

**Genetic Diversity in Supplemented North Fork Stillaguamish River
Chinook Salmon: 1980 - 2001**

Report to the Northwest Indian Fisheries Commission

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FINAL

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Background

The Stillaguamish Tribe initiated a conservation program for depressed North Fork Stillaguamish River summer chinook in 1986 at the Harvey Creek Hatchery to increase the abundance and preserve genetic diversity in the depressed population. At the same time the Tribe stopped fishing on this stock to avoid further decline. The Tribe would like to use the conservation program to maintain the effective population size (N_e) and minimize domestication in the population, and avoid incorporating non-native genes. Fish that originated in the hatchery program as well as fish that originated in the wild are taken for broodstock each year to foster genetic exchange between the two components and minimize potential domestication due to hatchery rearing. Both components also spawn in the wild each year.

Historically, Green River fall chinook salmon were stocked in the Stillaguamish River in substantial numbers until 1974. Most managers believe that these plants contributed few returns because fish were planted mostly as green eggs or unfed fry, which tend to produce few returning adults in chinook salmon. But this assumption has never been tested in the Stillaguamish River. Hatchery reform funding provided an opportunity for the Stillaguamish Tribe to evaluate the effectiveness of the hatchery program at maintaining genetic diversity and to test for the presence of Green River fall chinook salmon in the Stillaguamish River.

Methods

Scales, fin clips or liver tissues were already available from chinook salmon sampled in the Tribal in-river fishery, hatchery broodstock, or on the spawning grounds in the Stillaguamish River between 1980 and 1996, additional fin clips were collected in 2001 (Table 1 and Table 2). All samples were from early returning adults believed to be North Fork summer chinook as opposed to the South Fork fall chinook also in the system. We subcontracted to the Washington Department of Fish and Wildlife to characterize the genetic diversity in the samples. They used standard microsatellite and allozyme technology to generate genotype information. Using the genotypes generated by WDFW and additional allozyme genotypes already available for North Fork Stillaguamish Chinook, we evaluated within-year population structure by testing for Hardy-Weinberg equilibrium and linkage equilibrium using the computer program POWER MARKER; and when there was evidence for population structure, we assigned individuals to their most likely cluster of origin using a Bayesian approach (STRUCTURE). We then calculated global and pair-wise F_{st} and G-test statistics between all years (GENEPOP for most tests, POWER MARKER was used to calculate 95% confidence interval of F_{st}) to test for genetic differences between years; and when samples were available, we compared genetic diversity in program with natural origin fish, and fish sampled in the broodstock with fish sampled on the spawning grounds using the same pair-wise tests to test for within year genetic differences. We described genetic diversity each year (average heterozygosity and average number of alleles, POP TOOLS, an Excel add-in) and calculated the effective population size over different time periods (N_e ESTIMATOR) to test for change in genetic diversity over time. We also conducted an assignment test using Stillaguamish River chinook and Green River fall chinook raised at the Kendall Creek Hatchery in the Nooksack River to test for the presence of Green River chinook (WHICHRUN).

Results and Discussion

Unfortunately, the data from the 1980 samples was insufficient for our analysis because of apparent degradation of larger DNA fragments (Table 40). Absence of the 1980 samples notwithstanding, we made some noteworthy findings. Within year genetic diversity in North Fork Stillaguamish River summer chinook salmon has been maintained since supplementation started in 1986. Between 1985 and 2001 the number of alleles and the average heterozygosity has not changed significantly, although the trend is slightly negative for the number of microsatellite alleles (Figure 1). The number of alleles and average heterozygosity was equivalent to a relatively large hatchery population of Green River chinook salmon, albeit one with a long history of hatchery influence (Table 3). In addition, the effective population size determined genetically was consistent with the demographic estimate determined from census number of spawners indicating that genetic diversity is faithfully passed on (Table 4). No legacy of Green River chinook introductions was detected in the fishery, broodstock or on the spawning grounds in the Stillaguamish River during the years tested (Figure 2). There were some irregularities in the genetics that may cause concern, however.

In 1996 the program and natural origin returns were genetically indistinguishable, but by 2001 the program and natural origin returns had significantly different allele frequencies at microsatellite markers ($F_{st} = 0.005$, Table 5 and Figure 3). This level of divergence does not necessarily indicate life history or biological differentiation, but that concern does exist. For example, this level of divergence is comparable to the divergence between two hatchery populations of Green River Chinook, one in the Soos Creek Hatchery and the other in the Kendall Creek Hatchery ($F_{st} = 0.007$, Table 7 DNA Characterization of Nooksack River Chinook, WDFW Report, Nov. 2002). This level of divergence was also seen between two year classes of sockeye in Lake Ozette spawning in the same location, which overwhelmingly return as four year olds (Olsen beach 1999 vs. Olsen beach 2000 $F_{st}=0.007$, Genetic Characterization of Lake Ozette Sockeye, Report to the HSRG 2001).

Genetic divergence between two components, in this case the hatchery and natural origin summer chinook, generally indicates a reduction in geneflow. It is possible that genetic exchange between the fish from the hatchery and fish from the spawning grounds is unbalanced despite the Tribe's efforts to completely integrate program and natural origin fish (Figure 4). Program fish have been observed on the spawning grounds in large numbers, 10-60% of all spawners, but they may not perform as well as natural origin fish. We estimated 54 genetic migrants between the two components per generation among 2001 returns (Table 6). However, if the components have yet to reach equilibrium of genetic drift and geneflow, the real rate of geneflow between program origin and natural origin chinook may be even lower.

A potential cause of reduced geneflow between fish spawned in the hatchery and fish that spawn naturally is domestication selection, which favors performance in the hatchery and reduces performance in the wild. Power was insufficient to evaluate domestication, although it was encouraging to see that in a test for parentage of 2001 returns by 1996 hatchery brood all four mating types were identified: program x program, natural x natural, program x natural and natural x program (Table 12). If selection is

occurring, it does not completely preclude integration of natural origin fish into the broodstock.

Alternatively, the program and natural origin chinook may diverge if non-target chinook adapted to a different system were incorporated into the broodstock. There was strong evidence for population structure among the 1988 broodstock and 1996 hatchery origin component (Table 7). It is possible that individuals with ancestries outside the Stillaguamish River were collected for broodstock in 1988 and 1996. The 1988 sample may have been composed of one cluster of 13 individuals and a second cluster of 3 individuals (Table 8 and Table 10). The 1996 hatchery origin component was most likely composed of 41 individuals in one cluster and 7 individuals in a second cluster (Table 8 and Table 9). Interestingly, all seven individuals in the second cluster from 1996 were hatchery origin, presumably from the Harvey Creek Hatchery, as indicated by a fin clip or coded wire tag in the snout applied as juveniles. By comparison, there was no evidence for population structure among the natural origin fish in 1996 (Table 7). PSMFC records indicated that in 1996 one chinook was captured for broodstock carrying a tag from the Kendall Hatchery spring chinook program, although our records were insufficient to determine if this was one of the fish we identified as an outlier. PSMFC records also indicated that four fish from the Marblemount Hatchery in the Skagit River had also been captured for broodstock in 1994 (Table ##).

It is also possible that the fish in the second cluster from 1996 were not strays, but were from the North Fork Stillaguamish summer chinook population. Four of the seven individuals in the second cluster appeared to be siblings. Unequal reproductive success (low N_e/N) can lead to linkage disequilibrium¹, which we used as an indicator of population structure. By 2001 the fish in the second cluster appeared to be completely integrated into the hatchery origin component, one fish used for broodstock in 2001 was the offspring of one of the 1996 outliers and another natural origin fish (Table 12), and there was no evidence for population structure (Table 7).

In the future genetic diversity should continue to be monitored among Stillaguamish River chinook because of potential reduction in genetic diversity in the long term. In 1996 we identified four apparent siblings that were the offspring of fish spawned in a hatchery in 1993 (Table 9). If offspring from these parents returned in equal proportions to the Stillagumaish River as two, three, four and five year olds it is possible that a total of 43 siblings from the same parent-pair returned to spawn in the river, much higher than the two offspring per parent-pair expected for a stable population. Over time, large variance in reproductive success will lead to a loss of genetic diversity in the population.

Two individuals sampled in the 1983 fishery were unlikely North Fork summer chinook. Between the two of them they contained five microsatellite alleles not seen in any other individual (Table 13). Their true origin could not be determined, although the fishery occurs early in the year in the lower river and these fish may have been unlucky wanderers. Had these fish not been caught in the fishery, it is not clear that they would have spawned in the Stillaguamish River, so we are not attaching high significance to detecting them.

¹ Waples, R. and Teel, D. 1990. Conservation genetics of Pacific salmon I. Temporal changes in allele frequency. *Conservation Biology*. 4: 144-156.

In conclusion, the Stillaguamish Tribe's supplementation program for North Fork Stillaguamish River summer chinook is succeeding at maintaining genetic diversity. Also, Green River fall chinook are not established in the North Fork Stillaguamish River. There is cause for concern of genetic divergence between hatchery origin and natural origin fish, and variance in reproductive success. The Tribe has already taken efforts to address most of these issues. The Tribe shifted the location of broodstock collection and reads coded-wire tags prior to spawning to reduce the chance of incorporating non-target fish. The Tribe also adopted a modified "matrix" spawning protocol to reduce the variance in reproductive success between families. The Tribe might also consider mimicking the natural environment in the hatchery to reduce domestication and continue genetic monitoring of the wild component for geneflow with program origin fish. It is possible that the genetic divergence observed in 2001 was a sampling artifact or has already been alleviated by the efforts taken in the past few years.

Acknowledgements

We thank the Stillaguamish Tribe for help with tissue sample collection and providing biological information of Stillaguamish River chinook. We also thank John Sneva of WDFW for providing historical scale samples, and the WDFW genetics lab for providing allozyme genotypes and biological information from 1987, 1988 and 1996 Stillaguamish River chinook and for generating additional allozyme and microsatellite genotypes. The WDFW also provided microsatellite genotypes for Green River chinook salmon raised at the WDFW Kendall Creek Hatchery. Ken Currens, Kerry Naish, Fred Utter and many others provided helpful comments along the way.

Genetic Samples

Table 1 Allozyme and microsatellite tissue samples from Stillaguamish River chinook salmon. Individuals scored at nine or more microsatellite loci were used in further analysis.

Year	WDFW Code	Allozymes samples	Microsatellite samples (used)	Sampling location	Tissue type
1980	80AA		105(74)	In-river fishery	Scales
1983	83AA		1(1)	In-river fishery	Scales
	83AB		2(1)	In-river fishery	Scales
1984	84AA		4(3)	In-river fishery	Scales
1985	85AA		20(20)	Spawning grounds	Scales
	85AB		17(16)	In-river fishery	Scales
	85AC		52(39)	Spawning grounds	Scales
1987	87AK	70	70(69)	Broodstock	Liver and scales
1988	88QN	36	26(16)	Broodstock	Scales
1996	96EB	108	108(99)	Broodstock	Liver and scales
2001	01DY	115	118(114)	Broodstock	Fin clips
	01DZ		79(28)	Spawning Grounds	Fin clips

Table 2 Breakdown of 1996 and 2001 samples into hatchery, wild and unknown origin.

	Allozyme	Microsatellite
1996H	53	48
1996W	55	51
2001H	36	42
2001W	79	91
2001U	0	9

Escapement, Heterozygosity and Number of Alleles Over Time

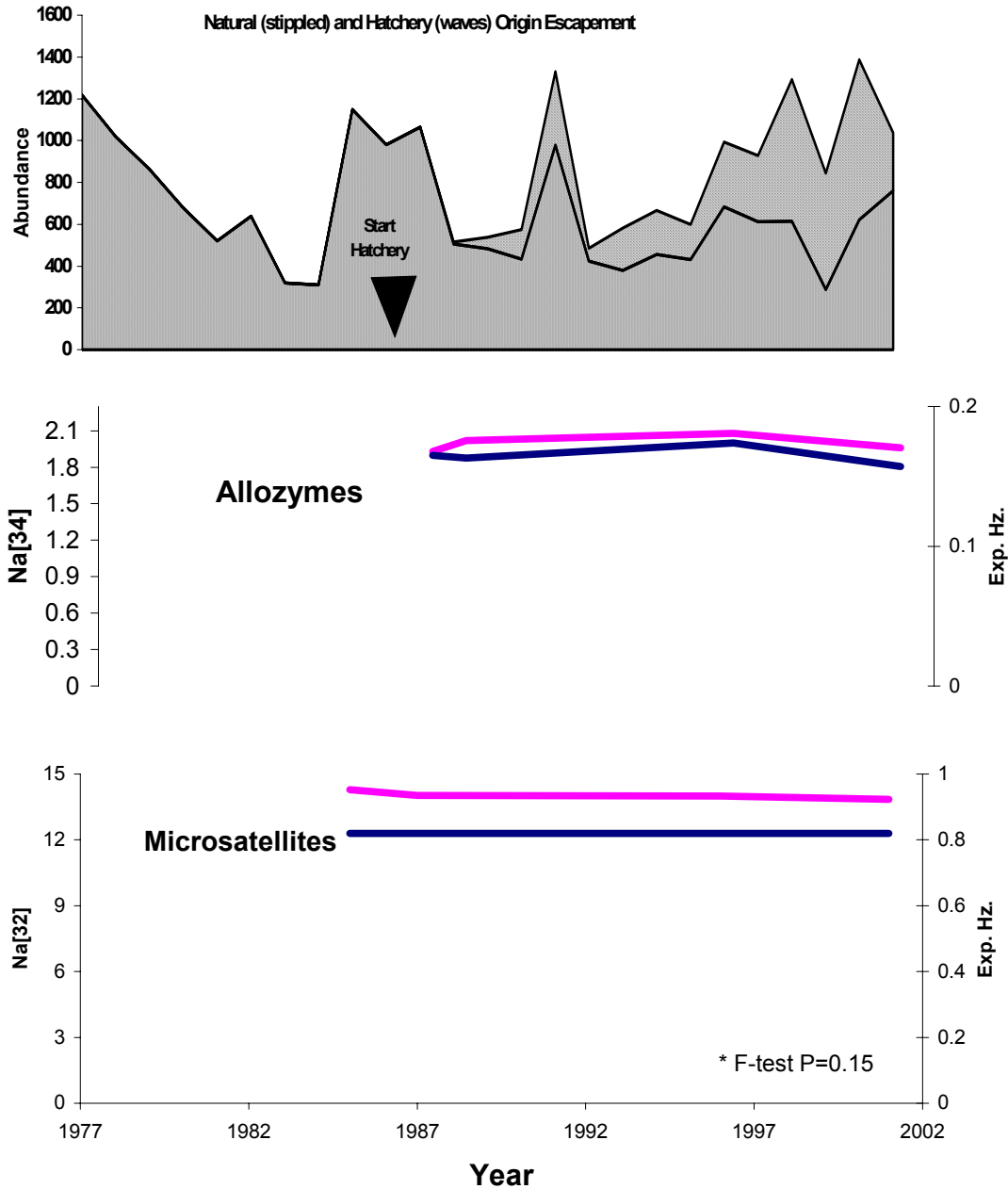


Figure 1 Stillaguamish summer chinook salmon natural and hatchery origin escapement (top) and genetic diversity standardized for a common number of samples (in brackets on Y-axis). Middle chart is based on 30 polymorphic allozyme loci from broodstock sampled in 1987, 1988, 1996 and 2001. Bottom chart is based on 16 microsatellite loci from broodstock and spawning ground samples collected in 1985, 1987-88, 1996 and 2001 (no fishery samples were included). Trends in number of alleles (Na) or expected heterozygosity (Exp. Hz.) were not significantly different than zero (F-Test).

Chinook Genetic Diversity

Table 3 Average allelic richness and expected heterozygosity at six microsatellite loci in Stillaguamish chinook salmon and Green River fall chinook at the Kendall Creek Hatchery.

	1980	1985	1987-8	1996	2001	Green River
Na[23]	9.6	11.0	10.0	10.9	10.7	10.2
Hz	0.75	0.80	0.82	0.82	0.82	0.81

Effective population size

Table 4 Effective population size (and 95% confidence interval).

	N	Nb- demographic	Nb- Temporal	Generation (yrs.)	Generations
1977- 1986	618	184		3.59	
1985- 1987			20 (11-63)		1
1985- 1996			99 (59-204)	3.59	3
1985- 2001			127 (86-206)	3.59	5
1987- 1996			144 (74-557)	3.59	3
1987- 2001	754	209	228 (118-780)	3.54	4
1996- 2001			100 (53-335)	3.54	1.5

Note 1 Demographic $N_b = 0.3 * 4 * (\text{Males} + \text{Females}) / (\text{Males} * \text{Females})$. The ratio of Males to Females each year on the spawning grounds was estimated from the hatchery broodstock records; N_b composite = N_b Hatchery + N_b Wild; N_b -Temporal was estimated using the approach of Waples 1990 using the computer program Ne Estimator.

Population Structure

Table 5 Microsatellite pair-wise Fst and 95% confidence intervals.

H v. W	1987	1996H	1996W	2001H
1996H	0.0024 (-0.0007, 0.0057)			
1996W	-0.0006 (-0.0026, 0.0012)	0.0025 (0.0000, 0.0053)		
2001H	0.0020 (-0.0019, 0.0065)	0.0010 (-0.0023, 0.0043)	0.0018 (-0.0014, 0.0053)	
2001W	0.0019 (-0.0002, 0.0043)	0.0017 (-0.0006, 0.0043)	0.0009 (-0.0012, 0.0030)	0.0046 (0.0005, 0.0090)

Genetic migration rate

Table 6 Estimated number of migrants per generation between the hatchery and spawning grounds

	Fst	Nm
1996 H and W	0.0025	100
2001 H and W	0.0046	54

Note 2 $F_{st} = 1 / (4Nm + 1)$

Population Structure

Table 7 Numbers of pairs of loci out of linkage equilibrium, H-hatchery origin, W-natural origin, A and C- spawning grounds, in 1985 B – fishery, and in 2001 B- broodstock. See Figure 5 to Figure 8 for results for specific markers.

	P > 0.05	P < 0.05	P < 0.01	P < 0.001
<i>Allozymes</i>				
1987	419	15	1	0
1988	424	10	0	1
1996 All	417	10	6	2
1996H	422	7	5	1
1996W	418	15	2	0
2001 All	425	8	2	0
2001H	423	9	3	0
2001W	428	6	1	0
<i>Microsatellites</i>				
1980	114	4	2	0
1983	28	0	0	0
1984	112	0	0	0
1985 All	112	4	2	2
1985A	120	0	0	0
1985B	113	5	2	0
1985C	114	5	1	0
1987	113	7	0	0
1988 All	101	16	2	1
1988A	120	0	0	0
1988B	105	0	0	0
1996 All	110	5	3	2
1996H	102	11	3	4
1996W	119	0	1	0
2001 All	110	8	1	1
2001H	112	7	1	0
2001W	112	6	2	0
2001A	111	6	3	0
2001B	103	12	5	0

Population Structure

Table 8 Results of STRUCTURE analysis for 1988 fish (16) and 1996 hatchery origin fish (48). User inputs number of clusters to test and STRUCTURE divides individuals among that number of clusters to maximize Hardy-Weinberg equilibrium and linkage equilibrium. Models with the maximum likelihood (closest to zero for negative numbers) are most consistent with the data.

	No. Clusters	Likelihood	Cluster 1	Cluster 2	Cluster 3
1988	1	-889.1	16	-	-
	2	-976.6	13	3	-
	3	-943.1	13	3	0
1996 H	1	-3077.5	48	-	-
	2	-3061.6	41	7	-
	3	-3446.5	37	11	0

Note 3 The likelihood is the average of three simulations

Table 9a 1996 broodstock in second cluster as indicated by computer program STRUCTURE, * indicates possible siblings.

	Origin	Age	Length (cm)	Sex
96EB0018*	H	3	77	F
96EB0051	H	-	97	F
96EB0075*	H	-	73	F
96EB0076*	H	3	75	F
96EB0079	H	-	71	M
96EB0083*	H	3	75	F
96EB0086	H	-	71	M

Table 9b Genotypes of apparent siblings from 1996 broodstock

Individual	Ocl-1	Ogo-2	Ogo-4	One-114	One-13M	One-6	One-8	Ots-1	Ots-100	Ots-101	Ots-107	Ots-108	Ots-2M	Ots-3M	Ots-G474	Ssa-197
96EB0018	160/164	221/221	132/137	???	229/189	205/201	166/180	???	295/305	214/153	???	???	156/152	149/151	181/157	255/150
96EB0075	164/164	227/221	132/161	350/285	229/189	205/205	159/166	188/192	295/305	222/153	232/232	96/105	156/133	136/145	165/157	259/171
96EB0076	164/164	221/221	137/151	350/285	229/189	205/205	159/166	192/192	295/305	214/153	228/232	105/125	152/133	136/149	169/165	171/150
96EB0083	160/164	221/221	151/161	350/281	191/189	???	166/180	???	295/327	222/206	196/232	96/105	133/133	149/151	165/157	255/150

Table 10 1988 individuals in second cluster as indicated by computer program STRUCTURE.

	Origin	Age	Length (cm)	Sex
88QN0010	N	4	90	F
88QN0018	N	5	94	F
88QN0020	N	-	86	F

Strays

Table 11 Coded wire tagged fish originating outside the North Fork Stillaguamish River observed on the spawning grounds or in the broodstock between 1989 and 1997. PSMFC database.

Return Year	Broodstock	Spawning Grounds	Stock
1989		1	BY 1985 Marblemount Hatchery spring chinook
		1	BY 1986 Capitol Lake fall chinook
1994	4		BY 1990 Marblemount Hatchery spring chinook
1996		2	BY 1993 Tulalip spring chinook
	1		BY 1992 Kendall Hatchery spring chinook
1997	3	1	BY 1993 Tulalip spring chinook
	1	1	BY 1993 Kendall Hatchery spring chinook
	1		BY 1994 Kendall Hatchery spring chinook
	1		BY 1994 Marblemount Hatchery spring chinook

Parentage Assignment

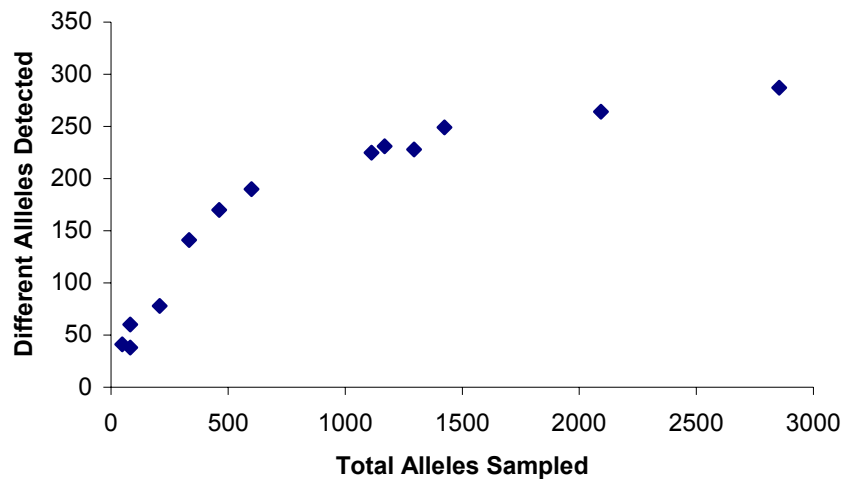
Table 12 Parentage assignment of 2001 returns to 1996 broodstock parents using 16 microsatellite loci. Assignments were made using the program CERVUS. Matches were supported at all loci.

Offspring	Sex/ Origin	Father	Origin	Age/Length (cm)	Mother	Origin	Age/Length (cm)
01DY0002	F/H	96EB0092	N	-/68	96EB0072	H	4/84
01DY0003	F/H	96EB0079	H	-/71	96EB0082	N	-/88
01DY0017	M/H	Unknown			96EB0025	N	-/90
01DY0056	F/H	96EB0045	N	-/90	96EB0033	N	-/87
01DY0081	F/H	96EB0008	H	-/66	96EB0030	H	-/72

Different Types of Alleles and Private Alleles Per Sample

Table 13 Number of different types of alleles and private alleles (alleles seen in no other sample) detected within each sample at 16 microsatellite loci in groups of chinook from the Stillaguamish River between 1983 and 2001.

		Alleles sampled	Different alleles detected	Private alleles
1983		48	41	5
1984		82	60	0
1985	1985A	600	190	1
	1985B	462	170	3
	1985C	1168	231	7
1987		2092	264	5
1988	1988A	334	141	5
	1988B	82	38	1
1996	1996HA	1112	255	2
	1996HB	208	78	0
	1996W	1424	249	6
2001	2001H	1294	228	2
	2001W	2854	287	16
	2001U	262	129	1



Allele sampling for 16 microsatellite loci in Stillaguamish River chinook salmon collected between 1980 and 2001.

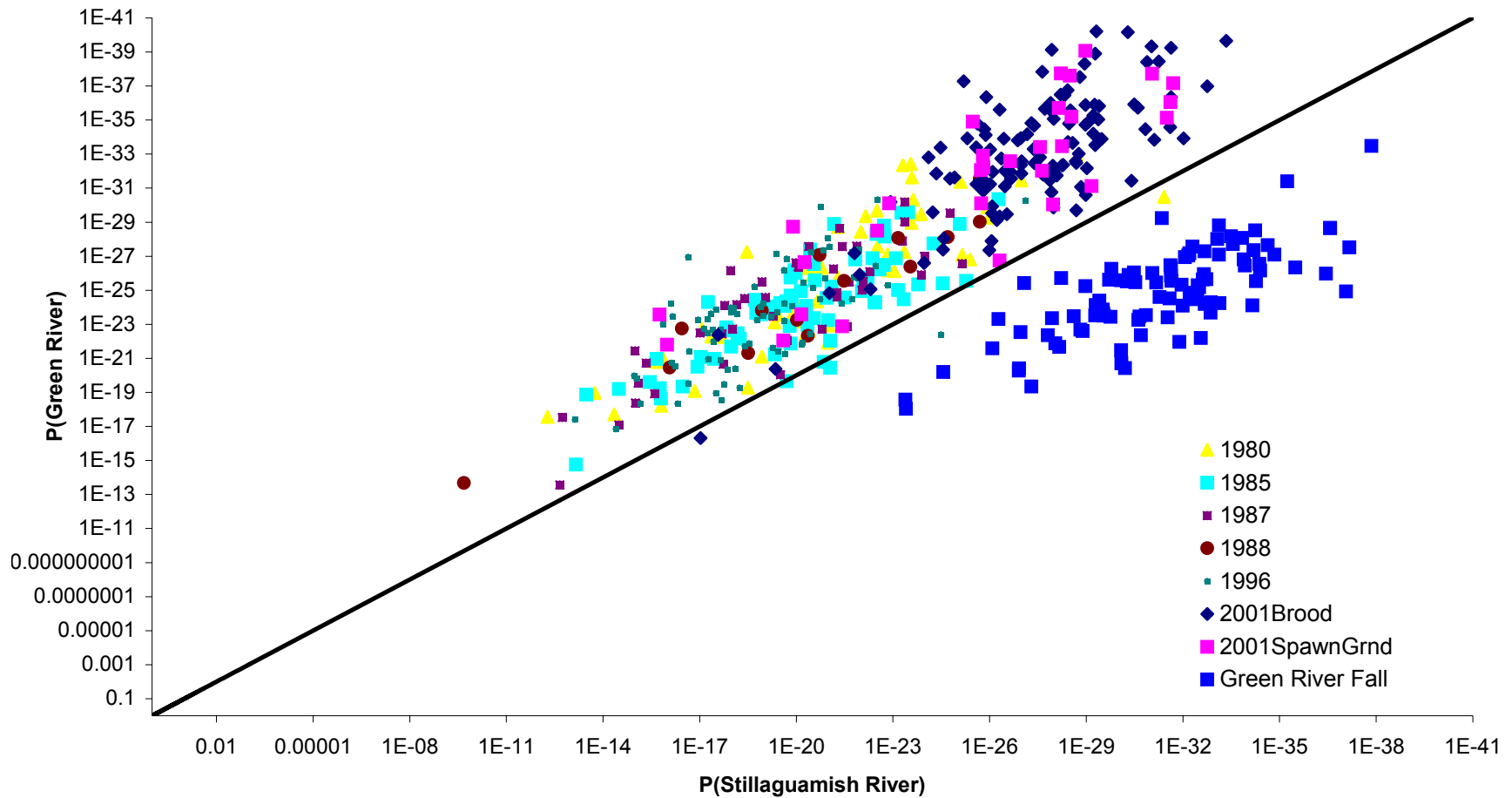


Figure 2 Assignment probabilities for chinook salmon from the Stillaguamsih River and Green River (reared at the WDFW Kendall Creek Hatchery on the North Fork Nooksack River) based on sixteen microsatellite loci. Points above line are more likely Stillaguamish River origin and points below line are more likely Green River origin. The 2001 brood was used as the genetic baseline for Stillaguamish River chinook (WHICHRUN).

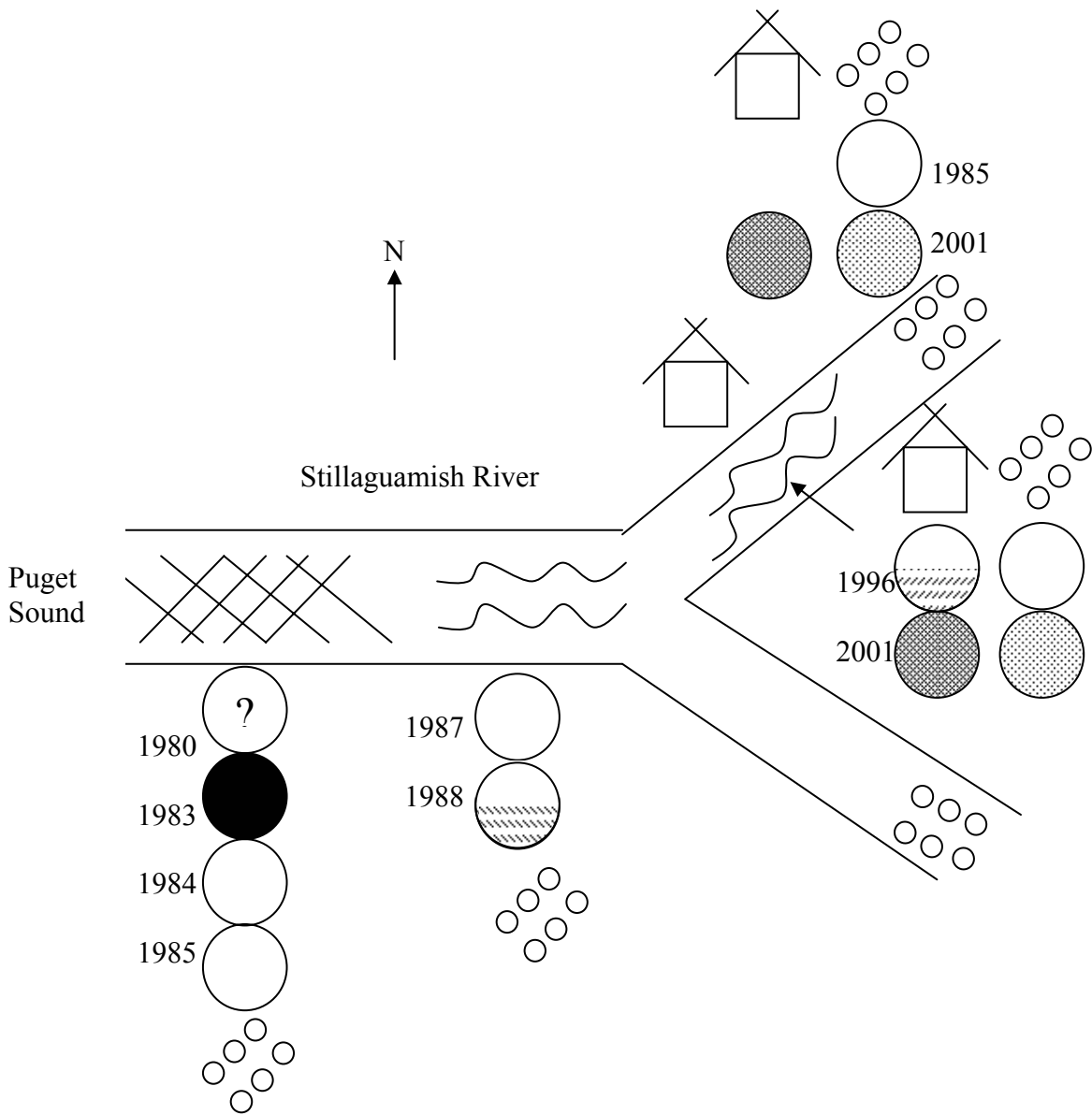


Figure 3 Relationship among chinook salmon returning to the Stillaguamish River between 1980 and 2001 as indicated by pair-wise F_{st} . Circle location indicates approximate location within the river the sample was collected, House indicates hatchery origin and cobble indicates natural origin. Like colored circles are most similar. Fish in 1984, 1985, 1987, and natural origin fish in 1996 were most similar to each other. Fish in 1980 could not be compared because of apparent DNA degradation. Two fish were sampled in 1983 that were probably not from the North Fork Stillaguamish River based on genetic differences. The 1988 broodstock and 1996 hatchery origin fish may have included individuals from the North Fork Stillaguamish River and another group of unknown origin. The 2001 hatchery origin and natural origin fish were genetically different from each other, but both groups were similar to earlier returns. See Tables 1 and 2 for samples size information.

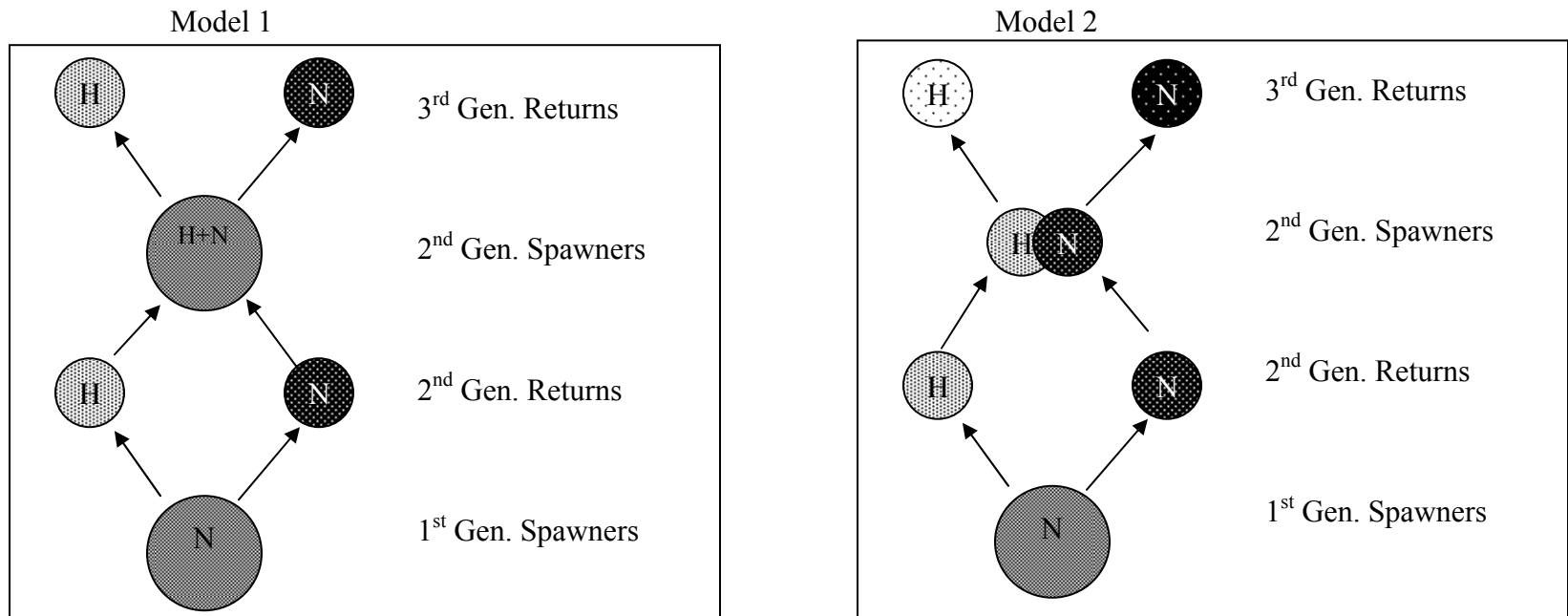


Figure 4 Alternative models for the distribution of genetic diversity as it progresses through Hatchery (H) and Natural (N) components. Under model 1, complete gene flow, hatchery and natural components are integrated during spawning. Hatchery origin parents are equally productive in the hatchery and on the spawning grounds, and similarly for natural origin parents. Under model 2, restricted gene flow or divergent selection, hatchery and natural components are weakly isolated during spawning. Hatchery origin parents are more productive in the hatchery than on the spawning grounds, and vice versa for natural origin parents. Under model 2 reproductively isolated groups will diverge genetically due to genetic drift.

Appendix

Table 14 Allozyme heterozygosity for polymorphic allozyme loci. Deviations from Hardy Weinberg equilibrium indicated by * $P < 0.05$ or ** $P < 0.01$.

<i>Marker</i>	<i>Year</i>							
	1987		1988		1996		2001	
	Obs. Hz	Exp. Hz	Obs. Hz	Exp. Hz	Obs. Hz	Exp. Hz	Obs. Hz	Exp. Hz
<i>mAAT1</i>	0.229	0.305	0.361	0.383	0.276	0.323	0.298	0.323
<i>mAAT2</i>	0.243	0.264	0.206	0.187	0.320	0.322	0.286	0.288
<i>sAAT2</i>	0.086	0.131*	0.139	0.128	0.111	0.136	0.096	0.106
<i>SAAT3</i>	0.061	0.058	0.167	0.194	0.094	0.089	0.092	0.087
<i>sAAT4</i>	0.134	0.124	0.194	0.176	0.107	0.133	0.048	0.065
<i>ADA1</i>	0.286	0.243	0.306	0.325	0.243	0.240	0.157	0.158
<i>ADA2</i>	0.071	0.068	0.083	0.079	0.074	0.071	0.061	0.059
<i>mAH4</i>	0.157	0.144	0.056	0.053	0.113	0.106	0.078	0.075
<i>sAH</i>	0.329	0.309	0.278	0.240	0.420	0.407	0.322	0.354
<i>FDHG</i>	0	0	0	0	0	0	0.017	0.017
<i>GPIA</i>	0.086	0.082	0.139	0.128	0.068	0.086	0.096	0.091
<i>GPIB2</i>	0	0	0	0	0.010	0.010	0.044	0.043
<i>GPIr</i>	0	0.028**	0	0.053*	0	0.021**	0	0
<i>GR</i>	0.014	0.014	0.056	0.053	0.019	0.018	0	0
<i>sIDHP1</i>	0.100	0.095	0.028	0.027	0.120	0.114	0.070	0.067
<i>sIDHP2</i>	0.114	0.107	0.056	0.053	0.150	0.153	0.061	0.059
<i>LDHC</i>	0.064	0.061	0.056	0.053	0.069	0.067	0.011	0.010
<i>sMDHB2</i>	0.057	0.055	0.111	0.105	0.074	0.080*	0.078	0.075
<i>sMEP1</i>	0.543	0.457	0.583	0.486	0.505	0.500	0.439	0.473
<i>MPI</i>	0.386	0.451	0.361	0.407	0.406	0.421	0.456	0.407
<i>PEPA</i>	0.029	0.028	0	0	0.047	0.046	0.026	0.026
<i>PEPB1</i>	0.500	0.443	0.417	0.407	0.574	0.455**	0.583	0.469*
<i>PEPD2</i>	0	0	0	0	0	0	0.009	0.009
<i>PEPLT</i>	0.029	0.028	0.083	0.079	0.022	0.021	0.061	0.059
<i>PGK2</i>	0.557	0.489	0.417	0.488	0.470	0.471	0.368	0.467*
<i>PGMI</i>	0	0	0	0	0.028	0.028	0	0
<i>sSOD1</i>	0.386	0.405	0.417	0.336	0.417	0.377	0.426	0.444
<i>sSOD2</i>	0.329	0.342	0.177	0.204	0.404	0.376	0.295	0.356
<i>TPI3</i>	0.043	0.042	0.028	0.027	0.037	0.036	0	0
<i>TPI4</i>	0.100	0.094	0.083	0.079	0.056	0.054	0.087	0.083
Average	0.164	0.162	0.160	0.158	0.174	0.172	0.152	0.156

Note 4 No individuals were heterozygous at the GPIr locus. Three individuals were homozygous for the rare allele, one in each of the three samples out of HWE. All other individuals were homozygous for the common allele. .

Table 15 Microsatellite heterozygosity, deviations from Hardy-Weinberg equilibrium indicated by * P < 0.05, ** P < 0.01, *** P < 0.001.

Marker	Year													
	1983		1984		1985		1987		1988		1996		2001	
	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.
<i>Ocl-1</i>	1.000	0.250	1.000	0.660	0.781	0.780	0.830	0.797	0.786	0.761	0.816	0.805	0.852	0.799
<i>Ogo-2</i>	1.000	0.250	1.000	0.563	0.783	0.805	0.773	0.755	0.800	0.808*	0.740	0.770	0.758	0.785
<i>Ogo-4</i>	1.000	0.250	0.500	0.391	0.764	0.799	0.768	0.788	0.750	0.797**	0.781	0.779	0.777	0.794
<i>One-114</i>	1.000	0.250	0.500	0.281	0.818	0.936*	0.836	0.920	0.786	0.877*	0.954	0.938	0.922	0.938*
<i>One-13M</i>	1.000	0.563	1.000	0.626	0.920	0.883	0.884	0.897	0.700	0.780	0.785	0.849	0.911	0.885
<i>One-6</i>	0.000	0.000	0.333	0.232	0.212	0.253	0.279	0.248	0.200	0.162	0.219	0.197	0.184	0.185
<i>One-8</i>	1.000	0.250	0.500	0.281	0.887	0.850	0.841	0.824	0.600	0.704*	0.832	0.846	0.812	0.832
<i>Ots-1</i>	0.000	0.250	1.000	0.560	0.487	0.486	0.515	0.598***	0.643	0.614	0.621	0.621	0.619	0.628
<i>Ots-100</i>	0.500	0.391	1.000	0.660	0.986	0.955	0.924	0.948	1.000	0.845	0.938	0.955*	0.964	0.959
<i>Ots-101</i>	1.000	0.563	1.000	0.694	0.920	0.934	0.954	0.928	0.867	0.872*	0.968	0.943	0.964	0.938
<i>Ots-107</i>	0.500	0.391	1.000	0.694	0.973	0.937	0.941	0.930	0.923	0.837	0.829	0.927*	0.942	0.921
<i>Ots-108</i>	0.000	0.000	1.000	0.563	0.873	0.918	0.923	0.913*	0.833	0.829	0.857	0.906	0.905	0.920
<i>Ots-2M</i>	1.000	0.563	1.000	0.563	0.865	0.869	0.866	0.884**	0.500	0.841***	0.870	0.898	0.906	0.883
<i>Ots-3M</i>	1.000	0.521	1.000	0.626	0.784	0.787	0.803	0.797	0.813	0.775*	0.798	0.800	0.836	0.834*
<i>Ots-G474</i>	1.000	0.563	0.667	0.498	0.680	0.694	0.696	0.736*	0.636	0.730	0.798	0.751	0.659	0.723
<i>Ssa-197</i>	1.000	0.250	0.500	0.391	0.800	0.933**	0.887	0.912	0.933	0.883	0.969	0.935	0.907	0.929
Average	0.750	0.331	0.813	0.518	0.783	0.801	0.795	0.805	0.736	0.757	0.798	0.808	0.807	0.810

Tests for population subdivision: All years

Table 16 Global tests for population subdivision among all samples.

All years	Allozymes	Microsatellites
Exact Test	0.0623	0.0000
G-Test	0.9996	0.0000

Table 17 Allozyme pair-wise exact test P-values

All years	1987	1988	1996
1988	.63206		
1996	.99801	.41029	
2001	.43188	.16208	.15404

Table 18 Allozyme pair-wise G-test P-values

All years	1987	1988	1996
1988	0.70611		
1996	0.99382	0.44993	
2001	0.45519	0.17593	0.21568

Table 19 Allozyme pair-wise Fst values and 95% confidence intervals.

All years	1987	1988	1996
1988	0.0002 (-0.0041, 0.0055)		
1996	-0.0016 (-0.0038, 0.0010)	0.0062 (-0.0019, 0.0157)	
2001	-0.0007 (-0.0029, 0.0018)	0.0078 (0.0014, 0.0153)	0.0012 (-0.0018, 0.0048)

Table 20 Microsatellite pair-wise exact test P-values, only samples with more than 10 individuals were compared.

All years	1985	1987	1988	1996
1987	0.00756			
1988	0.00002	0.00000		
1996	0.00050	0.07943	0.00000	
2001	0.00000	0.00129	0.00000	0.01924

Table 21 Microsatellite pair-wise G-test P-values, only samples with more than 10 individuals were compared.

All years	1985	1987	1988	1996
1987	0.06047			
1988	0.00008	0.00065		
1996	0.00204	0.1282	0.00002	
2001	0.00000	0.00449	0.00000	0.01844

Table 22 Microsatellite pair-wise Fst values and 95% confidence intervals only samples with more than 10 individuals were compared.

All years	1985	1987	1988	1996
1987	0.0026 (0.0000, 0.0055)			
1988	0.0110 (0.0036, 0.0187)	0.0055 (-0.0001, 0.0108)		
1996	0.0029 (0.0003, 0.0056)	0.0002 (-0.0015, 0.0018)	0.0076 (0.0019, 0.00130)	
2001	0.0041 (0.0022, 0.0068)	0.0012 (-0.0002, 0.0027)	0.0086 (0.0018, 0.0167)	0.0000 (-0.0011, 0.0010)

Tests for population subdivision: Hatchery vs. wild

Table 23 Allozyme pair-wise exact test P-values.

H v. W	1987	1988	1996H	1996W	2001H
1988	0.63265				
1996H	0.99809	0.28731			
1996W	0.56607	0.41773	0.61451		
2001H	0.94565	0.88381	0.79790	0.96919	
2001W	0.58643	0.45101	0.26890	0.37705	0.98030

Table 24 Allozyme pair-wise G-test P-values.

H v. W	1987	1988	1996H	1996W	2001H
1988	0.69205				
1996H	0.99939	0.31821			
1996W	0.50747	0.40283	0.75843		
2001H	0.91291	0.91261	0.79262	0.95004	
2001W	0.58136	0.47651	0.43521	0.47044	0.94984

Table 25 Allozyme pair-wise Fst values and 95% confidence intervals.

H v. W	1987	1988	1996H	1996W	2001H
1988	0.0002 (-0.0039, 0.0054)				
1996H	-0.0046 (-0.0064, -0.0025)	0.0045 (-0.0048, 0.0163)			
1996W	0.0049 (-0.0036, 0.0180)	0.0117 (-0.0039, 0.0356)	0.0059 (-0.0049, 0.0210)		
2001H	-0.0048 (-0.0074, -0.0017)	0.0033 (-0.0038, 0.0106)	-0.0036 (-0.0074, 0.0012)	0.0003 (-0.0075, 0.0088)	
2001W	-0.0005 (-0.0034, 0.0028)	0.0080 (0.0003, 0.0175)	0.0015 (-0.0032, 0.0070)	0.0055 (-0.0025, 0.0158)	-0.0050 (-0.0087, 0.0007)

Table 26 Microsatellite pair-wise exact test P-values, only samples with more than 10 individuals were compared.

H v. W	1985A	1985B	1985C	1987	1988	1996H	1996W	2001H
1985B	0.08501							
1985C	0.37397	0.01154						
1987	0.00481	0.10807	0.00276					
1988	0.00874	0.00720	0.00001	0.00001				
1996H	0.00011	0.00000	0.00001	0.00003	0.00000			
1996W	0.38324	0.13365	0.15856	0.67242	0.00023	0.00037		
2001H	0.00000	0.00053	0.00000	0.00000	0.00004	0.00625	0.00659	
2001W	0.00196	0.00861	0.00003	0.01165	0.00003	0.00816	0.04399	0.00028

Table 27 Microsatellite pair-wise G-test P-values, only samples with more than 10 individuals were compared.

H v. W	1985A	1985B	1985C	1987	1988	1996H	1996W	2001H
1985B	0.07062							
1985C	0.70910	0.03304						
1987	0.07714	0.26227	0.02388					
1988	0.03726	0.06945	0.00026	0.00066				
1996H	0.00024	0.00025	0.00003	0.00015	0.00000			
1996W	0.64781	0.22833	0.18234	0.60873	0.00166	0.00042		
2001H	0.00282	0.00143	0.00001	0.00031	0.00017	0.00419	0.00384	
2001W	0.02048	0.01895	0.00004	0.01779	0.00020	0.00538	0.03813	0.00032

Tests for population subdivision: Within Year Comparisons

1985

Table 28 Microsatellite global test for population structure among 1985 samples.

1985	Microsatellites
Exact test	0.0420
G-Test	0.1213

Table 29 Microsatellite pair-wise exact test P-values

1985	1985A	1985B
1985B	0.08368	
1985C	0.37871	0.01024

Table 30 Microsatellite pair-wise G-test P-values.

1985	1985A	1985B
1985B	0.07027	
1985C	0.69011	0.03965

Table 31 Microsatellite pair-wise Fst values and 95% confidence intervals.

1985	1985A	1985B
1985B	0.0035 (-0.0035, 0.0102)	
1985C	0.0008 (-0.0049, 0.0079)	0.0052 (-0.0012, 0.0114)

Tests for population subdivision: 1988

Used computer program STRUCTURE to assign 16 individuals from 1988 broodstock into two most likely groups (88A- 13 individuals, 88B- 3 individuals (88QN0010, 88QN0018, 88QN0020))

Table 32 Global test for population subdivision among 1988 samples.

1988	Microsatellites
Exact test	0.0000
G-Test	0.0000

Table 33 Microsatellite pair-wise exact test P-Values of two 1988 groups and 1987 sample.

1988	1987	1988A
1988A	0.00083	
1988B	0.00000	0.00001

Table 34 Microsatellite pair-wise G-test P-values of two 1988 groups and 1987.

1988	1987	1988A
1988A	0.01397	
1988B	0.0000	0.00051

Table 35 Microsatellite pair-wise Fst and 95% confidence intervals of two 1988 groups and 1987.

1988	1987	1988A
1988A	0.0016 (-0.0043, 0.0080)	
1988B	0.1129 (0.0606, 0.1756)	0.1157 (0.0543, 0.1821)

Tests for population subdivision: 1996

Used computer program STRUCTURE to assign 48 hatchery origin individuals from 1996 broodstock into two most likely groups (1996HA- 41 individuals 1996HB- 7 individuals (96EB18, 51, 75, 76, 79, 83, 86)).

Table 36 Global tests for population structure

1996	Microsatellite
Exact Test	0.0000
G-Test	0.0000

Table 37 Microsatellite pair-wise exact test P-values

1996	1996HA	1996HB
1996HB	0.00000	
1996W	0.01121	0.00000

Table 38 Microsatellite pair-wise G-Test P-values

1996	1996HA	1996HB
1996HB	0.00000	
1996W	0.01957	0.00000

Table 39 Microsatellite pair-wise Fst values and 95% confidence intervals

1996	1996HA	1996HB
1996HB	0.0556 (0.0309, 0.0794)	
1996W	0.0018 (-0.0015, 0.0054)	0.0557 (0.0334, 0.0777)

Suspect Microsatellite Heterozygosity from 1980

Table 40 Microsatellite heterozygosity within suspect 1980 sample, deviations from Hardy-Weinberg equilibrium indicated by * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.

Marker	1980	
	Obs.	Exp.
<i>Ocl-1</i>	0.779	0.784
<i>Ogo-2</i>	0.828	0.790*
<i>Ogo-4</i>	0.838	0.789
<i>One-114</i>	0.737	0.918***
<i>One-13M</i>	0.686	0.862***
<i>One-6</i>	0.121	0.262**
<i>One-8</i>	0.792	0.844
<i>Ots-1</i>	0.433	0.353
<i>Ots-100</i>	0.882	0.948*
<i>Ots-101</i>	0.879	0.906**
<i>Ots-107</i>	0.818	0.910***
<i>Ots-108</i>	0.917	0.903
<i>Ots-2M</i>	0.875	0.874**
<i>Ots-3M</i>	0.855	0.745
<i>Ots-G474</i>	0.786	0.686
<i>Ssa-197</i>	0.875	0.936***
Average	0.756	0.782

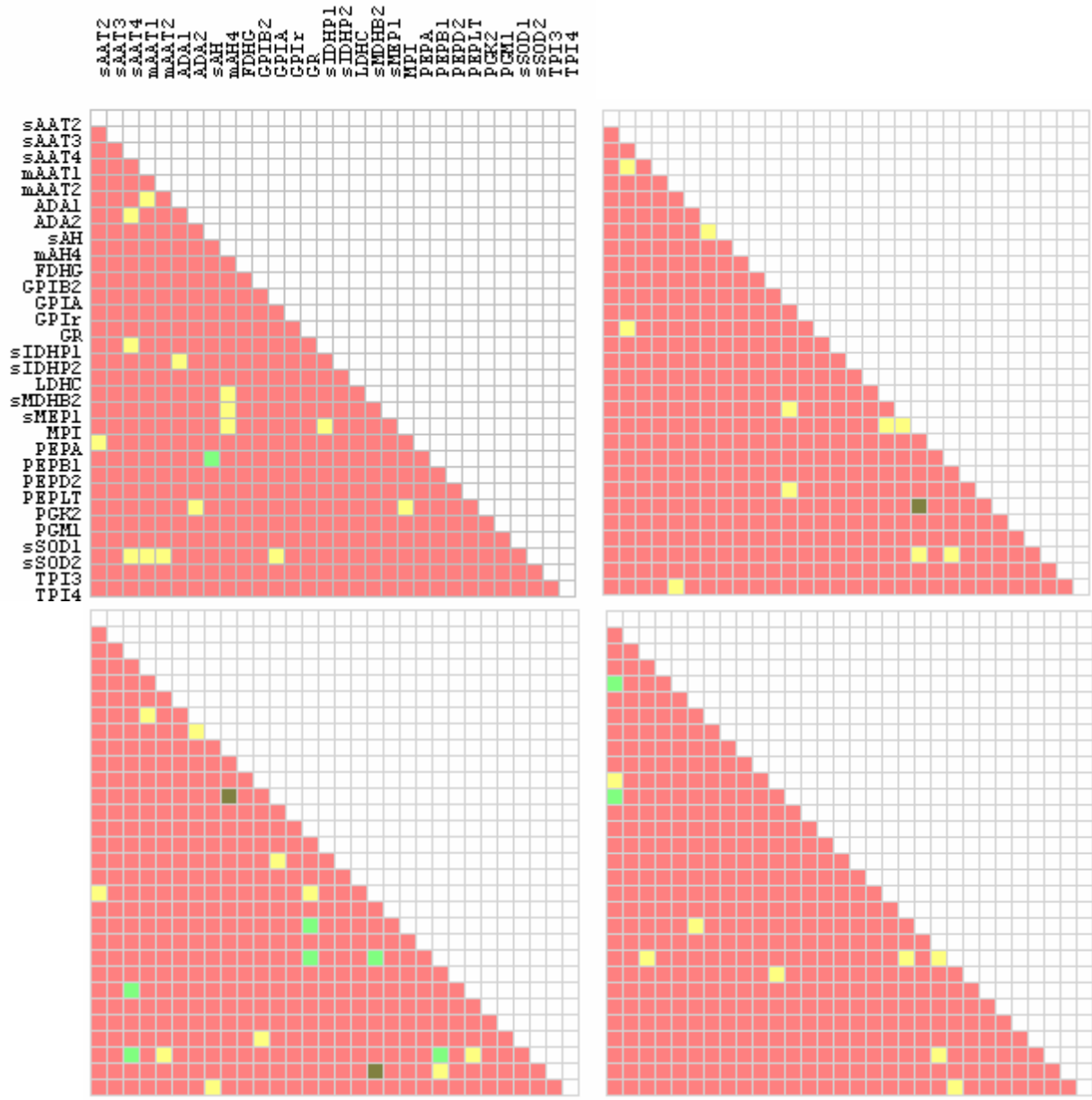


Figure 5. Allozyme linkage disequilibrium in northfork Stillaguamish summer chinook salmon. Exact Test p-values, red: $p > 0.05$, Yellow: $p < 0.05$, light green: $p < 0.01$, dark green: $p < 0.001$. Clockwise from top left: 1987, 1988, 2001 and 1996.

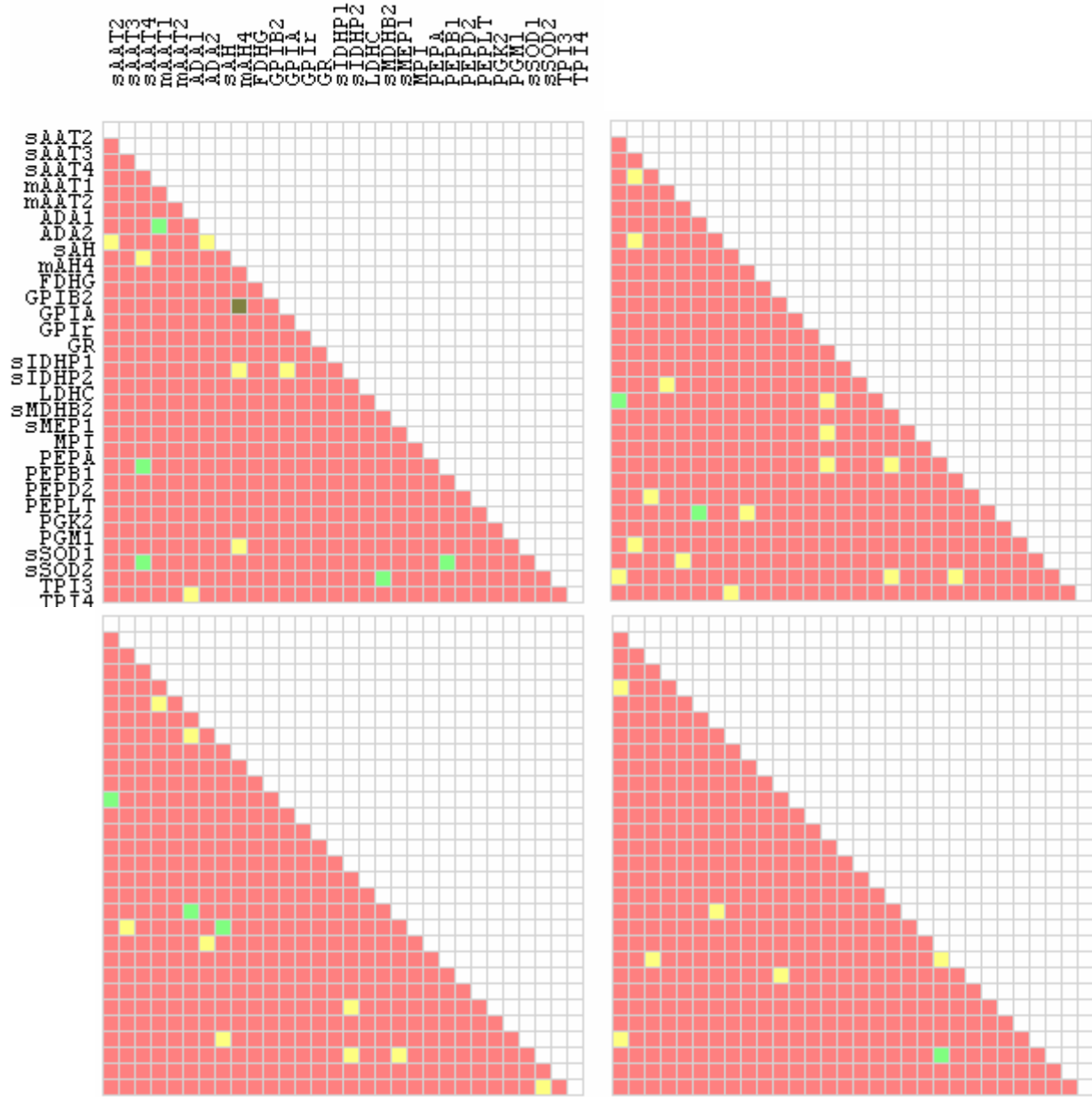


Figure 6. Allozyme linkage disequilibrium in northfork Stillaguamish River summer chinook salmon. Exact Test p-values, red: $p > 0.05$, Yellow: $p < 0.05$, light green: $p < 0.01$, dark green: $p < 0.001$. Clockwise from top left: 1996 hatchery, 1996 wild, 2001 wild and 2001 hatchery.



Figure 7. Microsatellite linkage disequilibrium in northfork Stillaguamish River summer chinook salmon. Exact Test p-values, red: $p > 0.05$, yellow: $p < 0.05$, light green: $p < 0.01$, dark green: $p < 0.001$, white not tested. Clockwise from top left: 1985, 2001, 1996, 1988 and 1987.

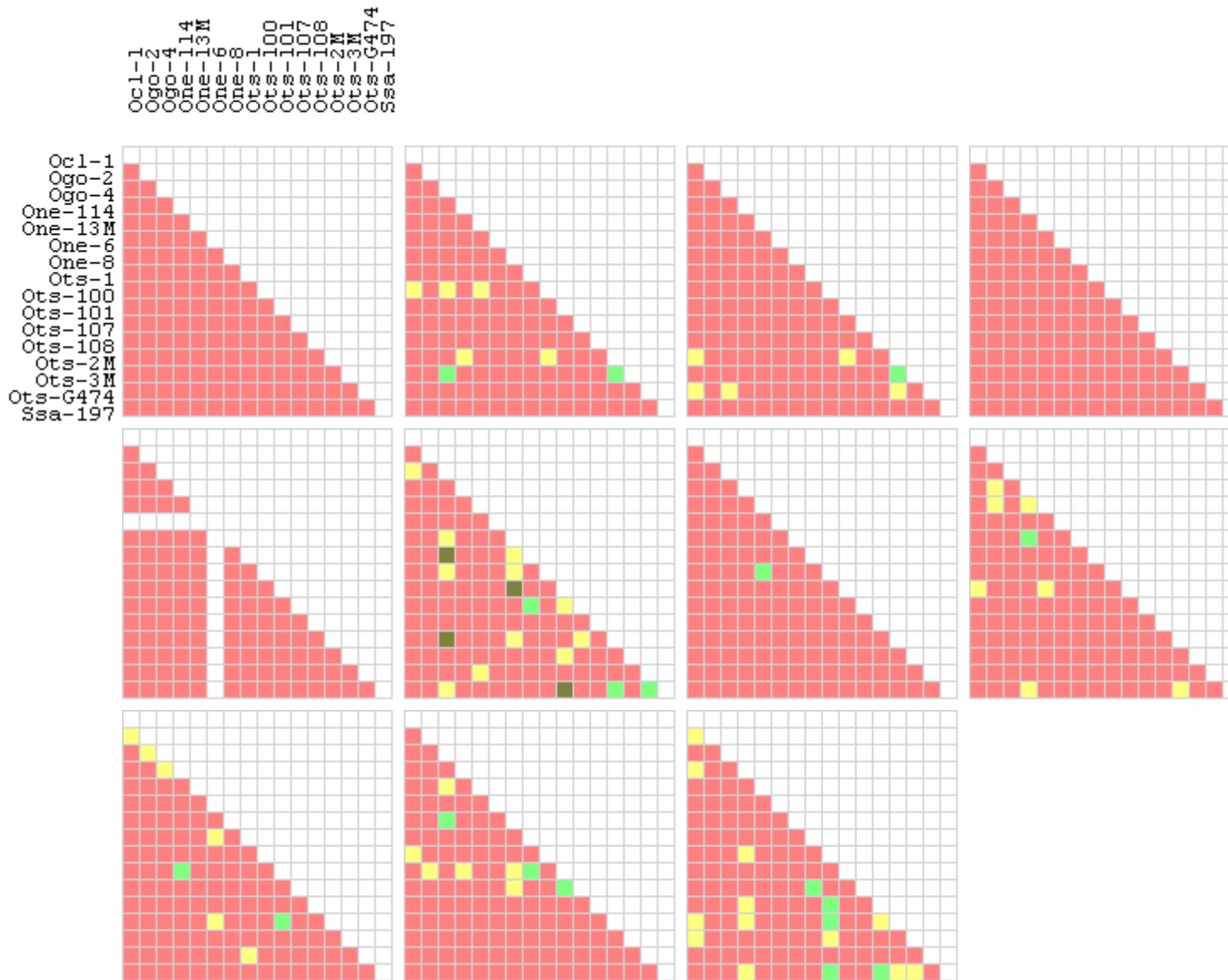


Figure 8 Microsatellite linkage disequilibrium in northfork Stillaguamish River summer chinook salmon. Exact Test p-values, red: $p > 0.05$, Yellow: $p < 0.05$, light green: $p < 0.01$, dark green: $p < 0.001$, white not tested. Left to right from top left: 1985 NF spawning grounds, 1985 fishery, 1985 upper NF spawning grounds, 1988A, 1988B, 1996 hatchery, 1996 wild, 2001 hatchery, 2001 wild, 2001 broodstock, 2001 spawning grounds.

Table 41 Allele frequencies at 16 microsatellite loci in Stillaguamish chinook over time

a- number of different alleles in sample

n- number of individuals scored at the particular locus

N- number of individuals sampled

Marker	Allele	1980	1983	1984	1985	1987	1988	1996	2001
Ocl-1	147	0	0	0	0	0	0	0.0051	0
Ocl-1	152	0.0147	0	0.1667	0.0391	0.0472	0	0.0102	0.0141
Ocl-1	154	0.0294	0	0	0.0313	0.0189	0	0.0051	0.007
Ocl-1	156	0.2059	0.5	0.1667	0.2266	0.0943	0.0357	0.1327	0.1408
Ocl-1	158	0.0956	0	0	0.1094	0.2358	0.3214	0.1837	0.1725
Ocl-1	160	0.2647	0.5	0.3333	0.3281	0.2642	0.25	0.25	0.2887
Ocl-1	162	0.0662	0	0.1667	0.0469	0.0849	0.1071	0.0765	0.0458
Ocl-1	164	0.2868	0	0	0.1953	0.2264	0.1429	0.2602	0.2465
Ocl-1	166	0.0074	0	0.1667	0.0078	0	0	0.0561	0.0141
Ocl-1	168	0	0	0	0	0	0	0	0.0035
Ocl-1	170	0.0074	0	0	0.0156	0.0189	0.0714	0.0051	0.0317
Ocl-1	174	0.0221	0	0	0	0.0094	0.0714	0.0153	0.0352
	a	10	2	5	9	9	7	11	11
	n	70	2	3	75	69	10	93	135
	N	74	2	3	75	69	16	99	142

Marker	Allele	1980	1983	1984	1985	1987	1988	1996	2001
Ogo-2	207	0	0	0	0	0	0	0	0.0114
Ogo-2	211	0.0234	0	0	0.0145	0.0152	0.0333	0.0205	0.0189
Ogo-2	213	0.0078	0	0	0.0145	0.0152	0	0.0137	0.0152
Ogo-2	215	0.1484	0	0.25	0.1522	0.1439	0.1667	0.1301	0.0871
Ogo-2	217	0.0234	0	0	0.0725	0.0455	0.0333	0.0479	0.0682
Ogo-2	219	0.2344	0.5	0.25	0.2681	0.2273	0.2333	0.2055	0.2311
Ogo-2	221	0.3203	0	0.25	0.2681	0.3788	0.2	0.3767	0.3598
Ogo-2	223	0.0156	0	0.25	0.0362	0.0076	0.0667	0.0274	0.0417
Ogo-2	225	0.0078	0	0	0	0.0076	0	0.0137	0.0114
Ogo-2	227	0.1484	0.5	0	0.1159	0.1439	0.1667	0.137	0.1174
Ogo-2	229	0	0	0	0.0145	0	0	0.0068	0.0152
Ogo-2	231	0.0234	0	0	0	0.0076	0	0	0
Ogo-2	233	0.0078	0	0	0.0217	0	0.0333	0	0.0038
Ogo-2	235	0.0234	0	0	0.0217	0	0	0.0205	0.0114
Ogo-2	237	0.0156	0	0	0	0.0076	0	0	0.0076
Ogo-2	255	0	0	0	0	0	0.0667	0	0
	a	13	2	4	11	11	9	11	14
	n	64	1	2	69	66	15	73	132
	N	74	2	3	75	69	16	99	142

Marker	Allele	1980	1983	1984	1985	1987	1988	1996	2001
Ogo-4	126	0	0	0	0	0	0.0625	0	0
Ogo-4	132	0.3108	0.5	0.5	0.2986	0.2971	0.25	0.2344	0.2698
Ogo-4	137	0.2162	0	0.25	0.1875	0.2754	0.2813	0.3177	0.2914
Ogo-4	139	0.0878	0	0	0.0278	0.0362	0.0625	0.0365	0.0396
Ogo-4	141	0	0	0	0	0	0	0	0.0072
Ogo-4	143	0	0	0	0	0.0072	0	0	0.0072
Ogo-4	151	0.0135	0	0	0.0694	0.0217	0.0938	0.0573	0.054
Ogo-4	153	0.0068	0	0	0.0069	0.0217	0	0.026	0.0216
Ogo-4	155	0	0	0	0.0069	0	0	0	0
Ogo-4	157	0.0203	0	0	0.0069	0.0072	0	0	0.0108
Ogo-4	159	0.0135	0	0	0.0278	0.0217	0.0938	0.0052	0.018
Ogo-4	161	0.2162	0.5	0.25	0.2222	0.1594	0.0625	0.224	0.1835
Ogo-4	163	0.0405	0	0	0.0278	0.0435	0.0313	0.0365	0.018
Ogo-4	167	0.0743	0	0	0.1181	0.1087	0.0313	0.0625	0.0791
Ogo-4	171	0	0	0	0	0	0.0313	0	0
	a	10	2	3	11	11	10	9	12
	n	74	1	2	72	69	16	96	139
	N	74	2	3	75	69	16	99	142

Marker	Allele	1980	1983	1984	1985	1987	1988	1996	2001
One-114	233	0	0	0	0	0	0	0.0057	0.0035
One-114	237	0	0	0	0.0227	0	0	0.0115	0.0035
One-114	241	0	0	0	0	0	0	0.0057	0.0035
One-114	245	0	0	0	0	0	0.0714	0	0.0035
One-114	249	0	0	0	0	0	0.0714	0	0
One-114	253	0	0	0	0.0076	0	0	0.0115	0.0035
One-114	257	0	0	0	0.0076	0.0075	0	0.0057	0.0071
One-114	261	0	0	0	0	0.0075	0	0.0172	0.0142
One-114	265	0.0175	0	0	0.0227	0.0149	0	0.0057	0.0035
One-114	269	0.0351	0.5	0	0.0455	0.0075	0.1429	0.0115	0.0248
One-114	273	0.0702	0	0	0.0455	0.0075	0.0714	0.0172	0.0816
One-114	277	0.0351	0	0	0.0303	0.0522	0	0.0632	0.0745
One-114	281	0.1053	0	0	0.0606	0.0373	0	0.0862	0.0638
One-114	285	0.0789	0	0	0.0833	0.0672	0.0714	0.0517	0.0745
One-114	289	0.114	0	0	0.053	0.1194	0.1071	0.046	0.078
One-114	293	0.114	0	0.25	0.0455	0.0821	0	0.0862	0.0709
One-114	297	0.0439	0.5	0.75	0.0227	0.0746	0.0357	0.046	0.0674
One-114	301	0.0439	0	0	0.0909	0.0821	0.0357	0.046	0.0603
One-114	305	0.0702	0	0	0.0682	0.0746	0.0714	0.1149	0.0993
One-114	310	0.0526	0	0	0.0909	0.0448	0.0714	0.0345	0.0177
One-114	314	0.0526	0	0	0.0682	0.1194	0.0357	0.0632	0.039
One-114	318	0.0614	0	0	0.053	0.0448	0.1071	0.0345	0.0355
One-114	322	0.0439	0	0	0.053	0.0522	0	0.046	0.0284
One-114	326	0.0263	0	0	0.0152	0.0522	0	0.0632	0.0213
One-114	330	0.0175	0	0	0.0303	0	0.0714	0.0115	0.0426
One-114	334	0	0	0	0.0076	0	0	0	0
One-114	338	0.0088	0	0	0	0.0075	0	0	0
One-114	342	0	0	0	0	0	0	0	0.0035
One-114	346	0	0	0	0.0076	0.0075	0	0.0057	0.0035
One-114	350	0	0	0	0	0	0	0.0172	0.0142
One-114	354	0	0	0	0.0076	0	0	0.0115	0.0035
One-114	358	0.0088	0	0	0.0303	0.0149	0	0.0057	0.0035
One-114	370	0	0	0	0	0.0075	0.0357	0.0115	0
One-114	377	0	0	0	0.0076	0	0	0	0
One-114	393	0	0	0	0.0076	0	0	0	0
One-114	397	0	0	0	0	0	0	0	0.0035
One-114	413	0	0	0	0	0	0	0.0115	0
One-114	433	0	0	0	0	0	0	0	0.0035
One-114	437	0	0	0	0.0076	0.0075	0	0.0057	0.0035
One-114	441	0	0	0	0	0	0	0	0.0035
One-114	445	0	0	0	0	0	0	0.0287	0.0071
One-114	449	0	0	0	0	0	0	0.0057	0.0142
One-114	461	0	0	0	0.0076	0	0	0.0057	0.0071
One-114	469	0	0	0	0	0	0	0	0.0035
One-114	477	0	0	0	0	0.0075	0	0.0057	0

One-114	501	0	0	0	0	0	0	0	0.0035
	a	19	2	2	28	24	14	34	38
	n	57	1	2	66	67	14	87	141
	N	74	2	3	75	69	16	99	142

Marker	Allele	1980	1983	1984	1985	1987	1988	1996	2001
One-13M	179	0.0214	0	0	0.0333	0.0362	0	0.0323	0.0481
One-13M	187	0.1	0	0.1667	0.1533	0.1739	0.1	0.2366	0.163
One-13M	189	0.2071	0.25	0.3333	0.1467	0.1377	0	0.1237	0.1333
One-13M	191	0.1357	0	0	0.12	0.1087	0.3	0.2151	0.1852
One-13M	199	0.1786	0	0.1667	0.08	0.0942	0	0.0968	0.0963
One-13M	201	0	0	0	0	0	0.1	0.0054	0.0111
One-13M	203	0.05	0	0	0.0467	0.0362	0	0.043	0.0481
One-13M	205	0.1286	0.25	0.3333	0.18	0.1087	0.2	0.1183	0.1185
One-13M	207	0.0643	0	0	0.0733	0.0725	0.05	0.0323	0.0519
One-13M	209	0.0357	0.25	0	0.02	0.0435	0.05	0.0108	0.0296
One-13M	211	0	0	0	0	0	0	0	0.0037
One-13M	213	0	0	0	0	0	0.05	0	0
One-13M	215	0.0071	0	0	0.0333	0.0435	0	0.0108	0.0074
One-13M	217	0	0	0	0	0	0	0	0.0037
One-13M	219	0.0071	0	0	0.04	0.0362	0.1	0.0215	0.0148
One-13M	225	0	0	0	0	0	0.05	0	0
One-13M	229	0	0	0	0.0067	0.029	0	0.0215	0.0296
One-13M	235	0.0071	0	0	0	0	0	0	0
One-13M	237	0	0	0	0	0	0	0.0054	0
One-13M	249	0	0	0	0.0067	0	0	0	0.0037
One-13M	251	0	0	0	0	0	0	0	0.0074
One-13M	260	0	0	0	0	0	0	0	0.0037
One-13M	284	0.0429	0	0	0.02	0.0072	0	0	0.0037
One-13M	286	0	0	0	0	0.0072	0	0	0
One-13M	292	0.0071	0	0	0.0067	0.0145	0	0.0161	0.0222
One-13M	304	0	0	0	0.02	0.0072	0	0.0054	0.0074
One-13M	310	0.0071	0.25	0	0.0067	0.0072	0	0.0054	0
One-13M	316	0	0	0	0	0.0145	0	0	0
One-13M	322	0	0	0	0	0.0072	0	0	0
One-13M	328	0	0	0	0.0067	0.0145	0	0	0.0037
One-13M	340	0	0	0	0	0	0	0	0.0037
	a	15	4	4	18	20	9	17	23
	n	70	2	3	75	69	10	93	135
	N	74	2	3	75	69	16	99	142

Marker	Allele	1980	1983	1984	1985	1987	1988	1996	2001
One-6	199	0.0758	0	0.1667	0.0455	0.0588	0	0.0313	0.0074
One-6	201	0.0758	0	0	0.0985	0.0809	0.1	0.0781	0.0956
One-6	205	0.8485	1	0.8333	0.8561	0.8603	0.9	0.8906	0.8971
	a	3	1	2	3	3	2	3	3
	n	33	1	3	66	68	5	32	136
	N	74	2	3	75	69	16	99	142

Marker	Allele	1980	1983	1984	1985	1987	1988	1996	2001
One-8	155	0.0069	0	0	0	0	0	0	0
One-8	157	0	0	0	0.0141	0	0	0	0
One-8	159	0.1667	0	0	0.0915	0.1304	0.1	0.1158	0.1087
One-8	161	0	0	0	0.007	0	0	0	0
One-8	163	0.0208	0.5	0	0.0141	0.0072	0.0333	0.0263	0.0145
One-8	166	0.0208	0	0	0.0282	0.029	0.0667	0.0474	0.0362
One-8	168	0.125	0.5	0	0.0986	0.1377	0	0.0842	0.1304
One-8	170	0.1181	0	0	0.1197	0.0797	0	0.1421	0.2101
One-8	172	0.0903	0	0.75	0.1479	0.1667	0.1	0.1632	0.1377
One-8	174	0.2639	0	0.25	0.2676	0.3043	0.4667	0.2684	0.2609
One-8	176	0.1042	0	0	0.1127	0.058	0.0667	0.0684	0.0543
One-8	178	0	0	0	0	0.0072	0.0333	0.0053	0.0036
One-8	180	0.0347	0	0	0.0211	0.0072	0	0.0263	0.0145
One-8	182	0.0069	0	0	0	0.0145	0	0	0
One-8	184	0	0	0	0.007	0.0072	0	0.0053	0.0036
One-8	186	0.0417	0	0	0.0563	0.0507	0.1333	0.0316	0.0217
One-8	192	0	0	0	0.0141	0	0	0.0158	0.0036
	a	12	2	2	14	13	8	13	13
	n	72	1	2	71	69	15	95	138
	N	74	2	3	75	69	16	99	142

Marker	Allele	1980	1983	1984	1985	1987	1988	1996	2001
Ots-1	158	0	0	0	0.0068	0	0	0	0
Ots-1	164	0	0.5	0	0	0	0	0	0
Ots-1	180	0.0083	0	0	0.027	0.0152	0.0714	0.0682	0.0597
Ots-1	182	0.175	0	0.3333	0.2027	0.303	0.3214	0.2727	0.291
Ots-1	184	0.0083	0	0	0	0	0	0	0
Ots-1	186	0	0.5	0.1667	0.0405	0.0682	0.0357	0.0682	0.0858
Ots-1	188	0	0	0	0.0068	0.0152	0.0357	0.0152	0.0037
Ots-1	192	0.7833	0	0.5	0.6824	0.5455	0.5	0.5379	0.5224
Ots-1	194	0.025	0	0	0.0338	0.053	0.0357	0.0379	0.0373
	a	5	2	3	7	6	6	6	6
	n	60	2	3	74	66	14	66	134
	N	74	2	3	75	69	16	99	142

Marker	Allele	1980	1983	1984	1985	1987	1988	1996	2001
Ots-100	170	0	0.5	0	0	0	0	0	0
Ots-100	239	0	0	0	0	0	0	0.0052	0
Ots-100	243	0.0098	0	0	0	0	0	0	0
Ots-100	247	0.0196	0	0	0	0.0303	0	0.0206	0.0109
Ots-100	252	0.0294	0	0.1667	0.0137	0.0303	0	0.0052	0.0073
Ots-100	256	0.0784	0	0	0.0274	0.0303	0.0714	0.0258	0.0292
Ots-100	260	0.0294	0	0	0.0616	0.0833	0	0.0567	0.0657
Ots-100	262	0	0	0	0.0068	0	0	0	0
Ots-100	264	0.0098	0	0	0.0137	0.0152	0.1429	0.0206	0.0146
Ots-100	268	0.0294	0	0	0.0068	0.0227	0	0.0155	0
Ots-100	270	0	0	0	0.0137	0	0.0714	0.0052	0.0109
Ots-100	272	0.0196	0	0	0.0068	0.0152	0	0.0052	0.0146
Ots-100	274	0.0196	0	0	0.0068	0	0	0.0103	0.0073
Ots-100	276	0.0098	0	0	0.0342	0.0682	0.0714	0.0103	0.0474
Ots-100	278	0.0392	0	0	0.0205	0.0152	0	0	0.0109
Ots-100	280	0	0	0	0.0479	0	0	0.0361	0.0036
Ots-100	282	0.0686	0	0	0.0274	0.0379	0	0.0412	0.0255
Ots-100	284	0.0196	0	0	0.0274	0.0152	0	0.0361	0.0219
Ots-100	286	0.0098	0	0	0.0342	0.0076	0	0.0309	0.0073
Ots-100	288	0.0196	0	0	0.0274	0.0076	0.0714	0.0155	0.0073
Ots-100	291	0	0	0	0.0274	0.0152	0	0.0515	0.0511
Ots-100	293	0.0588	0	0	0.0274	0.0379	0	0.0206	0.0328
Ots-100	295	0.0196	0	0	0	0.0076	0	0.0619	0.0365
Ots-100	297	0.0294	0	0.3333	0.0479	0.0455	0.0714	0.0309	0.0438
Ots-100	299	0	0	0	0.0068	0	0	0.0155	0.0036
Ots-100	301	0.0784	0	0.1667	0.0616	0.0606	0	0.0206	0.0474
Ots-100	303	0.0098	0	0	0.0068	0	0	0	0.0036
Ots-100	305	0	0	0	0.0479	0.0303	0	0.0773	0.062
Ots-100	310	0.0392	0	0	0.0479	0.0758	0	0.0567	0.0219
Ots-100	314	0.0392	0	0.1667	0.0274	0.0303	0.0714	0.0309	0.0584
Ots-100	318	0.049	0	0	0.0548	0.0758	0.0714	0.0567	0.0292
Ots-100	322	0.049	0	0	0.0548	0.0455	0.0714	0.0567	0.0584
Ots-100	327	0.0294	0	0	0.0274	0.0227	0.1429	0.0258	0.0365
Ots-100	331	0.0196	0	0	0.0068	0.0076	0	0.0155	0.0182
Ots-100	333	0	0	0	0	0	0	0	0.0036
Ots-100	335	0.0294	0	0.1667	0.0205	0.0379	0.0714	0.0206	0.0401
Ots-100	337	0.0098	0	0	0	0.0076	0	0.0052	0.0109
Ots-100	339	0.0098	0	0	0.0342	0.0152	0	0.0052	0.0109
Ots-100	341	0	0.25	0	0.0068	0.0076	0	0	0.0036
Ots-100	343	0.0098	0.25	0	0	0.0076	0	0.0206	0.0036
Ots-100	345	0.0098	0	0	0.0068	0.0227	0.0714	0.0052	0.0182
Ots-100	347	0.049	0	0	0.0616	0.0227	0	0.0052	0.0219
Ots-100	349	0.0098	0	0	0.0137	0	0	0	0.0109
Ots-100	351	0.0098	0	0	0.0205	0.0152	0	0.0412	0.0109
Ots-100	355	0.0098	0	0	0	0	0	0	0.0109

Ots-100	357	0	0	0	0	0	0	0.0052	0.0073
Ots-100	369	0	0	0	0.0068	0	0	0.0155	0.0328
Ots-100	373	0.0098	0	0	0	0	0	0	0
Ots-100	376	0	0	0	0	0.0227	0	0.0103	0.0219
Ots-100	378	0	0	0	0	0	0	0	0.0036
Ots-100	380	0.0098	0	0	0	0.0076	0	0	0
Ots-100	384	0	0	0	0.0068	0	0	0.0052	0
	a	37	3	5	38	35	12	40	44
	n	51	2	3	73	66	7	97	137
	N	74	2	3	75	69	16	99	142

Marker	Allele	1980	1983	1984	1985	1987	1988	1996	2001
Ots-101	153	0.0227	0	0	0.0133	0.0308	0	0.0579	0.0288
Ots-101	157	0	0	0	0	0	0	0	0.0036
Ots-101	161	0.0152	0	0	0.02	0.0077	0	0.0158	0
Ots-101	165	0	0	0	0.0333	0	0	0.0211	0.018
Ots-101	169	0	0	0	0.0067	0	0	0	0
Ots-101	173	0	0	0	0.0067	0	0	0	0
Ots-101	174	0	0	0	0.0067	0.0154	0	0.0053	0.0216
Ots-101	178	0	0	0	0.0267	0.0231	0.0333	0.0211	0.0144
Ots-101	182	0	0	0.1667	0.0067	0.0231	0.1	0.0368	0.0252
Ots-101	186	0.0152	0	0	0.0067	0.0231	0	0.0105	0.0252
Ots-101	190	0.0076	0	0	0.02	0.0077	0	0.0053	0.0108
Ots-101	194	0.0379	0	0	0.0333	0.0308	0.0667	0.0737	0.0504
Ots-101	198	0.053	0	0.1667	0.0533	0.0385	0	0.0368	0.0899
Ots-101	202	0.0455	0.25	0	0.0533	0.0692	0.0333	0.0316	0.0468
Ots-101	206	0.0909	0	0.1667	0.1067	0.1	0.1	0.1	0.0827
Ots-101	210	0.1515	0	0.1667	0.06	0.0462	0.1333	0.0579	0.0791
Ots-101	214	0.1667	0	0	0.12	0.0615	0.1667	0.0684	0.0899
Ots-101	218	0.0682	0	0.1667	0.0733	0.1385	0.0667	0.0789	0.0863
Ots-101	222	0.0833	0	0	0.06	0.0308	0	0.0474	0.0504
Ots-101	226	0.0606	0	0.1667	0.0667	0.1	0.0667	0.0211	0.0827
Ots-101	230	0.0379	0	0	0.0267	0.0538	0.0667	0.0263	0.0324
Ots-101	234	0.0227	0.25	0	0.04	0.0308	0.0667	0.0421	0.0288
Ots-101	238	0.0227	0	0	0	0.0385	0.0667	0.0421	0.0108
Ots-101	242	0	0	0	0.0067	0	0	0.0105	0.0144
Ots-101	246	0.0076	0	0	0.0533	0.0154	0	0.0474	0.0252
Ots-101	251	0	0	0	0.0067	0.0154	0.0333	0	0
Ots-101	255	0	0	0	0.0067	0	0	0.0105	0
Ots-101	259	0	0	0	0.0067	0.0462	0	0.0579	0.0144
Ots-101	263	0.0303	0	0	0.02	0.0077	0	0.0263	0.0288
Ots-101	267	0	0.25	0	0.0067	0	0	0.0211	0.0072
Ots-101	271	0.0303	0	0	0.0133	0.0231	0	0.0158	0.0144
Ots-101	275	0.0152	0	0	0.0333	0.0154	0	0.0053	0
Ots-101	279	0.0076	0	0	0	0.0077	0	0	0.0108
Ots-101	283	0	0	0	0.0067	0	0	0	0.0072
Ots-101	287	0.0076	0	0	0	0	0	0	0
Ots-101	291	0	0	0	0	0	0	0.0053	0
Ots-101	320	0	0.25	0	0	0	0	0	0
	a	22	4	6	31	26	13	29	28
	n	66	2	3	75	65	15	95	139
	N	74	2	3	75	69	16	99	142

Marker	Allele	1980	1983	1984	1985	1987	1988	1996	2001
Ots-107	172	0.0273	0	0	0.027	0.0147	0	0.0461	0.018
Ots-107	176	0	0	0	0.0405	0.0074	0	0.0132	0.0144
Ots-107	180	0.0455	0	0	0.0473	0.0956	0.0769	0.0263	0.0576
Ots-107	184	0.1818	0.25	0	0.1014	0.1103	0.2692	0.1118	0.1475
Ots-107	188	0.0545	0	0	0.0068	0.0074	0.0385	0.0197	0.018
Ots-107	192	0.0636	0	0.1667	0.0203	0.0294	0.0385	0.0329	0.0288
Ots-107	196	0.0636	0	0.1667	0.027	0.0515	0	0.0263	0.0324
Ots-107	200	0.0545	0	0	0.0811	0.0809	0.1538	0.1053	0.0683
Ots-107	204	0.0727	0	0	0.0743	0.0662	0.0769	0.0658	0.0576
Ots-107	208	0.0091	0	0	0	0	0	0	0
Ots-107	212	0	0	0	0	0.0074	0	0	0
Ots-107	216	0	0	0	0.0068	0.0147	0.0385	0	0.0144
Ots-107	220	0.0182	0	0	0.0338	0.0221	0.0769	0.0066	0.0288
Ots-107	224	0.0182	0	0	0.0135	0.0294	0	0.0132	0.0216
Ots-107	228	0.1091	0	0.1667	0.0608	0.0368	0	0.0921	0.036
Ots-107	232	0.0455	0.25	0.1667	0.0608	0.0588	0.0385	0.0855	0.1367
Ots-107	236	0.0273	0	0.1667	0.0676	0.0441	0.0769	0.0658	0.0504
Ots-107	240	0.0636	0	0	0.0405	0.0588	0	0.0592	0.0576
Ots-107	244	0.0091	0	0.1667	0.0405	0.0662	0.0385	0.0526	0.0396
Ots-107	248	0.0727	0	0	0.0541	0.0882	0.0385	0.0526	0.0971
Ots-107	253	0.0182	0.5	0	0.0608	0.0441	0	0.0395	0.036
Ots-107	257	0.0091	0	0	0.0541	0.0221	0.0385	0.0066	0.0108
Ots-107	261	0.0091	0	0	0.0068	0	0	0	0.0144
Ots-107	265	0.0182	0	0	0.0473	0.0147	0	0.0263	0
Ots-107	269	0.0091	0	0	0.0135	0.0221	0	0.0329	0.0072
Ots-107	293	0	0	0	0	0	0	0	0.0036
Ots-107	323	0	0	0	0	0.0074	0	0	0
Ots-107	327	0	0	0	0.0068	0	0	0.0132	0
Ots-107	331	0	0	0	0	0	0	0	0.0036
Ots-107	335	0	0	0	0.0068	0	0	0	0
Ots-107	339	0	0	0	0	0	0	0.0066	0
	a	22	3	6	25	24	13	23	24
	n	55	2	3	74	68	13	76	139
	N	74	2	3	75	69	16	99	142

Marker	Allele	1980	1983	1984	1985	1987	1988	1996	2001
Ots-108	105	0.0167	0	0	0.0397	0.0231	0	0.0325	0.0438
Ots-108	109	0.1333	0	0.25	0.1508	0.0846	0.1667	0.1623	0.1095
Ots-108	113	0.0167	0	0	0.0238	0.0231	0	0.0195	0.0182
Ots-108	117	0.1833	0	0	0.1111	0.1231	0.1667	0.1558	0.1387
Ots-108	121	0.075	0	0.25	0.0317	0.0462	0	0.026	0.0182
Ots-108	125	0.05	1	0	0.0635	0.1538	0.125	0.0844	0.0839
Ots-108	129	0.0167	0	0	0.0159	0.0077	0.0417	0.013	0.0219
Ots-108	133	0.0083	0	0	0.0079	0	0	0	0
Ots-108	138	0.1	0	0.25	0.119	0.1077	0.0833	0.1104	0.1168
Ots-108	142	0	0	0	0.0238	0.0154	0	0.0455	0.0146
Ots-108	147	0	0	0	0.0238	0	0	0	0
Ots-108	155	0.0417	0	0	0.0397	0.0077	0	0.0195	0.0073
Ots-108	160	0.025	0	0.25	0.0079	0.0538	0.0417	0.0195	0.0182
Ots-108	164	0.0083	0	0	0.0159	0.0308	0	0	0.0036
Ots-108	168	0.0333	0	0	0.0159	0.0538	0	0.039	0.0803
Ots-108	172	0.0667	0	0	0.0714	0.0769	0.0417	0.0649	0.0766
Ots-108	176	0.0333	0	0	0.0397	0.0308	0	0.0195	0.0146
Ots-108	180	0	0	0	0.0556	0.0077	0	0.026	0.0401
Ots-108	184	0.0167	0	0	0.0238	0.0385	0.0417	0.039	0.0292
Ots-108	188	0.0167	0	0	0.0079	0	0	0.0065	0
Ots-108	192	0	0	0	0.0079	0	0	0.0065	0.0109
Ots-108	196	0	0	0	0	0.0077	0	0.0065	0.0073
Ots-108	200	0.0083	0	0	0.0238	0	0	0	0
Ots-108	204	0.0167	0	0	0.0079	0.0077	0.0417	0.0195	0.0365
Ots-108	208	0.0167	0	0	0.0159	0.0462	0.0417	0.0325	0.0182
Ots-108	212	0.0083	0	0	0	0	0	0	0.0146
Ots-108	216	0.0083	0	0	0	0.0077	0	0	0.0036
Ots-108	220	0.0083	0	0	0	0.0077	0	0	0.0109
Ots-108	96	0.0917	0	0	0.0556	0.0385	0.2083	0.0519	0.062
	a	24	1	4	25	23	11	22	25
	n	60	1	2	63	65	12	77	137
	N	74	2	3	75	69	16	99	142

Marker	Allele	1980	1983	1984	1985	1987	1988	1996	2001
Ots-2M	125	0.0078	0	0	0	0.0075	0	0.0054	0
Ots-2M	133	0.2188	0	0.25	0.2365	0.1642	0.0938	0.1467	0.1486
Ots-2M	135	0.0234	0	0	0.0135	0.0448	0.0625	0.0326	0.029
Ots-2M	137	0.1172	0	0.25	0.0743	0.0672	0.1563	0.0924	0.1051
Ots-2M	143	0	0	0	0	0	0	0.0054	0
Ots-2M	145	0.0703	0	0.25	0.0608	0.0224	0.1875	0.0543	0.0725
Ots-2M	147	0.0938	0.25	0	0.0676	0.1269	0.1563	0.0924	0.1304
Ots-2M	150	0.0781	0.25	0	0.0878	0.0672	0.0625	0.0543	0.0507
Ots-2M	152	0	0	0	0.0405	0.0373	0	0.0543	0.0543
Ots-2M	154	0	0	0	0.0203	0.0149	0	0.0272	0.0072
Ots-2M	156	0.1172	0	0	0.1216	0.1716	0.0625	0.1522	0.1594
Ots-2M	158	0.0625	0	0	0.0338	0.0597	0.0625	0.0598	0.029
Ots-2M	160	0	0	0	0	0	0.0313	0	0.0036
Ots-2M	162	0.0156	0	0	0.0135	0.0149	0	0.0109	0
Ots-2M	164	0.0156	0	0	0.0068	0.0075	0	0.0054	0.0109
Ots-2M	166	0.0078	0	0	0.0068	0	0	0.0054	0
Ots-2M	168	0.1328	0.25	0.25	0.1689	0.1343	0	0.1359	0.1594
Ots-2M	170	0.0234	0	0	0.0203	0.0149	0.0938	0.0163	0.0109
Ots-2M	172	0	0	0	0.0135	0.0149	0	0.0109	0.0145
Ots-2M	174	0.0156	0.25	0	0.0135	0.0299	0.0313	0.038	0.0145
	a	15	4	4	17	17	11	19	16
	n	64	2	2	74	67	16	92	138
	N	74	2	3	75	69	16	99	142

Marker	Allele	1980	1983	1984	1985	1987	1988	1996	2001
Ots-3M	130	0	0	0	0	0	0	0	0.0036
Ots-3M	134	0	0.25	0	0	0	0	0	0
Ots-3M	136	0.0652	0.5	0	0.0811	0.0758	0.0313	0.0859	0.125
Ots-3M	138	0	0	0	0	0	0	0.0101	0
Ots-3M	139	0	0	0	0	0	0	0	0.0107
Ots-3M	140	0.0217	0	0	0	0	0	0.0051	0.0071
Ots-3M	143	0.1014	0	0.3333	0.1081	0.1212	0.1875	0.1212	0.1714
Ots-3M	145	0.2754	0.25	0.1667	0.3446	0.3333	0.2188	0.3283	0.2571
Ots-3M	147	0.3841	0	0.1667	0.1486	0.1439	0.2188	0.1111	0.0929
Ots-3M	149	0.087	0	0	0.1486	0.1439	0.25	0.1616	0.1464
Ots-3M	150	0	0	0	0	0.0076	0	0	0.0286
Ots-3M	151	0.0652	0	0.3333	0.1622	0.1515	0.0625	0.1667	0.1429
Ots-3M	153	0	0	0	0.0068	0.0227	0.0313	0.0101	0.0143
	a	7	3	4	7	8	7	9	11
	n	69	2	3	74	66	16	99	140
	N	74	2	3	75	69	16	99	142

Marker	Allele	1980	1983	1984	1985	1987	1988	1996	2001
Ots-G474	153	0.0071	0.25	0	0.0067	0	0.1818	0.0101	0
Ots-G474	157	0.4929	0	0.5	0.46	0.4348	0.3636	0.3889	0.4203
Ots-G474	165	0.0786	0	0.1667	0.0467	0.1087	0.0909	0.0859	0.0906
Ots-G474	169	0.1714	0	0.3333	0.26	0.1667	0.1364	0.2525	0.2681
Ots-G474	173	0.1714	0	0	0.1267	0.1594	0.1818	0.1263	0.0978
Ots-G474	177	0.0143	0.25	0	0.0267	0.0217	0	0.0202	0.0072
Ots-G474	181	0.0286	0.25	0	0.0533	0.0507	0.0455	0.0808	0.0833
Ots-G474	185	0.0214	0	0	0.0067	0.0145	0	0.0101	0.0072
Ots-G474	189	0.0071	0	0	0.0133	0.029	0	0.0202	0.0145
Ots-G474	193	0.0071	0	0	0	0.0145	0	0.0051	0.0109
Ots-G474	205	0	0.25	0	0	0	0	0	0
	a	10	4	3	9	9	6	10	9
	n	70	2	3	75	69	11	99	138
	N	74	2	3	75	69	16	99	142

Marker	Allele	1980	1983	1984	1985	1987	1988	1996	2001
Ssa-197	137	0.0313	0	0	0.02	0.0094	0	0.0052	0
Ssa-197	141	0	0	0	0	0.0189	0	0.0309	0.0143
Ssa-197	146	0.0156	0	0	0.02	0.0094	0	0.0155	0.0179
Ssa-197	150	0	0	0	0.01	0.0094	0	0.0155	0.0107
Ssa-197	155	0.1016	0	0	0.07	0.0283	0.1	0.0361	0.0321
Ssa-197	159	0.0234	0	0	0	0.0094	0	0	0.0214
Ssa-197	163	0	0.5	0	0	0	0	0.0206	0.0214
Ssa-197	167	0.0313	0	0	0.03	0	0	0.0052	0.0036
Ssa-197	171	0.0469	0.5	0	0.08	0.0472	0	0.0412	0.0786
Ssa-197	175	0.0234	0	0	0.07	0.0094	0.0667	0.0464	0.0286
Ssa-197	179	0	0	0	0	0	0	0.0052	0
Ssa-197	183	0	0	0	0.01	0	0	0.0052	0.0036
Ssa-197	191	0	0	0	0.01	0.0189	0	0.0052	0.0036
Ssa-197	195	0.0859	0	0	0.03	0	0.0333	0.0103	0
Ssa-197	199	0.0156	0	0	0.02	0.0189	0.0333	0.0206	0.0143
Ssa-197	203	0.0234	0	0	0.03	0.0094	0	0.0052	0.0107
Ssa-197	207	0.0156	0	0.25	0.02	0.0094	0	0	0.0036
Ssa-197	211	0.0078	0	0	0	0	0.0333	0	0.0071
Ssa-197	215	0.0313	0	0	0.05	0	0.0333	0.0361	0.0179
Ssa-197	219	0.0078	0	0	0	0	0	0.0103	0.0071
Ssa-197	223	0.0313	0	0	0.08	0.0283	0.0333	0.0412	0.025
Ssa-197	227	0.0938	0	0	0.05	0.0377	0	0.0309	0.0214
Ssa-197	231	0.0859	0	0.25	0.07	0.1509	0.1333	0.1392	0.1393
Ssa-197	235	0.0703	0	0	0.05	0.1132	0.1	0.0773	0.0929
Ssa-197	239	0.0547	0	0	0.1	0.1226	0.0667	0.0619	0.0857
Ssa-197	243	0.0313	0	0	0.04	0.0943	0.0667	0.0619	0.0964
Ssa-197	247	0.0313	0	0	0.04	0.0472	0.0333	0.0155	0.0321
Ssa-197	251	0.0313	0	0	0	0.066	0.0333	0.0412	0.0214
Ssa-197	255	0.0313	0	0	0.05	0.0566	0.1333	0.0619	0.0643
Ssa-197	259	0.0391	0	0.5	0.02	0.0377	0.1	0.0722	0.0643
Ssa-197	263	0.0234	0	0	0.01	0.0283	0	0.067	0.0321
Ssa-197	267	0	0	0	0.01	0.0094	0	0	0.0036
Ssa-197	272	0	0	0	0	0.0094	0	0.0052	0.0107
Ssa-197	276	0.0078	0	0	0	0	0	0	0
Ssa-197	280	0.0078	0	0	0.01	0	0	0	0
Ssa-197	296	0	0	0	0	0	0	0.0103	0.0143
	a	27	2	3	26	25	15	30	31
	n	64	1	2	50	53	15	97	140
	N	74	2	3	75	69	16	99	142