

January 12, 1984

Dr. Robert J. Behnke Department of Fishery and Wildlife Biology Colorado State University Fort Collins, Colorado 80523

Dear Bob:

Thanks for the manuscript on artic charr. I certainly agree with you that Nyman's conclusions drawn from a single esterase locus are farcical at best. I really cannot understand how he was able to get such conclusions published.

I have enclosed a copy of the galleys for the hybrid manuscript. Our limited data from bull trout populations indicates that in contrast to brook trout the bull trout apparently have low amounts of intraspecific genetic variation. Thus, you might want to revise this point in your manuscript.

This past summer we collected a fish that was undoubtedly the progeny from a brook trout-bull trout hybrid x brook trout mating. This conclusively demonstrates that some of these hybrids are fertile, although it appears that only a very small percentage are. Our data indicate about one percent.

We are working on a manuscript describing the heritabilities of eight meristic characters in a rainbow trout population. Many of these have unusually high heritabilities, greater than 0.80. I will send you a copy as soon as the manuscript is ready to submit for publication.

Sincerely,

Robb Lang

Robb Leary

RL/cs Encl.



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

June 13, 1986

Robert Behnke Fish and Wildlife Biology Colorado State University Fort Collins, Colorado 80523

Bob:

At long last here are the <u>Salvelinus</u> electrophoretic data. The samples were obtained from the following locations with sample sizes in parentheses: Bull trout, <u>S. confluentus</u> - South Fork Lolo Creek, Montana (34); Dolly Varden, <u>S. malma</u> - Bear Lake (1), Fox River (12), and Mystery Creek (1) from the Kenai Peninsula, Alaska; Arctic Char, <u>S. alpinus</u> - Clam Lake (1), Dolly Varden Lake (4), East Finger Creek (4), and Moose Lake (1) from the Kenai Penisula, Alaska and a single specimen from an unknown source in Sweden; Brook trout, <u>S. fontinalis</u> - Harriman Trout Company, St. Ignatius, Montana (14), Lake trout, <u>S. namaycush</u> - Lewis Lake strain maintained at the Jackson National Fish Hatchery, Jackson, Wyoming (50).

We determined the genotype of each individual at 42 protein encoding loci (Table 1) and of these 18 can be used to differentiate among the taxa (Table 2). Most of these loci, however, distinguish the brook trout and lake trout from the other three species. Only two loci, <u>Me2</u> and <u>Sod</u> unambiguously differentiate the bull trout from the Dolly Varden and Arctic char. These latter two species share alleles at all loci examined and thus cannot be distinguished with these data.

In Table 3, we have listed the allele frequencies at those loci that showed evidence of inter and intraspecific genetic variation in these samples with sample sizes greater than one plus the Swedish char. The inclusion of the Swedish char is justified based on the work of Nils Ryman and his colleagues. In an extensive survey of Swedish char they found that all populations analyzed clustered together at a Nei's genetic distance of 0.01. This indicates that there is relatively little electrophoretically detectable genetic differentiation among these fishes and thus a single specimen can be considered a valid representation of them.

Considering the Artic char, the allele frequencies in Table 3 have a couple of noteworthy points. At <u>Aatl</u>, the Swedish and Alaska char are completely divergent. The Swedish char have the allele common to the Dolly Varden while the Alaskan char have the allele characteristic of the bull trout. Although we did not detect the <u>Gpi3(108)</u> allele in the two samples of Alaskan char included in Table 3, we did detect this allele in the other two Alaskan specimens. Thus the allele frequencies at this locus are widely divergent Behnke June 13, 1986 Page 2

among populations of Arctic char. The 108 allele being common in Swedish populations the 103 allele common in some Alaskan populations, and both alleles apparently being common in other Alaskan populations.

We calculated Nei's genetic distance between all pairs of samples in Table 3. The dendrogram (Fig. 1) produced by cluster analysis of the genetic distance matrix (Table 4) shows rather nicely the confusing nature of the data. Note that the Swedish char clusters with Dolly Varden before it clusters with the Alaskan char. This indicates that there is as much electrophoretically detectable genetic divergence among Arctic char included in our samples as there is between the Arctic char and Dolly Varden. In contrast to this mess, the bull trout, lake trout, and brook trout are clearly distinct from each other as well as from the Arctic char - Dolly Varden complex. The available data, therefore, support the specific status of the bull trout.

Sincerely,

-Robb Leans

Robb Leary

Enclosures

RL:sf

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|--|----|---|---|---|---|
|--|----|---|---|---|---|

Enzymes and loci examined in samples of Salvelinus

| Loci | Tissue |
|----------------------|--|
| Adkl,2 | м |
| Adh | L |
| Aatl,2 Aat(3,4) | L M |
| Ckl,2 Ck3 | M E |
| Gpi1,2,3 | М |
| Gap(3,4) | E |
| G3p1,2 | L |
| G11,2 | E |
| Idhl,2 Idh(3,4) | M L |
| Ldhl,2 Ldh3,4,5 | M E |
| Lgg | E |
| Mdhl, 2 Mdh(3, 4) | L M |
| Me1,2,3 Me4 | M L |
| Pgml,2 | М |
| 6Pg | М |
| Sdh | L |
| Sod | L |
| | Adk1,2 Adh Aat1,2 Aat(3,4) Ck1,2 Ck3 Gpi1,2,3 Gap(3,4). G3p1,2 G11,2 Idh1,2 Idh1,2 Idh1,2 Idh1,2 Idh1,2,3 Mdh1,2 Mdh1,2,3 Me4 Pgm1,2 GPg Sdh |

Note: E = eye, L = liver, M = muscle. The pairs of loci listed in parentheses are electrophoretically indistinguishable in at least one taxon so they are considered to be single tetrasomic loci in all analyses.

| Taxa and alleles | | | | | | | | |
|------------------|-----------------|--------------|-------------|----------|----------|--|--|--|
| Locus | Bull | Dolly Varden | Arctic Char | Brook | Lake | | | |
| Aatl | 54 100,54 | | 100,54 | 100 | 100, nul | | | |
| Adk2 | 100 | 100,20 | 20 | 100 | 100 | | | |
| Ckl | 85 | 85 | 85 | 100 | 85 | | | |
| Ck2 | 86 | 86 | 86,100 | 100 | 86 | | | |
| Gpil | 100 | 100 | 100 | 100 | 108 | | | |
| Gpi3 | 108 | 103,108 | 103,108 | 108 | 108 | | | |
| Ldhl | 54 | 54 | 54 | 0 | 0 | | | |
| Ldh2 | 91 | 91 | 91 | 91 | 88 | | | |
| Ldh4 | 76 [.] | 76 | 76 | 28 | 76 | | | |
| Mdhl | 145 | 145 | 145 | 110 | 145 | | | |
| Mdh3,4 | 86 | 86 | 86 | 86,93 | 53,86 | | | |
| Mel | 145 | 145 | 145 | 56 | 127 | | | |
| Me2 | 145 | 175 | 175 | 145 | 125 | | | |
| Me4 | 95,97 | 95 | 95 | 97 | 97 | | | |
| Pgml | 100 | 100,138 | 75,100 | 100,null | 100 | | | |
| Sdh | 120 | 120 | 120 | 200 | 120 | | | |
| Sod | 190 | 177,142 | 177 | 97 | 190,177 | | | |

Loci that can be used to distinguish among members of the genus <u>Salvelinus</u>. Allelic mobilities are relative to the common allele at the homologous locus in rainbow trout, <u>Salmo gairnderi</u>.

Note: When more than one allele is observed at a locus within a species the most common allele is listed first.

TABLE 2

| | | Taxa and allele frequencies | | | | | | | |
|----------------|---------|-----------------------------|------------------------|---|-------------------|-------------|----------|------------|--|
| | | Bull | Dolly <u>Varden</u> | Arctic Char | | | Brook | Lake | |
| Locus | Alleles | S.F.Lolo | Fox Rvr | East Finger Crk | Dolly Varden Lake | Sweden | Harriman | Lewis Lake | |
| Aatl | 54 | 1.000 | 0.208 | 1.000 | 1.000 | | | | |
| | 100 | | 0.792 | | | 1.000 | 1.000 | 0.684 | |
| | null | | | | | | | 0.316 | |
| | 6.0 | 1 | 1 | 0.540 | | | | | |
| Aat3,4 | | 1.000 | 1.000 | 0.563 | 0.688 | 1.000 | 0.679 | 0.500 | |
| | 100 | | | | | | | 0.495 | |
| | 80 | | | | | | 0.321 | 0.005 | |
| | 40 | | | 0.437 | 0.312 | | | | |
| Adk2 | 100 | 1.000 | 0.708 | | | | 1.000 | 1.000 | |
| | 20 | | 0.292 | 1.000 | 1.000 | 1.000 | | | |
| | | | | | | | | | |
| Ckl | 85 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | | 1.000 | |
| | 100 | | | | | | 1.000 | | |
| Ck2 | 86 | 1.000 | 1.000 | 0.875 | 0.500 | 1.000 | | 1.000 | |
| | 100 | | | 0.125 | 0.500 | | 1.000 | | |
| Gap3,4 | 125 | 1.000 | 0.979 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | |
| Gaps,4 | 100 | 1.000 | 0.021 | | | | 1.000 | | |
| Company | | | | | | | | | |
| G3pl | 105 | 1.000 | 1.000 | 0.500 | 0.750 | 1.000 | 0.679 | 1.000 | |
| | 89 | | | 0.500 | 0.250 | | 0.321 | | |
| Gpil | 100 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | | |
| OPII | 108 | | | | | | | 1.000 | |
| | | | | | | | | | |
| Gpi3 | 108 | 1.000 | 0.042 | | | 1.000 | 1.000 | 1.000 | |
| | 103 | | 0.958 | 1.000 | 1.000 | | | | |
| Idhl | 200 | 0.853 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | |
| and starting | 333 | 0.147 | | | | | | | |
| Idh3,4 | 106 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 0.375 | 1.000 | |
| 14115,4 | 135 | 1.000 | | | | | 0.465 | | |
| 111111 | 82 | | | | | | 0.405 | | |
| and the second | | | | | | | | | |
| | null | | | (1) (1) (1) (1) (1) (1) (1) (1) (1) (1) | | | 0.035 | | |
| Ldhl | 54 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | | | |
| | 0 | | | | en entre ston Al | | 1.000 | 1.000 | |

Allele frequencies at those loci that showed evidence of genetic variation in sample of the genus <u>Salvelinus</u>.

TABLE 3

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TABLE 3 -- Continued

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| Ldh2 | 91 88 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 |
|--------|--------------------------|----------------|------------------------|-------------------|-------------------|-------------------|------------------------|------------------------|
| Ldh3 | 135 95 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 0.750 0.250 | 1.000 |
| Ldh4 | 76 28 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 |
| Ldh5 | 100 95 | 1.000 | 0.583 0.417 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 |
| Mdhl | 145 110 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 |
| Mdh3,4 | 86 93 53 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 0.839 0.161 | 0.005 0.995 |
| Mel | 145 127 56 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 |
| Me2 | 145 175 125 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 |
| Me4 | 95 97 | 0.941 0.059 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 |
| Pgml | 100 138 75 null | 1.000 | 0.833 0.167 | 1.000 | 1.000 | 1.000 | 0.750 0.250 | 1.000 |
| Pgm2 | 100 122 90 | 0.971 | 0.833 0.167 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 |
| Sdh | 120 200 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 |
| Sod | 190 177 142 97 | 1.000 | 0.917 0.083 | 1.000 | 1.000 | 1.000 | 1.000 | 0.950 0.050 |
| | | | | | | | | |

TABLE 4

Arctic Char Bull Dolly Varden East Finger Dolly Varden Sweden Brook Dolly Varden 0.109 ---Arctic Char East Finger 0.159 0.051 Dolly Varden 0.158 0.050 0.005 Sweden 0.143 0.047 0.068 0.066 ---Brook 0.342 0.406 0.497 0.471 0.412 ---Lake 0.238 0.288 0.399 0.400 0.318 0.386

Nei's genetic distance between members of the genus Salvelinus

Figure 1 -- Dendrogram produced by cluster analysis of the Nei's genetic distance matrix.

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Robb heary Department of Toology Viversity of Montana Missoula, Mantana 59812



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Robert Behuhe Fish and Wildlife Biology Colorado State University Font Colling Colorado 80523

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