University of Montana
Department of Zoology • Missoula, Montana 59812 • (406) 243-5122

April 29, 1986

RefID = 86748

Wayne Hadley
Montana Department of Fish,
Wildlife, and Parks
Box 835
Deer Lodge, Montana 59722

#2908

Wayne:

We have completed the electrophoretic analysis of the sample of Salmo (N=22) you collected from Upper Powell Reservoir (T10W, R7N, S16) September 25, 1985. The protein products encoded by 45 loci were analyzed for the presence of genetic variation (Table 1). At those loci that can be used to differentiate the rainbow, Salmo gairdneri, westslope cutthroat, S. clarki lewisi, and Yellowstone cutthroat trout, S. c. bouvieri, (Table 2) we detected only the presence of westslope cutthroat trout genetic material in the sample. We are capable of detecting as little as one percent rainbow trout genetic material in a population 95 percent of the time and as little as one percent Yellowstone cutthroat trout genetic material 99 percent of the time with a sample size of 22 individuals. Thus, the sample almost undoubtedly came from a 'genetically pure' population of westslope cutthroat trout.

The allele frequencies at those loci at which we detected evidence of genetic variation are given in Table 3. Although the Sdh(100) allele is characteristic of both the rainbow and Yellowstone cutthroat trout, its presence in the sample is not likely indicative of introgression because we did not detect alleles characteristic of these species at any other loci in Table 2. If the Sdh(100) allele truly represented nine precent rainbow or Yellowstone cutthroat trout genetic material in the population, the probability that we would not detect evidence of this genetic material at any other locus is one in a billion. The presence of the Sdh(100) allele, therefore, almost certainly represents westslope cutthroat genetic variation.

Sincerely,

Robb Leary

RL:sf

TABLE 1

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

Enzyme	Loci	Tissue
Adenylate kinase (AK)	Ak1,2	M
Alcohol dehydrogenase (ADH)	Adh	L
Aspartate aminotransferase (AAT)	Aat1,2	L
	Aat(3,4)	M
Creatine kinase (CK)	Ck1,2	M
	Ck3,CkC1,2	E
Glucose phosphate isomerase (GPI)	Gpi1,2,3	M
Glyceraldehyde-3-phosphate dehydrogenase (GAP)	Gap3,4	E
Glycerol-3-phosphate dehydrogenase (G3P)	G3p1,2	L
Glycyl-leucine Peptidase (GL)	Gl1,2	E
Isocitrate dehydrogenase (LDH)	Idh1,2	M
	Idh3,4	L
Lactate dehydrogenase (LDH)	Ldh1,2	M
	Ldh3,4,5	E
Leucyl-glycyl-glycine peptidase (LGG)	Lgg	E
Malate dehydrogenase (MDH)	Mdh(1,2)	L
	Mdh(3,4)	M
Malic enzyme (ME)	Me1,2,3	M
	Me4	L
Phosphoglucomutase (PGM)	Pgm1,2	M
6-Phosphogluconate dehydrogenase (6PG)	6Pg	M
Sorbitol dehydrogenase (SDH)	Sdh	L
Superoxide dismutase (SOD)	Sod	L
Xanthine dehydrogenase (XDH)	Xdh	L

Note: The protein products of the pairs of loci in ( ) are electrophoretically indistinguishable. Thus, they are considered to be single tetrasomic loci in all analyses.

TABLE 2

Loci that can be used to differentiate rainbow, westslope cutthroat, and Yellowstone cutthroat trout. Alleles are designated as the proportional migration distance in the gel relative to the distance traveled by the common allele in rainbow trout which is given a mobility of 100.

	Alleles		
Loci	Rainbow	Westslope	Yellowstone
Aatl	100	200,250	165
Ck2	100	84	84
CkCl	100,38	100,38	38
Gll	100,115,90	100	101
Gpi3	100	92	100
Idhl	100	100	-75
Idh3,4	100,114,71,40	100,86,71,40,Null	100,71
Lgg	100,135	100	135
Mel	100,55	88	100
Me3	100,75	100,75	90
Me4	100	100	110
Pgml	100,Null	100,Null	Null
Sdh	100,200,40	40,100	100

TABLE 3

Allele frequencies at those loci that showed evidence of genetic variation in westslope cutthroat trout from Upper Powell Reservoir, Montana

Locus	Alleles	Frequencies
Idh4	100	0.341
	40	0.659
Sdh	40	0.909
	100	0.091
Proportion polymorphic loci		0.050
Average expected heterozygosity		0.015