

## REFERENCE SLIP

4/11/83

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Bob Behnke

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REMARKS

Bob - here is copy of some revised pages on Mark Martin's report. Insert them into your copy. Do they make any diff. in your comments? Thanks for your comments - I'll keep them here with me - Did I ever send you a copy of the Stream Bible? Cheers! Don Duff

FROM



THE ELECTROPHORETIC ANALYSIS OF CUTTHROAT TROUT  
SUBSPECIES IN SELECTED UTAH WATERS

Abstract

Recent discoveries of native cutthroat trout (Salmo clarki Richardson) in Utah have prompted research by both State and Federal agencies. To help facilitate this research, the U.S. Forest Service located 39 Utah streams in which they suspected relict populations of native cutthroat existed. A total of 550 cutthroat from 31 streams was examined to identify strains and to investigate the degree of genetic differentiation. Horizontal starch gel electrophoresis was used to assay four protein systems from populations of Colorado River (S. c. pleuriticus), Bonneville (S. c. utah) and Yellowstone (S. c. bouvieri) cutthroat trout. Population differentiation was determined using cluster analysis. Deep Creek, North Fork of North Creek (Sevier River drainage, Beaver County), Moffit Creek (Weber River drainage, Summit County), Carter Creek, Meadow Creek, Mckenzie Creek (Bear River drainage, Summit County) and Sugarpine Creek (Bear River drainage, Rich County) contain native populations of the Bonneville cutthroat trout (S. c. utah). The Middle and West Forks of Beaver Creek and Brush Creek on the north slope of the Uinta mountains in the Green River drainage are largely inhabited by populations of Colorado River cutthroat trout (S. c. pleuriticus).



not absolute indicators of the species present because not all trout introductions into area waters have been documented.

### Results-Discussion

Loudenslager and Gall (1980a,b,c, 1981) discovered that locus IDH-3 differentiated some cutthroat strains and may also indicate rainbow hybridization. Cutthroat trout native to Utah are usually fixed for IDH-3 (100) and IDH-4 (140) but some variation may occur so IDH alone is not definitive for rainbow hybridization. Rainbow have IDH-3 at (170 and 60). LGG and ME at position 100 correspond to rainbow alleles, while cutthroat had alleles at 160 and 125 respectively (Loudenslager and Gall 1981). Two criteria are used to identify  $F_1$  rainbow x cutthroat hybrids from backcross rainbow x cutthroat hybrids. Trout heterozygous for either ME or LGG are classified as  $F_1$  hybrids. Individuals homozygous for a cutthroat or rainbow allele at one locus and either homozygous or heterozygous for the alternate allele at the other locus were backcross hybrids. The sorbitol dehydrogenase protein system (locus 1 and 2) was found to separate cutthroat strains. At locus 1 (SDH-1) allele 40 is predominant in the Yellowstone and Bear River Bonneville cutthroat. SDH-1 (0) is predominant in Colorado River and Snake Valley Bonneville cutthroat. Loudenslager and Gall (1980b) found pure populations of Snake Valley Bonneville from the Deep Creek drainages to be homozygous for SDH-1 (0) (Goshute and Pine Creeks) or slightly heterozygous for SDH-1 (0) (Trout Creek, 0 = 0.984, 40 = 0.016). Their Colorado River cutthroat population was homozygous for the 0 allele. Variation seen in the Snake Valley Bonneville at SDH-1 implied that pure populations of this variety



Behnke (1980b) to be 95 percent pure Bear River Bonneville (with possible cutthroat variations), while our results showed it to be 100 percent pure Bear River Bonneville because all trout contained the 40 allele at SDH-1. However, in Boundary Creek heterozygosity was noted in IDH-3 where 11 percent of the bands were positioned at allele 170 and 89 percent at allele 100. This may indicate rainbow hybridization. Rainbow x cutthroat trout genes were noted in 25 percent of the 100 allele in ME and 32 percent of the 100 allele in LGG of Boundary Creek. Cutthroat strains located in Meadow Creek had a frequency of 1.00 at SDH-1 position 40. At the IDH-3 locus 3 percent of the population contained the 170 allele and 97 percent had the 100 allele. This variation of the IDH-3 locus may indicate rainbow trout hybridization. A rainbow trout allele (LGG) appeared in 5 percent of the trout alleles sampled from Mill Creek (rainbows were stocked in Mill Creek). Heterozygous cutthroat trout alleles (locus SDH-1) existed in the Mill Creek trout population at 0.55 for 40 and 0.45 for 0. Behnke (1980b) reported this population to be 90 percent pure Bear River Bonneville (2 of 32 trout examined contained rainbow characteristics). Our study indicates the population is 95 percent cutthroat, but they are intermediate between the Bear River and Snake Valley forms.

Bunchgrass Creek was the only stream sampled in the Logan River drainage. No stocking records existed for this stream. However, downstream the Logan River has been planted with rainbow and brown trout and a rainbow allele ME (100) appeared in 5 percent of the population sampled from Bunchgrass Creek. One hundred percent of this population had the SDH-1 and 2 locus at alleles 40 and 100 respectively. This Bonneville at SDH-1 locus that pure populations of this variety



identity level of 0.988 and contained Kabell, Mill, Fifth Water, Nebo, Wanrhodes, Little Diamond and Muddy Creeks and Strawberry River above Strawberry Reservoir. The second was distinct at the genetic identity level of 0.970 and contained Thompson, Deep, the North Fork of North Creek, and the Middle and West Forks of Beaver, Brush, Moffit, Joulious, Greetesen, and Middle Fork of Blacks, Red Pine and Hy Hunt Creeks and the North Fork of American Fork River. The third cluster was distinct at the genetic identity level of 0.969 and contained Mckenzie, Carter, Sugarpine, the Left Fork of Hobble, Case, Shinglemill and Bunchgrass Creeks. The first cluster included a mixture of streams represented by Bear River Bonneville, Colorado River, Snake Valley Bonneville and Yellowstone cutthroat trout. Their alleles exhibited a high degree of both rainbow hybridization and heterozygosity within cutthroat strains as determined by SDH-1 (40) and (0). The second cluster contained streams with Snake Valley Bonneville and Colorado River cutthroat that had frequencies of the SDH-1 (0) allele. The third cluster included streams containing populations of either Yellowstone or Bear River Bonneville cutthroat trout. A high degree of homozygosity in SDH-1 at position 40 was dominant in this group. However, some heterozygosity existed with allele SDH-1 (0). A close genetic relationship between the Bear River drainage cutthroat populations and S. c. bouvieri was evidenced by the cluster. Also, a high genetic identity was implied between Snake Valley S. c. utah and S. c. pleuriticus because of the clustering of the Colorado River streams with the Snake Valley Bonneville streams. This same relationship can be seen by comparing the similarities of cutthroat populations between the various drainages.



Bunchgrass Creek (ME: 0.03, Logan River drainage), Wannhodes Creek (ME: 0.09, Spanish Fork River drainage), Nebo Creek (LGG: 0.13, Spanish Fork River drainage) and Hy Hunt Creek (LGG: 0.20, Sevier River drainage). The remaining 24 streams contained cutthroat trout populations which showed no electrophoretic evidence of rainbow hybridization. Based on SDH-1 allelic frequency, drainage location and cluster analysis, we divided the cutthroat populations into several categories. The first major category contains populations classified as "pure". These were defined by lacking rainbow hybridization and showing complete or nearly complete (0.90) homozygous conditions with an SDH-1 allele. These pure populations were further subdivided depending upon which SDH-1 allele dominated. A dominance of SDH-1 (0) characterized the Colorado River cutthroat and the Snake Valley form of Bonneville cutthroat. A dominance of SDH-1 (40) is indicative of either Yellowstone or Bear River Bonneville populations. A final subdivision of pairs is dependent upon the drainage from which the population was sampled. The "pure" populations in the Colorado River system were in the West Fork of the Beaver River, the Middle Fork of the Beaver River and Brush Creek. All 3 streams are located in the Wasatch Forest on the north slope of the Uinta mountains. Populations which are pure Snake Valley type Bonneville were found in Deep Creek (Sevier River drainage near Antimony, Utah), North Fork of North Creek, (Sevier River drainage near Beaver, Utah) and Moffit Creek in the Weber River drainage. Those populations that showed complete (100 percent) homozygosity for SDH-1 (40) were considered pure for either the Bear River form of the Bonneville cutthroat or the Yellowstone cutthroat. Populations in the



TABLE 1. Localities, numbers and status of trout collected in Utah.

Sample no.	Sample site	Trout present	No. indiv.	Status
1.	Kabell Creek	Y-BRG, CR	4	2
2.	Thompson Creek	CR, R	16	3
3.	M. Fk. Beaver Creek	CR	9	1
4.	W. Fk. Beaver Creek	CR	20	1
5.	Joulious Creek	Y-BRG, CR	17	2
6.	M. Fk. Blacks Creek	Y-BRG, CR	24	2
7.	Brush Creek	SVB	22	1
8.	Mckenzie	Y-BRB	12	1
9.	Mill Creek	SVB, Y-BRB, R	22	2,3
10.	Carter Creek	Y-BRB	17	1
11.	Boundary Creek	Y-BRB, R	20	3
12.	Meadow Creek	Y-BRB	19	1
13.	Moffit Creek	SVB	18	1
14.	Sugarpine Creek	Y-BRB	19	1
15.	Bunchgrass Creek	Y-BRB, R	19	3
16.	Durfee Creek		0	
17.	Greetsen Creek	SVB, Y-BRB	3	2
18.	Red Pine Creek	SVB, Y-BRB	18	2
19.	N. Fk. American Fk. River	SVB, Y-BRB	5	2
20.	Silver Creek	EB	0	
21.	L. Fk. Hobble Creek	Y-BRB	21	1
22.	Strawberry River	Y-BRB, CR	60	2
23.	Shinglemill Creek	Y-BRB	16	1
24.	Chase Creek	Y-BRB	4	1
25.	Fifth Water Creek	SVB, Y-BRB	11	2
26.	Indian Creek		0	
27.	Wanrhodes	SVB, Y-BRB, R	11	2,3
28.	Little Diamond Creek	SVB, Y-BRB	17	2
29.	Tie Fork Creek		0	
30.	Holman Creek	Y-BRB	27	2
31.	Nebo Creek	SVB, Y-BRB, R	23	2,3
32.	Mendenhall Creek		0	
33.	North Creek		0	
34.	Bear Canyon Creek		0	
35.	Willow Creek		0	
36.	Muddy Creek	Y-BRB, CR	5	2
37.	Deep Creek	SVB	16	1
38.	Hy Hunt Creek	SVB, R	25	2,3
39.	N. Fk. North Creek	SVB	30	1

Snake Valley Bonneville = SVB, Yellowstone or Bear River Bonneville = Y-BRB, Colorado River = CR, Rainbow = R, Eastern Brook = EB

1 = Pure: based on 90% or higher frequency of a single allele

2 = Heterozygous: allelic frequency between 11 and 89%

3 = Hybridized: rainbow x cutthroat cross



TABLE 2. Continued.

		Streams									
Locus		N. Fk. Am. Fk.	L. Fk. Hobble	Strawberry	Shinglemill	Chase	Fifth Water	Wanrhodes	Little Diamond	Holman	
SDH-1	100	----	----	----	----	----	----	----	----	----	
	40	0.25	1.00	0.50	0.97	1.00	0.50	0.36	0.35	0.85	
	0	0.75	----	0.50	0.03	----	0.50	0.64	0.65	0.15	
SDH-2	250	----	----	----	----	----	----	----	----	----	
	100	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	
IDH-3	170	----	----	0.01	----	----	----	----	----	----	
	100	1.00	1.00	0.99	1.00	1.00	1.00	0.95	1.00	1.00	
	60	----	----	----	----	----	----	0.05	----	----	
IDH-4	140	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	
LGG	160	1.00	1.00	1.00	1.00	1.00	1.00	0.91	1.00	1.00	
	100	----	----	----	----	----	----	0.09	----	----	
ME	125	1.00	1.00	1.00	1.00	1.00	1.00	0.91	1.00	1.00	
	100	----	----	----	----	----	----	0.09	----	----	



TABLE 2. Continued.

		Streams								
Locus		Mill	Carter	Boundary	Meadow	Moffit	Sugarpine	Bunchgrass	Greetsen	Red Pine
SDH-1	100	----	----	----	----	----	----	----	----	----
	40	0.55	1.00	1.00	1.00	0.03	1.00	1.00	0.17	0.25
	0	0.45	----	----	----	0.97	----	----	0.83	0.75
SDH-2	250	----	----	----	0.13	----	----	----	----	----
	100	1.00	1.00	1.00	0.87	1.00	1.00	1.00	1.00	1.00
IDH-3	170	----	----	0.11	0.03	0.08	----	----	----	----
	100	1.00	1.00	0.89	0.97	0.92	1.00	1.00	1.00	1.00
	60	----	----	----	----	----	----	0.03	----	----
IDH-4	140	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
LGG	160	0.95	1.00	0.68	1.00	1.00	1.00	1.00	1.00	1.00
	100	0.05	----	0.32	----	----	----	----	----	----
ME	125	1.00	1.00	0.75	1.00	1.00	1.00	1.00	1.00	1.00
	100	----	----	0.25	----	----	----	0.03	----	----



TABLE Continued.

		Streams				
Locus		Nebo	Muddy	Deep	Hy Hunt	N. Fk. North
SDH-1	100	----	----	----	----	----
	40	0.54	0.40	----	0.20	----
	0	0.46	0.60	1.00	0.80	1.00
SDH-2	250	----	----	----	----	----
	100	1.00	1.00	1.00	1.00	1.00
IDH-3	170	----	----	----	0.04	----
	100	1.00	1.00	1.00	0.96	1.00
	60	----	----	----	----	----
IDH-4	140	1.00	1.00	1.00	1.00	1.00
LGG	160	0.87	1.00	1.00	0.80	1.00
	100	0.13	----	----	0.20	----
ME	125	0.91	1.00	1.00	0.86	1.00
	100	0.09	----	----	0.14	----



