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Bob:

We have completed the electrophoretic analysis of the four samples of kokanee salmon, *Oncorhynchus nerka*, collected from Kootenay Lake in British Columbia. Samples were collected from the North, South, and West arms of the lake as well as a Central location between the North and South arms. Horizontal starch gel electrophoresis was used to determine the genotype of each fish at 45 genes that code for proteins present in eye, liver, or muscle tissue (Table 1). The data from these loci were used to determine if genetic differences exist between age classes within samples and between samples. The polymorphic loci observed are listed in Table 2.

Contingency table Chi-square analysis between age classes within samples indicated that there were no significant genetic differences between the age classes. Thus, in the remaining analyses, all age classes within each sample were combined.

Contingency table Chi-square analysis of the allele frequencies between the North and West, North and Central, South and West, South and Central, and West and Central samples indicate that significant allele frequency differences exist between them (Table 3). These samples, therefore, do not appear to have been collected from a randomly mating population, but rather from three reproductively isolated populations. This is further supported by the presence of the LDH-A2 *120 allele which was only observed in kokanee collected from the Central location in the lake. If these fish were derived from a mixture of kokanee from the North, South, and West arms then it is highly unlikely that the LDH-A2 *120 allele would not have been observed in the other samples (X^2 = 16.993, df = 1, P = 0.0004). Thus, from a management standpoint the kokanee from these locations should be treated as individual populations.

Contingency table Chi-square analysis of the allele frequencies between the North and South arm samples, however, were statistically homogenous at the five polymorphic loci observed (Table 3). Thus, there is no evidence to suggest that genetic differences exist between these samples. A situation not unexpected, if in fact the fish that occur in the South Arm are derived from North Arm fish as suspected (Lisa Thompson, British Columbia Ministry of Environment, pers. comm.). From a management standpoint, therefore, the North and South arm fish can be treated as one spawning population.

With regards to the question of whether kokanee from Lake Koocanusa are migrating into Kootenay Lake I can not currently answer that question because no data on the genetic population structure of the kokanee in Kootenay Lake exists prior to the possibility of kokanee from Lake Koocanusa migrating there. Thus, even though no significant allele frequency differences were observed between the North and South arm fish and those collected in Montana from Lake Creek and the Kootenai River, I can not be certain that the lack of differences between these samples is the result of mixing between the populations. The lack of any significant differences may simply be a historical coincidence. However, because significant genetic differences were observed between the kokanee collected from the West and Central locations and those collected from Lake Creek and the Kootenai River it should be possible to determine in the future whether kokanee from Lake Koocanusa are contributing to the kokanee population in Kootenay Lake.

Sincerely,

George K. Sage

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Table 3

2 X 2 Contingency table chi-square tests of allele frequencies between samples. NS indicates that the allele frequency differences between the samples were not significant. NA indicates that the samples being compared were fixed for the same allele at that locus.

Population	Locus					
	AAT-3,4*	ALAT*	GPI-A*	LDH-A2*	PGM-1*	PGM-2*
North Arm vs South Arm	NS	NS	NS	NA	NS	NS
North Arm vs West Arm	NS	***	*	NA	NS	NS
North Arm vs Central Area	NS	NS	NS	**	NS	NS
South Arm vs West Arm	NS	**	NA	NA	NS	NS
South Arm vs Central Area	NS	NS	NS	*	NS	NS
West Arm vs Central Area	NS	**	NS	*	*	NS

Note: * indicates $P < 0.05$, ** indicates $P < 0.01$, *** indicates $P < 0.001$.

Table 2

Allele frequencies at the genetically variable loci in the 1993 samples of kokanee salmon collected from Kootenay Lake in British Columbia.

Locus	Alleles	N = 15 1+ N. Arm Tr. #3	N = 20 3+ N. Arm M. Cr.	N = 21 1+ S. Arm Tr. #5	N = 04 2+ S. Arm Tr. #5	N = 10 2+ W. Arm R. Cr.	N = 13 3+ W. Arm K. Cr.	N = 12 1+ Central Tr. #6	N = 10 2+ Central Tr. 3,5&6	N = 12 3+ Central Tr. #3
AAT-3,4*	100	0.983	1.000	0.988	1.000	1.000	1.000	1.000	1.000	0.917
	86	-	-	0.012	-	-	-	-	-	0.083
	112	0.017	-	-	-	-	-	-	-	-
ALAT*	100	0.367	0.575	0.619	0.250	0.850	0.961	0.636	0.650	0.500
	97	0.300	0.225	0.119	0.500	0.050	-	0.046	0.150	0.330
	89	0.333	0.200	0.262	0.250	0.100	0.039	0.318	0.200	0.170
GPI-A*	107	0.900	0.925	1.000	1.000	1.000	1.000	0.917	1.000	0.833
	110	0.100	0.075	-	-	-	-	0.083	-	0.167
LDH-A2*	100	1.000	1.000	1.000	1.000	1.000	1.000	0.917	0.850	1.000
	120	-	-	-	-	-	-	0.083	0.150	-
PGM-1*	100	0.533	0.542	0.622	1.000	0.684	0.610	0.592	0.367	0.183
	null	0.447	0.458	0.378	-	0.316	0.390	0.408	0.633	0.817
PGM-2*	64	0.867	0.825	0.905	1.000	0.850	0.885	0.958	0.950	0.833
	85	0.133	0.150	0.095	-	0.100	0.115	0.042	0.050	0.167
	43	-	0.025	-	-	0.050	-	-	-	-

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*	L
	sAAT-3,4*	M
Creatine kinase	CK-A1*, CK-A2*	M
	CK-B*, CK-C1*, CK-C2*	E
Dipeptidase	PEPA*	E
Glucose-6-phosphate isomerase	GPI-A*	E
	GPI-B1*, GPI-B2*	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*	M
	sIDHP-1*, sIDHP-2*	L
Lactate dehydrogenase	LDH-A1*, LDH-A2*	M
	LDH-B1*, LDH-B2*, LDH-C*	E
Malate dehydrogenase	sMDH-A1,2*,	L
	sMDH-B1,2*	M
Malic enzyme	mMEP-1*, mMEP-2*, sMEP-1*	M
	sMEP-2*	L
Phosphoglucomutase	PGM-1*, PGM-2*	M
Phosphogluconate dehydrogenase	PGDH*	M
Superoxide dismutase	sSOD-1*	L
Tripeptide aminopeptidase	PEPB*	E
Xanthine dehydrogenase-like	XDH7	L