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Thurston:

The electrophoretic analysis of the adult kokanee salmon, *Oncorhynchus nerka*, collected from Ashley Lake (N=48, col. 12\5\91), Little Bitterroot Lake (N=25; col. 12\12\91), Lake Mary Ronan (N=49; col. 12\3\91), and Swan Lake (N=50; col. 12\4\91) in Montana, and the progeny spawned in 1991 from Wyoming's New Fork Lake (N=50) and Colorado's Granby Reservoir (N=50) broodstocks has been completed. In the Colorado and Wyoming samples, horizontal starch gel electrophoresis was used to determine each fishes genotype at 45 loci coding for proteins present in eye, liver, or muscle tissue (Table 1). In the Montana populations, only the polymorphic loci observed in the Wyoming (ALAT-1*, LDH-A2*, sMEP-1*, and PGM-2*) and Colorado (ALAT-1* and PGM-2*) samples were analyzed (Table 2). Further electrophoretic analysis of the Montana populations was not conducted because data obtained from 70 loci in 1976 and 1977 revealed no additional useful polymorphisms in these populations (Steve Phelphs, University of Montana, Masters Thesis). The data obtained from these loci were then used to determine if significant genetic differences exist between the Wyoming, Colorado, and Montana populations, and to determine if significant genetic changes had occurred within the Montana populations.

Contingency table chi-square analysis between the New Fork Lake Wyoming population and the other populations indicates that the allele frequencies are statistically heterogenous between these populations at all polymorphic loci except ALAT-1* in the Little Bitterroot Lake sample (Table 3). Thus, genetic differences exist between these populations. These differences are also not trivial. They account for a moderate amount, 10.8%, of the total genetic diversity detected, and most likely reflect the different origins of the fish used to establish these populations. The New Fork Lake population was indirectly established with fish originating from Meadow Creek, a tributary to Kootenay Lake, while the Flathead Lake population, from which all the other populations sampled were derived, was established with kokanee obtained from the Quannat Salmon Hatchery in Oregon. In addition, because the LDH-A2*120 and sMEP-1*95 alleles are unique to the Wyoming population, it should be relatively easy to determine if these fish are contributing to future spawning runs.

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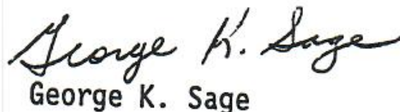
Contingency table chi-square analysis also indicates that significant allele frequency differences exist between the Ashley Lake sample and the Colorado sample, and the Ashley Lake sample and the other Montana samples, but not between the remaining Montana samples and the Colorado sample (Table 3). In contrast to the above situation, however, these differences are small, accounting for only 2.9% of the total genetic diversity detected. In addition, because no unique alleles were observed in any of these populations, our ability to determine their genetic contribution to lakes where they are stocked is limited. In order to estimate their contribution, we must know both the proportion of these fish stocked into a given lake and the allele frequencies of any existing kokanee population in the lake prior to their introduction.

Finally, we used contingency table chi-square analysis to determine if significant allele frequency changes had occurred within the Montana populations. No significant differences were observed within the Swan, Bitterroot, and Lake Mary Ronan spawning runs, but a significant difference was observed between the two Ashley Lake samples (Table 3). Several factors may be responsible for this change. It may be due to sampling error, or it could reflect either random changes caused by genetic drift or differential selection in response to different environmental parameters. Lacking information regarding the sizes, specific locations, or periods of the spawning runs from which the 1976 and 1977 samples were collected, however, makes it difficult to determine which of the above explanations, if any, are the most plausible.

Sincerely,



George K. Sage

Table 1

Loci and enzymes examined. E = eye, L = liver, M = muscle.

Enzyme	Loci	Tissue
Adenylate kinase	AK-1*, AK-2*	M
Alanine aminotransferase	ALAT*	M
Alcohol dehydrogenase	ADH*	L
Aspartate aminotransferase	sAAT-1*, sAAT-2* sAAT-3,4*	L M
Creatine kinase	CK-A1*, CK-A2* CK-B*, CK-C1*, CK-C2*	M E
Dipeptidase	PEPA*	E
Glucose-6-phosphate isomerase	GPI-A* GPI-B1*, GPI-B2*	E M
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH-3*, GAPDH-4*	E
Glycerol-3-phosphate dehydrogenase	G3PDH*	L
Iditol dehydrogenase	IDDH-1*, IDDH-2*	L
Isocitrate dehydrogenase	mIDHP-1*, mIDHP-2* sIDHP-1*, sIDHP-2*	M L
Lactate dehydrogenase	LDH-A1*, LDH-A2* LDH-B1*, LDH-B2*, LDH-C*	M E
Malate dehydrogenase	sMDH-A1,2*, sMDH-B1,2*	L M
Malic enzyme	mMEP-1*, mMEP-2*, sMEP-1* sMEP-2*	M L
Phosphoglucomutase	PGM-1*, PGM-2*	M
Phosphogluconate dehydrogenase	PGDH*	M
Superoxide dismutase	sSOD-1*	L
Tripeptide aminopeptidase	PEPB*	E
Xanthine dehydrogenase-like	XDH?	L

Table 2

Allele frequencies at the genetically variable loci in the 1992 Wyoming and Colorado kokanee broodstocks, and in the four kokanee populations sampled in Montana in 1976, 1977, and 1992. Note: the ALAT* locus was not analyzed in the samples collected in 1976 and 1977.

Locus	Alleles	Wyoming (1992)	Colorado (1992)	Ashley (1992)	Swan (1992)	Bitterroot (1992)	Mary Ronan (1992)	Ashley (76-77)	Swan (76-77)	Bitterroot (76-77)	Mary Ronan (1977)
ALAT*	100	0.622	0.390	0.375	0.370	0.500	0.469	-	-	-	-
	97	0.174	0.170	0.417	0.200	0.200	0.123	-	-	-	-
	89	0.204	0.440	0.208	0.430	0.300	0.408	-	-	-	-
LDH-A2*	100	0.620	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	120	0.380	-	-	-	-	-	-	-	-	-
sMEP-1*	100	0.900	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	95	0.100	-	-	-	-	-	-	-	-	-
PGM-2*	60	0.960	0.700	0.865	0.800	0.840	0.806	0.755	0.755	0.811	0.882
	80	0.040	0.300	0.135	0.200	0.160	0.194	0.245	0.245	0.189	0.118

Table 3

Results of the 2 X 2 contingency table chi-square tests for homogenous allele frequencies between samples. The missing values at the ALAT* locus indicate that no information was available for those comparisons. NA indicates that the locus was fixed for the same allele in both samples. NS indicates that the allele frequency differences between the samples were not significant. * = P < 0.050, ** = P < 0.010, *** = P < 0.001.

Locus			ALAT*	LDH-A2*	sMEP-1*	PGM-2*
Wyoming	vs	Colorado	***	***	**	***
		Ashley 92	***	***	**	*
		Swan 92	***	***	**	***
		Bitterroot 92	NS	***	*	*
		Mary Ronan 92	**	***	**	***
Colorado	vs	Ashley 92	***	NA	NA	**
		Swan 92	NS	NA	NA	NS
		Bitterroot 92	NS	NA	NA	NS
		Mary Ronan 92	NS	NA	NA	NS
Ashley 92	vs	Ashley 76/77	___	NA	NA	*
		Swan 92	***	NA	NA	NS
		Bitterroot 92	*	NA	NA	NS
		Mary Ronan 92	***	NA	NA	NS
Swan 92	vs	Swan 76/77	___	NA	NA	NS
		Bitterroot 92	NS	NA	NA	NS
		Mary Ronan 92	NS	NA	NA	NS
Bitterroot 92	vs	Bitterroot 76/77	___	NA	NA	NS
		Mary Ronan 92	NS	NA	NA	NS
Mary Ronan 92	vs	Mary Ronan 77	___	NA	NA	NS
Ashley 76/77	vs	Swan 76/77	___	NA	NA	NS
		Bitterroot 76/77	___	NA	NA	NS
		Mary Ronan 77	___	NA	NA	NS
Swan 77	vs	Bitterroot 76/77	___	NA	NA	NS
		Mary Ronan 77	___	NA	NA	NS
Bitterroot 76/77	vs	Mary Ronan 77		NA	NA	NS