Dr. Robert Behnke
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Dear Bob:

I apologize for being so slow in answering your letter. I've been on the road lately and heavily involved in the Yukon River negotiations between the U.S. and Canada.

We've looked at a number of char populations across the North Slope of Alaska and Canada the past few years for a genetic stock identification study. I've enclosed a draft copy of our report. Unfortunately, we just haven't had the time or resources to do any serious comparisons with any Dolly Varden populations. We are currently doing electrophoretic work on approximately 8,000 samples from the North Slope, Yukon River, and Bristol Bay. As a result, we've been rather overwhelmed. We did look at some Dolly Varden samples from a couple of interior rivers and from Karluk Lake a few years ago and found no fixed differences between these samples and the North Slope char. There were, however, some major frequency differences.

We hope to get a short breather this winter and plan to write up a couple of publications on the char work - one on just the electrophoretic results with comparisons with Dolly Varden and other char populations, and a second on the genetic stock identification results. When we get a manuscript together, I will send you a copy for review.

On another note, we are having difficulty finding someone to fill a GS-9 Geneticist position. We recent advertized the position and had no takers. If you know of anyone who might be interested, please have them contact me. We are re-advertizing the position and I've enclosed the announcement.

I hope we can get back to you this winter with some more definitive comparisons between the Arctic char and Dolly Varden. Have a good holiday season.

Sincerely,

Dick

Richard L. Wilmot

POPULATION GENETIC STRUCTURE OF ARCTIC CHAR (*Salvelinus alpinus*) FROM RIVERS OF THE NORTH SLOPE OF ALASKA AND CANADA

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INTRODUCTION

Potential problems with oil exploration and development on the North Slope of Alaska include the effects of offshore causeways, other structures, and development activities on anadromous species such as Arctic char (Salvelinus alpinus) and Arctic cisco (Coregonus autumnalis). In offshore areas, these species are in mixed aggregations, making it difficult to determine specifically which stocks could be at risk during what time period. In the tributaries, development activities such as river crossings or water removal from pools vital to overwintering could also affect migration, spawning, or rearing areas.

Arctic char are of special interest because of their relatively low abundance, limited range in a narrow band of coastal waters, and their importance in subsistence fisheries. Studies (e.g., Furniss 1975; Craig and McCart 1975) characterizing the marine and freshwater phases of Arctic char life history emphasize the importance of the coastal area of the Beaufort Sea. Populations of Arctic char migrate from freshwater, springfed spawning and overwintering areas to nearshore marine feeding grounds. Migration studies using mark and recapture techniques indicate that movements are generally limited to an area adjacent to the river of origin (Furniss 1975). However, examples of extended migration and overwintering in drainages other than those used for spawning have been documented (Craig and McCart 1976; Glova and McCart 1974).

In order to determine which stocks could be affected by

development, and possibly to predict how they would be affected, we need to understand the stock structure of both the inland and offshore stages of the Arctic char life history. By studying the amount and pattern of genetic variation in the populations while they are associated with their natal drainages, we can make inferences about the evolutionary history of northern Arctic char, and predict their ability to respond to changing environmental conditions. Using samples from spawning populations of the tributaries, we can genetically characterize these individual stocks, determine their relationships to each other, and form a baseline.

With baseline information, we can estimate the composition of mixed stocks using genetic stock identification methods to compare the "genetic types" of the baseline to the mixed stock samples. Electrophoretic detection of protein variation makes it possible to discriminate among stocks using quantifiable characters having a genetic basis.

Electrophoretically distinguishable characters have generally proven to be stable characteristics of fish stocks that have been studied (see Utter et al. 1980; Grant et al. 1980; Milner et al. 1980; Campton and Utter 1987; and Robin Waples, National Marine Fisheries Service, personal communication). Exceptions have been observed in Alaska sockeye (Wilmot, U.S. Fish and Wildlife Service, unpublished data) and in chinook of the Columbia River, Washington (Milner et al. 1980). In the latter case, shifts apparently related to straying from transplantation and migration, though selection is a possible explanation.

If the species of concern has a suitable stock structure, biochemical genetics methods can be used to estimate the percent composition of various stocks represented in mixed aggregations sampled from offshore areas. This type of information can provide site-specific information on stocks at risk from habitat alteration, and biological data at migratory stages of the life cycle of these natural populations.

Background

The objectives of the first year of this study were to: 1) characterize the amount and pattern of genetic variation in populations of anadromous Arctic char from major drainages of the North Slope of Alaska, 2) determine whether the population structure of North Slope char is such that genetic stock identification of mixed populations collected from offshore waters would be possible, and 3) describe how a sampling program would be designed to use genetic stock identification to determine which stocks would be affected by specific development projects.

In 1986, samples of juvenile Arctic char from 15 populations were collected from 10 tributaries to the Beaufort Sea. We used horizontal starch-gel electrophoresis to identify protein products of 42 loci coding for 20 enzymes in three tissues. We measured the amount of variation, the pattern of variation (genotypic distribution) within population samples, the similarity between populations, their heterogeneity, and the degree of gene diversity among groups.

We found that northern Alaska Arctic char have more genetic variation than might be expected given the relatively narrow range of waters they inhabit and the harsh environmental conditions. With an average heterozygosity per locus of 5.1%, they are typical of fish species in general; at the upper end of the range observed in other salmonid fishes; and higher than most other Arctic char populations that have been studied.

The genetic identities (Nei 1972; 1978) among riverine North Slope Arctic char populations studied are high (>0.987), indicating fairly recent common ancestry. High similarity values do not imply lack of significant differences between populations. Heterogeneity tests between populations indicated the distinctness of the populations and the complexity of the relationships between them. Almost all North Slope Arctic char populations studied are significantly genetically distinct from each other. The implication of this information is that fish from different drainages are reproductively isolated, and are most likely true to their spawning streams.

Since anadromous char do mix to some unknown degree in feeding areas, the differences that have been established between stocks are likely maintained by homing behavior. Populations of each drainage are probably discrete, locally adapted units. It is not clear at this time how non-migratory forms are related to anadromous stocks. Various authors maintain differences within drainages.

It is unlikely that loss of any one stock would be mitigated by substitution of another. While the actual loci we have studied may be selectively neutral, underlying variation that is marked by these loci

may be highly selected for in different environments, corresponding generally to different drainages. As such, Arctic char stocks of the North Slope should be managed as individual, unique gene pools.

North Slope Arctic char do not have the magnitude of difference between groups exhibited by the non-migratory char of northern Europe. They do, however, compare with the population structure of anadromous Pacific salmon. To do genetic stock identification there must be sufficient detectable genetic variation between populations of different major drainages, combined with a low within-group variability.

Our data (Everett and Wilmot 1987) indicate that North Slope char have a relatively large amount of genetic variation; there are significant differences among populations; and the observed variation is partitioned such that there is as much difference between char from different drainages as there is among populations of sockeye and chum salmon where genetic stock identification has been used successfully. As such, we could anticipate successful application of this technique to the identification of char at specific offshore sites, and designed a project to collect additional samples for baseline data, plus offshore samples from Beaufort Sea mixed aggregations near Endicott Causeway, Prudhoe Bay, and Camden Bay.

Objectives

The goals of the 1987 Arctic Fish Habitats and Sensitivities Study are to understand the genetics of the anadromous North Slope Arctic

char populations, and to determine which of the populations using certain offshore areas of the Beaufort Sea would be affected by development projects in that area.

The objectives of the genetic stock identification study are to: 1) analyze additional populations of Arctic char that are major contributors to the offshore mixed stock of the Beaufort Sea, 2) compare the Arctic char of the drainages of the Chukchi Sea to those of the Beaufort Sea, and 3) collect samples of Arctic char from the mixed stock in the Beaufort Sea and estimate the percent composition of fish from the baseline populations we have studied that contribute to mixed stock collections.

To accomplish these objectives, we collected samples of Arctic char from several additional river sites for baseline information, and acquired samples from mixed stocks at the mouth of the Sagavanirktok Drainage at the Endicott Causeway and from the Camden Bay area. We did electrophoretic analysis of protein variation for all these fish, and did statistical analyses to determine the relationships of the collections to each other (over space, time, and resident versus non-resident populations). We then used the baseline data to do computer simulations to determine the accuracy and precision of our database, and then did actual stock-composition analyses of the samples from the Endicott area.

METHODS

Baseline Collections

U.S. Fish and Wildlife Service crews used electroshockers and minnow traps to sample for Arctic char at 22 sites on 16 rivers. Char were found at 12 sites on eight rivers (Table 1, Figure 1). Sample sizes ranged from 21 to 97 fish captured. Service personnel took the fish, on ice, back to Deadhorse, Alaska. They were frozen, then shipped to the Service lab in Anchorage. There they were held at -80°C until muscle, liver, eye, and heart tissues were dissected. Long term storage of tissues is also at -80°C.

Offshore Collections

Our target was 200 fish collected from one location during a five-day period, three times during the summer season. Our sample sizes were determine by availability during that five-day period. Samples were collected from near Prudhoe Bay in the area around Endicott causeway June 24-26, July 29 - August 1, and September 8 - 11, 1987 by Envirosphere Company personnel using fyke traps. Service personnel worked at Envirosphere's Deadhorse laboratory to dissect and freeze samples before shipping them back to the Service laboratory in Anchorage.

Samples were collected from the Camden Bay area at Kongaevik Point and Simpson Cove on July 1, 1987 by personnel of the Service's

Table 1.- Populations of Arctic char collected from rivers of the North Slope of Alaska and Canada with site location, number of samples collected from each site, and date of collection.

Population	UTM coordinates			Number of char	Date
	Grid	Latitude	Longitude		
Aichilik River					
Site 1	7W	7699000	419000	40	9/86
Site 2	7W	7688000	419000	70	8/87
Anaktuvuk River	5W	7626000	565000	40	5/86
Babbage River					
Site 1	7W	7626000	579000	53	8/87
Site 2	7W	7619000	575000	21	8/87
Canoe River	7W	7611000	593000	35	9/86
Canning River					
Site 1	6W			27	5/86
Site 2	6W	7716000	525000	70	8/87
Site 3	6W	7691000	516000	62	8/87
Marsh Fork	6W	7665000	539000	29	5/86
Shublik Spring	6W	7698000	535000	59	8/87
Echooka River	6W	7685000	489000	24	4/86
Egaksrak River	7W	7700000	435000	41	5/86
Firth					
Site 1	7W	7625000	506000	64	8/87
Site 2	7W	7610000	495000	47	8/87
Joe Creek	7W	7646000	501000	40	9/86
Hula Hula River					
Site 1	6W	7741000	614000	15	10/85
Site 2	6W	7712000	609000	37	10/85
Site 3	6W	7692000	598000	59	10/85
Site 4	6W	7735000	613000	97	8/87
Ivishak River	6W	7690000	519000	50	9/86
Kavik River	6W	7690000	519000	40	9/86
Kongakut River					
Site 1	7W	7710000	473000	40	9/86
Site 2	7W	7668000	465000	90	8/87
Lupine River	7W	7659000	439000	48	8/87
Ribdon River	7W	7615000	460000	40	5/86
Sadlerochit Spring	6W	7730000	595000	62	8/87

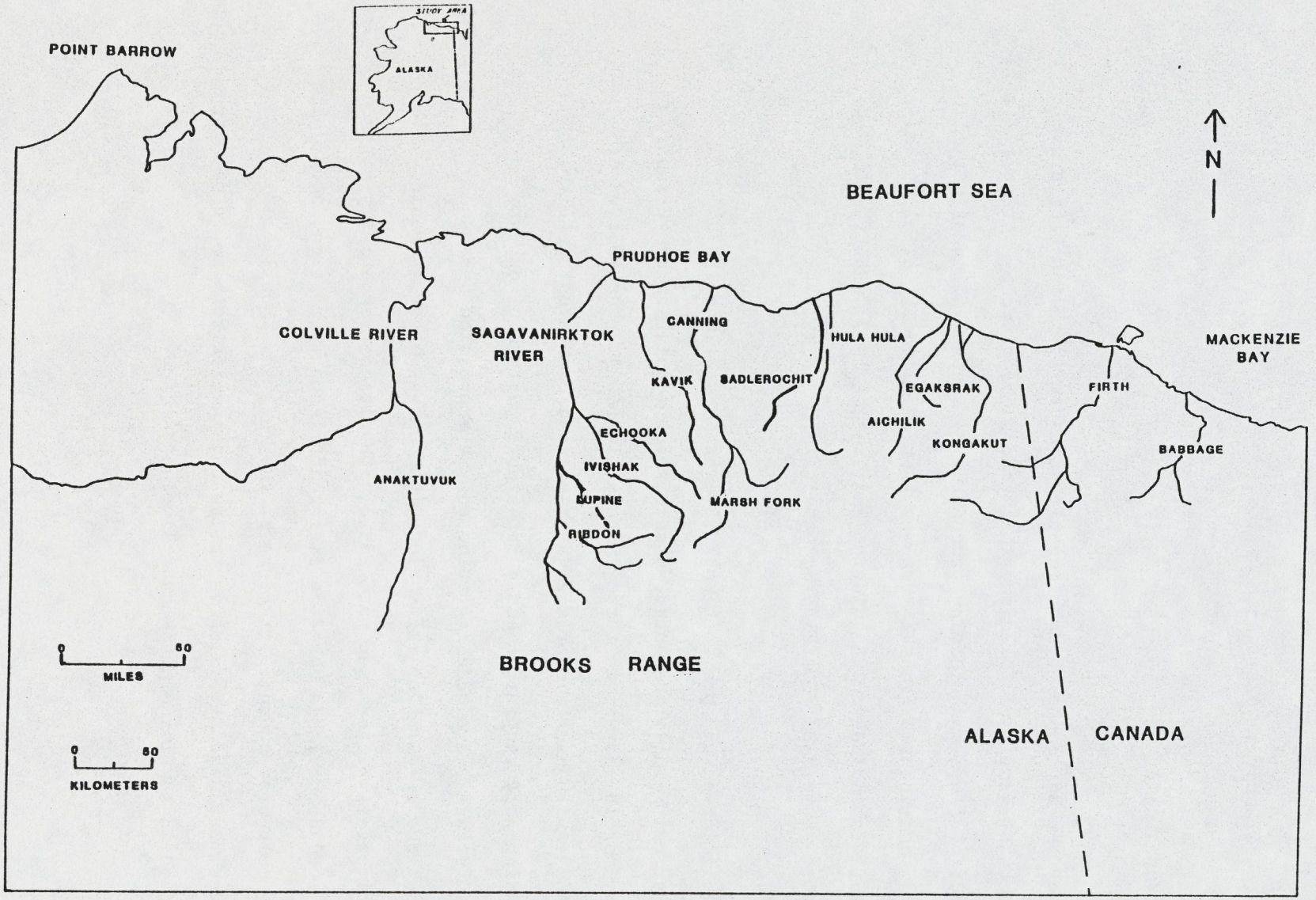

Figure 1.- Sampling sites for Arctic char genetics research.

Fairbanks Fisheries Assistance Office.

Electrophoresis

We used horizontal starch-gel electrophoresis to identify protein products of gene loci following the methods described by Utter et al. (1974). Buffers and staining procedures were after Allendorf et al. (1977), and isozyme nomenclature was that of Allendorf et al. (1983). Gel buffers included: AC (Clayton and Tretiak 1972) pH 6.1, 6.8; AC+ (AC plus 30 mg NAD); RW (Ridgway et al. 1970) pH 8.2; EBT (Boyer et al. 1963) pH 8.5.

Building on our previous work (Everett and Wilmot 1987), statistical results are based on successful resolution of 42 loci coding for 19 enzymes in three tissues (Table 2). The loci we used are those with nearly complete data sets and consistent results, including good resolution and a repeatable pattern of expression.

Inferences were made regarding enzyme expression based on: 1) assumptions of parallel expression with that of other salmonids with experimentally determined patterns of inheritance (especially Johnson 1984), 2) comparisons based on different tissue expression, and 3) the known molecular subunit structure of the enzymes. Mobilities of enzymes were measured relative to the common electrophoretic phenotype observed in samples of Anaktuvuk River Arctic char.

Table 2.- Enzymes, Enzyme Commission (E.C.) numbers[a], and loci examined in samples of Arctic char collected from northern Alaska in 1987. Buffers include: AC (Clayton and Tretiak 1972), pH 6.1 and pH 6.8; AC+ = AC + NAD; RW (Ridgway et al. 1970), pH 8.2; and EBT (buffer of Boyer et al. 1963, modified by Washington Department of Fisheries biologists), pH 8.5. Tissues include muscle (M), liver (L), and eye (E). The pairs of loci listed in parentheses are electrophoretically indistinguishable (isoloci; Allendorf and Thorgaard 1984). For these analyses, each member of a locus pair was treated as an individual locus with variation assigned to one of the two loci.

Enzyme	E.C. number	Loci	Buffer	Tissue
Adenylate kinase	2.7.4.3	Adk1	AC 6.8	M
Alcohol dehydrogenase	1.1.1.1	Adh1	RW	L
Aconitate hydratase	4.2.1.3	Aco4	AC 6.8	L
Aspartate aminotransferase	2.6.1.1	Aat1,2	RW	L,E
		Aat(3,4)	RW	M
Creatine kinase	2.7.3.2	Ck1,2	RW	M
		Ck3	RW	E
Fumarate hydratase	4.2.1.2	Fh1[b]	AC 6.8	M
ß-Ga	3.2.1.30	Hex1[b]	AC 6.8	L
Glucose phosphate isomerase	5.3.1.9	Gpi(1,2)	RW	M
		Gpi3	RW	M
Glutathione reductase	1.6.4.2	Gr1	RW	L
Glyceraldehyde-3-phosphate dehydrogenase	1.2.1.12	Gap3,4	AC 6.1	E
Glycerol-3-phosphate dehydrogenase	1.1.1.8	G3p1,2	AC 6.1,RW	M,L
Glycyl-leucine peptidase	3.4.11.	PepGL1	EBT	M
Isocitrate dehydrogenase	1.1.1.42	Idh1,2	AC 6.8	M
		Idh(3,4)	AC 6.1,6.8	L,E
Lactate dehydrogenase	1.1.1.27	Ldh1,2	RW	M
		Ldh3,4,5	RW	E
		Ldh	RW	L
Leucyl-glycyl-glycine peptidase	3.4.13.	PepLGG1	EBT	M
Malate dehydrogenase	1.1.1.37	Mdh(1,2)	AC 6.1	M
Malate dehydrogenase		Mdh(3,4)	AC 6.1	M
(NADP-dependent)	1.1.1.40	Mdhp1,2,3	AC 6.1	M
Phosphoglucomutase	2.7.5.1	Pgm1,2	RW	M
		Pgm(3,4)	AC 6.1	L,M
6-Phosphogluconate dehydrogenase	1.1.1.44	6Pg1	AC 6.8	M,L,E
Sorbitol (iditol) dehydrogenase	1.1.1.14	Sdh(1,2)	RW	L
Superoxide dismutase	1.15.1.1	Sod1	RW	L
Xanthine dehydrogenase	1.2.3.2	Xdh1[b]	RW	L

[a] Enzyme Commission, IUCBN. (citation).

[b] Variation was observed at these loci but poor resolution in many samples prevented inclusion in the analyses.

STATISTICAL METHODS

Amount of Genetic Variation

The amount of genetic variation is estimated by determining the percent of loci that are polymorphic (P), and the mean percent of heterozygous loci per individual (H). Expected average heterozygosity for each locus is calculated using allele frequencies of observed genotypes in each population and expected random mating (Hardy-Weinberg) proportions:

$$H = 1 - \left(\sum_{j=1}^{L} \sum_{i=1}^{A_j} P_{ij}^2 \right) / L$$

where L is the number of loci, A_j is the number of alleles at the jth locus, and P_{ij} is the frequency of the ith allele at the jth locus.

The standard criteria for polymorphism (P) is the percent of the loci examined in a population in which the frequency of the common allele is less than or equal to 0.99.

For this and subsequent analyses, isoloci (duplicated locus pairs with indistinguishable mobilities) were counted as two individual loci and all observed variation was attributed arbitrarily to only one locus of the pair.

Genotypic Distribution

Observed genotypes in samples were tested for conformance to random mating (Hardy-Weinberg) proportions. A chi-square test was

used to determine whether the frequency of genotypes for each locus equal those expected from calculations of probable combinations of alleles (with the frequencies we observed) joining at random. For each population sampled, a multiple simultaneous chi-square test was done by summing the chi-square values over all the variable loci, summing the degrees of freedom, and comparing these values to a chi-square distribution.

Genetic Heterogeneity

Criteria for joining collections is based on a joint resolution by the West Coast interagency working group doing genetic stock identification of Pacific salmon. It has been agreed that the criteria for joining collections from the same drainage is a probability greater than 0.05 that the collections -- made at different sites or in different years -- are not significantly different using a chi-square or log likelihood ratio (G-test) statistic.

Collections from different geographic areas are not joined before basic analyses. After estimates of percent composition are made, populations can be joined to reflect biological and/or management groups, and the bootstrap variances are recalculated.

To test the heterogeneity between paired populations, we used multiple simultaneous G-tests (Sokal and Rohlf 1981). G-tests were performed for each locus, and G-values and degrees of freedom for each locus were summed over all loci in all pairs and tested against a

chi-square distribution. Because of the robustness of the test, only cells with expected values less than 1.0 were combined (Felsenstein 1967).

When making all possible pairwise comparisons for an overall G-test, the large number of non-independent pairwise comparisons (120) makes it possible that a percentage of the comparisons could appear significantly different by chance. Consequently, the probability value required to demonstrate a significant difference among all collections was modified for this analysis according to Cooper (1968) to eliminate spurious correlations. This involves increasing the criteria for a significant test to reflect the number of tests, such that a probability of 0.05 would be divided by the number of tests (here 120). It would then be necessary to get a chi-square value from the table that corresponded to a probability value less than 0.0004 for a comparison to be considered significantly different.

Genetic Similarity

The genetic similarity among baseline collections was determined using computer programs by Donald Campton of University of Florida. The program calculates Nei's index of genetic identity (1972; 1978) using the probability of identity of gene pairs between populations averaged over all loci. We report the results of the analyses that compensate for the unequal sample sizes of the collections (Nei 1978).

The normalized identity of genes between two populations, X and Y, is defined as:

$$I = J_{XY} / SQRT (J_X J_Y);$$

where J_X, J_Y, and J_{XY} are the arithmetic means over all loci of the probabilities of identity between gene pairs among populations.

Identity values are scaled from 0.0 to 1.0; 0.0 corresponds to complete allele substitution at all loci, and 1.0 to populations that are electrophoretically indistinguishable at all loci studied. Genetic distance is calculated as the negative natural log of the identity value.

Genetic identity values were used in a clustering algorithm (UPGMA: Sneath and Sokal 1973) modified by Donald Campton to produce a dendrogram of relationships among populations. The average linkage method of clustering was used, and this analysis was also weighted to reflect unequal sample sizes.

Gene Diversity Analysis

Gene diversity analysis determines the source of observed variation, i.e., what proportion of the observed variation is between individuals within populations, as opposed to differences among populations or groups of populations. Our analysis was done with a computer program by Donald Campton based on the work of Nei (1973) and Chakraborty (1980). Modifications include use of simple unweighted arithmetic averages of population samples within sites rather than weighting gene frequencies within sites by the number of samples.

Sample data were analyzed by individual subpopulations (sites), by

subpopulations of different drainages, and by the combined populations of a region. The combined total amount of genetic variation of all populations studied was partitioned into within- and between-subpopulation diversity components. The total gene diversity (H_T) over all subpopulations equals the average heterozygosity within the subpopulations (H_S) plus the average gene diversity between subpopulations (D_{ST}). The diversity between subpopulations (D_{ST}) can be broken down to differences between sites within a drainage (D_{BS}) and differences between populations of different drainages (D_{BD}). The relative magnitude of gene differentiation among populations (G_{ST}) was estimated as D_{ST} / H_T or $(D_{BS} + D_{BD}) / H_T$, and can be expressed as a percentage.

Genetic Stock Identification

Genetic stock identification was done using a maximum-likelihood estimate program modified by Sam Nelson and Jerome Pella (National Marine Fisheries Service, Auke Bay, Alaska) with the expectation maximization (EM) algorithim as used by Milner et al. (1983), and refined by Millar (1987). Estimates and standard errors are obtained using a bootstrap technique (Demster 19??, Efron 1982) whereby the mixture is resampled 100 to 200 times.

Simulations

We used genetic stock identification methods four ways to evaluate

their effectiveness for North Slope Arctic char. First, we constructed an artificial mixed stock by combining all baseline data. The baseline data characterizes each fish stock; it is used for a reference by which the artificial mixed stock fish are assigned as a percent composition to the stock-of-origin. The program gives point estimates and variances of the estimates for a sample of known composition. The actual contribution of each populations to the artificial mixture is determined by sample size. We are then able to compare estimated percent composition of the artificial mixed stock to actual expected values using a chi-square statistic using number of fish estimated to have come from each stock, compared to number of fish expected (actual mixture composition).

Second, we did incremental mixed-stock simulations where each baseline population was added to an artificial mixture at 20% increments, with baseline data from other populations used to total 100%. This tests the accuracy and precision of the estimates for each stock over the range of possible contributions from 0 to 100%. Point estimates and standard errors are graphed with actual contributions in known estimates for comparison.

Third, we did simulations where each baseline stock, one at a time, was used to make up an artificial mixed stock. When tested against the baseline made up of all stocks, these simulations indicate how the fish are allocated, and to which stocks incorrectly allocated fish are assigned.

Endicott Samples

We also did estimates of the percent composition of mixed fishery samples taken from Prudhoe Bay adjacent to the Endicott Causeway in June, July, and August of 1987. We used baseline data from 14 Arctic char populations and bootstrap resamplings to determine mean estimate and the error around the mean of the estimates.

Populations with an estimated stock contribution of 1% or less are not used. They are considered spurious, as the maximum likelihood analysis program always assigns some fish to each baseline specified as a possible contributor.

RESULTS

We have information on population parameters compared among baseline populations, computer simulations on known samples for accuracy and precision, and mixed-fishery composition estimates for Endicott samples.

1987 Collections

Most Arctic char captured are juveniles, with some small resident adults. A small sample of char was collected upstream from the waterfall on the Babbage River (site number 2) for comparison of these resident fish with anadromous populations. Firth River sampling site number 2 is in Alaska, and was included for comparison of upstream and downstream populations in this drainage. Upstream Firth fish were

small, and many appeared to have mature gonads.

No Arctic char were captured at sites that were sampled near the Chukchi Sea, including the Singaruak, Walakpa, and Kugrua rivers. No Arctic char were captured at the Shaviovik River, the downstream end of the Colville River, or the Anaktuvuk, which is tributary to the Colville.

Approximately 232 Arctic char were collected from Prudhoe Bay in late June, 137 in late July, and 166 in early September. From the Camden Bay area, 50 char were collected near Kongaevik Point and 50 from Simpson Cove.

Amount of Genetic Variation

Of the 46 gene loci we examined, 15 are variable and were used in the analysis. Allele frequencies were calculated for each population, and relative mobility of allelic variants were measured (Appendix A). Four additional enzyme loci (Hex1, FH1, Pgm3,4, and Xdh1) are known to be variable in these Arctic char. Aat1, Hex1, and Xdh1 were scored in 1986, when we had live fish to sample in the lab. However, these gene loci are particularly sensitive to sample handling and storage, and consistently good resolution could not be obtained in 1987 when samples were brought from the field frozen. The other 27 loci studied are monomorphic in all populations.

Percent of loci polymorphic (P) and average heterozygosity per locus (H) for the 16 populations of Arctic char sampled were calculated for combined 1986 and 1987 collections (Table 3). The

Table 3.- Expected average percent of fish heterozygous per locus (H), and percent of loci examined that were polymorphic (P) in 16 populations of Arctic char sampled from rivers of the North Slope of Alaska in 1986 and 1987. Samples in some drainages were combined if G-test $p > 0.05$. The average value of H is weighted by sample size. Heterozygosities were recalculated in 1988 to include only loci that were studied in both years. Hex, XXO, and FH were excluded.

Drainage / Sites	Year	Max N	% H	% P
Aichilik River	1986/1987	85	5.04	23.81
Colville River				
Anaktuvuk	1986	40	3.81	19.05
Babbage River				
Canoe River	1986	35	2.51	9.76
Site #1	1987	53	2.48	11.90
Site #2	1987	21	2.43	7.14
Canning River				
5 Sites	1986/1987	212	4.13	26.19
Egaksrak River	1986	41	4.32	21.43
Firth River				
3 Sites	1986/1987	132	4.29	28.57
Hula Hula River				
Site #1	1986/1987	95	4.57	23.81
Site #2	1986	54	4.66	22.50
Kavik River	1986	40	3.14	14.29
Kongakut River				
2 Sites	1986/1987	85	4.54	21.40
Sadlerochit River	1987	45	1.63	7.14
Sagavanirktok River				
Ivishak/Echooka	1986	74	3.62	26.19
Lupine	1987	45	4.36	19.05
Ribdon	1986	40	5.16	21.95
Average		1097	3.79 ± 1.02	19.01 ± 6.68

values of P range from 7.1 to 35.7% (average: 19%). The average population heterozygosity ranges from 1.6 to 5.2% for the combined 1986 and 1987 collections, and the weighted average heterozygosity per individual over all populations is 3.8%.

Genotypic Distributions

Significant deviation from expected values can indicate non-random mating, unequal fertility among parents, unequal viability among offspring (selection), migration from other populations, or failure to collect a random sample from the population. Within the collections of Arctic char we studied, individual loci were occasionally out of equilibrium. However, when all loci for a population were considered, there was no evidence of departure from the expected genotypic distributions in any population. The parental generations have apparently been mating at random (no more than one population was detected in any sample), and the collections appear to represent random samples of the populations.

Genetic Heterogeneity

Heterogeneity tests between North Slope Arctic char populations were done first between collections from the same drainage at different sites and in different years. The data for the differing sites and years of collection within the Aichilik, Canning, Firth, and Kongakut Rivers char subsamples were combined (Appendix A) as they are

not detectably different from each other (Table 4). The char collected from the upstream sites (number 2 and number 3) of the Hula Hula River are not distinct genetically, and were combined as site number 2. Samples from Hula Hula site number 1 in 1986 and 1987 are not significantly different, and were combined as site number 1. The five sites in the Canning River Drainage include char from the Marsh Fork and Shuklik Springs.

The three collections from the Babbage River Drainage (from the Canoe River, from a site downstream from the waterfall, and from a site above the waterfall) could not be combined because they are significantly differentgenetically. The populations of the major tributaries of the Sagavanirktok River are significantly genetically distinct, though the collection from the Ivishak River is not distinct from that of its tributary, the Echooka. This results in a total of 16 baseline populations for all analyses excepting genetic stock identification procedures, where a baseline of 14 stocks is used.

When data from the 16 collections are compared, most of 120 pairwise comparisons indicate significant genetic differences ($p < 0.01$) among North Slope char populations when corrected for the number of non-independent tests (Table 5). A summary G-test, including all populations and all 15 variable loci, shows that the Arctic char studied are highly different from each other ($G = 1237$ with 143 degrees of freedom; $p << 0.001$).

Genetic Similarity

Table 4.- Log likelihood ratio (G-tests) heterogenity tests among populations sampled at different sites and/or different years. Probability of P>0.05 was used as criteria for combination of samples within a drainage. Degrees of freedom (df) reflects the number of loci in the comparisons.

Population	Year	Sites	G	df	P
Aichilik	1986/1987	2	12.45	11	0.330
Babbage	1986/1987	3	46.95	7	<0.001
Canning	1986/1987	5	19.31	8	0.132
Ivishak	1986	2	11.99	8	0.152
Firth	1986/1987	3	31.64	23	0.108
Hula Hula	1986/1987	2	29.41	9	<0.001
Kongakut	1986/1987	2	5.71	10	0.839

Table 5.- Matrix of genetic heterogeneity, tested pairwise among Arctic char populations of the North Slope, Alaska and Canada. G-values, with degrees of freedom are in parentheses. The significance level was modified according to Cooper (1968) to compensate for the number of pairwise tests (120).

1 Canoe 86	X															
2 Babbage 87-1	19.4 (4)	X														
3 Babbage 87-2	38.8 (3)	17.0 (4)	X													
4 Firth	110.7 (11)	96.1 (12)	60.7 (9)	X												
5 Kongakut	100.0 (10)	106.9 (10)	70.9 (9)	54.4 (13)	X											
6 Egaksrak	46.0 (8)	102.6 (8)	73.1 (8)	97.6 (14)	45.6 (11)	X										
7 Aichilik	49.1 (10)	136.5 (11)	92.5 (10)	135.5 (14)	75.0 (13)	33.1 (11)	X									
8 Hula 1	81.7 (9)	150.7 (11)	87.7 (8)	139.6 (14)	46.6 (12)	25.7 (13)	73.5 (14)	X								
9 Hula 2	99.8 (8)	154.4 (9)	91.8 (8)	128.2 (10)	59.6 (10)	29.5 (9)	97.5 (10)	29.4 (9)	X							
10 Sadlerochit	99.2 (4)	75.4 (5)	66.6 (5)	164.4 (11)	180.8 (10)	179.6 (7)	212.5 (11)	247.2 (10)	226.6 (8)	X						
11 Canning	87.7 (10)	129.6 (10)	63.8 (9)	125.9 (14)	75.6 (13)	43.2 (12)	72.9 (14)	59.8 (13)	100.7 (9)	208.2 (10)	X					
12 Kavik	124.3 (6)	60.4 (6)	32.6 (5)	78.4 (10)	61.8 (10)	70.4 (9)	124.2 (11)	68.5 (9)	56.2 (9)	132.8 (6)	87.2 (10)	X				
13 Ivishak	134.4 (9)	72.3 (9)	38.9 (7)	69.4 (13)	46.2 (11)	70.6 (10)	144.8 (12)	53.8 (11)	70.7 (10)	155.7 (8)	65.4 (12)	39.3 (10)	X			
14 Ribdon	89.3 (10)	85.8 (10)	77.7 (10)	55.6 (11)	48.3 (12)	61.2 (11)	133.0 (13)	80.5 (13)	66.3 (10)	156.7 (9)	113.4 (12)	80.9 (10)	51.5 (11)	X		
15 Lupine	22.4 (6)	75.5 (7)	74.5 (7)	53.8 (13)	38.3 (12)	38.9 (8)	48.5 (12)	56.6 (11)	74.7 (9)	141.7 (7)	66.1 (11)	79.0 (8)	51.1 (10)	26.0 (10)	X	
16 Anaktuvuk	94.5 (10)	63.0 (9)	63.0 (9)	68.7 (13)	79.9 (12)	75.4 (13)	103.4 (13)	85.2 (13)	128.8 (12)	108.8 (8)	29.5 (11)	88.5 (10)	57.2 (11)	96.7 (13)	64.2 (10)	X
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16

No allele substitutions were observed at any locus. Genetic identities are high between North Slope char populations. All pairwise comparisons have values greater than or equal to 0.981, corresponding to a genetic distance of 0.019. The Sadlerochit River population is responsible for the lowest identity values among the char studied. Without this unique population, the identity values among anadromous North Slope char are 0.989 or higher, ranging up to complete identity, 1.000 (Table 6).

A dendrogram (Figure 2) illustrates the genetic relationships among Arctic char populations of tributaries of the Beaufort Sea. Again, the Sadlerochit River char are the most unlike the other populations.

Gene Diversity Analysis

The absolute and relative magnitude of the diversity among subpopulations was analyzed hierarchically (Table 7). Approximately 8% of the observed variation is due to differences among the populations of the 11 drainages sampled. Less than 1% is due to differences among populations of different sampling sites within drainages. Variation among individuals within populations accounts for 91.1% of the total gene diversity.

Genetic Stock Identification

Artificial Mixed Stock Simulations.- For these genetic stock

Table 6.- Matrix of Nei's (1978) gene identity values pairwise among 16 populations of Arctic char sampled from the North Slope of Alaska rivers in 1986 and 1987.

	Population															
1	Canoe 86	1.000														
2	Babbage 87-1	0.998	1.000													
3	Babbage 87-2	0.995	0.999	1.000												
4	Firth	0.999	0.998	0.996	1.000											
5	Kongakut	0.999	0.997	0.996	0.999	1.000										
6	Egaksrak	0.998	0.994	0.994	0.996	0.999	1.000									
7	Aichilik	0.999	0.996	0.995	0.998	1.000	0.999	1.000								
8	Hula 1	0.998	0.995	0.995	0.996	0.999	1.000	1.000	1.000							
9	Hula 2	0.997	0.989	0.991	0.991	0.996	0.999	0.997	0.998	1.000						
10	Sadlerochit	0.989	0.996	0.996	0.993	0.990	0.985	0.989	0.986	0.981	1.000					
11	Canning	0.997	0.998	0.997	0.999	0.999	0.998	0.999	0.999	0.995	0.991	1.000				
12	Kavik	0.996	0.998	0.999	0.997	0.998	0.998	0.998	0.998	0.996	0.992	0.999	1.000			
13	Iviskak	0.997	0.998	0.998	0.998	0.999	0.998	0.999	0.999	0.994	0.991	1.000	0.999	1.000		
14	Ribdon	1.000	0.997	0.995	0.999	1.000	0.998	0.999	0.998	0.995	0.989	0.998	0.997	0.998	1.000	
15	Lupine	0.999	0.997	0.995	0.999	0.999	0.997	0.999	0.997	0.993	0.991	0.998	0.996	0.997	1.000	1.000
16	Anaktuvuk	0.996	0.998	0.997	0.999	0.998	0.995	0.997	0.996	0.990	0.993	0.999	0.998	0.999	0.996	0.997	1.000
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16

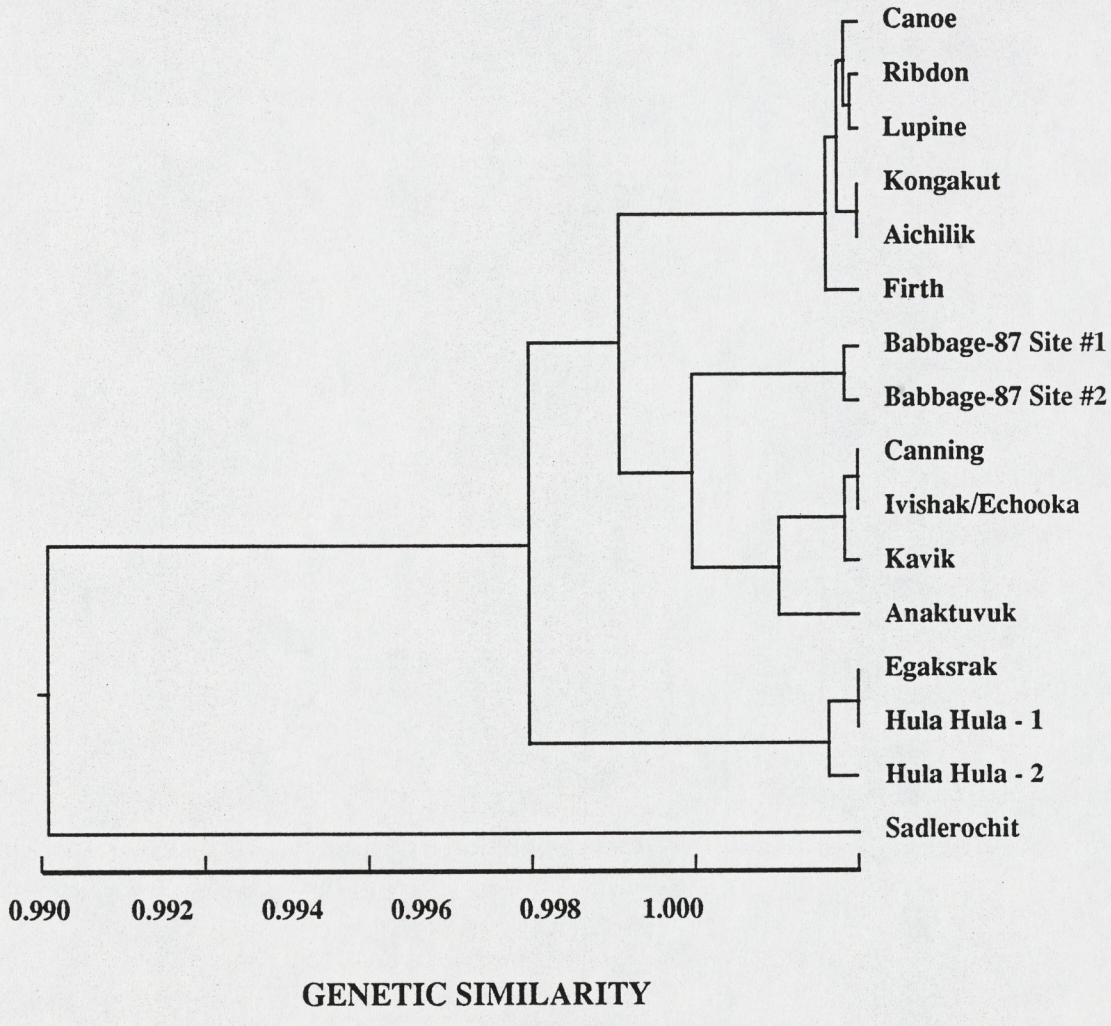

Figure 2.- Relationships based on Nei's (1978) index of genetic identity of 16 populations of Arctic char from rivers of the North Slope of Alaska and Canada.

Table 7.- Gene diversity analysis (Nei 1973; Chakraborty 1980) among populations of Arctic char from rivers of the North Slope of Alaska and Canada. The average values represent data from all 16 populations from the 11 drainages studied in 1986 and 1987.

		Absolute gene diversity				Relative diversity (%)		
Drainage	# of sites	Within sites	Between sites	Between drainages	Total	Within sites	Between sites	Between drainages
Babbage River	3	0.0256	0.0020	---	0.0276	92.9	7.1	
Hula Hula River	2	0.0463	0.0009	---	0.0472	98.1	1.9	
Sagavanirktok	3	0.0429	0.0013	---	0.0442	97.1	2.9	
Average	16	0.0383	0.0004	0.0033	0.0420	91.1	0.9	8.0

identification analyses, data from 14 stocks were used as a baseline. The Sadlerochit char were excluded from the analyses, as they are not anadromous. Fish from Babbage River upstream of the waterfall were also excluded from the GSI analyses as they probably contribute little to migratory stocks.

Artificial Mixture.- We used the data from baseline spawning populations to make an artificial mixture (N = 1032) of known composition. The actual values for 7 of 14 populations were within an 80% confidence interval (point estimate ±1.28 standard deviations) of the estimated allocation from GSI (Appendix C and Figure 3).

Canoe, Hula Hula site #2, and Ribdon River populations were estimated at essentially zero while actually present at 3, 5, and 4% respectively. Eighty percent confidence intervals for estimated values included zero for Egaksrak, Lupine, and Anaktuvuk River populations.

Babbage, Egaksrak, Kavik, and Lupine char point allocations are not significantly different than actual values (χ^2: $p > 0.5$). Kongakut and Anaktuvuk River composition estimates are significantly different than actual composition (χ^2: $P < 0.05$), but if corrections are made for the number of non-independent tests (Cooper 1968) are not. The actual contributions to the artificial mixed stock of the populations listed above are within the 80% confidence intervals around the estimated values. Only the actual contributions of Canoe, Hula Hula site #2, and Ribdon River fish (erroneously estimated at zero contribution to the mixture) and Canning River fish are not

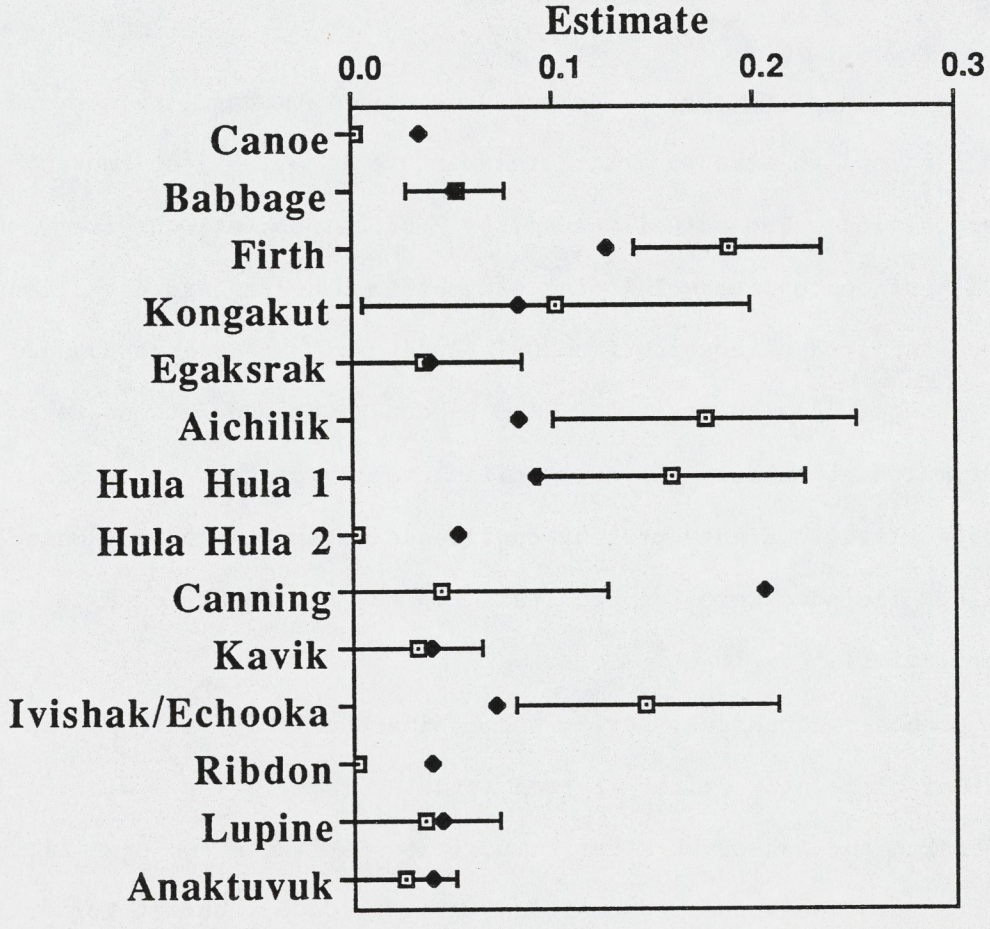

Figure 3.- Maximum likelihood method of genetic stock identification on an artificial mixed stock of North Slope Arctic char. Estimated numbers of fish (❐) are given with 1.28 standard deviations calculated from bootstrap resampling. Actual values (♦) are numbers of fish from each stock in the artificial mixture.

within two standard deviations (95% confidence interval) of their estimates.

Incremental Simulations.- Incremental artificial mixed stock simulations showed that some populations of char are identifiable within a whole range of contributions to a simulated mixed fishery (Appendix D and Figures 4a-n). Data for 14 populations was used to identify, sequentially, each population as 100% of an artificial mixture. In the simulations, each population studied was identified as making up 78% or more of its mixture. Eight of 14 stocks were greater than 90% correct, and three were greater than 95% correct.

Fourteen percent of the Babbage Drainage Canoe River fish were incorrectly allocated to the Babbage mainstem population. Over 12% of Kongakut fish were incorrectly allocated to Aichilik and Egaksrak River, and conversely, 16.5% of Aichilik fish were incorrectly allocated to Kongakut and Egaksrak. Eight percent of Hula Hula site #1 fish were allocated to Egaksrak, as were 7% of Hula Hula site #2 fish. Twelve percent of Canning fish were incorrectly allocated, as were 16% of the Ribdon char. Twelve percent of Ribdon fish were allocated to Lupine River, of the same drainage. The Anaktuvuk population was properly allocated 98% of its fish by the GSI technique.

Twenty Percent Incremental.- When different populations were used to make up different percentages of mixture files, in 20% increments from 0 to 100%, several populations were correctly allocated throughout the range of the simulations (Figures 5a-n). These were

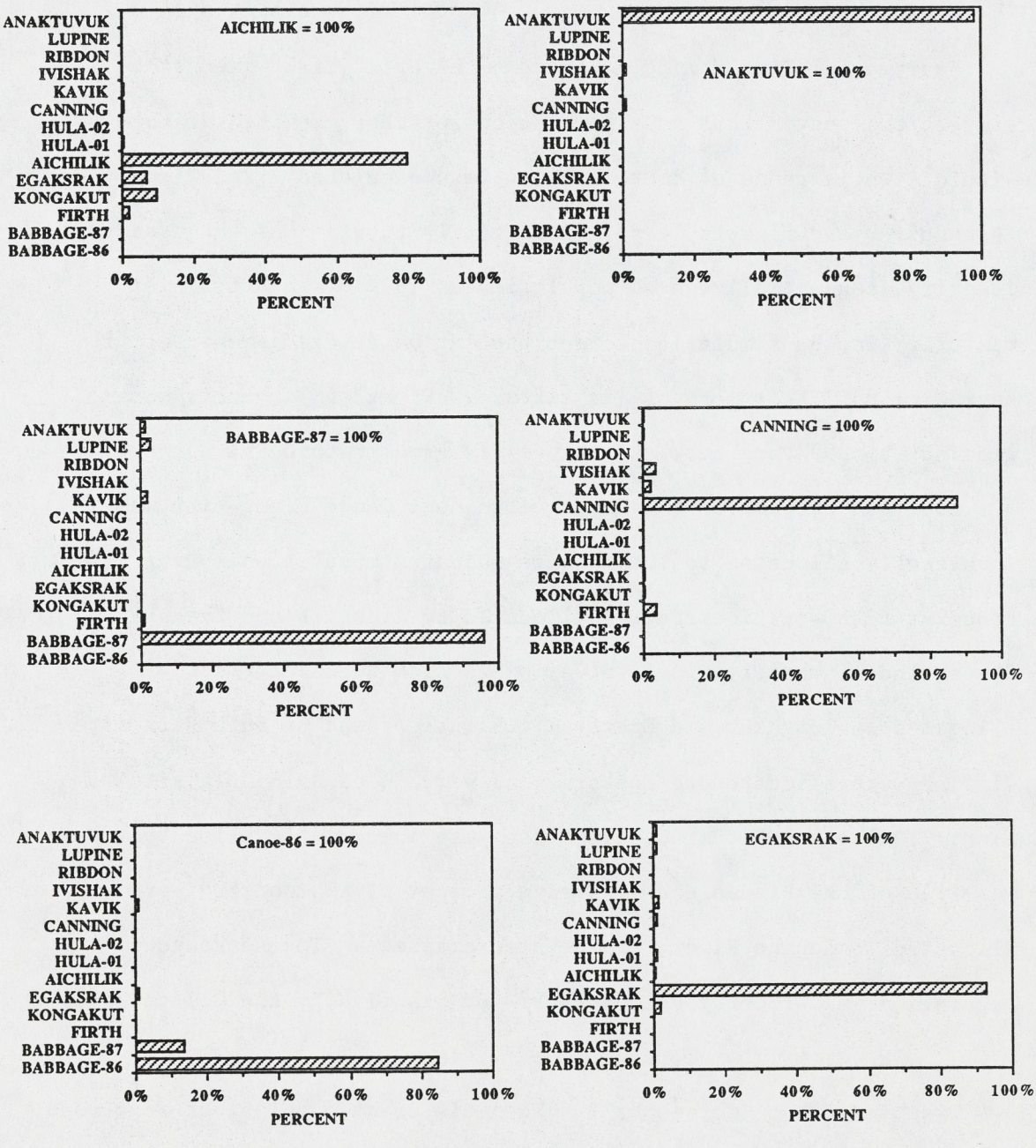

Figure 4.- Incremental artificial mixed stock simulations for each of 14 populations of North Slope Arctic char. Estimated using maximum likelihood techniques with 200 bootstrap resamplings.

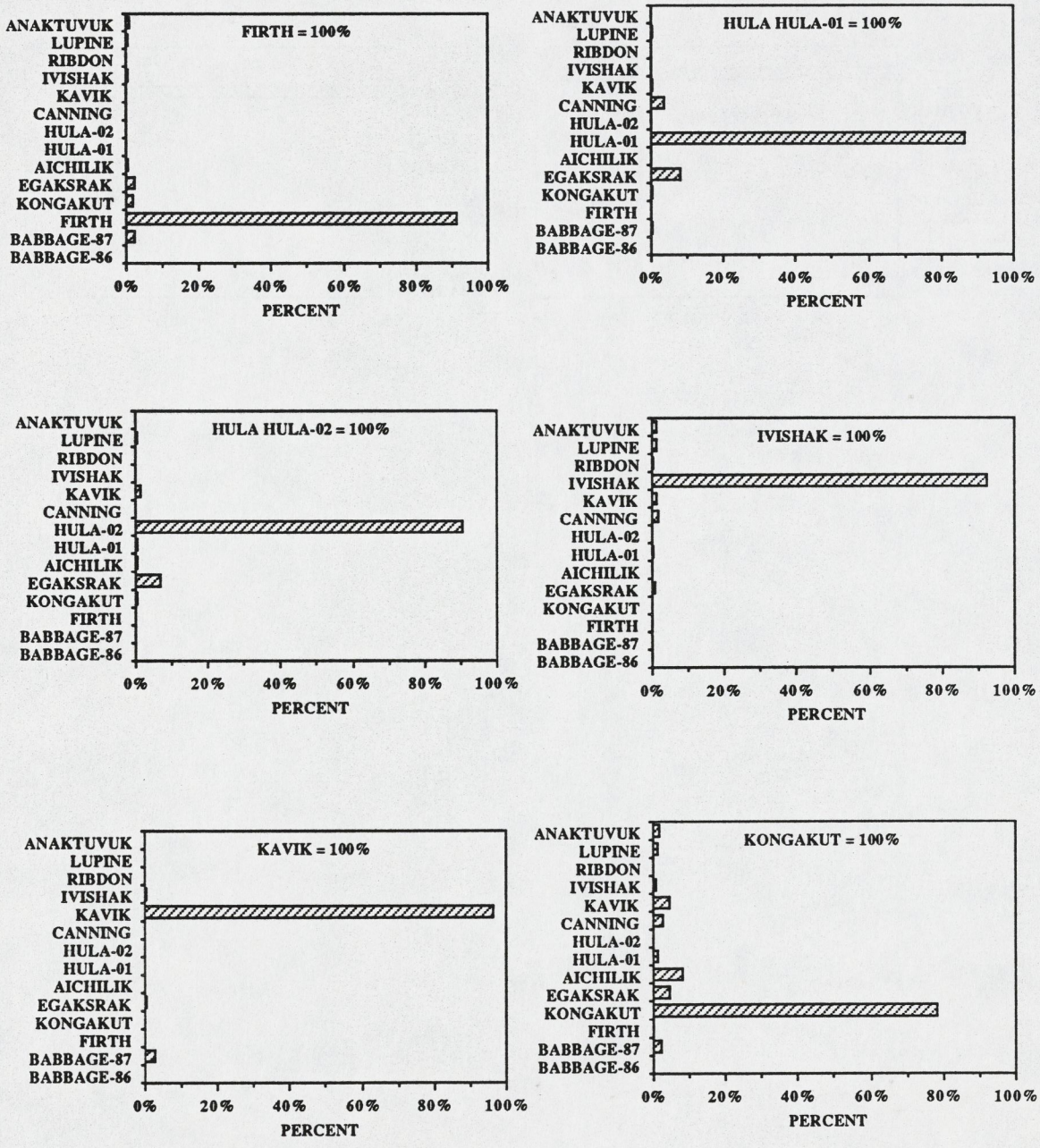

Figure 4.- Continued.

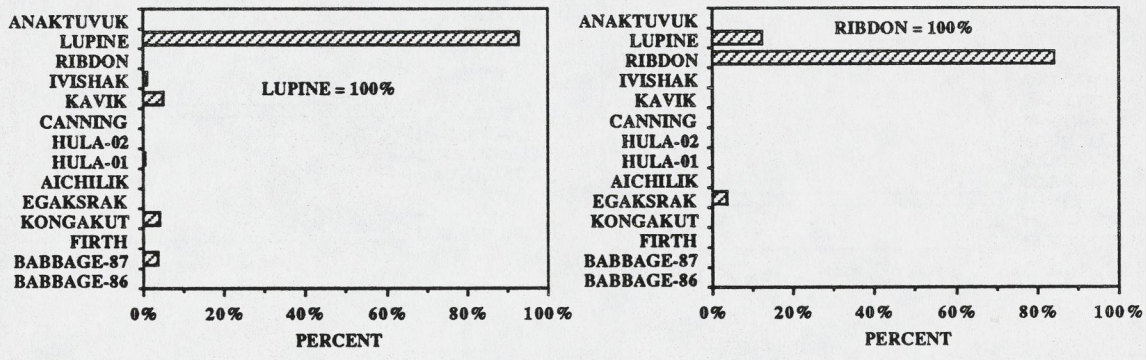

Figure 4.- Continued.

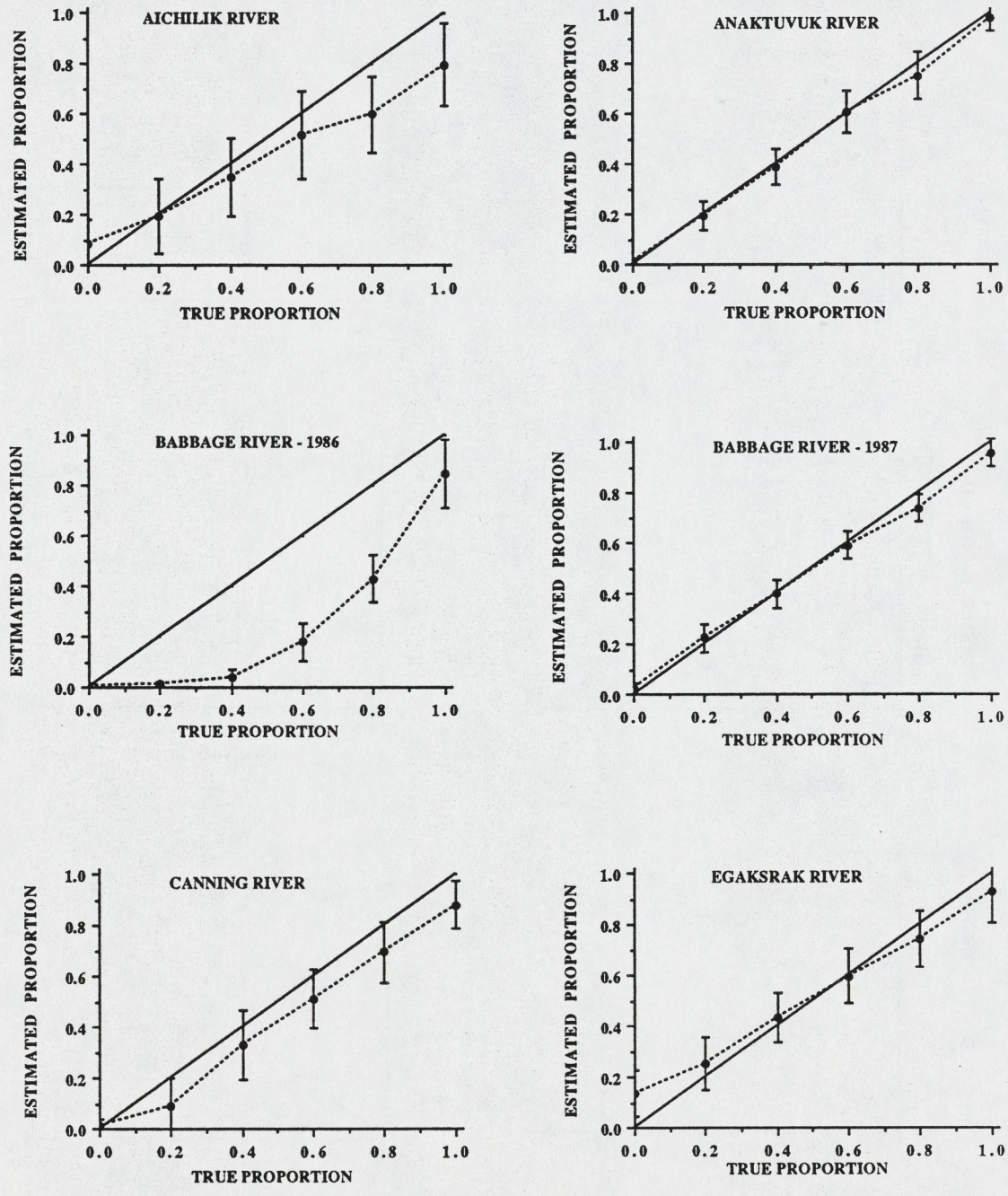

Figure 5.- Incremental artificial mixed stock simulations for each of 14 populations of North Slope Arctic char. Contributions of each population, in 20% increments, are estimated using maximum likelihood techniques with 200 bootstrap resamplings.

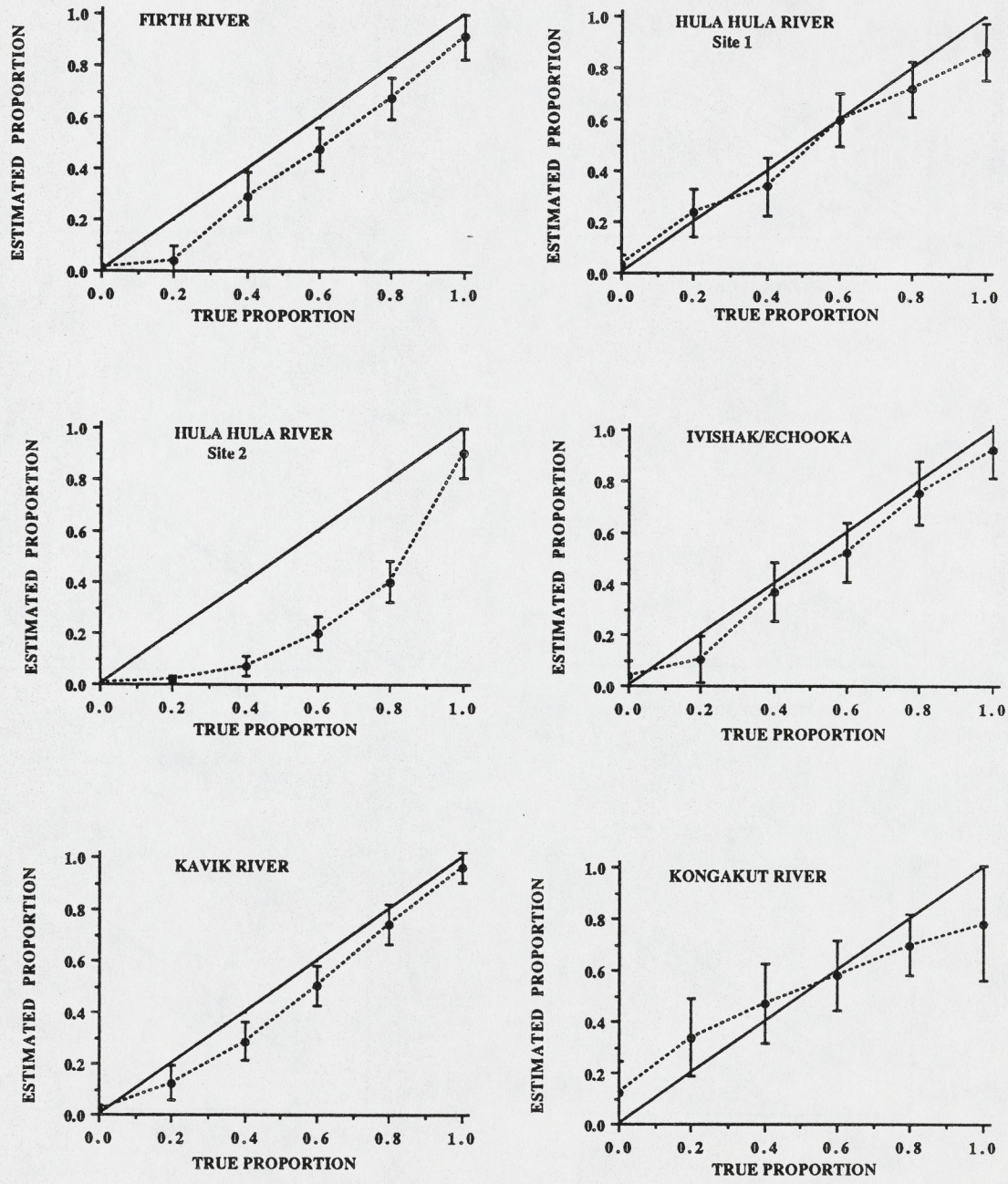

Figure 5.- Continued.

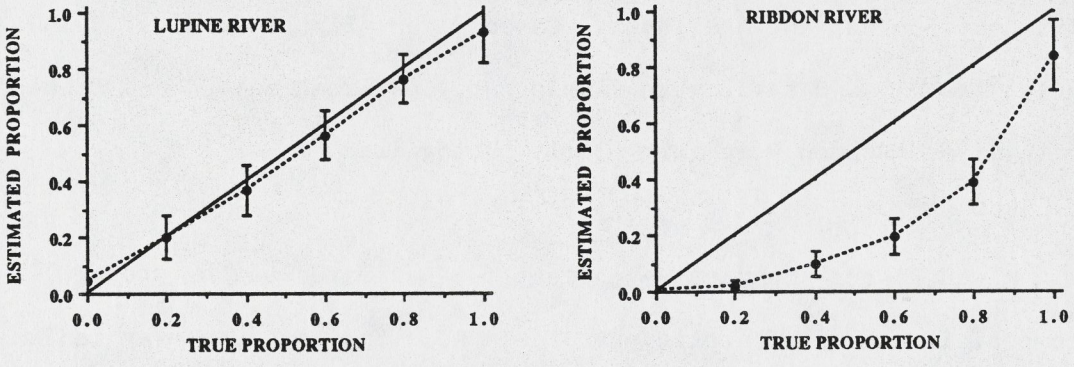

Figure 5.- Continued.

Babbage site #2 and Sadlerochit River char (neither of which were used in the GSI analyses); Kongakut, Egaksrak, Aichilik, Hula Hula site #1, Ivishak, Lupine, and Anaktuvuk. Canoe River, Firth, Canning, Hula Hula site #2, and Kavik were consistently underestimated, and Babbage site #1 and Ribdon were very poorly "recognized."

Mixed Fishery Samples -- Endicott.- Estimates of the stock composition of mixed Arctic char taken near Endicott Causeway in June (N = 208), July (N = 126), and August 1987 (N = 166), were made using maximum likelihood estimation, bootstrap resampling, and the 14-stock baseline already described. Eight percent confidence intervals were generated around the point estimates for each population (estimate ±1.28 standard deviations); and for each month (tabulated in Appendices E, F, G, and graphed as Figures 6, 7, and 8).

For June, only Ivishak, Lupine, and Anaktuvuk estimates did not include zero in the 80% confidence interval. When the contribution of the Sagavanirktok fish (Ivishak, Lupine, and Ribdon) are summed and the variances recalculated, they contribute 66% ±20.9%. Anaktuvuk contributes an additional 14% ±10.9%, together accounting for 80% of the fish sampled.

In July, four populations made contributions where zero was not within the 80% confidence interval. Hula Hula site #1 (12% ±10.2%) and Kavik (10% ±8.3%) drop out of the estimates if a 95% confidence interval is used, as zero would be included in that interval. When the estimates of the three Sagavanirktok tributaries are allocated, then summed and the variances recalculated, the contribution is 42%

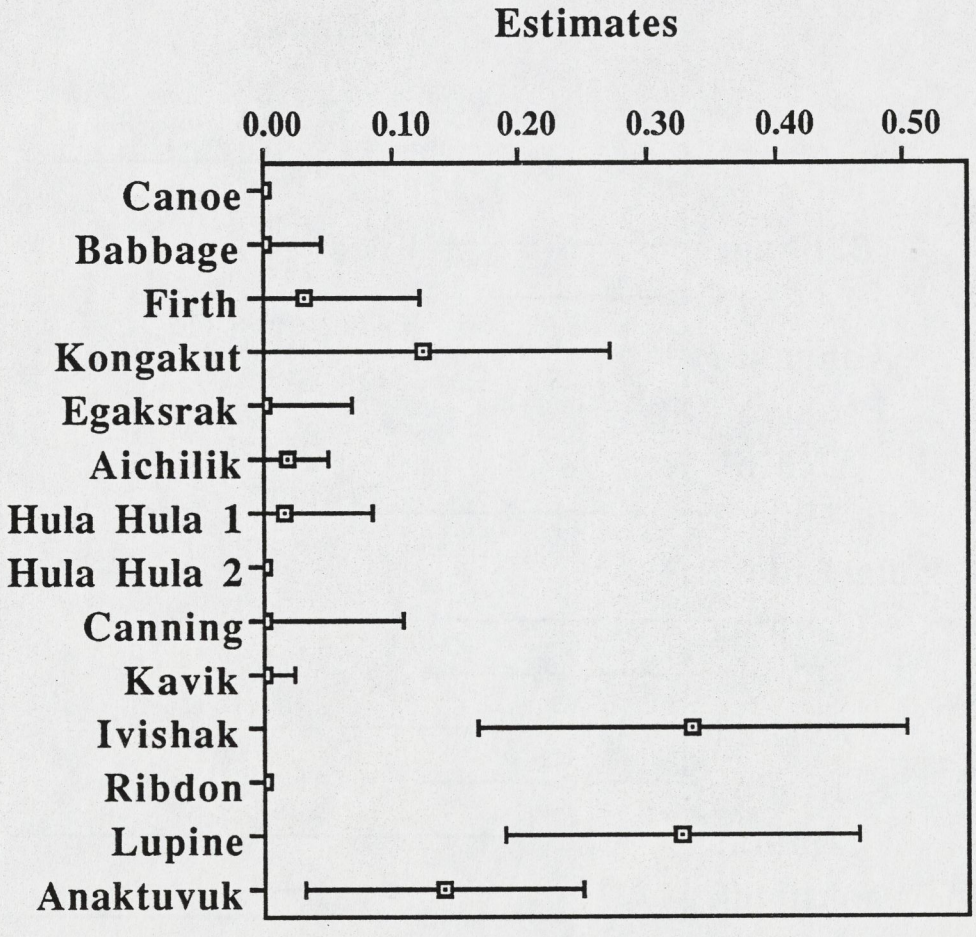

Figure 6.- Estimated composition (±1.28 standard deviation) of a mixed fishery sample from Prudhoe Bay, Alaska, collected in June 1987. Estimates are made using maximum likelihood techniques with 200 bootstrap resamplings and a 14-stock genetic baseline.

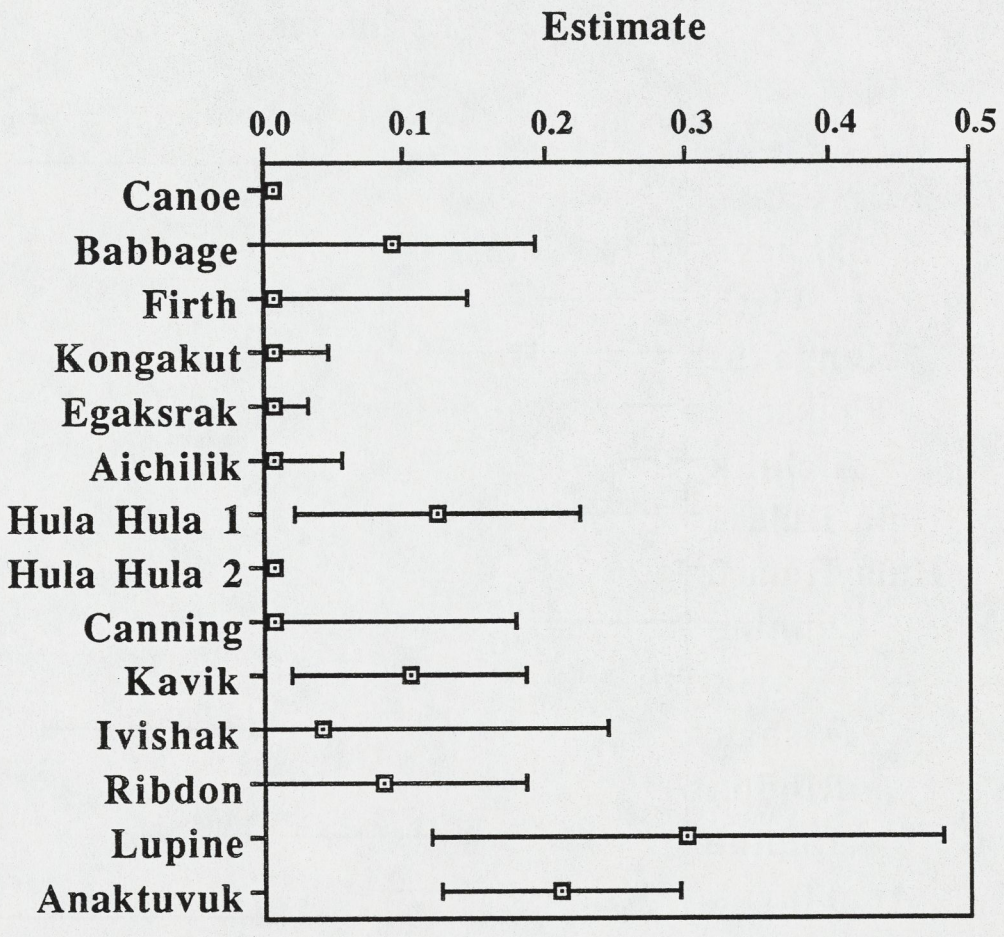

Figure 7.- Estimated composition (±1.28 standard deviation) of a mixed fishery sample from Prudhoe Bay, Alaska, collected in July 1987. Estimates are made using maximum likelihood techniques with 200 bootstrap resamplings and a 14-stock genetic baseline.

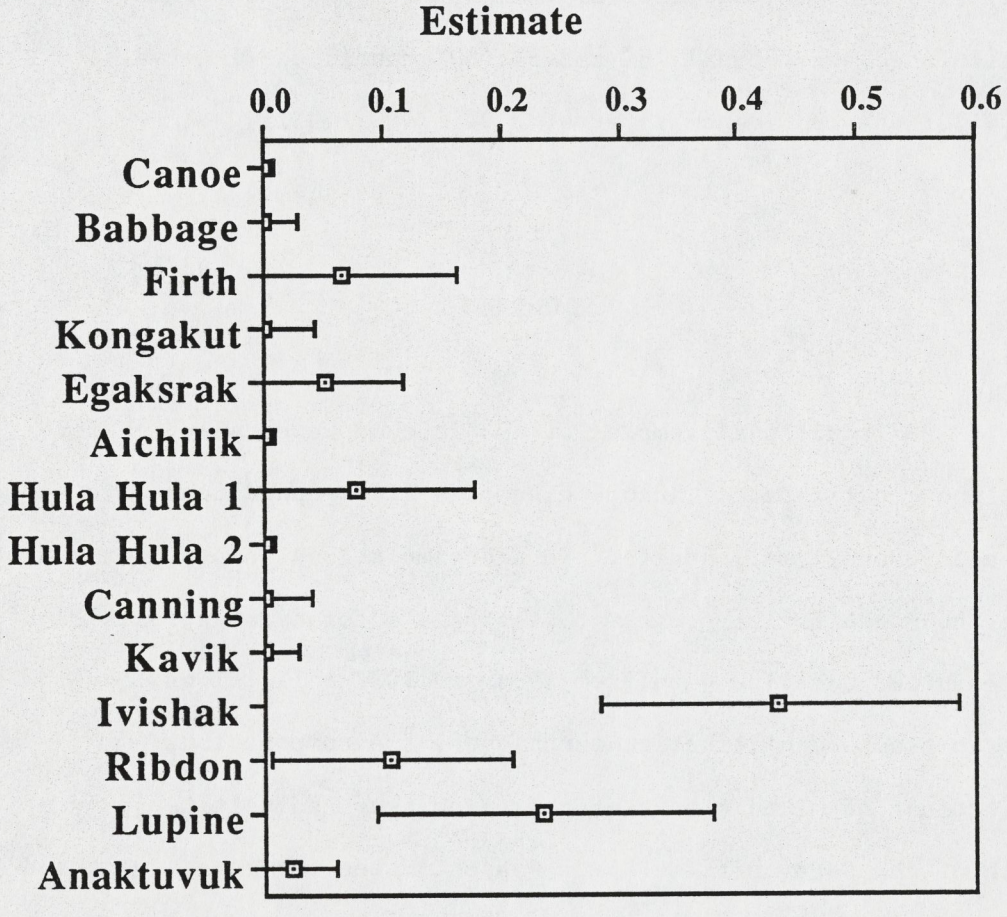

Figure 8.- Estimated composition (±1.28 standard deviation) of a mixed fishery sample from Prudhoe Bay, Alaska, collected in August 1987. Estimates are made using maximum likelihood techniques with 200 bootstrap resamplings and a 14-stock genetic baseline.

±17.3%. Anaktuvuk contributes 21% ±8.5%. Sagavanirktok and Anaktuvuk fish, then, account for 63% of the fish sampled in July.

In the August sample, all three Sagavanirktok tributary stocks are represented. When the allocations of Ivishak, Ribdon, and Lupine fish (43%, 11%, and 24%, respectively) are summed and the variance recalculated, they equal 78% ±13.3% (80% confidence interval: 0.6078 - 0.9472; 95% confidence interval: 0.5176 - 1.0375).

DISCUSSION

In 1987 additional samples of Arctic char were collected for baseline genetic data, including samples from populations with non-adadromous, small adults. We did simulations using the maximum likelihood estimation program to test the accuracy and precision of our combined baseline data from 1986 and 1987 collections. Using genetic stock identification techniques, the compositions of collections of mixed stocks of char from near Endicott Causeway at the mouth of the Sagavanirktok River was estimated for June, July, and August 1987. With this information, we are able to discuss population characteristics of North Slope Arctic char, the quality and potential of our current baseline data, and the possible implications of the estimates of Endicott char stock composition, plus direction and capabilities for further study.

Collections

Our genetic baseline for Arctic char covers the major migratory stocks from the McKenzie River of Canada to Point Barrow in Alaska. Our mixed stock samples are limited to the area around Endicott Causeway, at the mouth of the Sagavanirktok River, Alaska. Collections of char taken near Barter Island are too small to be useful.

Sampling additional char necessitated modifying our 1986 baseline data sets, and the enzyme protocol we used. In 1988 we were more conservative in the number of loci we considered to be reliably scoreable. Many of the char samples we obtained in 1986 were brought back alive, and consequently were of very high quality when analyzed electrophoretically. Though every effort was made in 1987 to bring back quality samples from the field, frozen samples are not likely to be as good. In 1987 we were unable to consistently score two highly variable loci, Hex1 and Xdh1.

Fish from more sites in freshwater tributaries; second samples from same or similar sites; and larger sample sizes were collected. No Arctic char were found in three rivers draining to the Chukchi Sea in August 1987, or in certain other rivers of the Beaufort Sea area. We did collect char representing different forms associated with non-migratory life history.

Amount of Genetic Variation

The amount of genetic variation in North Slope Arctic char is typical of fish species in general (Nevo 1978), and slightly higher

than average among salmonids that have been studied (Utter et al. 1981). Our overall estimate of variability, measured as average heterozygosity, for char from our combined 1986 and 1987 collections is slightly lower than that for 1986 alone. Two loci were excluded from the 1987 analyses, and samples from populations from small, isolated populations in springs and from upstream in the Babbage and Firth River Drainages were included.

Combining Baseline Data

With the exception of the Babbage, Hula Hula, and Sagavanirktok River systems, we found that collections of Arctic char made in different years and in different parts of the same drainage are not significantly different in allele frequencies (G-test: $p < 0.01$) and could be combined. Multiple samples taken in 1986 and 1987 from the different sites within the Canning, Firth, Aichilik, Kongakut, and Ivishak are not significantly different in allele frequencies. It is best to combine baseline information for stocks that are both genetically and geographically similar.

The amount of precision in genetic stock identification estimates has been shown to be consistent with the level of divergence among stocks (Milner et al. 1981). Collections of fish that have not diverged significantly should be combined, particularly since larger numbers of baselines result in smaller percentage contributions allocated to a greater number of stocks. Smaller estimates typically have relatively large errors (comparable as coefficients of

variation). Milner et al. (1986) found that stock composition estimates of less than 5% for a given population generally are poor. With many baselines, it is likely that more stocks will be identified in smaller percentages than if more baselines are used.

Though we sometimes find genetically similar stocks from different drainages or even regions, they should not be combined before analyses. Geographically remote stocks should be combined after the fact because we know that the EM algorithm is unable to discriminate between them, and will assign fish to one or both of them. Wood et al. (1987) have done simulations showing that estimates should be made for individual stocks that are genetically similar but unrelated geographically. These estimates can be pooled, and the variances recalculated. Recalculated variances are smaller than the sum of the individual variances.

Collections from drainages supporting both resident and migratory forms of char can apparently be combined in the case of Firth and of Canning River char. We found no evidence that these life history forms represent separate populations. If genetic differences were detected between resident and migratory forms it could be due either to separate evolutionary lines or recent reproductive isolation. Recent divergence may be due to behavioral or physical isolation, which allows genetic differences to accumulate. It is certainly possible that similarities among geographically isolated groups may be due to selection, founding events, or by chance convergence of electrophoretic phenotypes at structural loci.

In other salmonid populations that have been studied, e.g.,

rainbow trout (Allendorf and Utter 1979) and brown trout (Ryman and Stahl 1981), only a small percentage of the divergence among populations is due to the ecological distinction between resident and migratory forms. Resident populations of North Slope Arctic char could either be composed of a separately evolved group with physiological or behavioral isolating mechanisms from migratory groups, or they could have arisen independently in various drainages where condition made it unfavorable or impossible to migrate.

With the exception of the Babbage River, the Arctic char populations of a given drainage had no detectable statistical difference between fish known to include residents (small adults) and juveniles from the main range of the anadromous adults. Within collections with both dwarf adults and juveniles of unknown life history propensities towards anadromy, we found no evidence of disequilibrium of allele frequencies that might be expected if more than one ecologically distinct breeding population was included in one collection.

The fish collected from the Sadlerochit Springs area are thought to be entirely non-migratory (Craig 1977), and were consequently excluded from mixed-stock fisheries analyses. They are genetically distinct in allele frequencies from other North Slope char populations, though there are no major differences such as allele substitutions. This distinction from other populations could be easily explained by isolation in a closed system, and periodic episodes of low effective population size. They are geneticaly distinct, but may well have become so by losing genetic variation.

Loss of genetic variation is often a symptom of low population size and random genetic drift.

Thus, resident groups could either resemble each other across the North Slope, or could most closely resemble the migratory groups in their drainage, with local divergence due to selection or genetic drift (random changes) in presumably small populations. We found that residents generally resembled those populations "expected" to be anadromous within the drainage, or in the case of the physically isolated Sadlerochit Springs char, to be quite different.

Genetic Differences Among Populations Within Drainages

We studied three collections of char from the Babbage Drainage. Those of the Canoe River, those from below the waterfall, and those from above the waterfall have all apparently diverged. The distinction may be less one of Taxonomy than relatively recent reproductive isolation and genetic drift. Bain (1974) has observed small adults spawning with anadromous char below the falls. While the downstream group may have emigrants coming in, the group above has no migration in. If condistions were unfavorable upstream and the population size became severely reduced, a shift in allele frequencies could occur due to random processes without strong directional selective forces being responsible.

The population sampled downstream of the Babbage Falls probably receives at least one successful migrant per generation, enough to prevent species divergence (Allendorf and Phelps 1980). The upstream

group meanwhile is probably diverging in allele frequencies due to a small effective population size. Though divergence between char of these sites on the Babbage has been observed, genetic similarities between them still results in their closeness on a dendrogram showing genetic relationships among populations.

The distinctness of the Canoe River population, from a tributary to the Babbage River, may relate to the small sample size (N = 21) available from that population. Sampling error could have resulted in the inclusion of a non-random sample, also indicated by disequilibrium at the Gpi3 locus.

The Sagavanirktok is a large system, with a number of tributaries and considerable char populations. Of the collections we made in 1986 and 1987 from four tributaries, two are genetically similar. The Echooka is tributary to Ivishak River, and Echooka char are not significantly different genetically from the Ivishak fish. The others are distinct, though Lupine and Ribdon are relatively closely related using a genetic similarity index, and simulations show that Ribdon fish are allocated to Lupine.

The Hula Hula River char from two different sites are genetically distinct. Though this river is apparently not complicated by different tributary stocks, it is possible that the two different sites are used preferentially by different char, with spatial and/or temporal variation in spawning. Some reproductive isolation is apparent, though they do cluster together fairly closely on a dendrogram of genetic similarities.

The complicating factor in the discussion of Hula Hula River char

is that Egaksrak River char are even more similar, on average, to Hula Hula River site #1 fish than are Hula Hula River site #2 char. The Egaksrak River is actually between and very close to the Aichilik and Kongakut rivers. The char of the latter rivers are very similar genetically, while those of the Egaksrak most closely resemble those of the Hula Hula River. Though this is not "tidy,", it may well be that the colonizers of the Hula Hula River were from the Egaksrak (or vice versa), or the similarity may be due to chance convergence of allele frequencies, or possibly selection.

The relationship between Canning and Ivishak River Drainage char populations also require discussion. From Craig's work (1971) it is apparent that there is migration of Arctic char between the Canning and Ivishak Rivers. Non-spawners were tagged in the Ivishak, and were observed spawning in the Canning. Non-spawners in the Canning were tagged, and were seen in spawning condition in the Ivishak. Though we have no evidence of individual fish spawning in both places, it is interesting that we are currently unable to discriminate genetically between the Ivishak and Canning River char populations we sampled. Though actual interbreeding between char of these populations may be taking place, it is also possible that we sampled actual Ivishak fish from the Canning, or actual Canning fish in the Ivishak. Chance convergence of genotypes is certainly a possible explanation, as is directional selection.

Genetic Divergence Among Populations

After combining collections within drainages, most North Slope Arctic char populations from different drainages are significantly genetically distinct from each other (with the exceptions noted) using a heterogeneity test that emphasizes the effect of variable loci. This information indicates that fish from different drainages are not freely interbreeding, and are most likely true to their spawning streams.

Although we have quantified significant genetic differences among populations of char within the Babbage and Sagavanirktok River systems, and among populations of different drainages, the overall genetic similarity among all char studied -- migratory and non-migratory -- is high. On the scale of similarities used (Nei 1972; 1978), both the variable enzymes and the number of enzymes that are consistently monomorphic are considered in evaluating relatedness among stocks. The measured differences among these populations only reflect what is recognized in other taxa as "local" differences (see Ayala and Kiger 1980, or Hartl 1980), relating to fairly recent divergence. We found no fixed differences among populations that would identify them as different taxa. Sadlerochit Springs fish are the most unlike other populations, but this could be explained by loss of genetic variation in a small closed system.

Most of the diversity in North Slope Arctic char is between individuals within subpopulations, and a seemingly small percent is due to differences between subpopulations. Among the char populations we collected in 1986 and 1987, only 8% of the variation is due to statistically detectable differences among fish from different

drainages. This amount, however, is similar to the 7% difference that has been quantified among human racial groups, again indicating current reproductive isolation and considerable difference among stocks.

Genetic Stock Identification: Simulations

Simulations are particularly needed with North Slope char studies. Other types of information on population dynamics are generally used with GSI to verify or validate what is seen for estimates. Since these other means are not available to address the accuracy and precision of our estimates we must rely on simulations and on limited amount of biological data available. There are currently no large-scale, comprehensive studies of population dynamics, escapements, enhancement, tagging, or scale pattern analyses that include the entire Beaufort Sea area. Certain studies target specific areas, such as Barter Island (Service) or Prudhoe Bay (oil company consultants). Past work did include tagging studies across the North Slope area, but tag returns were limited.

To evaluate the accuracy and precision of our baseline for Arctic char genetic stock identification, a simulation estimating the composition of a known stock was done. Less than half the stocks contributing to this known mixture, composed of baseline data, were allocated to the correct baseline using the GSI technique. Four stocks were estimated at zero contribution.

Poor stock discrimination could be due, in part, to the fact that

this type of estimate is a special case, where all stocks are present in low percentages. Estimates of stock compositon are more precise when less stocks are in higher percentages in a mixture. As large variances around small estimates often include zero, it is not then possible to presume accuracy in near-zero estimates, even though several stocks may be making small positive contributions to a fishery.

Given that low percentage estimates are predictably poor, 100% incremental simulations, which use known baseline from an individual stock as a mixture, should represent the best case. Though all baselines tested were at least 78% correct, and one was actually 95% correct, it is apparent from these simulations that certain populations are not well identified using GSI methods. It is probably a factor that the sample sizes for these simulations are small, as several baselines were composed of only forty samples, and some were less.

Incremental simulations do effectively give some indication of where fish are incorrectly allocated by the program. There is some pattern in the way certain char are assigned, e.g., simulations show that some fish are incorrectly assigned to other populations in their own drainage, for instance. The 100% simulation shows that Canning fish that are not allocated to the Canning baseline go to Ivishak and Firth Rivers. In the artificial mixed stock analysis, Canning is underestimated, and Ivishak and Firth stocks are overestimated by a corresponding amount.

The Canning River population allocation might be explained or improved in the future if certain points were considered. In the case

of the Canning River baseline, we combined data from five different sites collected over two different years and including at least two morphotypes representing different life history strategies. Though a test of heterogeneity signified that these collections did not represent significantly different breeding stocks, it is possible that the test was not sufficiently rigorous in defining differences.

Another potential problem with the Canning stock identification is indicated by the incremental simulation representing different percentages of contribution by the Canning stock in an artificial mixture. At 20%, which corresponds to the actual percentage of Canning data in the artificial mixed stock simulation, Canning was the most underestimated.

Most important, it is possible that the Canning char stock, as represented by our baseline, is just not sufficiently diverged from other stocks -- especially the Ivishak -- to be recognized by the GSI program. Perhaps it does not have unique genotypes. It is also possible that either our baselines from these two areas have included fish from the wrong stocks, or spawning fish are actually mixing in these two rivers.

In other cases it is not apparent where and why fish are allocated when the estimates and actual values are unlike. In some stocks that are underestimated, the stocks that the simulations show that they should be allocated to are not corresponsingly overestimated. Other types of simulations, exploring other cases with different numbers of char artificial stocks, could be designed to eliminate problems we understand or recognize or expect.

Evaluating Genetic Divergence

There are different ways of evaluating the degree of genetic divergence among stocks to predict the success with genetic stock identification techniques. It can be done with a scaled index of similarity, such as that of Nei (1972) or with a test of heterogeneity, such as the log likelihood ratio test of Sokal and Rohlf (1981), also called the G-test statistic. Genetic divergence (G_{ST}, Nei 1973) also gives an estimate of the divergence among stocks.

We used G-statistics and G_{ST} to predict that GSI would work to discriminate the composition of mixed stocks of North Slope char. The G-tests indicated that most populations are strongly distinct, even when corrected for the number of independent pairwise tests. G_{ST} levels are similar to the G_{ST} levels of salmon species where GSI is used in Washington, D.C., and California. However, Wood et al. (1987) suggest that a modified index of genetic similarity (Nei 1972), or a proportional difference in allele frequencies would be better predictors of successful stock discrimination. Though the G-tests and G_{ST} are significant, our similarity values are higher than those seen, for instance, in Columbia River chinook.

Milner et al. (1983) evaluated genetic stock identification techniques with actual chinook salmon electrophoretic data. They had baseline, mixed stocks, and other methods, such as escapement counts, coded wire tags, and life history data with which to validate their results. The GSI results are consistent with other types of data. The indices of relatedness, measured as Nei (1972) index of genetic

distance, between chinook population pairs ranged from 0.000 to 0.0737, with an average value of 0.0205. The maximum distance value between North Slope char populations is 0.0192, approximately equal to the average value for chinook. The distance between chinook groups ranged from 0.008 to 0.015, whereas Arctic char distance between groups is approximately 0.003. The within-group variation for chinook ranged from 0.0015 to 0.0382 and averaged 0.0112, compared to 0.04 for North Slope char that were studied. The work of Wood et al. (1987) and comparisons with the chinook data of Milner et al. (198?) suggest that using G-statistics for predicting success in population identification may not be the best method.

Genetic Stock Identification: Endicott Samples

In the June and August collections, all population contribution estimates where zero was not included in an 80% confidence interval were identified as Sagavanirktok River populations (Ivishak, Lupine, Ribdon) or the Colville River population (Anaktuvuk). In the July collection, Kavik and Hula Hula site #1 fish also had positive estimates of contribution to the mixed stock sample. For the July sampling period, the sample size was smaller, and the confidence intervals were wider. Though the error terms are large, the presence of additional stocks in the July collection is realistic given what is known about offshore char migration in the Beaufort Sea area in summer.

Arctic char migrate from freshwater rivers to offshore feeding areas in early summer. There they mix in feeding aggregations, and

return to spawn and/or overwinter in late summer. Because of the small size of captured char, it is not surprising that fish caught in large enough concentrations for GSI nearshore are apparently juveniles from the Sagavanirktok River system. High apparent contributions from the Colville system are interesting. Simulations show that Anaktuvuk char are effectively identified using GSI methods, so the presence of Anaktuvuk char near Prudhoe Bay should be considered.

Populations with larger percentage estimated contributions to the mixed stock have relatively smaller standard errors, emphasizing the fact that the program works best with a few major contributors. With a 95% confidence interval, only Ivishak and Lupine fish persist in the June and August mixtures.

Because of the large errors associated with small estimates, it is not possible to determine conclusively whether percent composition estimates from the other populations are real, e.g., the presence of Babbage char in Prudhoe Bay in the July sample. Only Lupine and Anaktuvuk River char estimates are non-zero in a 95% confidence interval in this collection.

From simulations we know that Canning River char are underestimated, and are probably assigned to the Ivishak River population which it resembles in genetic characteristics. It is possible that those identified as Ivishak fish in the Endicott collections are actually Canning char.

Through predominance of Sagavanirktok and Anaktuvuk fish in non-zero estimates is reasonable considering what is known of the biology of North Slope Arctic char, the estimates would be more useful

if the standard errors around the means of the estimates were smaller. The mixed stock sample sizes obtained are probably all too small for a 14-stock baseline. The work by Wood et al. (1987) shows with simulations that a mixed stock collection should contain 50 samples for each baseline. For computational ease, his work only included three stocks. Other researchers, such as Milner et al. (198?), using more than 20 stocks, have found that this rule is too extreme. The sample sizes necessary to answer specific questions can be calculated from the empirically-determined level of divergence in the target species, the number of variable loci, and the management goals for precision. The relationship of number of samples needed is not an arithmatic function of the number of baselines, but rather a function of the level of divergence of the species, and what is acceptable to management.

The basis of genetic stock identification is electrophoretically detectable differences in genotype frequencies between stocks. To do genetic stock identification (GSI) there must be sufficient detectable genetic variation in the stocks to be studied. Variation between groups of populations, e.g., between those of major drainages, should be relatively high combined with a low within-group variability. Also, the baseline should represent the major populations contributing to the mixed stock to be analyzed.

The level of divergence among populations that is detected using electrophoretic methods depends on the species and area. Different species have different levels of detectable differences (e.g., sockeye salmon are low, chinook are typically high). The species in question

may be at the center or edge of its range, and the relationships among populations of a species may reflect the evolutionary history of that species is in that area. Isolated populations and those colonized by a limited number or those experiencing stochastic fluctuations in number are more likely to have a low level of variability. Because of genetic drift, they may be different because of low variability or different because uncommon genotypes increased in a small population by chance.

The number of genetic loci that are studied can affect the accuracy and precision of genetic stock identification. Although the loci used in any study are meant to represent a random sample of the genome, and any sample of genetic characters should give similar estimates of the relationships among populations, the possibility exists that additional variable loci may introduce unique genotype combinations identifiable using maximum likelihood statistics.

Milner et al. (1983) used electrophoretic data from chinook salmon to simulate the addition of loci. They observed a 60% increase in accuracy with an increase from 10 to 25 loci. Wilmot (1988) found that the point estimates for chum salmon allocations to United States versus Canada stocks changed markedly when the number of variable loci was increased from 7 to 12.

The number of loci and the sample size needed are correlated in an inverse relationship. This relationship can be used either to increase accuracy and precision by increasing both number of characters measured and the sample size, or decrease the number of samples required to get similar levels of accuracy and precision.

Implications for Management

North Slope Arctic char have an above average amount of genetic variation compared to other salmonids. The pattern of variation shows distinctness among different populations, but the differences do not correspond to migratory versus resident life history strategies that have been postulated.

The pattern of divergence indicated by comparisons, pairwise, by log likelihood ratio statistics (G-tests) and by a calculation of gene diversity (G_{ST}) indicated that char populations are genetically distinct. These statistics measure diversity, but may not be good indicators of the level of divergence among populations that is required to do genetic stock identification.

Genetic stock identification techniques have potential for North Slope Arctic char biology and management, but need improvements. The reliability of the estimates is hard to verify. With little data on population dynamics from other sources, we have relied mainly on simulations for indications of the accuracy and precision in our estimates.

Simulations show that certain populations of Arctic char are allocated correctly, but that others are not. Though lack of precision is typical in composition estimates where many stocks contribute a small amount to a mixture, certain population of North Slope char are still not identified accurately in the 40 to 80% composition range. It suggests that the detected level of divergence in North Slope char populations is not sufficient to distinguish all

populations using our current baseline. This is also supported by the high levels of genetic similarity (Nei 1972) observed among certain population pairs.

Despite inaccuracies and imprecision we have observed in our simulations with GSI for North Slope Arctic char, the allocations made by the program with actual data from mixed fishery stocks from the Endicott area are supported by biological data. The collections in June, July, and August 1987 were made near the mouth of the Sagavanirktok River. The stocks identified in these mixtures are predominatly from the Sagavanirktok River Drainage, particularly in June and August when these fish would first be outmigrating to feed, then returning to overwinter. The July sample apparently included fish from other drainages, supporting data that shows that Arctic char migrate considerable distances and mix offshore during the summer season.

It is possible to improve both the accuracy and precision of GSI estimates. This can be done by increasing the completeness of the baseline; the number of loci in baseline and mixed stock samples; and the sample size of baseline and mixed fishery samples.

We believe we have major stocks, though more questions could be addressed if more collections were made within certain drainages with numerous spawning stocks, and with additional non-migratory stocks. Data from more baseline, spawning populations may need to be collected in the future to allow us to increase the number of loci in the analyses.

More loci studied would correspond to more data from each fish

sampled, and therefore smaller sampled sizes would be necessary to get the same level of precision. Additional loci are possible with an increase in sample quality and effort.

Increased sample sizes in mixed fishery samples improve both the accuracy and precision of GSI estimates. Increasing both the number of loci and the sample sizes would do the most for increasing both accuracy and precision in mixed stock identification procedures.

It has been determined that the Beaufort Sea environment is highly changeable, and that the dynamics of fish populations is highly dependent on wind conditions from year to year. In order to understand the distribution and timing of the migratory North Slope Arctic char it will be necessary to sample numerous places offshore, and at more times during the summer season when they migrate. This would allow us to determine how these fish use the area, predict how our activities may affect them, and use consideration for them in our plans for development.

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Appendix A.- Gene frequencies of variable loci in 12 populations of Arctic char collected in 1987 from the North Slope of Alaska and Canada. Variants of duplicated loci were arbitrarily assigned to one locus of the duplicated pair. Names of enzyme loci (abbreviated here) are in Table 2.

		Populations											
Loci		AICH	BAB1	BAB2	CAN1	CAN2	FIR1	FIR2	HULA	KONG	LUPI	SADL	SHUB
AAT1	100	0.975	1.000	1.000	0.975	0.956	ND	0.947	0.981	1.000	1.000	1.000	0.956
	33	0.025	0.000	0.000	0.025	0.044	--	0.053	0.019	0.000	0.000	0.000	0.044
	N	40.00	53.00	21.00	40.00	45.00	46.00	38.00	80.00	45.00	45.00	44.00	45.00
AAT3	100	0.911	1.000	1.000	0.910	0.936	0.920	0.956	0.950	0.932	0.956	0.867	0.922
	75	0.089	0.000	0.000	0.090	0.064	0.080	0.033	0.050	0.068	0.044	0.133	0.078
	129	0.000	0.000	0.000	0.000	0.000	0.000	0.011	0.000	0.000	0.000	0.000	0.000
	N	45.00	53.00	21.00	50.00	55.00	44.00	45.00	80.00	44.00	45.00	45.00	45.00
ACO4	100	0.533	0.490	0.441	0.477	0.611	0.434	0.544	0.562	0.544	0.467	0.100	0.444
	115	0.211	0.019	0.000	0.244	0.167	0.196	0.200	0.219	0.189	0.211	0.011	0.233
	130	0.256	0.490	0.559	0.279	0.222	0.370	0.256	0.219	0.267	0.322	0.889	0.322
	N	45.00	52.00	17.00	43.00	45.00	46.00	45.00	80.00	45.00	45.00	45.00	45.00
FH	100	0.433	ND	ND	ND	ND	ND	ND	ND	0.422	0.619	0.444	0.578
	130	0.567	--	--	--	--	--	--	--	0.578	0.381	0.556	0.422
	N	45.00	53.00	21.00	55.00	55.00	45.00	46.00	80.00	45.00	42.00	45.00	45.00
GAP3	100	0.716	0.933	0.850	0.744	0.756	0.767	0.826	0.581	0.682	0.767	1.000	0.738
	Null	0.284	0.067	0.150	0.256	0.244	0.233	0.174	0.419	0.318	0.233	0.000	0.262
	N	44.00	52.00	20.00	43.00	45.00	43.00	46.00	80.00	44.00	45.00	45.00	42.00
GPI1	100	1.000	0.990	1.000	1.000	1.000	1.000	0.989	1.000	1.000	1.000	1.000	1.000
	55	0.000	0.010	0.000	0.000	0.000	0.000	0.011	0.000	0.000	0.000	0.000	0.000
	N	45.00	52.00	21.00	55.00	55.00	44.00	45.00	80.00	44.00	45.00	45.00	45.00
GPI3	100	0.744	0.846	1.000	0.891	0.927	0.659	0.667	0.819	0.733	0.589	0.844	0.822
	96	0.256	0.154	0.000	0.109	0.073	0.341	0.333	0.181	0.267	0.411	0.156	0.178
	N	45.00	52.00	21.00	55.00	55.00	44.00	45.00	80.00	45.00	45.00	45.00	45.00
IDH2	100	0.967	1.000	1.000	1.000	1.000	0.997	1.000	1.000	0.977	0.978	1.000	1.000
	220	0.033	0.000	0.000	0.000	0.000	0.023	0.000	0.000	0.023	0.022	0.000	0.000
	N	45.00	53.00	21.00	41.00	43.00	43.00	46.00	80.00	44.00	45.00	45.00	45.00
IDH3	100	0.889	1.00	1.00	0.977	0.978	0.935	0.946	0.975	1.000	1.000	1.000	0.944
	80	0.111	0.000	0.000	0.023	0.022	0.065	0.054	0.025	0.000	0.000	0.000	0.056
	N	45.00	53.00	21.00	44.00	45.00	46.00	46.00	79.00	45.00	45.00	45.00	45.00
LDH5	100	0.944	1.000	1.000	1.000	1.000	0.978	0.978	0.988	1.000	1.000	1.000	1.000
	97	0.056	0.000	0.000	0.000	0.000	0.022	0.022	0.012	0.000	0.000	0.000	0.000
	N	45.00	48.00	21.00	45.00	45.00	46.00	46.00	80.00	45.00	45.00	45.00	45.00
MDH1	100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	128	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	N	45.00	53.00	21.00	43.00	45.00	41.00	46.00	80.00	45.00	40.00	45.00	45.00
ME3	100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	69	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	N	45.00	53.00	21.00	45.00	45.00	46.00	46.00	80.00	45.00	45.00	45.00	45.00
6PG1	100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.989	1.000	1.000
	95	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.011	0.000	0.000
	N	45.00	53.00	21.00	45.00	45.00	46.00	46.00	80.00	45.00	45.00	45.00	44.00
PGM2	100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.975	1.000	1.000	1.000	1.000
	88	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.025	0.000	0.000	0.000	0.000
	N	45.00	51.00	21.00	45.00	45.00	44.00	44.00	80.00	45.00	45.00	45.00	45.00
SDH1	100	0.922	1.000	1.000	0.932	0.966	0.978	0.978	0.913	0.989	0.989	1.000	0.878
	43	0.078	0.000	0.000	0.068	0.034	0.022	0.022	0.087	0.011	0.011	0.000	0.122
	N	45.00	53.00	21.00	44.00	44.00	46.00	46.00	80.00	44.00	44.00	44.00	45.00
SOD1	100	0.944	0.944	0.857	0.973	0.973	1.000	1.000	0.900	0.978	0.911	1.000	0.967
	115	0.056	0.000	0.000	0.027	0.027	0.000	0.000	0.100	0.022	0.089	0.000	0.033
	87	0.000	0.056	0.143	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	N	45.00	53.00	21.00	55.00	50.00	46.00	46.00	80.00	45.00	45.00	45.00	45.00
XDH1	100	0.433	ND	ND	ND	ND	ND	ND	ND	0.422	0.619	0.444	0.578
	86	0.567	--	--	--	--	--	--	--	0.578	0.381	0.556	0.422
	N	45.00	53.00	21.00	55.00	55.00	45.00	46.00	80.00	45.00	42.00	45.00	45.00

AICH = Aichilik
BAB1 = Babbage Site 1
BAB2 = Babbage Site 2
CAN1 = Canning Site 1
CAN2 = Canning Site 2
FIR1 = Firth Site 2
HULA = Hula Hula
KONG = Kongakut
LUPI = Lupine
SADL = Sadlerochit
SHUB = Shublik

Appendix B.- Gene frequencies of variable loci in 16 populations of Arctic char collected in 1986 and 1987 from the North Slope of Alaska and Canada. Variants of duplicated loci were arbitrarily assigned to one locus of the duplicated pair. Names of enzyme loci (abbreviated here) are in Table 2.

		Populations														
Loci		AIC	ANA	BA1	BA2	CAN	CAO	EGA	FIR	HU1	HU2	IVI	KAV	KON	LUP	RIB	SAD
AAT1	100	0.988	0.975	1.000	1.000	0.969	1.000	0.986	0.921	0.981	ND	1.000	1.000	1.000	1.000	ND	1.000
	33	0.012	0.025	0.000	0.000	0.031	0.000	0.014	0.079	0.019	—	0.000	0.000	0.000	0.000	—	0.000
	N	80	40	53	33	179	21	35	76	80	00	22	37	85	45	00	44
AAT3	100	0.918	0.908	1.000	1.000	0.908	1.000	0.951	0.942	0.950	ND	0.966	ND	0.912	0.956	0.950	0.867
	75	0.082	0.092	0.000	0.000	0.092	0.000	0.049	0.050	0.050	—	0.034	—	0.088	0.044	0.050	0.133
	129	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.008	0.000	—	0.000	—	0.000	0.000	0.000	0.000
	N	85	38	53	35	206	21	41	130	80	00	72	00	85	45	40	45
ACO4	100	0.541	0.403	0.490	0.700	0.514	0.441	0.557	0.461	0.560	0.467	0.535	0.463	0.547	0.467	0.588	0.100
	115	0.194	0.292	0.019	0.029	0.216	0.000	0.243	0.211	0.220	0.239	0.174	0.137	0.177	0.211	0.112	0.011
	130	0.265	0.305	0.490	0.271	0.270	0.559	0.200	0.328	0.220	0.294	0.291	0.400	0.275	0.322	0.300	0.889
	N	85	36	52	35	183	17	35	128	91	46	72	40	85	45	40	45
GAP3	100	0.655	0.934	0.933	ND	0.754	0.850	0.500	0.883	0.560	0.325	0.775	0.706	0.714	0.767	0.730	1.000
	Null	0.345	0.066	0.067	—	0.246	0.150	0.500	0.177	0.440	0.675	0.225	0.294	0.286	0.233	0.270	0.000
	N	82	38	52	00	183	20	32	107	91	40	71	34	84	45	37	45
GPI1	100	1.000	0.950	0.990	1.000	0.998	1.000	1.000	0.981	1.000	1.000	0.993	1.000	1.000	1.000	0.923	1.000
	55	0.000	0.050	0.010	0.000	0.002	0.000	0.000	0.019	0.000	0.000	0.007	0.000	0.000	0.000	0.077	0.000
	N	85	40	52	35	211	21	41	129	95	51	74	40	85	45	39	45
GPI3	100	0.759	0.900	0.846	0.629	0.897	1.000	0.829	0.694	0.842	0.860	0.912	0.988	0.718	0.589	0.667	0.844
	96	0.241	0.100	0.154	0.371	0.123	0.000	0.171	0.306	0.158	0.140	0.088	0.012	0.282	0.411	0.333	0.156
	N	85	39	52	35	211	21	41	129	95	50	74	40	85	45	39	45
IDH2	100	0.982	1.000	1.000	1.000	0.997	1.000	1.000	0.981	1.000	0.990	0.986	0.975	0.988	0.978	0.950	1.000
	220	0.018	0.000	0.000	0.000	0.003	0.000	0.000	0.019	0.000	0.010	0.014	0.025	0.012	0.022	0.050	0.000
	N	85	37	53	35	149	21	35	129	95	51	74	40	85	45	40	45
IDH3	100	0.888	1.000	1.000	1.000	0.965	1.000	0.986	0.947	0.973	0.927	0.993	0.900	0.941	1.000	1.000	1.000
	80	0.122	0.000	0.000	0.000	0.035	0.000	0.014	0.053	0.027	0.073	0.007	0.100	0.059	0.000	0.000	0.000
	N	85	39	53	35	184	21	35	131	91	48	73	40	85	45	40	45
LDH5	100	0.946	1.000	1.000	0.986	0.995	1.000	0.929	0.973	0.989	0.941	0.973	0.988	0.965	1.000	0.923	1.000
	97	0.054	0.000	0.000	0.014	0.005	0.000	0.071	0.027	0.011	0.059	0.027	0.012	0.035	0.000	0.077	0.000
	N	83	35	53	35	188	21	35	132	95	51	73	40	85	45	39	45
MDH1	100	1.000	0.956	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	128	0.000	0.044	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	N	82	34	53	35	182	21	35	128	93	52	72	40	85	40	40	45
ME3	100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.981	1.000	1.000	1.000	1.000	1.000	1.000
	69	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.019	0.000	0.000	0.000	0.000	0.000	0.000
	N	85	40	53	35	197	21	35	132	95	54	74	40	85	45	40	45
6PG1	100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.993	1.000	1.000	0.989	0.988	1.000
	95	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.007	0.000	0.000	0.011	0.012	0.000
	N	85	40	53	35	197	21	35	132	95	51	74	40	85	45	40	45
PGM2	100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.996	0.979	0.971	1.000	1.000	1.000	1.000	1.000	1.000
	88	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.021	0.029	0.000	0.000	0.000	0.000	0.000	0.000
	N	85	35	51	28	161	21	39	128	95	51	50	40	85	45	40	45
SDH1	100	0.965	0.875	1.000	1.000	0.912	1.000	0.986	0.985	0.914	1.000	0.913	1.000	0.959	0.989	1.000	1.000
	43	0.035	0.125	0.000	0.000	0.088	0.000	0.014	0.015	0.086	0.000	0.087	0.000	0.041	0.011	0.000	0.000
	N	85	36	53	34	188	21	35	131	87	17	23	40	85	44	40	44
SOD1	100	0.947	1.000	0.944	0.957	0.974	0.857	0.943	0.996	0.914	0.907	0.972	1.000	0.976	0.911	0.888	1.000
	115	0.053	0.000	0.000	0.015	0.026	0.000	0.057	0.004	0.086	0.093	0.028	0.000	0.024	0.089	0.112	0.000
	87	0.000	0.000	0.056	0.028	0.000	0.143	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	N	85	35	53	35	212	21	35	132	93	54	72	40	85	45	40	45

AIC= Aichilik ANA= Anaktuvuk BA1= Babbage Site 1 BA2= Babbage Site 2 CAN= Canning CAO= Canoe
EGA= Egakarak FIR= Firth HU1= Hula Hula Site 1 HU2= Hula Hula Site 2 IVI= Ivishak KAV= Kavik
KON= Kongacut LUP= Lupine RIB= Ribdon SAD= Sadlerochit

Appendix C.- Mean estimate (with one bootstrap standard deviation) and actual proportion of an artificial mixed stock analyzed with maximum likelihood method of genetic stock identification. Estimates are listed in descending order, and those below the line are less than 1%.

	Population	Mean estimate	Standard deviation	Actual proportion	80% Confidence interval		95% Confidence interval	
1	Firth River	0.1874	0.0359	0.128	0.1415	0.2334	0.1170	0.2578
2	Aichilik	0.1756	0.0588	0.082	0.1003	0.2508	0.0603	0.2908
3	Hula Hula 1	0.1594	0.0517	0.092	0.0932	0.2255	0.0580	0.2607
4	Ivishak	0.1462	0.0507	0.072	0.0813	0.2111	0.0468	0.2456
5	Kongakut	0.1014	0.0756	0.082	0.0046	0.1981	-0.0468	0.2495
6	Babbage	0.0518	0.0197	0.051	0.0266	0.0771	0.0132	0.0905
7	Canning	0.0442	0.0648	0.205	-0.0388	0.1271	-0.0828	0.1712
8	Egaksrak	0.0353	0.0385	0.040	-0.0139	0.0846	-0.0401	0.1108
9	Lupine	0.0352	0.0289	0.044	-0.0018	0.0722	-0.0214	0.0919
10	Kavik	0.0323	0.0249	0.039	0.0004	0.0642	-0.0165	0.0811
11	Anaktuvuk	0.0246	0.0200	0.039	-0.0010	0.0502	-0.0146	0.0638
12	Hula Hula 2	0.0022	0.0016	0.053	0.0002	0.0043	-0.0009	0.0054
13	Ribdon	0.0022	0.0015	0.039	0.0003	0.0041	-0.0007	0.0052
14	Canoe	0.0022	0.0014	0.034	0.0004	0.0040	-0.0006	0.0049

Appendix D.- Percentage allocations to each of 14 North Slope Arctic char stocks when an artificial mixture of each stock is compared to baseline data using the maximum likelihood method of genetic stock identification.

	Site	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	Canoe R.	84.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
2	Babbage-87	13.5	95.8	2.2	2.2	0.0	0.0	0.3	0.0	0.0	2.7	0.2	0.1	3.8	0.0
3	Firth	0.0	0.8	91.5	0.0	0.0	2.0	0.1	0.0	3.4	0.0	0.0	0.0	0.0	0.2
4	Kongakut	0.0	0.0	1.7	78.4	1.7	9.5	0.4	0.4	0.5	0.0	0.0	0.1	4.1	0.0
5	Egaksrak	0.7	0.0	2.3	4.3	92.8	7.0	8.2	6.8	0.3	0.3	1.1	3.4	0.0	0.0
6	Aichilik	0.0	0.0	0.4	8.1	0.6	79.7	0.2	0.3	0.0	0.0	0.0	0.0	0.0	0.0
7	Hula-01	0.0	0.0	0.2	1.5	0.9	0.6	86.5	0.3	0.0	0.0	0.5	0.0	0.3	0.0
8	Hula-02	0.0	0.0	0.0	0.0	0.0	0.0	0.0	90.4	0.0	0.0	0.0	0.0	0.0	0.0
9	Canning	0.0	0.0	0.1	2.8	0.8	0.4	3.6	0.0	88.0	0.0	2.0	0.0	0.1	0.7
10	Kavik	0.8	1.7	0.0	4.5	1.2	0.6	0.4	1.5	2.4	96.4	1.4	0.0	4.9	0.0
11	Ivishak	0.2	0.0	0.3	1.1	0.0	0.0	0.0	0.0	3.8	0.4	92.2	0.1	1.1	0.8
12	Ribdon	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.3	84.1	0.0	0.0
13	Lupine	0.1	2.9	0.6	1.2	0.7	0.1	0.3	0.3	0.5	0.0	1.2	12.2	92.8	0.0
14	Anaktuvuk	0.0	1.2	0.7	1.9	1.0	0.0	0.0	0.0	0.6	0.2	1.2	0.0	0.1	98.3

Appendix E.- Mean estimates (with one bootstrap standard deviation) of the composition of the June sample of Arctic char (N = 208) taken from near the Endicott causeway. Estimates are listed in descending order, and those below the line are less than 1%.

	Population	Mean estimate	Standard deviation	80% Confidence interval		95% Confidence interval	
1	Ivishak	0.3346	0.1300	0.1682	0.5010	0.080	0.589
2	Lupine	0.3259	0.1081	0.1875	0.4643	0.114	0.538
3	Anaktuvuk	0.1409	0.0852	0.0318	0.2500	-0.026	0.308
4	Kongakut	0.1239	0.1158	-0.0243	0.2721	-0.103	0.351
5	Firth	0.0321	0.0708	-0.0585	0.1227	-0.107	0.171
6	Aichilik	0.191	0.0255	-0.0135	0.0517	-0.031	0.069
7	Hula Hula 1	0.0169	0.0541	-0.0523	0.0861	-0.089	0.123
8	Canoe	0.0009	0.0023	-0.0020	0.0038	-0.003	0.005
9	Babbage	0.0009	0.0349	-0.0438	0.0456	-0.068	0.069
10	Egaksrak	0.0009	0.0539	-0.0681	0.0699	-0.105	0.107
11	Hula Hula 2	0.0009	0.0023	-0.0020	0.0038	-0.004	0.005
12	Canning	0.0009	0.0842	-0.1069	0.1087	-0.164	0.166
13	Kavik	0.0009	0.0175	-0.0215	0.0233	-0.033	0.035
14	Ribdon	0.0009	0.0023	-0.0020	0.0038	-0.004	0.005

Appendix F.- Mean estimates (with one bootstrap standard deviation) of the composition of the July sample of Arctic char (N = 126) taken from near the Endicott causeway. Estimates are listed in descending order, and those below the line are less than 1%.

	Population	Mean estimate	Standard deviation	80% Confidence interval		95% Confidence interval	
1	Lupine	0.2993	0.1417	0.1180	0.4807	0.0216	0.5771
2	Anaktuvuk	0.2103	0.0663	0.1255	0.2952	0.0804	0.3403
3	Hula Hula 1	0.1236	0.0798	0.0215	0.2258	-0.0328	0.2800
4	Kavik	0.1029	0.0650	0.0197	0.1861	-0.0245	0.2303
5	Babbage	0.0917	0.0786	-0.0089	0.1923	-0.0623	0.2458
6	Ribdon	0.0842	0.0786	-0.0164	0.1848	-0.0698	0.2383
7	Ivishak	0.0412	0.1591	-0.1624	0.2449	-0.2706	0.3530
8	Canoe	0.0067	0.0046	0.0008	0.0125	-0.0024	0.0157
9	Firth	0.0067	0.1088	-0.1326	0.1459	-0.2066	0.2199
10	Kongakut	0.0067	0.0315	-0.0337	0.0470	-0.0551	0.0684
11	Egaksrak	0.0067	0.0201	-0.0191	0.0324	-0.0327	0.0461
12	Aichilik	0.0067	0.0387	-0.0429	0.0562	-0.0692	0.0825
13	Hula Hula 2	0.0067	0.0046	0.0008	0.0125	-0.0024	0.0157
14	Canning	0.0067	0.1335	-0.1642	0.1775	-0.2550	0.2683

Appendix G.- Mean estimates (with one bootstrap standard deviation) of the composition of the August sample of Arctic char (N = 126) taken from near the Endicott causeway. Estimates are listed in descending order, and those below the line are less than 1%.

	Population	Mean estimate	Standard deviation	80% Confidence interval		95% Confidence interval	
1	Ivishak	0.4345	0.1180	0.2835	0.5856	0.2033	0.6658
2	Lupine	0.2355	0.1110	0.0934	0.3775	0.0179	0.4530
3	Ribdon	0.1075	0.0790	0.0063	0.2086	-0.0474	0.2623
4	Hula Hula 1	0.0761	0.0801	-0.0264	0.1768	-0.0809	0.2331
5	Firth	0.0650	0.0762	-0.0325	0.1625	-0.0843	0.2144
6	Egaksrak	0.0509	0.0528	-0.0166	0.1185	-0.0525	0.1544
7	Anaktuvuk	0.0223	0.0292	-0.0151	0.0597	-0.0350	0.0795
8	Babbage	0.0012	0.0210	-0.0257	0.0281	-0.0400	0.0423
9	Canoe	0.0012	0.0058	-0.0063	0.0086	-0.0102	0.0125
10	Kongakut	0.0012	0.0327	-0.0407	0.0430	-0.0629	0.0653
11	Aichilik	0.0012	0.0059	-0.0064	0.0087	-0.0104	0.0127
12	Hula Hula 2	0.0012	0.0058	-0.0063	0.0086	-0.0102	0.0125
13	Canning	0.0012	0.0315	-0.0392	0.0415	-0.0606	0.0629
14	Kavik	0.0012	0.0211	-0.0258	0.0282	-0.0402	0.0425

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