Biological Sciences, Department of Zoology • Missoula, Montana 59812-1201 • (406) 243-5122

16 June 1988

Dr. Leo Marnell Glacier National Park P. O. Box 343 West Glacier, MT 59936

Dear Leo,

The purpose of this letter is to inform you of the results of our analysis of the fish that we collected from a hybrid swarm of westslope and Yellowstone cutthroat trout in Fish Lake last year. We caught 1 fish by angling and 29 fish with experimental gill nets on 6 September 1987. We exceeded our limit by 5 because we caught an unexpected total of 10 fish on our last set of the nets. The attached Table 1 presents the length, weight, condition factor, sex, and age of each fish collected.

This work is part of the dissertation research of Steve Forbes. I have enclosed a copy of his dissertation proposal which describes the objectives of his research and summarizes the results to date. Steve's results are based on samples from three populations of westslope X Yellowstone hybrid swarms: Fish Lake, Cataract Creek (a tributary of the Vermilion River in the lower Clark Fork drainage), and Forest Lake (Lewis and Clark National Forest).

I believe this is fundamentally important research. In addition, Steve's results have dramatically changed our view of hybrid swarms of trout in ways that have important management implications.

The most important result is that the frequency of Yellowstone genes has increased significantly in all three populations. We can see this by comparing Steve's results to the results of the 1979 sample from Fish Lake (see attached Table 2). Five loci were examined in both the 1979 and 1987 samples. The frequency of the westslope alleles has decreased at every one of these loci; this change is statistically significant at 3 of the 5 loci. On the average, the frequency of westslope genes in the population has decreased from 30% to 13%. The same trend was found in the other two populations as well.

The simplest explanation of these results is that natural selection is favoring Yellowstone chromosomes in these populations. Steve's results with mtDNA support this interpretation. The frequency of westslope mtDNA is greater than the frequency of westslope proteins in all three populations (see attached Table 3). The increase in frequency of Yellowstone genes is completely unexpected (at least by us), especially because the westslope is the native fish.

Steve also found an association between the gender of fish and their mtDNA type (westslope or Yellowstone). There is a deficit of males with westslope mtDNA in all three populations (see attached Table 3). These results suggest that there may be some genetic incompatibility between westslope mtDNA and Yellowstone nuclear genes.

We would like to be able to continue our work in Fish Lake. It is important to confirm our initial results so that we can begin to understand the dynamics of the genetic changes in these populations. You may recall that we initially requested permission to sample 50 fish. We would ideally like to sample an additional 50 fish this year. However, a sample of 25 fish would also be useful.

The letter from Superintendent Rusk last year requested prior notification of plans to publish this information. We are currently working on a manuscript describing these results that we intend to submit to a peer reviewed journal, probably the journal Genetics.

Best regards,

Fred W. Allendorf Professor of Zoology

Table 1. Length, weight, condition factor, sex, and age of Yellowstone X westslope cutthroat trout collected from Fish Lake, Glacier National Park, 6 September 1988.

Fish No.	lg (mm)	wt (g)	cf	sex	age
1	431	924	1.15	М	2+
2	420	940	1.26	M	3+
3	445	950	1.07	F	4+
4	417	858	1.18	F	4+
5	401	687	1.06	F	4+
6	376	697	1.31	M	3+
7	369	597	1.18	F	3+
8	368	580	1.16	M	2+
9	352	525	1.20	M	2+
10	368	634	1.27	F	4+
11	375	<u> 6</u> 90	1.30	F	4+
12	377	670	1.25	M	3+
13	356	545	1.20	F	3+
14	362	559	1.17	F	2+
15	357	522	1.14	F	3+
16	354	585	1.31	М	3+
17	368	568	1.13	М	2+
18	346	502	1.21	M	2+
19	320	412	1.25	F	2+
20	328	386	1.09	F	5+
21	291	293	1.18	M	2+
55	296	319	1.23	F	5+
23	282	270	1.20	F	3+
24	282	278	1.23	M	2+
25	275	271	1.30	F	2+
56	270	219	1.11	F	· 1+
27	246	175	1.17	F	1+
28	229	144	1.19	F	1+
29	214	124	1.26	F	1+
30	212	108	1.13	F	1+

Table 2. Allele frequencies in Yellowstone X westslope cutthroat trout collected in 1979 and 1987 from Fish Lake, Glacier National Park.

N = number of fish analyzed p(ws) = frequency of westslope allele $\Delta p(ws) = p(ws)(1987) - p(ws)(1983)$ 

<del></del>	1979		1		
Locus	N	p(ws)	N	p(ws)	<b>∆</b> p(ws)
·····	<del></del>	<del></del>	<del></del>		
Aat1	0		22	.227	
CkC1	0		30	.250	
Gpi3	31	.290	30	.100	19**
Idh1	31	.387	30	.267	12
Idh4	31	.242	30	.133	11
Lgg	0		30	.117	
Me-1,2	31	.258	30	.083	18*
Me3	0		30	.150	
Me4	31	.304	30	.050	26***
Sdh	0		29	.034	
Average		.297		.127	

\*P<0.05; \*\*P<0.01; \*\*\*P<0.001

Table 3. Nuclear and mtDNA gene frequencies in three hybrid swarms of westslope x Yellowstone cutthroat trout.

p(ws) = mean frequency of westslope nuclear alleles averaged over 10 diagnostic loci

m(ws) = frequency of westslope mtDNA

 $X^2$  is a 2x2 contingency chi-square for independence of mtDNA type versus sex of fish.

df = degrees of freedom for chi-square test

Collection	N	Gene Frequency		Number of Fish					
		Nuclea	r MtDNA	WS mtDNA		YS mtDNA			
	madelaris (1914)	p(ws)	m(ws)	female	male	female	male	χ=	df
Cataract Cr.	58	0.41	0.53	21	10	12	15	3.19	1
Fish L.	30	0.13	0.43	10	3	9	8	1.82	1
Forest L.		0.44	0.71	35	9	9	9	5.41*	1
Total	150		*** ***	66	55	30	32	10.42*	3

<sup>\*</sup>P<0.05