2007	1038-072	fa	fa	0.999	fa	1.000
2007	1038-073	fa	fa	1.000	fa	1.000
2007	1038-074	fa	fa	1.000	fa	0.998
2007	1038-075	fa	fa	0.989	sp	1.000
2007	1038-076	fa	fa	0.995	fa	0.995
2007	1038-077	fa	fa	1.000	sp	0.548
2007	1038-078	fa	fa	1.000	fa	1.000
2007	1038-079	fa	fa	1.000	fa	1.000
2007	1038-080	fa	fa	0.999	fa	0.960
2007	1038-081	fa	fa	1.000	fa	1.000
2007	1038-082	fa	fa	1.000	fa	1.000
2007	1038-083	fa	fa	0.984	fa	1.000
2007	1038-084	fa	fa	1.000	fa	0.996

Year	Sample ID	Phenotype	GAPS	P	HMSC	P
2007	1038-085	fa	fa	1.000	fa	1.000
2007	1038-086	fa	fa	1.000	fa	1.000
2007	1038-087	fa	fa	1.000	fa	1.000
2007	1038-088	fa	fa	1.000	fa	1.000
2007	1038-089	fa	fa	1.000	fa	1.000
2007	1038-090	wi	sp	1.000	sp	1.000
2007	1038-091	wi	wi	1.000	wi	1.000
2007	1038-092	fa	fa	0.999	fa	1.000
2007	1038-093	fa	fa	1.000	fa	1.000
2007	1038-094	fa	fa	1.000	fa	1.000
2007	1038-095	fa	fa	1.000	fa	1.000
2007	1038-096	fa	sp	1.000	sp	1.000
2007	1038-097	fa	fa	1.000	fa	1.000
2007	1038-098	fa	fa	1.000	fa	1.000
2007	1038-099	fa	fa	0.999	fa	1.000
2007	1038-100	fa	fa	0.997	fa	1.000
2007	1059-001	fa	fa	1.000	fa	1.000
2007	1059-002	fa	fa	0.993	fa	1.000
2007	1059-003	fa	sp	0.966	fa	0.533
2007	1059-004	fa	fa	1.000	fa	1.000
2007	1059-005	fa	sp	0.989	sp	1.000
2007	1059-006	fa	sp	0.999	sp	0.999
2007	1059-007	fa	fa	1.000	fa	1.000
2007	1059-008	wi	sp	1.000	sp	1.000
2007	1059-009	fa	fa	1.000	fa	1.000
2007	1059-010	fa	fa	1.000	fa	1.000
2007	1059-011	fa	fa	1.000	fa	1.000
2007	1059-012	fa	sp	0.971	fa	1.000
2007	1059-013	fa	fa	1.000	fa	1.000
2007	1059-014	fa	fa	1.000	fa	0.997
2007	1059-015	fa	fa	1.000	fa	1.000
2007	1059-016	fa	fa	1.000	fa	1.000
2007	1059-017	fa	wi	0.999	wi	0.991
2007	1059-018	fa	fa	1.000	fa	0.998
2007	1059-019	fa	fa	0.996	fa	0.989
2007	1059-020	fa	fa	1.000	fa	1.000
2007	1059-021	fa	fa	1.000	sp	1.000
2007	1059-022	fa	fa	1.000	fa	1.000
2007	1059-023	fa	fa	1.000	sp	0.522
2007	1059-024	fa	fa	1.000	fa	1.000
2007	1059-025	fa	fa	1.000	fa	1.000
2007	1059-026	fa	fa	1.000	sp	0.612
2007	1059-027	fa	fa	0.982	fa	1.000
2007	1059-028	fa	fa	1.000	fa	1.000

Year	Sample ID	Phenotype	GAPS	P	HMSC	P
2007	1059-029	fa	fa	1.000	fa	1.000
2007	1059-030	fa	fa	1.000	fa	1.000
2007	1059-031	fa	fa	0.800	fa	0.921
2007	1059-032	fa	fa	1.000	fa	1.000
2007	1059-033	fa	fa	1.000	fa	1.000
2007	1059-034	fa	fa	1.000	fa	1.000
2007	1059-035	fa	fa	0.995	fa	1.000
2007	1059-036	fa	fa	1.000	fa	1.000
2007	1059-037	fa	fa	1.000	fa	1.000
2007	1059-038	fa	fa	1.000	fa	0.995
2007	1059-039	fa	fa	0.856	fa	0.968
2007	1059-040	fa	fa	1.000	fa	1.000
2007	1059-041	fa	fa	1.000	fa	1.000
2007	1059-042	fa	fa	0.995	fa	1.000
2007	1059-043	fa	fa	1.000	fa	1.000
2007	1059-044	fa	sp	0.869	sp	0.937
2007	1059-045	fa	sp	0.534	fa	0.999
2007	1059-046	fa	fa	1.000	fa	0.976
2007	1059-047	fa	fa	1.000	fa	1.000
2007	1059-048	fa	fa	0.999	fa	1.000
2007	1059-049	fa	fa	1.000	fa	1.000
2007	1059-050	fa	fa	1.000	fa	1.000
2007	1059-051	fa	fa	1.000	fa	0.800
2007	1059-052	fa	fa	0.990	fa	1.000
2007	1059-053	fa	fa	1.000	fa	1.000
2007	1059-054	fa	fa	1.000	fa	1.000
2007	1059-055	fa	fa	1.000	fa	0.994
2007	1059-056	fa	sp	0.535	fa	1.000
2007	1059-057	fa	fa	1.000	fa	1.000
2007	1059-058	fa	fa	1.000	fa	1.000
2007	1059-059	fa	fa	0.999	fa	1.000
2007	1059-060	fa	fa	1.000	fa	1.000
2007	1059-061	fa	fa	0.796	fa	1.000
2007	1059-062	fa	fa	1.000	fa	1.000
2007	1059-063	fa	fa	1.000	fa	1.000
2007	1059-064	fa	fa	1.000	fa	0.999
2007	1059-065	fa	fa	0.994	fa	0.998
2007	1059-066	fa	fa	1.000	fa	1.000
2007	1059-067	fa	fa	0.953	fa	0.984
2007	1059-068	fa	fa	1.000	fa	1.000
2007	1059-069	fa	fa	1.000	fa	1.000
2007	1059-070	fa	fa	0.912	fa	0.580
2007	1059-071	fa	fa	1.000	fa	1.000
2007	1059-072	fa	fa	1.000	fa	1.000

Year	Sample ID	Phenotype	GAPS	P	HMSC	P
2007	1059-073	fa	fa	1.000	fa	0.999
2007	1059-074	fa	fa	1.000	fa	1.000
2007	1059-075	fa	sp	0.546	sp	0.788
2007	1059-076	fa	fa	1.000	fa	0.988
2007	1059-077	fa	fa	1.000	fa	1.000
2007	1059-078	fa	fa	1.000	fa	1.000
2007	1059-079	fa	fa	0.997	fa	0.999
2007	1059-080	fa	fa	1.000	fa	1.000
2007	1059-081	fa	sp	0.659	fa	1.000
2007	1059-082	fa	fa	0.771	fa	1.000
2007	1059-083	fa	fa	1.000	fa	1.000
2007	1059-084	fa	fa	1.000	fa	1.000
2007	1059-085	fa	fa	1.000	fa	1.000
2007	1059-086	fa	fa	1.000	fa	0.995
2007	1059-087	fa	sp	0.999	sp	1.000
2007	1059-088	fa	fa	1.000	fa	1.000
2007	1059-089	fa	fa	1.000	fa	1.000
2007	1059-090	fa	fa	1.000	fa	1.000
2007	1059-091	fa	fa	0.992	fa	0.970
2007	1059-092	fa	fa	1.000	fa	0.888
2007	1059-093	fa	fa	1.000	fa	1.000
2007	1059-094	fa	fa	0.997	fa	1.000
2007	1059-095	fa	fa	1.000	sp	0.951
2007	1059-096	fa	fa	1.000	fa	1.000
2007	1059-097	fa	fa	1.000	fa	1.000
2007	1059-099	fa	sp	0.808	fa	0.951
2007	1059-100	fa	fa	1.000	fa	1.000
2007	980-001	wi	sp	0.643	sp	1.000
2007	980-002	wi	wi	1.000	wi	1.000
2007	980-003	wi	sp	0.995	sp	1.000
2007	980-004	wi	wi	1.000	wi	1.000
2007	980-005	wi	fa	0.999	fa	1.000
2007	980-006	sp	sp	0.994	sp	1.000
2007	980-007	sp	sp	1.000	sp	1.000
2007	980-008	sp	sp	1.000	sp	1.000
2007	980-009	wi	sp	0.948	fa	0.528
2007	980-010	sp	fa	1.000	fa	0.952
2007	980-011	sp	sp	1.000	sp	1.000
2007	980-012	wi	fa	1.000	fa	1.000
2007	980-013	wi	sp	1.000	sp	0.999
2007	980-014	wi	sp	0.860	sp	1.000
2007	980-015	sp	sp	1.000	sp	1.000
2007	980-016	sp	sp	0.974	sp	0.993
2007	980-017	wi	fa	1.000	fa	0.996

Year	Sample ID	Phenotype	GAPS	P	HMSC	P
2007	980-018	wi	sp	0.994	sp	1.000
2007	980-019	wi	fa	0.756	fa	0.999
2007	980-020	wi	fa	1.000	fa	0.987
2007	980-021	wi	sp	1.000	sp	1.000
2007	980-022	sp	sp	1.000	sp	1.000
2007	980-023	wi	wi	1.000	wi	1.000
2007	980-024	sp	sp	1.000	sp	1.000
2007	980-025	wi	sp	0.999	sp	1.000
2007	980-026	wi	wi	1.000	wi	1.000
2007	980-027	sp	sp	0.771	sp	0.839
2007	980-028	wi	fa	1.000	fa	1.000
2007	980-029	wi	fa	1.000	fa	1.000
2007	980-030	sp	fa	0.911	fa	0.996
2007	980-031	wi	fa	0.923	fa	0.975
2007	980-032	sp	fa	0.998	fa	1.000
2007	980-033	wi	fa	0.625	fa	0.993
2007	980-034	wi	fa	1.000	fa	1.000
2007	980-035	wi	sp	1.000	sp	1.000
2007	980-036	fa	fa	1.000	fa	1.000
2007	980-037	wi	fa	0.997	sp	1.000
2007	980-039	wi	fa	1.000	fa	1.000
2007	980-040	fa	fa	0.979	fa	1.000
2007	980-041	fa	fa	0.999	fa	1.000
2007	980-042	wi	fa	1.000	fa	1.000
2007	980-043	fa	fa	0.850	fa	1.000
2007	980-044	fa	fa	0.999	fa	0.999
2007	980-045	fa	fa	1.000	fa	1.000
2007	980-046	fa	fa	1.000	fa	1.000
2007	980-047	wi	fa	0.785	fa	0.932
2007	980-048	wi	fa	0.999	fa	1.000
2007	980-049	sp	sp	1.000	sp	0.886
2007	980-050	sp	fa	1.000	fa	0.985
2007	980-051	fa	fa	1.000	fa	0.985
2007	980-052	sp	fa	1.000	fa	1.000
2007	980-053	sp	fa	0.900	fa	1.000
2007	980-054	fa	fa	0.998	fa	0.908
2007	980-055	wi	fa	1.000	fa	0.991
2007	980-056	fa	fa	1.000	fa	1.000
2007	980-057	fa	fa	1.000	fa	1.000
2007	980-058	wi	fa	1.000	fa	1.000
2007	980-059	fa	fa	1.000	fa	0.996
2007	980-060	fa	fa	1.000	fa	1.000
2007	980-061	fa	sp	0.993	sp	0.997
2007	980-062	fa	fa	1.000	fa	1.000

Year	Sample ID	Phenotype	GAPS	P	HMSC	P
2007	980-063	sp	fa	1.000	fa	1.000
2007	980-064	fa	fa	1.000	fa	1.000
2007	980-065	sp	fa	1.000	fa	1.000
2007	980-066	wi	wi	1.000	wi	1.000
2007	980-067	wi	wi	1.000	wi	1.000
2007	980-068	fa	fa	1.000	fa	1.000
2007	980-069	fa	fa	1.000	fa	1.000
2007	980-070	sp	fa	1.000	fa	0.987
2007	980-071	fa	fa	1.000	fa	0.973
2007	980-072	sp	fa	1.000	fa	1.000
2007	980-073	fa	fa	1.000	fa	1.000
2007	980-074	sp	sp	1.000	sp	1.000
2007	980-075	fa	fa	1.000	fa	1.000
2007	980-076	fa	fa	1.000	fa	1.000
2007	980-077	fa	fa	1.000	fa	1.000
2007	980-078	fa	fa	0.993	fa	1.000
2007	980-079	fa	fa	1.000	fa	1.000
2007	980-080	fa	fa	1.000	fa	1.000
2007	980-081	sp	fa	1.000	fa	1.000
2007	980-082	fa	fa	1.000	fa	1.000
2007	980-083	wi	sp	0.998	sp	0.946
2007	980-084	fa	fa	1.000	fa	1.000
2007	980-085	fa	fa	1.000	fa	0.515
2007	980-086	fa	fa	1.000	fa	1.000
2007	980-087	fa	fa	1.000	fa	1.000
2007	980-088	fa	fa	1.000	fa	1.000
2007	980-089	fa	fa	1.000	fa	0.962
2007	980-090	fa	fa	1.000	fa	1.000
2007	980-091	fa	fa	1.000	fa	1.000
2007	980-092	fa	fa	1.000	fa	1.000
2007	980-093	fa	fa	0.985	fa	1.000
2007	980-094	wi	fa	1.000	fa	1.000
2007	980-095	fa	fa	1.000	sp	0.999
2007	980-096	fa	fa	0.966	fa	1.000
2007	980-097	sp	fa	1.000	fa	1.000
2007	980-098	fa	fa	1.000	fa	1.000
2007	980-099	fa	fa	1.000	fa	1.000
2007	980-100	fa	fa	1.000	fa	1.000
2007	981-001	fa	fa	0.999	fa	1.000
2007	981-002	sp	fa	1.000	fa	1.000
2007	981-003	fa	fa	1.000	fa	1.000
2007	981-004	fa	fa	1.000	fa	1.000
2007	981-005	fa	fa	0.978	fa	1.000
2007	981-006	fa	fa	0.999	fa	0.999

Year	Sample ID	Phenotype	GAPS	P	HMSC	P
2007	981-007	wi	fa	0.999	fa	0.595
2007	981-008	sp	fa	1.000	fa	1.000
2007	981-009	fa	fa	1.000	fa	1.000
2007	981-010	fa	fa	1.000	sp	1.000
2007	981-011	fa	fa	1.000	fa	0.999
2007	981-012	fa	fa	0.947	fa	0.999
2007	981-013	fa	fa	0.964	fa	0.978
2007	981-014	fa	fa	1.000	fa	1.000
2007	981-015	fa	fa	1.000	fa	1.000
2007	981-016	fa	fa	1.000	fa	1.000
2007	981-017	fa	fa	1.000	fa	1.000
2007	981-018	fa	fa	0.929	fa	1.000
2007	981-019	fa	sp	0.966	fa	0.533
2007	981-020	fa	sp	0.672	fa	0.996
2007	981-021	fa	fa	0.674	sp	0.990
2007	981-022	fa	fa	1.000	fa	1.000
2007	981-023	fa	sp	0.778	sp	1.000
2007	981-024	fa	fa	1.000	fa	1.000
2007	981-025	fa	fa	1.000	fa	1.000
2007	981-026	fa	fa	1.000	fa	1.000
2007	981-027	fa	fa	1.000	fa	1.000
2007	981-028	fa	fa	0.785	fa	1.000
2007	981-029	fa	fa	1.000	fa	1.000
2007	981-030	wi	wi	1.000	wi	1.000
2007	981-031	fa	fa	1.000	fa	1.000
2007	981-032	fa	fa	0.999	sp	0.980
2007	981-033	fa	sp	0.906	fa	1.000
2007	981-034	fa	fa	1.000	fa	0.960
2007	981-035	fa	fa	1.000	fa	1.000
2007	981-036	fa	fa	1.000	fa	1.000
2007	981-037	fa	fa	1.000	fa	1.000
2007	981-038	fa	fa	1.000	fa	1.000
2007	981-039	fa	sp	0.921	sp	1.000
2007	981-040	fa	fa	1.000	fa	1.000
2007	981-041	fa	fa	1.000	fa	1.000
2007	981-042	fa	fa	0.990	fa	0.999
2007	981-043	fa	fa	0.998	fa	0.888
2007	981-044	fa	fa	1.000	sp	0.767
2007	981-045	fa	fa	1.000	fa	1.000
2007	981-046	fa	fa	1.000	fa	1.000
2007	981-047	fa	fa	1.000	fa	0.991
2007	981-048	fa	fa	1.000	sp	0.847
2007	981-049	fa	fa	1.000	fa	1.000
2007	981-050	fa	fa	1.000	fa	1.000

Year	Sample ID	Phenotype	GAPS	P	HMSC	P
2007	981-051	fa	sp	0.553	fa	1.000
2007	981-052	fa	fa	1.000	fa	1.000
2007	981-053	fa	fa	1.000	fa	0.999
2007	981-054	fa	fa	0.997	fa	0.997
2007	981-055	fa	fa	1.000	fa	0.830
2007	981-056	fa	sp	1.000	sp	1.000
2007	981-057	fa	fa	1.000	fa	0.744
2007	981-058	fa	fa	1.000	fa	0.551
2007	981-059	fa	fa	0.999	sp	0.555
2007	981-060	fa	fa	1.000	fa	1.000
2007	981-061	fa	fa	1.000	fa	1.000
2007	981-062	fa	fa	1.000	fa	0.999
2007	981-063	fa	fa	1.000	fa	1.000
2007	981-064	fa	fa	1.000	fa	1.000
2007	981-065	fa	fa	1.000	fa	1.000
2007	981-066	fa	fa	1.000	fa	1.000
2007	981-067	fa	fa	0.502	fa	1.000
2007	981-068	fa	sp	0.636	fa	0.987
2007	981-069	fa	fa	1.000	fa	1.000
2007	981-070	fa	sp	0.989	fa	0.994
2007	981-071	fa	fa	1.000	sp	0.939
2007	981-072	wi	sp	0.997	sp	1.000
2007	981-073	fa	sp	1.000	sp	0.967
2007	981-074	wi	sp	1.000	sp	1.000
2007	981-075	fa	fa	1.000	fa	1.000
2007	981-076	fa	fa	0.899	fa	1.000
2007	981-077	fa	fa	1.000	fa	1.000
2007	981-078	fa	fa	1.000	fa	1.000
2007	981-079	fa	sp	1.000	sp	1.000
2007	981-080	fa	fa	1.000	fa	0.995
2007	981-081	fa	fa	0.988	sp	0.610
2007	981-082	fa	fa	0.984	fa	1.000
2007	981-083	wi	wi	1.000	wi	1.000
2007	981-084	fa	fa	1.000	fa	0.999
2007	981-085	fa	fa	0.751	fa	0.893
2007	981-086	fa	fa	1.000	fa	1.000
2007	981-087	fa	fa	1.000	fa	0.996
2007	981-088	fa	sp	0.592	sp	0.982
2007	981-089	fa	fa	1.000	fa	1.000
2007	981-090	fa	fa	0.999	fa	1.000
2007	981-091	fa	fa	1.000	fa	1.000
2007	981-092	fa	fa	0.970	fa	0.563
2007	981-093	fa	fa	1.000	fa	1.000
2007	981-094	wi	fa	0.994	fa	0.904

Year	Sample ID	Phenotype	GAPS	P	HMSC	P
2007	981-095	fa	fa	1.000	fa	1.000
2007	981-096	fa	fa	0.998	fa	0.934
2007	981-097	fa	fa	0.995	fa	1.000
2007	981-098	fa	fa	0.824	sp	0.979
2007	981-099	fa	fa	0.999	fa	0.982
2007	981-100	fa	fa	1.000	fa	0.999