NATIVE RAINBOW TROUT IN MONTANA

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ABSTRACT

Previous reports have indicated the absence of rainbow trout as native in Montana. All planted rainbow trout in Montana came indirectly from the McCloud River in California and were originally derived from a coastal steelhead trout population. Electrophoretic techniques can distinguish between inland and coastal steelhead trout. Using these techniques, along with evidence from hatchery records and geographical distribution, it is shown that rainbow trout are native in Callahan Creek and in the Yaak River. This is important in the consideration of fish planting measures because the gene pool of these natural populations could be jeopardized by plantings of hatchery stocks, thus eliminating fish which should be better adapted to the Montana enviornment.

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INTRODUCTION

The existence of native populations of rainbow trout, or Salmo gardeneri, in Montana is controversial. It is the contention of some that Montana is excluded from the world wide distribution of native rainbow trout (MacCrimmon, 1971), while others believe that there are indeed native populations there (Phillips, personal communication).

This paper is concerned with settling this controversy. Distribution studies have thus far excluded Montana, but it is possible that native rainbow trout could have gained access into Montana, thus establishing a native population. The history of planting of rainbow trout in Montana and the hatchery records offer evidence as to where possible natural populations exist or where they have possibly been contaminated. Electrophoretic work can establish genetic variation relationships within rainbow trout populations and between them; thus facilitating the comparison of native populations and planted ones. Along these three lines- distribution, hatchery plantings, and electrophoresis- we will attack the problem of native rainbow trout in Montana.

MATERIALS AND METHODS

DISTRIBUTION

Rainbow trout are generally considered native to Montana by many inhabitants in northwest Montana, in the Yaak and Kootenai River drainages although contrasting studies have been presented. One study, by MacCrimmon, indicates that non-anadromous native rainbow trout are widespread in the Fraser River watershed and in the Columbia River system, except for that portion of the Columbia drained by the Moyie, Elk and part of the Kootenai Rivers. In Idaho, rainbow trout are indigenous to the Snake River system up to Augar Falls and Mile 607 (near the present town of Twin Falls) and anadromous fish migrations terminate in the Snake River at Hell's Canyon Dam at River Mile 247 but resident rainbow trout are found throughout the former range (MacCrimmon,1971). This information limits the native distribution of rainbow trout to Idaho up to the Montana-Idaho border.

It is believed that rainbow trout in Canada are native to the Kootenay Lakes. Those that inhabit the south arm of the lake probably spawn in the Kootenai River, but neither it nor its tributaries have been investigated (Andrusak via May,personal communication). The understanding is that the British Columbia Fish and Wildlife Branch feels that rainbow trout are native in Kootenay Lakes and upstream from the Canadian border with Montana (Huston via Holton,personal communication). This information establishes the native distribution to British Columbia up to the Montana-Canadian border. Thus, Montana is excluded

Figure 1. Map showing the relationship of the Kootenai River to the Columbia River Drainage.

state hatcheries. In order to expand the gene pool, a brood stock was created by crossing the Missouri strain females with Donaldson strain males. Then, all original stock was disposed of. This cross was made in 1955 (Colley, et al.,1977). The Bozeman Hatchery station, a federal hatchery, records its earliest rainbow trout egg shipment in 1899 in which 50,000 eggs were recieved from Neosho Missouri (Piper via Holton,personal communication). Futhermore, Dr. Raymond C. Simon, former Director of the U.S. Fish and Wildlife Service Fish Genetics Laboratory in Beulah,Wyoming, feels that probably every rainbow trout brood stock used in federal fish hatcheries have been heavily influenced by coastal steelhead trout. This is based on records of exchanges of fish between hatcheries.(Simon via Holton,personal communication). Dr. F.W. Allendorf of the University of Montana feels that there is no reason to think that any hatchery brood stock used in Montana was derived from inland strains of rainbow or steelhead trout (Allendorf via Holton,personal communication). All of this information is significant in that we see the introduction of the coastal steelhead variety of rainbow trout via Missouri into Montana's hatcheries to serve as brood stocks for planting.

One can only speculate about the early distribution of hatchery fish in Montana since inadequate records were kept. Fish were shipped from federal fish hatcheries in the East to designated stations in the state. Their final destination, whatever the species, was left to the person who received the fish (Alvord,1977). However, recent planting records are useful in determining which streams consist of planted populations and which are not.

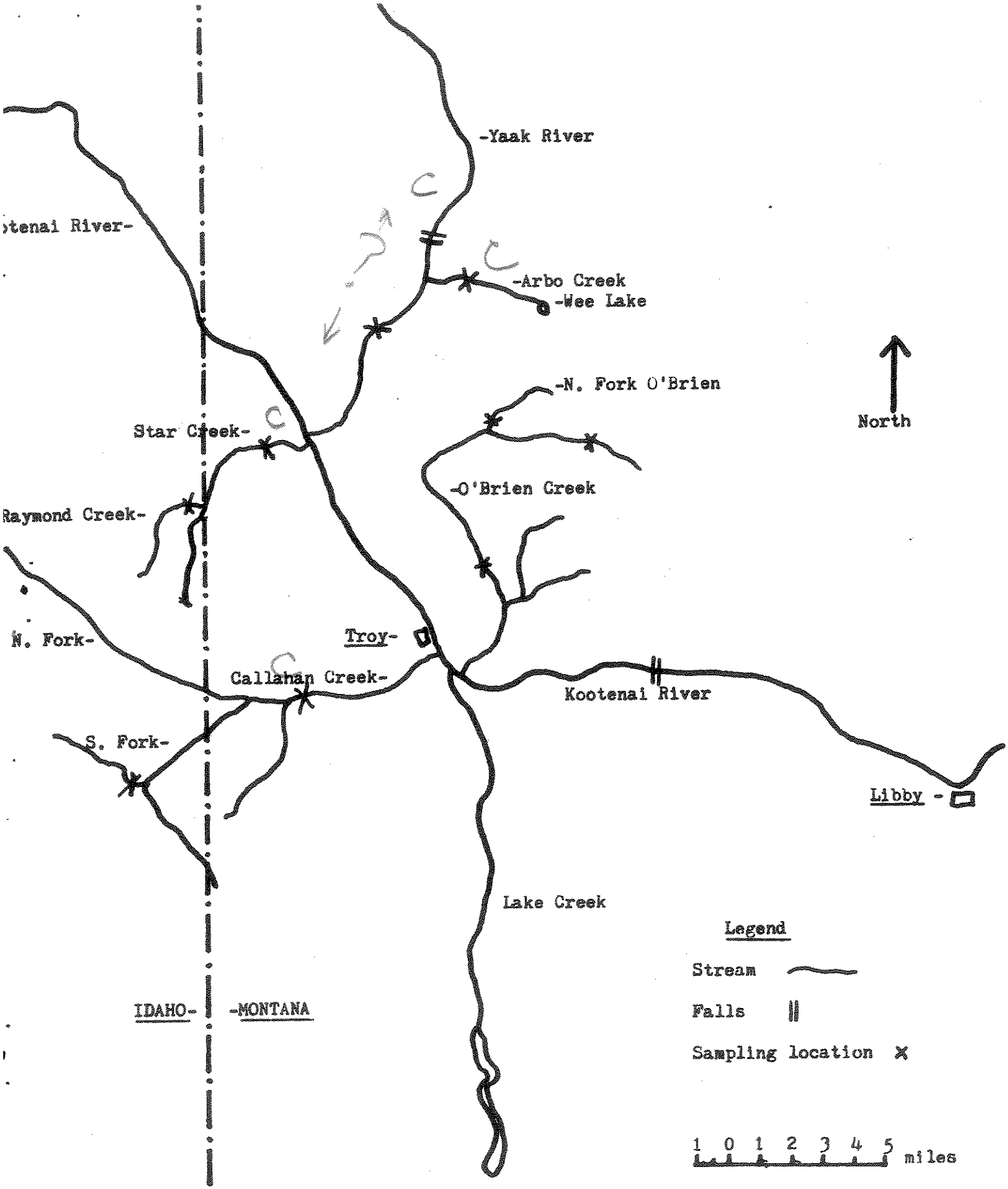

Figure 2. Map of sampling area.

inserts as small as 4X6 mm and placed side by side along the gel separated by 1 mm. In this manner, more than 40 samples can be tested on a single gel. After the inserts were in place, the smaller gel section was placed firmly against the larger section and inserts. The plastic wrap was folded back to expose about 1 cm at each end of the gel.

The buffer trays used were plastic dishes containing 150 to 200 ml of buffer. The tray buffer was transmitted to the gel with disposable utility cloths. The initial current for the electrophoresis was 250V. The sample inserts were removed and discarded following a 10 min preliminary electrophoresis. The gel sections were again placed firmly together. Ice packs composed of gelled refrigerant repackaged to fit on a gel-sized glass plate were placed on top of the gel and electrophoresis was continued until the dye marker or boundary migrated the appropriate distance- about 6 to 9 cm from its origin.

Staining Procedures

The gel was sliced horizontally into 4 sections by pulling tightly drawn monofilament sewing thread through the gel at 3 levels determined by 1/16th in plastic strips placed on both sides of the gel. The 4 resulting sliced were then placed into individual trays and stained.

The stains used were:

For LDH (Lactate Dehydrogenase)

NBT (5 mg)

PMS (10 mg)

NAD as cofactor (5 mg)

20 ml 0.5M DL-NA-Lactate

Sample	LDH-4 (1.00)	SOD (1.00)	MDH-3 (1.00)	(1.18)
Chambers Creek	.794	.651	.859	.000
Quinault River	.975	.575	.856	.000
McCreary	1	.500	.938	.006
West Virginia	1	.844	1	.000
Univ. of Wash	1	1	.981	.000
Deschutes River	.400	.962	.982	.000
Pahsimeroi River	.388	.938	.994	.006

(Allendorf, 1975)

Table 1. Frequencies of alleles for the LDH-4, SOD and MDH-3 loci in seven reference populations.

RESULTS

The frequency for the common alleles for LDH-4, SOD and MDH-3 were recorded for our samples. See Table 2. The common allele is designated as 1.00. This designation represents the migration distance of the protein coded for by this allele. MDH-3 shows polymorphism so we also indicated the frequency of the 1.18 allele. Also indicated in Table 1 is the chi square derived from the Hardy-Weinberg proportions for each stream for each protein. Using this data, we constructed table 3. The values represent a measure of the genetic similarity between corresponding streams averaged for the three proteins tested. The genetic similarity (S) is defined as 1-D. The genetic distance (D) is defined as:

$$D = \left[1/2 \sum_{j=1}^{A_i} (P_{ijx} - P_{ijy})^2 \right]^{1/2}$$

where A_i is the number of alleles at the i^{th} locus, and P_{ijx} and P_{ijy} are frequencies of the j^{th} allele at the i^{th} locus in populations x and y respectively (Rogers, 1972). The weighted average linkage method (WALM) was then applied to cluster the genetic similarities and elucidate the relationships between the populations (Sneath and Sokal, 1973). A dendrogram was then prepared using the data from the WALM analysis. See Table 4.

	Yaak River	Star Creek	Raymond Creek	Arbo Creek	Summit-Goat	Callahan Creek (Upper)	Callahan Creek (Lower)	Arlee Hatchery	Chambers	Quinault	West Virginia	U of Washington	McCreary	Deschutes	Pahsimeroi
Yaak River	1														
Star Creek	.836	1													
Raymond Creek	.883	.929	1												
Arbo Creek	.859	.899	.830	1											
Summit-Goat	.915	.863	.933	.853	1										
Callahan Creek (Upper)	.915	.763	.833	.774	.865	1									
Callahan Creek (Lower)	.893	.741	.810	.752	.870	.978	1								
Arlee Hatchery	.868	.875	.879	.910	.889	.784	.806	1							
Chambers	.845	.856	.788	.970	.824	.758	.735	.872	1						
Quinault	.758	.890	.822	.910	.775	.671	.648	.852	.913	1					
West Virginia	.867	.955	.961	.849	.897	.796	.777	.866	.820	.854	1				
U of Washington	.867	.909	.981	.800	.941	.838	.823	.844	.744	.808	.942	1			
McCreary	.753	.902	.834	.850	.770	.666	.643	.791	.854	.938	.865	.820	1		
Deschutes	.879	.722	.794	.727	.835	.941	.952	.728	.724	.637	.755	.787	.632	1	
Pahsimeroi	.878	.728	.789	.726	.826	.931	.832	.727	.723	.636	.763	.770	.631	.983	1

Table 3. Average genetic similarity matrix among fifteen populations for LDH-4, SOD, and MDH-3 loci.

DISCUSSION AND CONCLUSION

Electrophoresis and selective protein staining were used to distinguish between inland steelhead, coastal steelhead, and resident rainbow. The average gene frequencies for these populations for the three proteins tested for are presented on page 14. The loci LDH-4 and SOD separate the two steelhead groups the best. Some conclusions are based on a comparison of this information and Table 2. Most of our streams seem to follow similar frequencies as the resident rainbow and coastal steelhead. However, three of them appear distinctly different. Upper and lower Callahan Creek fish show a low LDH-4 and a high SOD frequency, very similar to the gene frequencies for inland steelhead trout. Also, the Yaak River appears to deviate from the other streams. The LDH-4 frequency of .7 is significantly lower than the .874 of the coastal steelhead. Also, the SOD frequency of .913 approximates the frequency of inland steelhead. Goat-Summit fish didn't appear to follow the pattern of inland steelhead. From this information, we conclude that Callahan Creek and the Yaak River have inland steelhead populations.

Our gene frequencies were also compared with those of the reference streams chosen. The genetic similarity clustering appears in Table 4. In analyzing this data, we see two distinct clustered groups. Group A contains the streams Quinault through West Virginia. This group actually consists of two subgroups. Group 1A is from Quinault to Chambers. Here we see Arlee Hatchery and Arbo Creek clustering with three coastal steelhead river systems. This clustering of Arlee Hatchery stock with coastal

of the streams we sampled, we come to the conclusion that there are no impassable barriers to the movement of populations. Hence, we find it not only possible, but probable that fish were able to migrate to Montana and establish native populations. We suggest that the Kootenai River provided the best access for these populations into Montana.

Application of this work comes in the managing of these resources. It is naturally desirable to maintain these native populations since they should be better adapted to the Montana environment than introduced brood stocks. In order to maintain these populations, we suggest no planting here where the natural gene pool will become jeopardized.

Simon, R. C. March 15, 1978. Telephone conversation with George Holton. Montana Fish and Game Files. Helena, Mt.

Sneath, P. H. and R. R. Sokal. 1973. Numerical Taxonomy. Freeman Press, San Francisco.