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GENETIC STOCK STRUCTURE OF ARCTIC CHAR (Salvelinus alpinus)
FROM DRAINAGES TO THE BEAUFORT SEA IN ALASKA AND CANADA

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ABSTRACT

To study anadromous Arctic char that maybe affected by oil and gas development activities in the Beaufort Sea area of Alaska and Canada, we have used protein electrophoresis to genetically characterize samples from spawning stocks and to identify the tributary-of-origin of mixed stocks. In 1986 and 1987 we collected samples of Arctic char from 11 tributaries to the Beaufort Sea. These collections were analyzed for 49 presumptive gene loci, 19 of which are variable. Twelve loci were used as baseline data. The average heterozygosity is 0.038 (SE=0.010); pairwise genetic identity values (Nei) exceed 0.98; and tests of genetic heterogeneity between stocks are generally significant. Computer simulations using maximum likelihood statistics were used to analyze the accuracy and precision of composition estimates of artificial mixed stocks of known proportions. These simulations indicate that certain Arctic char stocks are identifiable and others are not using the current baseline data. Analyses of actual mixed-stock samples of Arctic char collected during the summer of 1987 near Prudoe Bay, Alaska indicate that most of the fish came from nearby drainages, but that stocks from as far away as Canada were present. Development activities should show consideration for the genetic distinctness of populations of North Slope Arctic char and their patterns of migration.

Technical Summary

The genetic stock structure of Arctic char (Salvelinus alpinus) from the North Slope of Alaska and Canada (North Slope) was studied to determine which stocks could be at risk from oil and gas development activities. Arctic char are of particular interest in this area because they use both freshwater tributaries and coastal waters, and because they are important in subsistence fisheries in the United States and Canada. Development activities resulting in change to either the freshwater or the marine environment could affect Arctic char stocks.

Because Arctic char are migratory and because different stocks may be using areas that could be affected by development activities, we need to know more about the pattern of their use of Beaufort Sea waters. To supplement the collections from Beaufort Sea tributaries made in 1985 and 1986, we collected samples of Arctic char from several additional river sites for genetic baseline information in 1987. We also acquired samples of Arctic char from mixed stocks at the mouth of the Sagavanirktok River near the Endicott Causeway and from the Camden Bay area. No Arctic char were captured at sampling sites near the Chukchi Sea, including the Singaruak, Walakpa, and Kugrua Rivers and their tributaries. Repeated overflights looking for habitat apparently preferred by char, and several efforts at electrofishing produced no fish.

We did electrophoretic analysis of over 40 gene loci for the Arctic char that were captured, and did statistical analyses to determine the relationships of the collections from different freshwater sites and from different years. We then used this baseline data set in computer simulations to study the accuracy and precision of estimates of mixed-stock composition, and then analyzed the composition of mixed-stock Arctic char collections from the Endicott Causeway area.

The amount of genetic variation observed in North Slope Arctic char was typical of fish species in general, and close to average among salmonids that have been studied. In general, collections of Arctic char made in different years and in different parts of the same drainage were not significantly

different in allele frequencies and could be combined to represent the population of that drainage.

We found no evidence that resident and migratory life history forms of Arctic char represent separate populations in these collections. 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.

After combining data from collections of Arctic char from within each drainage, most North Slope populations from different drainages were significantly distinct genetically from each other. This information indicates that fish from different drainages are not freely interbreeding, and are generally true to their spawning streams.

Although we quantified significant genetic differences among populations of Arctic char of certain different drainages, the overall genetic similarity among all Arctic char studied, both migratory and non-migratory forms, was high. The measured differences among all populations studied reflect what is recognized in other taxa as "local differences, relating to fairly recent divergence. We found no fixed differences among populations that would identify them as different subspecies. Sadlerochit Springs Arctic char were most unlike other populations, but its distinctness could reflect loss of genetic variation in a small system, closed to immigration.

Tests of the accuracy and precision of stock composition estimates (using simulations) indicated general reliability of estimates but also some misallocation of stocks, though much of that was to geographically proximate stocks. Our inability to distinguish some populations from one another in this study suggests that the 12-locus baseline used for analyses may need to be expanded. However, this baseline is adequate to distinguish the more distinct populations, e.g., the Firth and Babbage River stocks of Canada, and the Kavik and Anaktuvuk River stock of the United States. Also, certain stock management groups are relatively distinct genetically from each other, i.e., the Sagavanirktok River stocks versus most of the Arctic National Wildlife Refuge stocks, with the exception of the Canning River Arctic char. That the U.S. and Canada Arctic char stocks are

genetically distinct is suggested by the general lack of misallocation between them.

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 predominately 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 higher percentages of Arctic char **from** other drainages, supporting tag return data that show that Arctic char migrate considerable distances and mix offshore during the summer season. These results demonstrate that development in the nearshore Prudhoe Bay area would likely affect mainly Sagavanirktok River Arctic char stocks, but that contributions by other stocks from as far away as the Arctic National Wildlife Refuge and Canada are not negligible.

Although not all populations of Arctic char can be distinguished genetically using the methods of this study, the results do confirm the hypothesis that an Arctic char population is generally distinct to a watershed area. Given this conclusion, it is possible that human activity affecting a critical habitat such as an overwintering area or access to Beaufort Sea coastal feeding areas in summer could have significant impact on a unique population of Arctic char. The resource in each watershed area should be considered as having long term implications for Arctic char abundance in the area and for the genetic diversity of the region's Arctic char populations.

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INTRODUCTION

The genetic structure of Arctic char, (Salvelinus alpinus) from the North Slope of Alaska and Canada (North Slope) was studied to determine which stocks could be at risk from oil and gas development activities. Arctic char are of particular interest in this area because they use both freshwater tributaries and coastal waters, and because they are important in subsistence fisheries in the United States and Canada. Development activities resulting in change to either the freshwater or the marine environment could affect Arctic char stocks.

Fish and fishing are important to the people across the North Slope of Alaska (Jacobson and Wentworth 1982). Anadromous fish are harvested from coastal waters near the village of Kaktovik from late June to September, and from traditional fish camps on the Hulahula River in fall and winter. Many Arctic char are also harvested as part of the summer fishery in the Colville River near Nuiqsut (Moulton et al. 1986; Pedersen and Shishido 1988). Although there is much variability in numbers of fish harvested by North Slope residents in any given year, these differences may reflect both fish abundance and fishing effort (Craig 1989a).

Arctic char life history and migration patterns reflect an adaptive response to the limitations of the habitat of the North Slope and to the potential for variation in habitat availability. Arctic char populations vary widely in abundance from year to year as a consequence of extremely variable physical conditions (temperature, extent of ice formation, timing of spring thaw, etc.) in the North Slope region.

North Slope Arctic char spend most of their lives in tributaries to the Beaufort Sea where they spawn, rear, and overwinter. Char spawn in autumn in areas generally associated with perennial springs in or near the Brooks Range (McCart 1980), and eggs remain in the gravel until hatching in the spring. Juvenile char generally remain in tributaries year-round until three to five years of age (McCart 1980; Craig 1977a). Adults overwinter in freshwater after spawning; during the winter, marine waters are too saline and supercooled for Arctic char.

Only about two percent of tributary habitat, deep river pools and springs, remains available to fish by the end of winter (Craig 1989b), and these areas are shared by Arctic char at all life history stages. If an overwintering area fails, e.g. due to anoxia or freezing solid, fish are not able to move to a different refuge because connecting stream segments are frozen. The limited deep pool habitat in the tributaries is therefore critical to Arctic char population viability.

At spring thaw, adult Arctic char typically move to brackish food-rich nearshore waters to feed for the short (10-week) summer open water season. On the North Slope, Arctic char do not typically spawn until age five or six (Craig 1977a; Bain 1974). Although individual Arctic char can spawn repeatedly over their lifetime, each needs to reach the level of somatic reserves of energy required by early summer in order to spawn that year (Dutil 1986). Consequently, they seldom spawn every year.

Although springfed streams are very productive during the summer, intense feeding during the summer is necessary in order for Arctic char to meet the critical energy requirements for spawning, and much more food-producing habitat is available in coastal areas (Craig 1989b). Because little food is available in overwintering areas (Bain 1974; Glova and McCart 1974; McCart et al. 1972; Craig 1977a), Arctic char must maximize summer feeding opportunities. This makes migration to sea where the food source is more concentrated energetically critical for most segments of the adult char populations.

Migration is generally limited to the brackish waters near the river-of-origin (Furniss 1975), though examples of extended migration have been documented (Glova and McCart 1974; Craig 1977a; Furniss 1975; Jessop et al. 1974). Arctic char tagged in one stream in non-spawning condition have been found spawning in another stream in another year. Several Arctic char tagged in Beaufort Sea tributaries have been caught up to 300 kilometers away in coastal Native domestic fisheries. Tagging studies have shown that Arctic char caught near Barter Island originated from Alaska's Sagavanirktok and Canning Rivers, and Canada's Firth River (Craig and Haldorson 1981).

The high variation in Arctic char abundance in response to environmental changes (Craig 1989b) is an indication of the potential vulnerability of the population to perturbations as a result of development. Though Arctic char populations are adapted to the physical extremes of the Arctic by long life and repeat spawning, they also rely the availability of overwintering areas and on their ability to migrate. In the freshwater environment, water removal from overwintering sites for drilling, road construction, or other human use could deplete the limited overwintering resource used by all life history stages of Arctic char. Construction of river crossings, channelization, or removal of material from the rivers could affect migratory corridors and substrate quality.

In the estuarine environment used by Arctic char, food availability could be affected by development activities. Construction of physical barriers such as causeways or drilling islands could affect water movement, and therefore salinity stratification and temperature gradients. Changes in water currents could also affect food distribution, as well as affecting migratory routes

by fragmenting the habitat. This could be energetically costly to fish trying to maximize their food intake in **estuarine** environments.

Because Arctic char are migratory and because different stocks may be using areas that could be affected by development activities, we need to know more about the pattern of their use of **Beaufort** Sea waters. We used biochemical genetics techniques to study Arctic char collected from the freshwater and marine environments of the North Slope area. By studying the amount and pattern of genetic variation within and between stocks, we can determine how they are related to each other. Genetic data from these breeding populations allow us to establish a baseline for analyses of the composition of mixed-stock collections sampled from the marine environment. By sampling at different places and times, we can study the pattern of distribution and use of northern waters by Arctic char. Knowledge of the population genetic structure of North Slope Arctic char would allow us to identify which stocks could be affected by development activities on a **site-specific** basis.

Objectives

The goals of this portion of the Arctic Fish Habitats and Sensitivities Study were to understand the genetics of the **anadromous** North Slope Arctic char populations, and to determine which of these stocks using certain nearshore areas of the **Beaufort** Sea would be affected by development projects in that area.

The objectives of the 1987 study were 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** Seato those of the **Beaufort** Sea, and 3) collect samples of Arctic char from the coastal area of **Beaufort** Sea and estimate the percent composition of baseline populations we have studied that contribute to it.

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** River near 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 from different sites and different years to each other. We then used the baseline data in computer simulations to study the accuracy and precision of estimates of mixed-stock composition, and then analyzed the composition of Arctic char collections from the Endicott Causeway area.

METHODS

sampling

U.S. Fish and Wildlife Service (Service) crews located Arctic char by overflying tributaries to the Beaufort and Chukchi Seas with a helicopter to find suitable habitat (relatively clear water, some flow, and rocky or gravelly substrate). They used **electrofishing** units and minnow traps to sample for Arctic char,

Service personnel took Arctic **char** from the tributaries, on ice, to Deadhorse, Alaska where they were frozen, then shipped to the Service laboratory in Anchorage. Tissues were stored at -80°C .

The target mixed-stock sample size from **estuarine** waters was 200 Arctic char collected from each location during a five-day period, three times during the summer season. The actual sample sizes were determined by availability during that five-day period. The sampling protocol called for random sampling with regard to condition, sex, or size. Samples from the **Prudhoe Bay** area were collected by Envirosphere Company personnel with fyke traps in the area around Endicott Causeway. Service personnel dissected the Arctic char in Deadhorse, then froze the samples before shipping them to 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 Fairbanks Fisheries Assistance Office,

Electrophoretic methods

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; and EBT (**Boyer** et al. 1963) pH 8.5.

Building **on** our previous work (Everett and **Wilmot** 1987) and that of Andersen et al. (1983), we analyzed 49 gene **loci** coding for 20 enzymes in three tissues. The loci we used were 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; May 1980), 2) comparisons based on different tissue expression, and 3) the known molecular subunit structure of the enzymes. Nabilities of enzymes were measured relative to the common **electrophoretic** phenotype observed in samples of **Anaktuvuk River Arctic char**, which were chosen as a reference arbitrarily **from** among the populations sampled from the North Slope.

Statistical methods

The methods for analyzing the amount of genetic variation, pattern of genetic variation within and between stocks, artificial mixed-stock composition simulations, and actual mixed-stock identification are described below, and summarized in Appendix A.

Amount of genetic variation.- The amount of genetic variation was estimated by determining the percent of loci that were polymorphic (P), and the mean percent of **heterozygous** loci per individual (H). Expected average heterozygosity for each locus was calculated with 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 j th locus, and p_{ij} is the frequency of the i th allele at the j th locus.

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

For this and subsequent analyses, **isoloci** (Allendorf and Thorgaard 1984: duplicated locus pairs with indistinguishable nobilities) were counted as two individual loci and all observed variation was attributed arbitrarily to one locus of the pair.

Genotypic distribution. - Observed genotypes in samples were tested for conformance to Hardy-Weinberg (random mating) 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 pooling data **from** collections was based on a joint resolution by the West Coast interagency group for genetic stock identification of Pacific salmon. The criteria used for pooling data from collections from the same drainage was a probability greater than 0.05 that the collections, made at different sites or in different years, were not **significantly** different using a **chi-square** or log likelihood ratio statistic (G-test: **Sokal and Rohlf** 1981).

Baseline data from collections from different geographic areas (such as major drainages) were not pooled before the basic genetic analyses. After estimates of percent composition were made for mixed-stock samples, estimates from stocks of the same drainage were pooled. After pooling samples, the variances associated with the estimates were recalculated.

To test the heterogeneity between paired populations, we used multiple simultaneous G-tests. 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.

When making all possible pairwise tests between 16 different populations, the **large** number of non-independent pairwise comparisons 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 between each pair of collections was modified for this analysis according to Cooper (1968) to eliminate spurious correlations. This involves making the criteria for a significant test more rigorous, such that a probability of 0.05 would be divided by the number of pairwise tests (120 in a 16 by 16 matrix of collections). It would then be necessary to observe a **chi-square** value from the table that **corresponded** to a probability value less than 0.0004 for a comparison between collections to be considered significantly different.

Genetic similarity.- The genetic similarity among baseline collections was calculated with 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:

$$I = J_{XY} / \text{SQRT}(J_{XX} J_{YY});$$

where J_{XX} , J_{YY} , and J_{XY} are the arithmetic means overall loci of the probabilities of identity between gene pairs among populations relative to the probability that two randomly chosen alleles from the same population will be identical.

Pairwise 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) to produce a **dendrogram** of relationships among populations. The average linkage method of clustering was used and was weighted to reflect unequal sample sizes.

Gene diversity analysis. - Gene diversity analysis was used to determine the source of observed variation, i.e., what proportion of the observed variation was due to quantifiable genetic differences between individuals within populations, as opposed to differences among populations (Nei 1973; Chakraborty 1980).

Sample data were analyzed hierarchically by individual **subpopulations** (sites), by subpopulations of different drainages, and by all **subpopulations** of a region combined. The combined total amount of genetic variation of all subpopulations studied was partitioned into within- and between- subpopulation diversity components. The total gene diversity (H_T) overall 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 fish within a drainage (D_{BS}) and differences between subpopulations of different drainages (D_{BD}). The relative magnitude of gene differentiation among subpopulations (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. - To compute the conditional maximum likelihood estimate of the composition of mixed stocks, the **Genetic Iteratively Re-weighted Least Squares** model with an **Expectation Maximization** algorithm (GIRLS-EM) described in Pella (1986) was used. The program was **modified** in 1989 (Pella, unpublished). The baseline data set, or learning sample, was made up of allele frequency data (genetic characteristics) from each stock that could potentially contribute to the mixed fishery. Similar genetic data were characterized for each individual in a

mixed fishery. For simulations of mixed fisheries, artificial mixtures were made by combining known proportions of baseline data.

The GIRLS-EM program estimates the proportion of each baseline stock that would have to be included in a hypothetical mixture in order to produce the mixed-stock data being evaluated. This produces point estimates of the percentage of each baseline stock present in the mixed fishery. Standard errors were calculated using a bootstrap technique (Efron 1982) to resample the baseline data and the mixture data 100 to 200 times. This allowed us to evaluate the precision in the estimates of stock composition.

We used three types of simulated mixed stocks to evaluate the effectiveness of genetic stock identification for North Slope Arctic char with our baseline. A 14-stock baseline with twelve gene loci was used as the learning sample. In each simulation, bootstrap resampling was used to determine the standard error of the estimates.

Equal-contribution simulations.- To evaluate the accuracy of mixed-stock composition estimates, a single artificial mixed stock was constructed using nearly equal proportions of each baseline data set. The estimated percent composition of the artificial mixed stock was compared to actual expected values with a chi-square statistic using number of fish estimated to have come from each stock, compared to number of fish expected (actual mixture composition).

100% simulations.- To indicate how accurately the fish from each stock were allocated and to which stocks incorrectly allocated fish were assigned, each baseline stock, one at a time, was used to makeup an artificial mixed stock and tested against the baseline made up of all 14 stocks.

Incremental simulations.- To test the accuracy and precision of the estimates for each stock over the range of possible contributions, each baseline population data set was used to make an artificial mixture at 20% increments from 0 to 100%, with baseline data from other populations used to total 100%. The point estimates of contribution, with error bars for one standard deviation, were graphed against a line representing the actual values if the maximum likelihood program were to identify the stock accurately.

Endicott samples.- The percent composition of mixed fishery collections taken from coastal waters of the Beaufort Sea near Prudhoe Bay adjacent to the Endicott Causeway was determined using maximum likelihood statistics and bootstrap resampling. These collections were made in June,

July, and August of 1987. Sixty-eight and 95 percent confidence intervals were generated around the point estimates of the proportional contribution for each population for each sampling period.

RESULTS

sampling

Arctic char were sampled for at 22 sites on 16 rivers in 1987. They were found at 12 sites on eight rivers (Table 1, Figure 1). Sample sizes ranged from 21 to 97 fish. Sampling took place in August and early September, and most of the Arctic char captured in freshwater were juveniles, with some small resident adults. A small sample of Arctic char was collected upstream from the waterfall on the **Babbage River** (site #2) for comparison of these apparently non-migratory fish with **anadromous** populations. **Firth River** sampling site #2 was in **Alaska**, and was included for comparison of upstream and downstream populations in this drainage. Upstream **Firth River** fish were small, and many appeared to have mature gonads indicating that they **are** probably residents. No Arctic char were captured at the **Shaviovik River**, the downstream end of the **Colville River**, or the **Anaktuvuk River**, which is a tributary to the **Colville River**.

No Arctic char were captured at sampling sites near the **Chukchi Sea**, including the **Singaruaq**, **Walakpa**, and **Kugrua Rivers** and their tributaries. These drainages **are** low gradient tundra-draining rivers with silty substrates. Repeated overflights looking for habitat apparently preferred by char, and several efforts at **electroshocking** produced no fish.

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

Gene loci resolved and allelic variation

Of the 49 gene loci we examined (Table 2), 19 were variable in at least some populations and 30 were monomorphic. Complete data sets for all baseline and mixed-stock collections were not obtained. Incomplete data sets usually reflect sample quality. Up to eighteen variable loci were used in some of the pairwise analyses among baseline stocks, but only twelve loci were available in all collections. Mixed-stock simulations and estimates of the composition of **Endicott** samples were based on these twelve loci (indicated in Table 2).

Allele frequencies at each gene locus were calculated for each baseline population, and the relative nobilities of **allelic** variants were measured (Appendix B). **Aat4**, **Hex1**, and **Xdhl** were included in the analyses in 1986, when we had live fish to sample in the lab. However, these **geneloci** are particularly sensitive to sample handling and storage, and consistently good resolution

Table 1.- Collections of Arctic char sampled from the North Slope of Alaska and Canada with site location (Universal Transverse Mercator), number of samples, and date collected. Prudhoe Bay area collections represent mixed stocks from estuarine areas near the Endicott Causeway.

Collections	UTM Coordinates			N	Date
	Zone	Latitude	Longitude		
Beaufort Sea					
Aichilik River					
Site 1	7W	7699000	419000	40	9/86
Site 2	7W	7688000	419000	70	8/87
Anaktuvuk River	5W	7725000	576000	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	7755000	552500	27	5/86
Site 2	6W	7716000	525000	70	8/87
Site 3	6W	7691000	539000	62	8/87
Marsh Fork	6W	7665000	539000	29	5/86
Shublik Spring	6W	7698000	535000	59	8/87
Egaksrak River	7W	7700000	435000	41	5/86
Firth River					
Site 1	7W	7625000	506000	64	8/87
Site 2	7W	7610000	495000	47	8/87
Joe Creek	7W	7650000	501000	40	9/86
Hula Hula River					
Site 1	6W	7740000	609000	15	10/85
Site 2	6W	7711000	605000	37	10/85
Site 3	6W	7692000	598000	59	10/85
Site 4	6W	7753000	609000	97	8/87
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
Sadlerochit Spring	6W	7730000	600000	62	8/87
Echooka River	6W	7685000	489000	24	4/86
Ivishak River	6W	7690000	492000	50	9/86
Lupine River	6W	7659000	439000	48	8/87
Ribdon River	6W	7615000	460000	40	5/86
Prudhoe Bay					
Endicott Causeway	4W	7803000	465000	232	6/87
				137	7/87
				166	8/87
Chukchi Sea					
Kugrua River	4W	7840000	498000	0	8/87
Singaruak River	4W	7894000	579000	0	8/87
Walakpa River	4W	7884000	566000	0	8/87

Table 2.- Enzymes, IUBNC^a numbers, 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 or other protein	IUBNC	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 ^b	AC 6.8	L
Aspartate aminotransferase	2.6.1.1	Aat3,4	RW	E,L
		Aat(1,2)	RW	M
Creatine kinase	2.7.3.2	Ck1.2	RW	M
		Ck5 "	RW	E
Fumarate hydratase	4.2.1.2	Fh1	AC 6.8	M
b-Glucosaminidase	3.2.1.30	Hex1	AC 6.8	L
Glucose phosphate isomerase	5.3.1.9	Gpi(1,2) ^b	RW	M
		Gpi3 ^b	RW	M
Glutathione reductase	1.6.4.2	Grl	RW	L
Glyceraldehyde-3-phosphate dehydrogenase	1.2.1.12	Gap3 ^b ,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.	Dpep	EBT	M
Isocitrate dehydrogenase	1.1.1.42	Idh1 ^b ,2	AC 6.8	M
		Idh(3,4) ^b	AC 6.1,6.8	L,E
Lactate dehydrogenase	1.1.1.27	Ldhl,2	RW	M
		Ldh3,4,5 ^b	RW	E
		Ldh4	RW	L
Leucyl-glycyl-glycine peptidase	3.4.13.	Tapep	EBT	M
Malate dehydrogenase	1.1.1.37	Mdh(1,2) ^b	AC 6.1	M
		Mdh(3,4)	AC 6.1	M
Malate dehydrogenase (NADP-dependent)	1.1.1.40	Mdhpl,2,3	AC 6.1	M
Phosphoglucomutase	2.7.5.1	Pgml,2 ^b	RW	M
		Pgm(3,4)	AC 6.1	L,M
6-Phosphogluconate dehydrogenase	1.1.1.44	6Pg1 ^b	AC 6.8	M,L,E
Sorbitol (iditol) dehydrogenase	1.1.1.14	Sdh(1,2) ^b	RW	L
Superoxide dismutase	1.15.1.1	Sod1 ^b	RW	L
Triose-phosphate isomerase		Tpil,2,3,4	TG	E
Xanthine dehydrogenase	1.2.3.2	Xdhl	RW	L

^a International Union of Biochemistry, Nomenclature Committee, 1984.

^b These loci represent the twelve used for genetic stock identification analyses.

could not be obtained in 1987 when samples were brought **from** the field frozen. Pgm(3,4) is a duplicated monomer, and could not be reliably scored. Tpi2 variation was observed in mixed-stock samples, but not surveyed among baseline samples.

Statistical analyses

Amount of genetic variation.- The 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 values of P range from 7.1 to 35.7% (average 19%, SE= 6.68%). 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 was 3.8% (SE=1.02%). **Sadlerochit** River Arctic char have the least genetic variation at 1.6%.

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, particularly in the Canoe River collection from the **Babbage** River Drainage. 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 collection), and the collections appear to represent random samples of the populations.

Genetic heterogeneity.- Based on allele frequency comparisons of collections made within each drainage at different sites and in different years, the data sets from the **Aichilik**, Canning, Firth, Ivishak, and Kongakut River Arctic char **subsamples** were not detectably different from each other (Table 4), and were combined (Appendix C). The Arctic char collected from the upstream sites (#2 and #3) of the **Hulahula** River were not distinct genetically, and were combined as site #2. Collections from **Hulahula** River site #1 in 1986 and 1987 were not significantly different, and were combined as site #1. The five collections combined in the Canning River Drainage include Arctic char from the Marsh Fork and **Shublik** Springs.

The three Arctic char collections from the **Babbage** River Drainage, 1) from the Canoe River, 2) from a site downstream from the waterfall, and 3) from a site above the waterfall were significantly different genetically when tested pairwise, and could not be combined. The populations of 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. The average value of H is weighted by sample size (standard errors for average H and average P are in parentheses). Heterozygosities were calculated using only gene loci that were studied in both years.

Drainage /Sites	Year	N	% H	% P
Aichilik River	1986/1987	85	5.04	23.8
Colville River				
Anaktuvuk	1986	40	3.81	19.0
Babbage River				
Canoe River	1986	35	2.51	9.8
Site #1	1987	53	2.48	11.9
Site #2	1987	21	2.43	7.1
Canning River				
5 Sites	1986/1987	212	4.13	26.2
Egaksrak River	1986	41	4.32	21.4
Firth River				
3 Sites	1986/1987	132	4.29	28.6
Hula Hula River				
Site #1	1986/1987	95	4.57	23.8
Site #2	1986	54	4.66	22.5
Kavik River	1986	40	3.14	14.3
Kongakut River				
2 Sites	1986/1987	85	4.54	21.4
Sadlerochit River	1987	45	1.63	7.1
Sagavanirktok River				
Ivishak/Echooka	1986	74	3.62	26.2
Lupine River	1987	45	4.36	19.0
Ribdon River	1986	40	5.16	22.0
Average		1097	3.79 (1.02)	19.0 (6.7)

major tributaries of the **Sagavanirktok** River (**Ribdon**, **Lupine**, and **Ivishak** Rivers) were significantly different genetically, though the collection from the **Ivishak** River was not distinct from that of its tributary, the **Echooka** River.

When data from the 16 collections were compared, all but 13 of 120 pairwise comparisons indicated highly significant genetic differences ($P < 0.001$) among North Slope Arctic char populations when corrected for the number of non-independent tests (Appendix D). A summary **G-test**, including all populations and all variable loci, showed that the Arctic char studied were highly different from each other ($G = 1237$, $df = 143$; $P < 0.001$).

Table 4.- Log likelihood ratio genetic heterogeneity tests among populations of North Slope Arctic char sampled at different sites and/or different years. A probability of $P > 0.01$ was used as the criteria for combining collections within a drainage. Degrees of freedom (df) reflect 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	0.013
Firth	1986/1987	3	11.64	13	0.458
Hulahula	1986/1987	2	29.41	9	<0.001
Kongakut	1986/1987	2	5.71	10	0.839
Sagavanirktok	1986/1987	3	53.60	12	<0.001
Ivishak	1986	2	11.99	8	0.152

Genetic similarity.-No allele substitutions were observed at any locus. Genetic identities, calculated with corrections for unequal sample sizes (Nei 1978), were high between North Slope Arctic 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 was responsible for the lowest similarity values among the Arctic char studied Without this unique population, the identity values among anadromous North Slope Arctic char were 0,990 or higher, ranging up to complete identity, 1.000 (Table 5). *

A dendrogram (Figure 2) illustrates the genetic relationships among Arctic char populations of the Beaufort Sea area. The Sadlerochit River Arctic char were most unlike the other populations.

Gene diversity analysis.- Using hierarchical gene diversity analysis, the relative magnitude of the diversity among subpopulations of the 11 drainages sampled was approximately 8% of the total variation among North Slope Arctic char studied (Table 6). Less than 1% was due to differences among subpopulations of different sampling sites within drainages. Variation among individuals within populations accounts for 91.1 % of the total gene diversity.

Table 5.- Matrix of Nei's (1978) gene identity values pairwise among 16 populations of Arctic char sampled from the North Slope of Alaska and Canada rivers in 1986 and 1987.

Population																
1 canoe	1.000															
2 Bab 1	0.998	1.000														
3 Bab 2	0.995	0.999	1.000													
4 Firth	0.999	0.998	0.996	1.000												
5 Kongak.	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 Sadler	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 Ivishak	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 Anaktu.	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

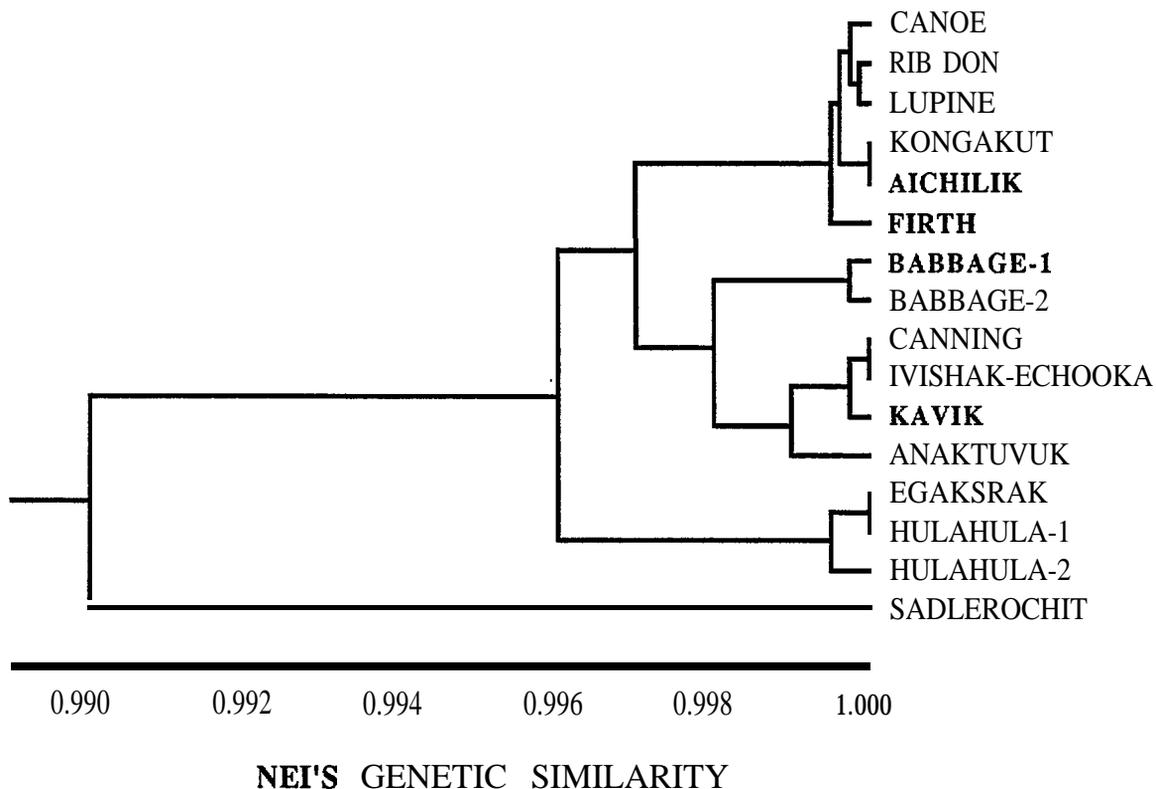


Figure 2.- Relationships based on Nei's (1978) index of genetic similarity of 16 populations of Arctic char from rivers of the North Slope among Alaska and Canada.

Genetic Stock Identification.- For genetic stock identification analyses, data from 14 populations were used as a baseline. The **Sadlerochit** River Arctic char were excluded from the analyses, as they are not **anadromous**. Data from the Canoe River stock (**Babbage** River Drainage) were also excluded as the sample size was so small and may not represent a random sample. For these fourteen stocks, data **from** twelve variable gene loci were complete and informative, and were used in the simulations and mixed-stock analyses.

Equal-contribution simulations.- The actual percent contributions for all 14 populations making up the artificial mixed **stock** were within one standard deviation of the estimated allocation using genetic stock **identification** procedures (Appendix E, Figure 3). A **chi-square** test between the

Table 6.- 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.

Drainage	# of sites	ABSOLUTE GENE DIVERSITY				RELATIVE DIVERSITY (%)		
		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

estimated and actual number of fish from each stock in the artificial mixture showed that the estimated contributions of only two stocks were significantly different from the actual values. The contribution of Aichilik to the artificial mixture was overestimated ($X^2=5.33$, $df=1$, $P<0.025$) and Canning fish were overestimated ($X^2=12.9$, $df=1$, $P<0.001$).

100% simulations.- With the 12-1ocus data set used, the program correctly identified over 90% of the fish for only one stock (Babbage site#2) (Appendix F and Figure 4). Babbage site #1, Kavik, and Anaktuvuk River stocks were allocated over 80% of their fish correctly, while Firth, Hulahula site #2, Canning, and Lupine River stocks were correctly allocated 70% or more fish. Kongakut, Egaksrak, and Aichilik were poorly identified (43 - 52% correct), and a large proportion of Ivishak fish were misallocated to the Canning River stock

Incremental simulations. - When each population was used to makeup 20% incremental proportions of artificial mixtures, Babbage River site #2, Sadlerochit, Kongakut, Egaksrak, Aichilik, Hulahula site #1, Ivishak, Lupine, and Anaktuvuk Rivers stocks were correctly allocated throughout the range of the simulations (Figure 5). Canoe, Firth, Canning, Hulahula site #2, and Kavik River populations were consistently underestimated, and Babbage River site #1 and Ribdon River Arctic char were poorly “recognized”.

Endicott samples.- After allocation, the point estimates for Babbage site #1 and #2; for Hulahula site #1 and #2; and for Ivishak, Lupine, and Ribdon sites were combined as Babbage, Hulahula, and Sagavanirktok River drainage contributions, and the variances were re-calculated. Maximum likelihood estimates of the stock composition of Arctic char taken near Endicott Causeway in June 1987 showed that Sagavanirktok, Canning, and Anaktuvuk River stocks (61, 26, and 11%) were the major contributors among Arctic char sampled (Appendices G, H, and I; Figures 6,7, and 8). In July, Canning (38%) and Sagavanirktok (31%) contributed 69% of the fish sampled at Endicott, with Canada stocks from the Firth and Babbage Rivers making up 23% of the mixture. In the August sample, all three Sagavanirktok River tributary stocks were represented, making up 78% of the sample from the Endicott area. Hulahula and Firth River stocks (9 and 7%) were also represented in the August mixture,

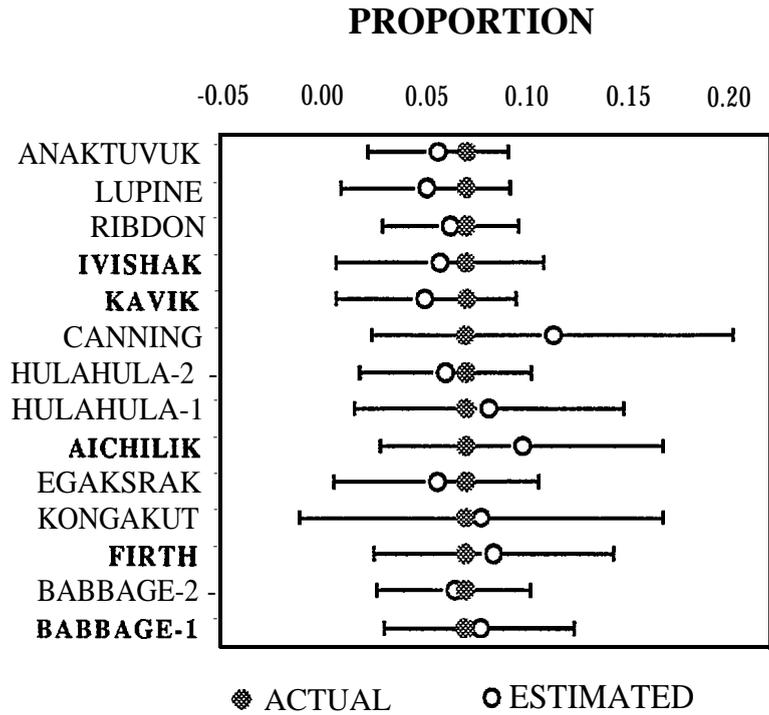


Figure 3.- Maximum likelihood method of genetic stock identification used to identify the composition of an artificial mixed stock of North Slope Arctic char (N = 500) made up of nearly equal proportions of each of 14 stocks sampled. Estimated numbers of fish (o) are given with one standard error. Actual values (*) are the proportion of fish from each stock in the artificial mixture.

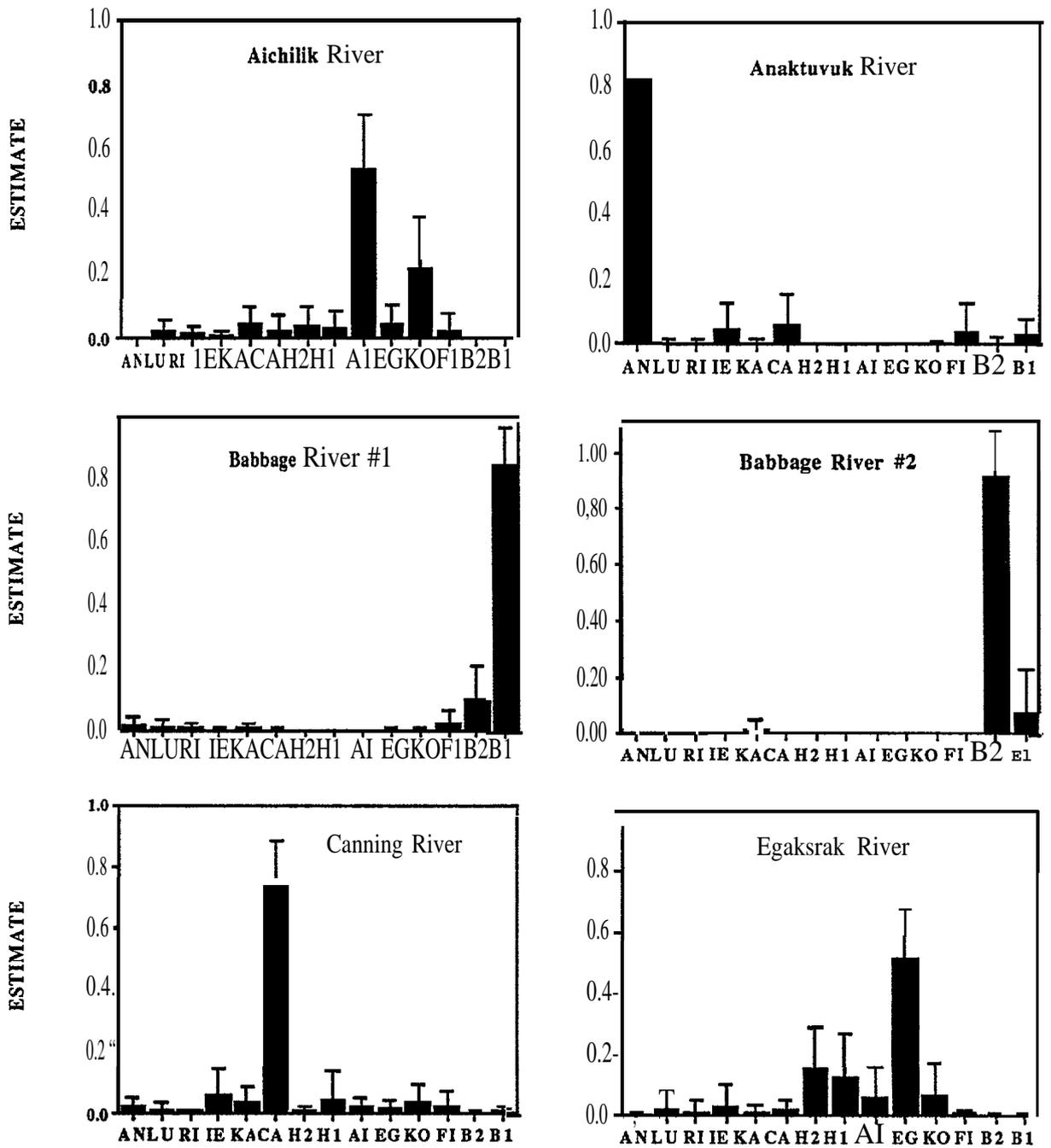


Figure 4.- Mixed stock simulations for each of 14 populations of North Slope Arctic char, each as 100% of an artificial mixture. Proportions were estimated using maximum likelihood techniques, and graphed with error bars representing one standard error. Stocks are graphed from left to right corresponding to west to east across the North Slope, and have 2-letter codes: Anaktuvuk (AN), Lupine (LU), Ribdon (RI), Ivishak (IE), Kavik (KA), Canning (CA), Hulahula site#2 (H2), Hulahula site#1 (H1), Aichilik (AI), Egaksrak (EG), Kongakut (KO), Firth (FI), Babbage River site#2 (B2), and Babbage River site#1 (B1).

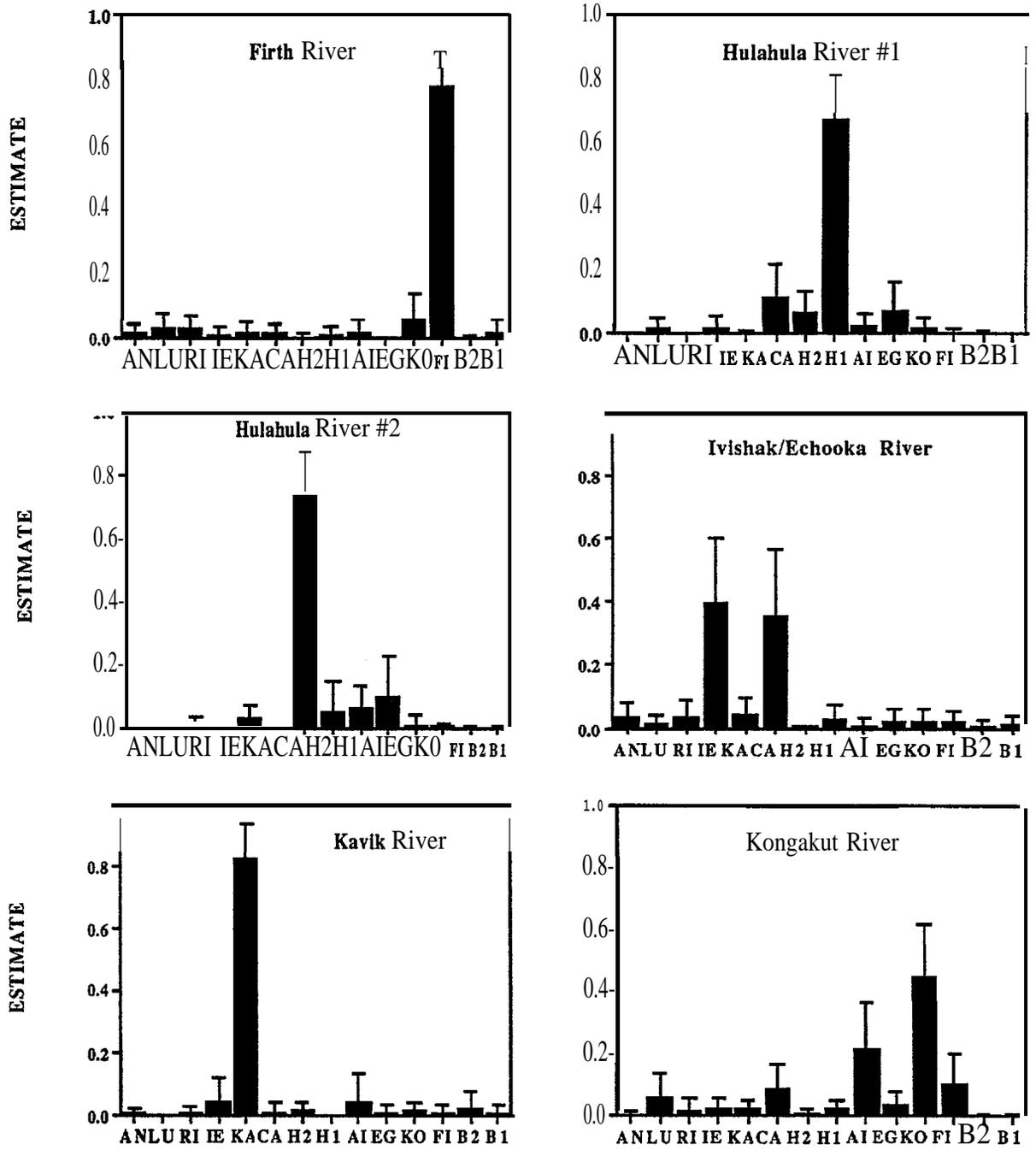


Figure 4,- Continued

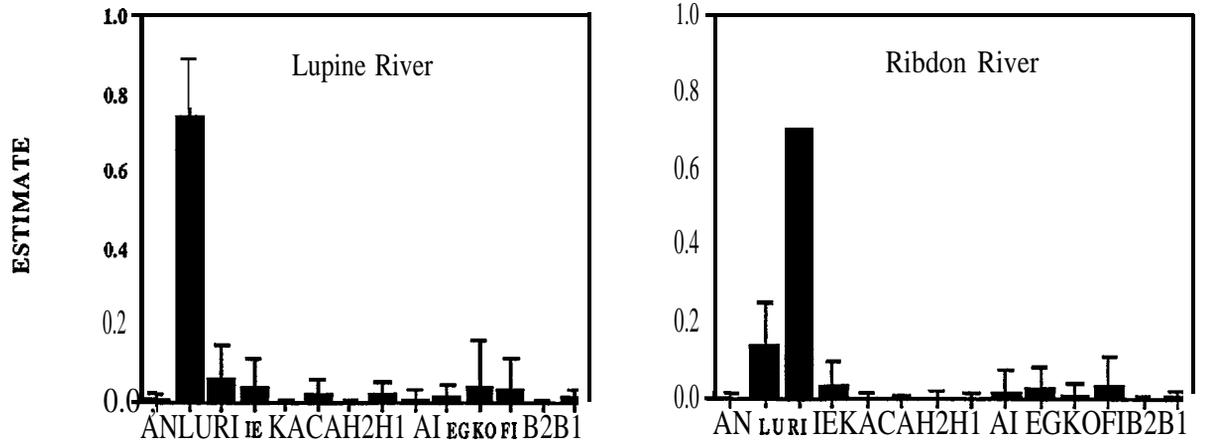


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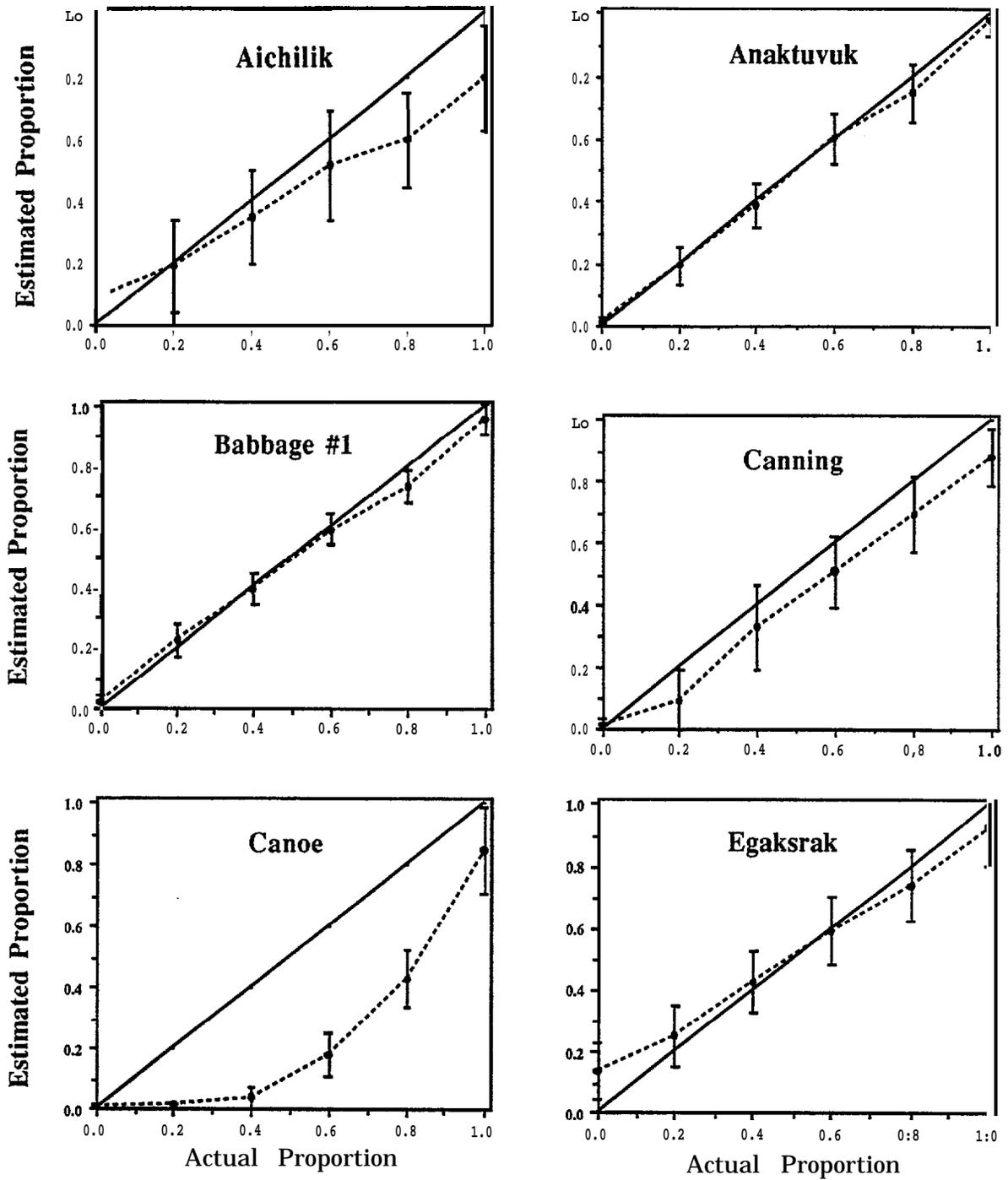


Figure 5.- Incremental mixed stock simulations for each of 14 populations of North Slope Arctic char. Contributions of each stock, in 20% increments, estimated using maximum likelihood techniques, and graphed with a 45 degree line representing the results if estimated proportions equaled actual values. Error bars represent one standard deviation of the mean of the estimates.

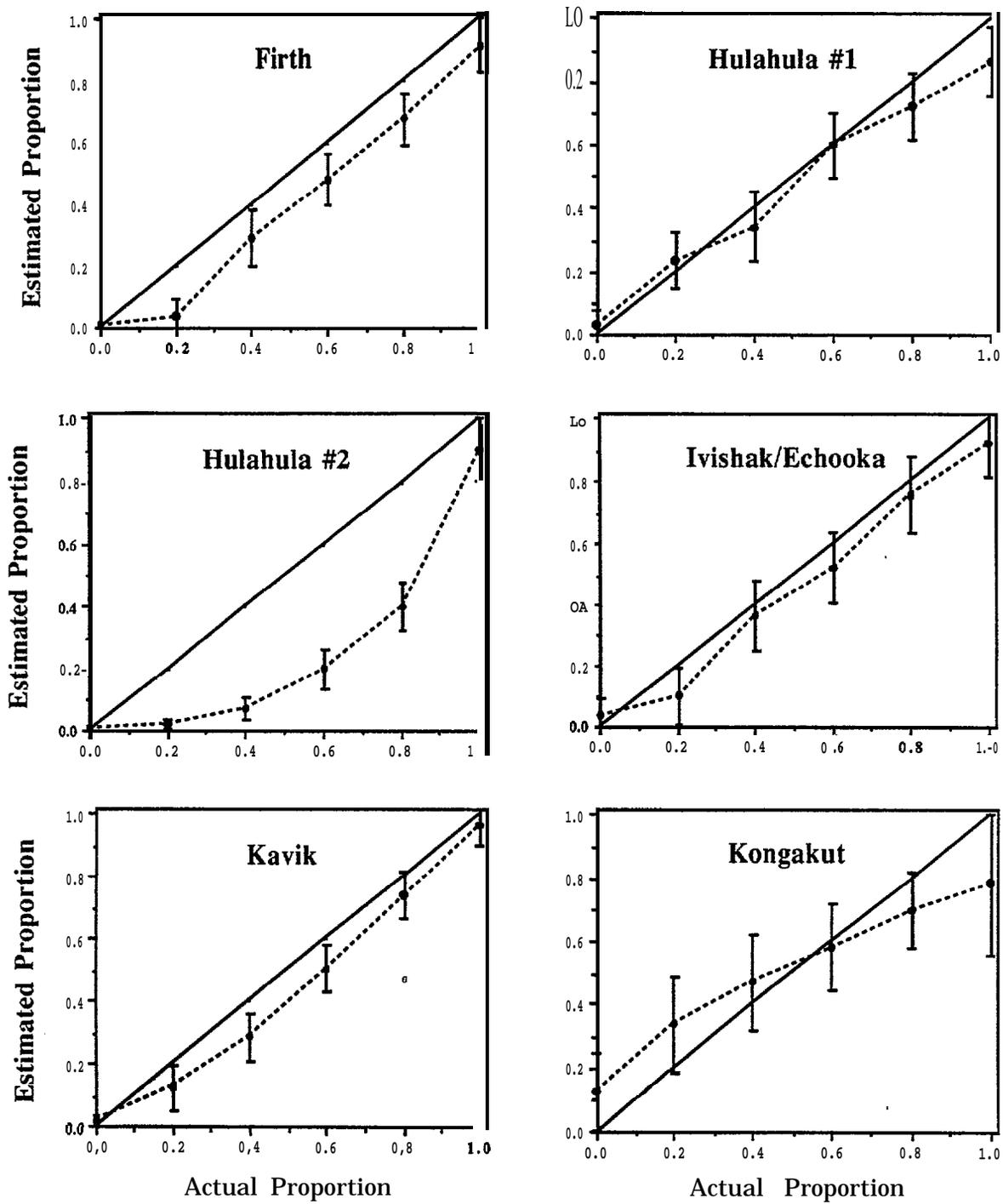


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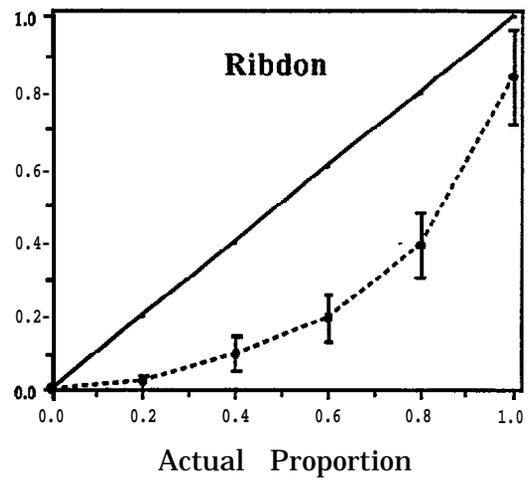
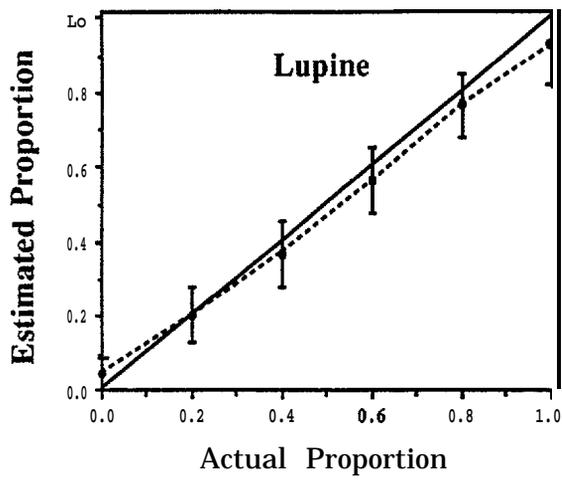


Figure 5.- Continued

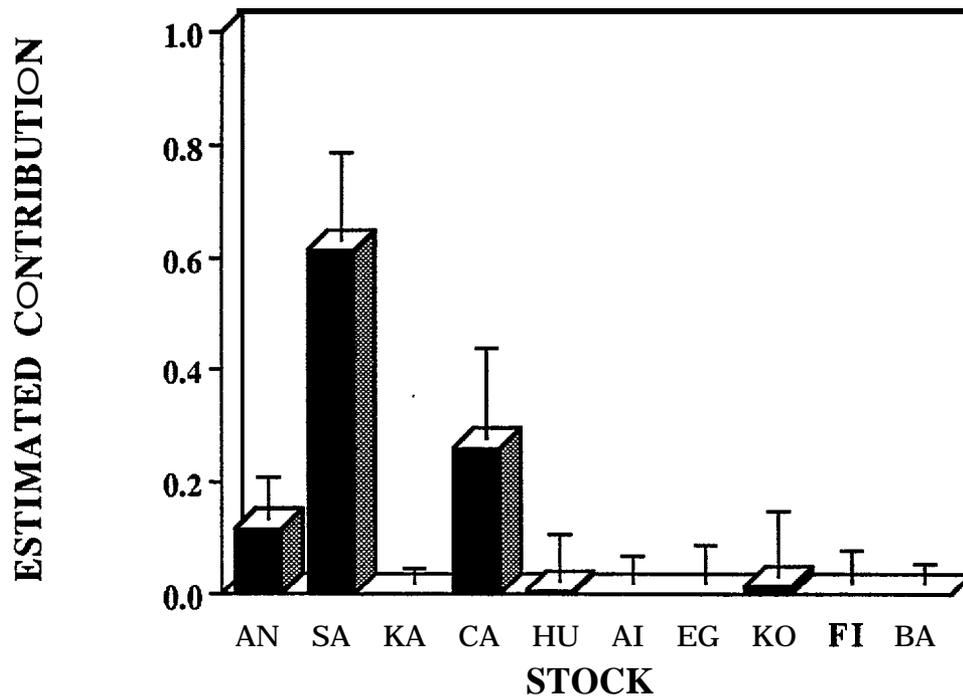


Figure 6.- Estimated composition (with one standard error) of a mixed fishery sample from the Prudhoe Bay, Alaska area collected in June 1987. Estimates are made using maximum likelihood techniques with a 14-stock genetic baseline. The stocks are arranged on the graphs from left to right as west to east along the North Slope of Alaska and Canada. Allocations from three sites are joined to make up the Sagavanirktok River drainage (SA), as are two sites from the Hulahula River (I-W), and two sites from the Babbage River drainage (BA). Anaktuvuk (AN), Kavik (KA), Canning (CA), Aichilik (AI), Egaksrak (EG), Kongakut (KO), and Firth (FI) Rivers are the other stocks in the genetic baseline.

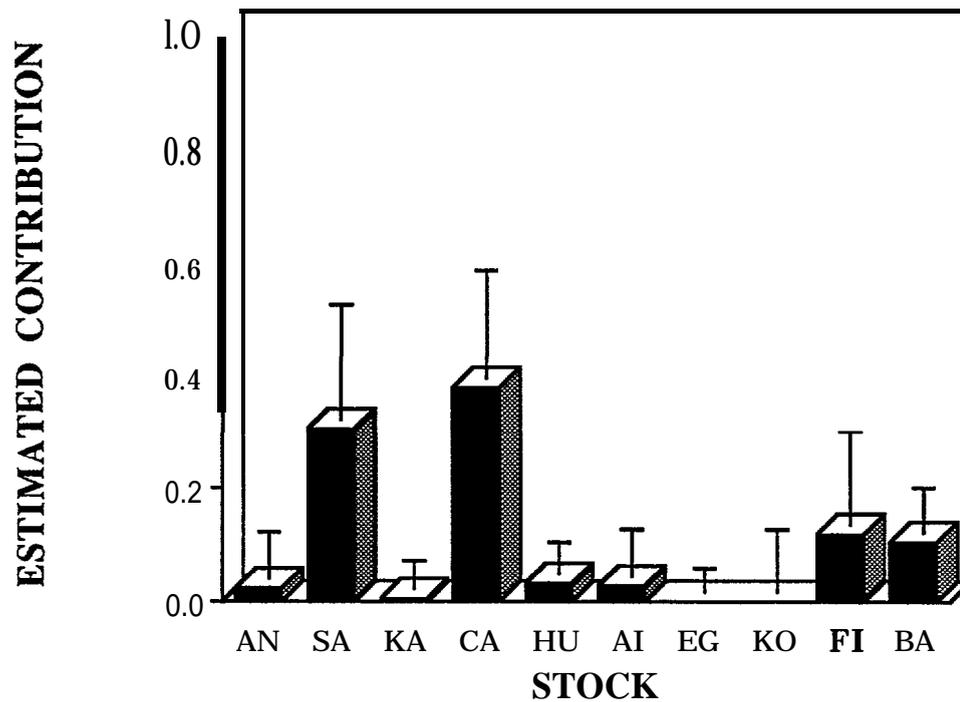


Figure 7,- Estimated composition (with one standard error) of a mixed fishery sample from the Prudhoe Bay, Alaska area collected in July 1987. Estimates are made using maximum likelihood techniques and a 14-stock genetic baseline. The stocks are arranged on the graph from left to right as west to east along the North Slope of Alaska and Canada. Allocations from three sites are joined to make up the Sagavanirktok River drainage (SA), as are two sites from the Hulahula River (HU), and two sites from the Babbage River drainage (BA). Anaktuvuk (AN), Kavik (KA), Canning (CA), Aichilik (AI), Egakrak (EG), Kongakut (KO), and Firth (FI) Rivers are the other stocks in the genetic baseline.

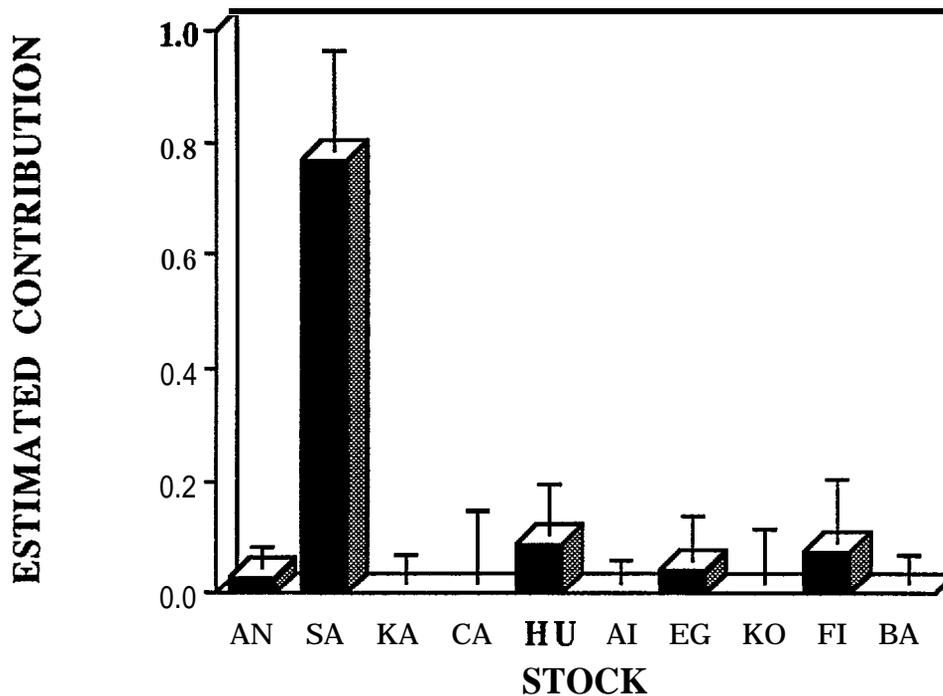


Figure 8.- Estimated composition (with one standard error) of a mixed fishery sample from the Prudhoe Bay, Alaska area collected in August 1987. Estimates are made using maximum likelihood techniques and a 14-stock genetic baseline. The stocks are arranged on the graphs from left to right as west to east along the North Slope of Alaska and Canada. Allocations from three sites are joined to make up the Sagavanirktok River drainage (SA), as are two sites from the Hulahula River (HU), and two sites from the Babbage River drainage (BA). Anaktuvuk (AN), Kavik (KA), Canning (CA), Aichilik (AI), Egaksrak (EG), Kongakut (KO), and Firth (FI) Rivers are the other stocks in the genetic baseline.

DISCUSSION

Sampling

The genetic baseline for this study of Arctic char included the major stocks between the McKenzie River of Canada and Point Barrow in Alaska. Collections made in 1987 include fish from more sites in freshwater tributaries, second samples from the same or similar sites, and larger sample sizes. Arctic char representing different morphotypes associated with non-migratory life history were included in the analyses.'

No Arctic char were found in three rivers draining to the Chukchi Sea in August 1987. Although these rivers were listed as char-producing streams in Alaska Department of Fish and Game catalogue of freshwater fish, we located no adults from the air, and found no juveniles by electrofishing. Adults maybe in estuarine waters inaccessible to sampling in August, and juveniles may be rearing in estuaries or in springs not sampled.

No Arctic char were captured in certain other rivers of the Beaufort Sea. We collected Arctic char from the Anaktuvuk River, tributary to the Colville River system in 1986 (Everett and Wilmot 1987), but located no Arctic char this trip, nor did we find any in the Colville River Delta area, Adult Arctic char could better be targeted in the lower Colville River in the fall subsistence or commercial catch as they migrate upstream to spawn. The Shaviovik River may not have a spawning population, and Arctic char that have been documented there in the past may be summer migrants.

Limitations in sample size and in tissue quality from some collections affected the analyses of some mixed-stock collections. The number of samples from Camden Bay in 1987 was too small and the samples of too poor quality to be used. Because some enzymatic proteins denature easily, two highly variable loci were not scored in 1987 that were included in the 1986 baseline (Everett and Wilmot 1987). Several loci were dropped from the mixed-stock fishery analyses due to incomplete data sets. Though it would have been informative to stratify the mixed-stock analyses by age-groups for the three Endicott Causeway collections, the numbers of samples were too small.

Amount of Genetic Variation

The amount of genetic variation observed in North Slope Arctic char was typical of fish species in general (Nevo 1978), and close to average among salmonids that have been studied (Utter et al. 1981). Our overall estimate of variability, measured as average heterozygosity, for Arctic char from our combined 1986 and 1987 collections is lower than that for 1986 alone. This is due to exclusion of some highly variable gene loci from the 1987 analyses and because several low-variability collections were added to the analyses. Isolated populations with small effective population numbers and little or no emigration often lose genetic variation due to random drift. When a breeding population is small, on average, not all genetic variation is included in the next generation by chance. Less frequently, relatively rare alleles can be increased in a small subpopulation by chance inclusion in the next generation.

Combining Baseline Data

In general, collections of Arctic char made in different years and in different parts of the same drainage were not significantly different in allele frequencies and could be combined to represent the population of that drainage. The exceptions include collections of Arctic char from different sites within the Babbage, Hulahula, and Sagavanirktok River drainages, which were genetically distinct and could not be combined before statistical analyses. Baseline information for stocks that are both genetically and geographically similar are combined to improve precision in genetic stock identification estimates.

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.

Though genetically similar stocks from different drainages or even regions are sometimes found, data from these stocks should not be combined before analyses (Wood et al. 1987). For genetic stock identification, the stock composition estimates for geographically separated stocks can be combined after allocation to the tributary-of-origin.

We found no evidence that resident and migratory life history forms of Arctic char represent separate populations in these collections. 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. Collections from drainages supporting both resident and migratory forms of Arctic char can be combined in the case of both Firth and of Canning River populations.

If genetic differences were detected between resident and migratory forms it could be due either to separate evolutionary lines or recent reproductive isolation. While similarities among geographically isolated groups may be due to selection, founding events, or by chance convergence of electrophoretic phenotypes at structural loci, recent divergence may be due to behavioral or physical isolation, which allows genetic differences to accumulate.

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 was due to the ecological distinction between resident and migratory forms. Resident populations of North Slope Arctic char could be composed of a separately evolved group with physiological or behavioral isolating mechanisms from migratory groups, but they could have arisen independently in various drainages where conditions made it unfavorable or impossible to migrate. Nordeng et al. (1983) found that in a brood of Arctic char raised and marked in a hatchery experiment then released in the wild, some individuals would mature early and remain small residents in response to a high feeding intensity. This could be explained by a growth-dependent maturity pattern (Jonsson and Hindar 1982).

The Arctic char from the Sadlerochit Springs area are thought to be entirely non-migratory (Craig 1977b), and were consequently excluded from mixed-stock fisheries analyses. They were genetically distinct in allele frequencies from other North Slope Arctic char populations, though there were no major differences such as allele substitutions where two stocks have no alleles in common at certain loci.

Genetic Differences Among Populations Within Drainages

Some reproductive isolation between North Slope Arctic char stocks was apparent from the level of genetic similarity that we observed among stocks. Arctic char from below the waterfall, from above the waterfall, and from the Canoe River of the Babbage River drainage have apparently diverged. Although divergence between Arctic char of these sites on the Babbage River has been

observed, genetic similarities between populations still resulted in their closeness on a dendrogram showing genetic relationships.

The distinction among mainstem Babbage River stocks (sites #1 and #2, below and above the waterfall) may be less one of natural selection than of relatively recent reproductive isolation and genetic drift. Bain (1974) observed small adult Arctic char spawning with large anadromous Arctic char below the Babbage River Falls. The population downstream of the Falls probably receives at least one successful migrant per generation from the upstream group, enough to prevent species divergence (Allendorf and Phelps 1981). The population upstream, with no emigration, periodic unfavorable conditions, and a reduced population size, could have experienced a shift in allele frequencies due to random processes with chance inclusion of rare alleles in high proportions.

The distinctness of the Canoe River population, from a tributary to the Babbage River, may relate to the small sample size (N=35) 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. For this reason, the Canoe River data set was excluded from the genetic stock identification baseline.

The Sagavanirktok River drainage is a large system, with a number of tributaries and substantial Arctic char populations. Of the collections we made in 1986 and 1987 from four tributaries, two are genetically similar. The Ehooka River is a tributary to the Ivishak River, and Ehooka River Arctic char are not significantly different genetically from the Ivishak River fish. The major stocks were genetically distinct, though Lupine and Ribdon River were relatively closely related using a genetic similarity index, plus simulations with mixed-stock analysis show that some Ribdon River fish were misallocated to the Lupine River stock.

The Hulahula River Arctic char from two different sites upstream and downstream were genetically distinct. Though all collections were made in the mainstem, it is possible that the two different sites are used preferentially by different subpopulations of Arctic char, with spatial and/or temporal variation in spawning.

Genetic Divergence Among Populations

After combining data from collections of Arctic char from within each drainage, most North Slope populations from different drainages were significantly genetically distinct from each other using a heterogeneity test that emphasizes the effects of variable loci. This information indicates

that fish from different drainages are not freely interbreeding, and are generally true to their spawning streams.

Although we quantified significant genetic differences among populations of Arctic char within the **Babbage**, **Hulahula**, and **S agavanirktok** River systems, and among populations of different drainages, the overall genetic similarity among all Arctic char studied, both migratory and non-migratory forms, was high. On the scale of similarities used (Nei 1972; 1978), both the variable enzymes (up to 15) and the enzyme loci that were consistently monomorphic (30) were considered in evaluating relatedness among stocks. The measured differences among these populations 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 subspecies. **Sadlerochit** Springs Arctic char were most unlike other populations, but its distinctness could reflect loss of genetic variation in a small system, closed to immigration.

The level of divergence observed among Arctic char populations indicates moderate differentiation and current reproductive isolation among stocks. Among the Arctic char populations we collected in 1986 and 1987, 8% of the variation was due to statistically detectable differences among fish from different drainages. Most of the diversity in North Slope Arctic char was between individuals within subpopulations, with a seemingly small percent due to differences between subpopulations. However, using this measure of divergence qualitatively, 15- 20% would be considered great differentiation, 5- 15% as moderate differentiation, and even 5% or less is not a negligible amount of differentiation among the populations of various taxa that have been studied (Wright 1978).

Genetic Stock Identification: Simulations

Other types of biological information on population dynamics are generally used with genetic studies to verify or validate estimates of mixed fisheries composition. In the Beaufort Sea area, certain studies including Arctic char have targeted specific coastal areas, such as Arctic National Wildlife Refuge lagoons (Fruge et al. 1989; West and Wiswar 1985; Wiswar and West 1985; Service, ongoing), Prudhoe Bay (Envirosphere 1985; 1986; LGL 1988; LGL, ongoing), or Phillips Bay, Canada (Bond and Erickson 1987). Craig (1984;1989b) and Craig and McCart (1976) have summarized the results of past Arctic char tagging experiments across the Beaufort Sea drainages, but tag returns have always been limited.

There are currently no large-scale studies of population dynamics, escapements, enhancement, tagging, or scale pattern analyses for Arctic char that include the entire Beaufort Sea area and that address the origins of Arctic char in mixed-stock aggregations in coastal waters. Since the usual means were not available to assess the accuracy and precision of our estimates of stock composition, we relied on computer simulations to supplement the limited amount of biological data available.

Tests of the accuracy and precision of stock composition estimates indicated general reliability of estimates but also some misallocation of stocks. The general accuracy of the estimates was supported by the analysis of an artificial mixture of equal proportions of baseline data from all 14 Arctic char stocks (equal-contribution simulation). When this mixture was evaluated for composition, only estimates from two stocks were significantly different from the actual proportion they contributed. The Canning River stock was overestimated, as was the Aichilik River stock contribution.

From incremental artificial mixtures of Arctic char baseline, it was apparent that several stocks were not very distinct genetically using this 12-locus database and genetic stock identification statistical methods. In this simulation, all stocks tested were allocated correctly 40 to 92% of their fish, but only Babbage sites#1 and #2, Kavik, and Anaktuvuk River stocks were correctly allocated more than 80% of their Arctic char. From experience with maximum likelihood estimation statistics, it is known that stocks in low frequency are overestimated at the expense of those in high frequency, which are consequently underestimated. This source of bias is expected, but seldom exceeds 5%; a correction for it is being developed (J. Pella, NMFS, personal communication).

Although there was misallocation among stocks in the 100% simulations, much of that was to geographically proximate stocks. There was allocation from one Babbage River stock to the other and from one Sagavanirktok River tributary stock to another. Kongakut, Egaksrak, Aichilik, and Hulahula River stocks have a high percentage of misallocation among them, but are geographically close as well as genetically similar to one another. That the U.S. and Canada Arctic char stocks are genetically distinct is suggested by the general lack of misallocation between them. Only the Kongakut River stock had as much as 10% misallocated to one of the Canada stocks, the Firth River Arctic char.

Unfortunately, a large proportion of Arctic char from the Ivishak River were misallocated to the Canning River stock in this simulation, which may explain overestimation of the Canning River stock in the first type of simulation. From Craig's work (1977a) it is apparent that there is migration of Arctic char between the Canning and Ivishak Rivers. In that study, non-spawners were tagged in the Ivishak River, and were observed spawning in the Canning River.

Non-spawners in the Canning River were tagged, and were seen in spawning condition in the Ivishak River.

Though we have no evidence of individual fish spawning in both the Canning and Ivishak River drainages, it is interesting that we have difficulty in discriminating genetically between these char populations. Since we sampled juvenile Arctic char from these rivers, which are smaller than those that typically migrate in coastal waters, it is unlikely that we sampled Ivishak River fish from the Canning River, or Canning River fish in the Ivishak River. Chance convergence of genotypes, natural selection, or common origin due to a founding event are other possible explanations for similarities of the Arctic char from these drainages.

Genetic Stock Identification: Endicott Samples

In the June and August Arctic char collections, Sagavanirktok River stocks (Ivishak, Lupine, and Ribdon Rivers) were identified as the major contributors to the mixed fishery. In June, the Canning River stock was also estimated to contribute 26% of the mixture, and 11% were identified from the Anaktuvuk River. In August, smaller contributions were made by the Hulahula, Firth, Egaksrak, and Anaktuvuk River stocks, but large standard errors around these estimates make them less reliable.

In the July collection, Canning River Arctic char stocks contribute 38%, with an additional 31% from the Sagavanirktok River, 12% from the Firth River stock, and 10% from the Babbage River. From the computer simulations with artificial mixed stock of known composition we learned that Ivishak River stocks, of the Sagavanirktok River drainage, are very similar to Canning River stocks genetically. For this reason, it would be parsimonious to assume that part of the large contributions allocated to the Canning River stock are likely of Ivishak River origin, making the total estimate for the Sagavanirktok River drainage stocks higher in June and July. Even though some Ivishak River Arctic char maybe misallocated to the Canning River population, the contributions of the Canning River stock to the mixed fishery near Endicott causeway is not negligible.

From the incremental mixed-stock simulation, it is apparent that Anaktuvuk River Arctic char were identified well in these analyses, so it is reasonable to conclude that Anaktuvuk River Arctic char do indeed migrate to the Sagavanirktok River Delta area. Firth River and Babbage River Arctic char, from Canada, are also well recognized by genetic stock identification techniques. Contributions of Arctic char of 12% from the Firth River in July and 7% in August, and contributions of almost 11 % from the Babbage River stocks in the July collection are likely even

with the large error terms associated with the estimates because of the accuracy with which they were identified in the simulations.

For the July sampling **period**, the sample size was smaller and the confidence intervals were wider. Though the error terms were large, the presence of several stocks in the July collection is realistic given that some Arctic char migrate extensively in coastal waters of the **Beaufort Sea** area in summer to **feed**. Because of the small size of Arctic char captured for this study, it is not surprising that most of the fish caught near mouth of the **Sagavanirktok** River in large enough numbers for genetic **stock** identification are apparently sub-adults from that river system.

Though predominance of **Sagavanirktok** River fish in collections made near the mouth of the **Sagavanirktok** River is reasonable, the **estimates** for stocks present in smaller proportions would be more useful if the standard errors 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 stock represented. For computational ease, his work included only three stocks and 150 samples. Other researchers, such as **Milner** et al. (1981), 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 less an arithmetic function of the number of baseline stocks, than a function of the level of divergence of the species, and what level of precision is acceptable to management.

Implications for Management

Certain methodological considerations should be kept in mind while evaluating the results reported here. The basis of genetic stock identification is **electrophoretically** detectable differences in genotype **frequencies** between stocks. To do genetic stock **identification** 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 salmon 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 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.

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. (1981) used **electrophoretic** data from chinook salmon to simulate the addition of variable gene loci. They observed a 60% increase in accuracy with an increase from 10 to 25 loci. Wilmot (unpublished data) found that the point estimates for Yukon River chum salmon allocations to United States versus Canada stocks changed markedly when the number of variable loci in the data set was increased from seven to twelve.

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.

Arctic char have an amount of genetic variation typical of **salmonids**. The pattern of variation in North Slope Arctic char shows distinctness among different populations, but the differences do not correspond to migratory versus resident life history strategies that have been postulated, nor to different subspecies classification.

Arctic char populations are genetically distinct **from** each other based on the pattern of divergence indicated by comparisons, pairwise, by log likelihood **ratio** statistics (G-tests) and by a calculation of gene diversity (**G_{ST}**). 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.

Our inability to distinguish some populations **from** one another in this study suggests that the 12-locus baseline used for analyses may need to be expanded. However, this baseline is adequate to distinguish the more distinct populations, e.g., the **Firth** and **Babbage** River stocks of Canada, and the **Kavik** and **Anaktuvuk** River stock of the United States. Also, certain stock management groups are relatively distinct genetically from each other, i.e., the Sagavanirktok River stocks

versus most of the Arctic National Wildlife Refuge stocks, with the exception of the Canning River Arctic char.

Despite inaccuracies and imprecision observed in simulations with genetic stock identification 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 predominantly 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 higher percentages of Arctic char from other drainages, supporting tag return data that show that Arctic char migrate considerable distances and mix offshore during the summer season. These results demonstrate that any impact on Arctic char stocks from development activities in the Prudhoe Bay area would affect mainly Sagavanirktok River Arctic char stocks, but that stocks from as faraway as the Arctic National Wildlife Refuge and Canada would also be affected.

Although not all populations of Arctic char can be distinguished genetically using the methods of this study, the results do confirm the hypothesis that an Arctic char population is generally distinct to a watershed area. Given this conclusion, it is possible that human activity affecting a critical habitat such as an overwintering area or access to Beaufort Sea coastal feeding areas in summer could have significant impact on a unique population of Arctic char. The resource in each watershed should be considered as having long term implications for Arctic char abundance in the area and for the genetic diversity of the region's Arctic char populations.

Though we have characterized the major stocks of North Slope Arctic char, 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 increase the number of gene loci characterized in the analyses. We are currently collecting data from two additional variable loci in our mixed-stock collections that are not represented in the baseline, and are aware of three other highly polymorphic loci in North Slope Arctic char that could be analyzed in high quality samples. More loci studied would correspond to more data from each fish sampled, and therefore smaller sample 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 genetic stock identification 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.

In order to understand the distribution and timing of the **migratory** North Slope Arctic char using coastal areas it will be necessary to sample numerous places offshore, and at more times during the summer season when they migrate. It has been determined that the Beaufort Sea environment is highly changeable, and that the dynamics of fish populations is highly dependent on climatic variables, especially wind conditions from year to year. Additional sampling would allow study of the pattern of use of the Beaufort Sea area by Arctic char, and enable us to predict which stocks development activities could affect at different locations and times during coastal migration.

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Appendix A.- Summary of analyses used for population genetics studies of fish.

Name	Input	Process	output
Percent of loci polymorphic.	Number of gene loci variable and total number of loci surveyed.	Number of gene loci variable divided by the total number of loci surveyed multiplied by 100	Relative number of variable loci for comparison with other populations or other species as a measure of the amount of genetic variation.
Average heterozygosity per individual per locus.	Observed allele frequencies for all loci.	In a two-allele system with the frequency of the common allele p and q = 1 - p , $(p + q)^2 = p^2 + 2pq + q^2$, solve for $2pq$ for each locus, and average overall loci and all individuals.	Amount of variation per locus per individual in a population for comparison with other populations or other species as a measure of the amount of genetic variation observed.
Random mating proportions (Hardy-Weinberg equilibrium).	Observed genotypes and observed allele frequencies for each variable locus.	Observed genotype counts are compared to expected numbers of each genotype when observed frequencies are used with binomial probability equation using the chi-square statistic.	Information regarding the randomness of the sample or random mating within the population.
Heterogeneity tests among collections.	Frequencies of all variable loci in collections from the same site in different years, or from the same drainage.	Log likelihood ratio test (G-test) used to compare among all variable loci pairwise between collections. G-value and degrees of freedom for each test are compared to the chi-square distribution to detect significant tests. If the probability is >0.05 , collections can be pooled.	Information on whether gene frequency data from two collections could have been drawn from the same population, and therefore whether or not they can be combined for future analyses.

Appendix A.- Continued

Name	Input	Process	output
Heterogeneity tests: 1) among all collections made, and 2) between population pairs.	Allele frequencies for all variable loci in all populations studied (using pooled frequencies for related collections where appropriate).	Log likelihood ratio test (G-test) used to compare allele frequencies: 1) among all variable loci in all collections, then 2) pairwise between collections. G-values and degrees of freedom for each test are compared to the chi-square distribution to detect significant differences between collections.	Information: 1) on whether all collections sampled could have been drawn from the same population, and 2) to detect a pattern of relatedness between population pairs.
Genetic similarity (Nei 1972).	Allele frequency data for all collections, after pooling like collections from geographically proximate sites.	Pairwise population comparisons based on the probability of drawing identical alleles from each.	Index of genetic similarity (or distance) among collections which indicates, on average, the degree of relatedness among populations.
47 Dendrogram.	Genetic similarity values among population pairs.	Unweighed pair-group method (UPGMA) of cluster analysis.	A graphic “tree” indicating the relationships, on average, among populations being studied.
Gene diversity analysis.	Genetic similarity values, pairwise , among populations studied.	Hierarchical evaluation of the amount of variation within versus between populations studied. Levels evaluated usually correspond to differences among individuals from the same site, different sites within drainages, different drainages within a region, and possibly comparisons among stocks of different regions.	Gives relative value of the amount of genetic difference between different population levels for comparison with other areas for the same species, or for comparison with different species.

Appendix A,- Continued

Name	Input	Process	output
Genetic stock identifi- cation.	Allele frequencies of variable loci in populations (baselines) that are evaluated as potential contributors to a mixed stock, and genotype data for the individual fish making up a mixture to be analyzed for percent composition.	Maximum likelihood statistics using the Genetic Iteratively Reweighted Least-Squares (GIRLS) algorithm (Nelson and Pella, NMFS) for estimating the percent composition of a mixture. The program determines the most likely proportions of the baselines provided that would result in the given mixture of genotypes being analyzed. Variances around the point estimates are determined by using a bootstrap analysis which resamples (with replacement) both the baselines and the mixture file 100 times. The variance of 100 estimates reflects sampling error in both the baseline file and the mixture file.	The point estimates are the proportional composition of the mixture as determined by maximum likelihood statistics. These estimates can be compared to data from other sources available regarding the composition of the mixture, or can be compared to values known if you are working with tagged fish or with an artificial mixture (sometimes made up for simulations from base-line data). By comparing the estimates obtained using maximum likelihood statistics with known information, you can evaluate the accuracy of the estimates. The boot-strapping procedure provides information on the precision of the estimates.
100% artificial mixture.	Baseline genetic	Maximum likelihood statistics and bootstrap resampling using the established baseline as the learning sample, and each stock in turn as an artificial mixture. The process is repeated for each baseline stock.	Proportional composition of each of the artificial mixtures, which shows how accurately each stock is “recognized” and to which stocks “misallocated” fish are assigned.

Appendix A.- Continued

Name	Input	Process	output
Incremental simulations.	Baseline genetic data for related stocks (as allele frequencies) and genotype data from each individual from each stock being evaluated as a proportion of a series of artificial mixtures.	Maximum likelihood statistics and bootstrap resampling using the established baseline as the learning sample, and each stock as part of an artificial mixture. The process is repeated for each baseline stock at each increment. The balance of each incremental mixture is made up of data from other populations.	Estimated contribution of each baseline to artificial mixtures compared to actual proportion. Shows how accurately each stock is “recognized” at different promotions in a mixture, and indicates amount and direction of bias. Bootstrap resampling describes the precision of the estimates.
Equal - contribution simulations	Baseline genetic data for related stocks (as allele frequencies) for a learning sample, and equal proportions of all stocks as an artificial mixture of known composition.	Maximum likelihood statistics and bootstrap resampling using the established baseline as the learning sample and an artificial mixture of known composition.	Estimated percent composition of the artificial mixture of baseline fish which can be compared to the actual percent composition to test the accuracy of the allocation using maximum likelihood statistics methods.

Appendix B.- Gene frequencies of variable loci in 12 populations of Arctic char sampled in 1987 from the North Slope of Alaska and Canada. Variants at duplicated loci were arbitrarily assigned to one locus of the duplicated pair. Names of **enz** yme loci (abbreviated here) are in Table 2. No data (ND) were available for some loci.

Loci/Mobility	Populations												
	AI	B1	132	C1	C2	F1	F2	HU	KO	LU	SA	SH	
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
AC04	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	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
GP13	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

AI = Aichilik B1 = Babbage Site#1 C1 = Canning Site#1 F1 = Firth Site#1 HU = Hulahula SA = Sadlerochit
 KO = Kongakut B2 = Babbage Site#2 C2 = Canning Site#2 F2 = Firth Site#2 LU = Lupine SH = Shublik

Appendix B.- Continued.

Loci/MobiJity		Populations											
		AI	B1	132	C1	C2	F1	F2	HU	KO	LU	SA	SH
IDH3	100	0.889	1.000	1.000	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
XDH1	100	0.433	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

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AI = Aichilik B1 = Babbage Site#1 C1 = Canning Site#1 F1 = Firth Site#1 HU = Hulahula SA = Sadlerochit
 KO = Kongakut B2 = Babbage Site#2 C2 = Canning Site#2 F2 = Firth Site#2 LU = Lupine SH = Shublik

Appendix C.- Gene frequencies of variable loci in 16 populations of Arctic char sampled 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. No data (ND) was available for some loci.

Loci/Mobility	POPULATIONS															
	A1	AN	B1	B2	CA	CA	EG	FI	H1	H2	IV	KA	KO	LU	RI	SA
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	21	179	33	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	21	206		41	130		00	72	00	85	45	40	45
AC04 100	0.541	0.403	0.490	0.411	0.514	0. % 0	0.557	0.461	0.5 % 0	0.467	0.535	0.463	0.547	0.467	0.588	0.100
115	0.194	0.292	0.019	0.000	0.216	0.029	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	0.559	0.270	0.271	0.200	0.328	0.220	0.294	0.291	0.400	0.275	0.322	0.300	0.889
N	85	36	52	17	183	35	35	128	91	46	72	40	85	45		
GAP3 100	0.655	0.934	0.933	0.850	0.754	ND	0.500	0.883	0.560	0.325	0.775	0.706	0.714	0.767	0.7 ? 0	1. (\$ 0
Null	0.345	0.066	0.067	0.150	0.246	--	0.500	0.177	0.440	0.675	0.225	0.294	0.286	0.233	0.270	0.000
N	82	38	52	20	183	00		32	107	91	40	71	34	84	45	37
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	21	211	35	41	129	95	51	74	40	85	45		45
GP13 100	0.759	0.900	0.846	1.000	0.897	0.629	0.829	0.694	0.842	0.860	0.912	0.988	0.718	0.589	0.6 % ' 7	0.844
96	0.241	0.100	0.154	0.000	0.123	0.371	0.171	0.306	0.158	0.140	0.088	0.012	0.282	0.411	0.333	0.156
N	85	39	52	21	211	35	41	129	95	50	74		40	85	45	39
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	21	149	35	35	129	95	51	74	40	85	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. (% 0	1. (% 0
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	21	184	35	35	131	91	48	73	40	85	4,5	40	45

AI= Aichilik B1=Babbage #1 CA= Canning EG= Egaksrak IV= Ivishak KA= Kavik KO= Kongakut HI= Hulahula #1
 AN= Anaktuvuk B2= Babbage #2 CN= Canoe FI= Firth LU= Lupine RI= Ribdon SA= Sadlerochit H2= Hulahula #2

Appendix C.- Continued

		POPULATIONS																	
Loci/Mobility	AI	AN	B1	B2	CA	CA	EG	FI	H1	H2	IV	KA	KO	LU	RI	SA			
LDH5	100	0.946	1.000	1.000	1.000	0.995	0.986	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	0.000	0.005	0.014	0.071	0.027	0.011	0.059	0.027	0.012	0.035	0.000	0.077	0.000		
	N		35	53	21	188	35	35	132	95	51	73	40	85		39	45		
MDH1	100	1.(%0	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.(%0	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	21	182	35	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	21	197	35	35	132		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	21	197	35	35	132	95	51	74	40	85	45	40	45	
PGM2	100	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	1.000		
	88	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	0.000		
	N		85	35	51	21	161	28	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	21	188	34	35	131	87	17	23	40	85	44	40	44	
SOD1	100	0.947	1.000	0.944	0.857	0.974	0.957	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	0.000	0.026	0.015	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	0.043	0.000	0.028	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
	N		85	35	53	21	212	35	35	132	93	54	72	40	85	45	40	45	

AI= Aichilik B 1=Babbage #1 CA= Canning EG= Egaksrak IV= Ivishak KA= Kavik KO= Kongakut H1= Hulahula #1
 AN= Anaktuvuk B2= Babbage #2 CN= Canoe FI= Firth LU= Lupine RI= Ribdon SA= Sadlerochit H2= Hulahula #2

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

1 Canoe 86	X	NS	NS	***	***	***	***	***	***	***	***	***	***	***	NS	***	
2 Babbage1	19.4	X	NS	***	***	***	***	***	***	***	***	***	***	***	***	***	
	(4)																
3 Babbage2	38.8	17.0	x	***	***	***	***	***	***	***	***	***	***	***	***	***	
	(3)	(4)															
4 Firth	110.7	96.1	60.7	X	***	***	***	***	***	***	***	***	***	***	***	***	
	(11)	(12)	(9)														
5 Kongakut	100.0	106.9	70.9	54.4	X	***	***	***	***	***	***	***	***	***	*	***	
	(lo)	(lo)	(9)	(13)													
6 Egaksrak	46.0	102.6	73.1	97.6	45.6	X	NS	NS	**	***	**	***	***	***	***	***	
	(8)	(8)	(8)	(14)	(11)												
7 Aichilik	49.1	136.5	92.5	135.5	75.0	33.1	X	***	***	***	***	***	***	***	***	***	
	(lo)	(11)	(lo)	(14)	(13)	(11)											
8 Hulahula1	81.7	150.7	87.7	139.6	46.6	25.7	73.5	X	NS	***	***	***	***	***	***	***	
	(9)	(11)	(8)	(14)	(12)	(13)	(14)										
9 Hulahula2	99.8	154.4	91.8	128.2	59.6	29.5	97.5	29.4	X	***	***	***	***	***	***	***	
	(8)	(9)	(8)	(lo)	(lo)	(9)	(lo)	(9)									
10 Sadleroch.	99.2	75.4	66.6	164.4	180.8	179.6	212.5	247.2	226.6	X	***	***	***	***	***	***	
	(4)	(5)	(5)	(11)	(10)	(7)	(11)	(10)	(8)								
11 canning	87.7	129.6	63.8	125.9	75.6	43.2	72.9	59.8	100.7	208.2	X	***	***	***	***	NS	
	(lo)	(lo)	(9)	(14)	(13)	(12)	(14)	(13)	(9)	(lo)							
12 Kavik	124.3	60.4	32.6	78.4	61.8	70.4	124.2	68.5	56.2	132.8	87.2	X	**	***	***	***	
	(6)	(6)	(5)	(lo)	(lo)	(9)	(11)	(9)	(9)	(6)	(10)						
13 Ivishak	134.4	72.3	38.9	69.4	46.2	70.6	144.8	53.8	70.7	155.7	65.4	39.3	X	***	***	***	
	(9)	(9)	(7)	(13)	(11)	(10)	(12)	(11)	(10)	(8)	(12)	(10)					
14 Ribdon	89.3	85.8	77.7	55.6	48.3	61.2	133.0	80.5	66.3	156.7	113.4	80.9	51.5	X	NS	***	
	(lo)	(lo)	(lo)	(11)	(12)	(11)	(13)	(13)	(lo)	(9)	(12)	(lo)	(11)				
15 Lupine	22.4	75.5	74.5	53.8	38.3	38.9	48.5	56.6	74.7	141.7	66.1	79.0	51.1	26.0	x	***	
	(6)	(7)	(7)	(13)	(12)	(8)	(12)	(11)	(9)	(7)	(11)	(8)	(10)	(10)			
16 Anaktuvuk	94.5	63.0	63.0	68.7	79.9	75.4	103.4	85.2	128.8	108.8	29.5	88.5	57.2	96.7	64.2	x	
	(10)		(9)	(9)	(13)		(12)	(13)	(13)	(13)	(13)	(12)	(8)	(11)	(10)	(11)	(13)
	1		2	3	4		5	6	7		8	9	10	11	12	13	14
																	15
																	16

NS = not significant

* = ≤ 0.05

** = ≤ 0.01

*** = < 0.001

Appendix E.- Estimated proportions (with one standard error) of each baseline stock represented in a simulated mixed-stock sample of Arctic char (N = 500) composed of nearly equal proportions of all baseline stocks. Actual contribution of each of 14 stocks was 0.071, except Anaktuvuk at 0.077. Estimates are listed in descending order.

Population	Estimate	SE	68%		95%	
			Confidence Interval		Confidence Interval	
canning	0.1138	0.0887	0.0251	0.2025	-0.0601	0.2877
Aichilik	0.0985	0.0690	0.0295	0.1675	-0.0367	0.2337
Firth	0.0852	0.0587	0.0265	0.1439	-0.0299	0.2003
Hulahula-1	0.0824	0.0660	0.0164	0.1484	-0.0470	0.2118
Kongakut	0.0786	0.0895	-0.0109	0.1681	-0.0968	0.2540
Babbage- 1	0.0781	0.0464	0.0317	0.1245	-0.0128	0.1690
Babbage-2	0.0655	0.0375	0.0280	0.1030	-0.0080	0.1390
Ribdon	0.0632	0.0332	0.0300	0.0964	-0.0019	0.1283
Hulahula-2	0.0605	0.0423	0.0182	0.1028	-0.0224	0.1434
Ivishak	0.0586	0.0510	0.0076	0.1096	-0.0414	0.1586
Anaktuvuk	0.0567	0.0343	0.0224	0.0910	-0.0105	0.1239
Egaksrak	0.0566	0.0504	0.0062	0.1070	-0.0422	0.1554
Lupine	0.0514	0.0418	0.0096	0.0932	-0.0305	0.1333
Kavik	0.0512	0.0444	0.0068	0.0956	-0.0358	0.1382

Appendix F.- Percentage allocations (with standard errors) to each of 14 North Slope Arctic char stocks. Each of the 14 baseline data sets is used as simulated mixed fishery and is analyzed using the maximum likelihood method of genetic stock identification. Each vertical column is the results of one analysis, and the percentage of each stock correctly allocated to itself is on the diagonal of the matrix.

Site	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1 Babbage 1	84.5 (11.4)	7.1 (16.4)	1.9 (3.7)	0.2 (0.9)	0.1 (0.4)	0.0 (0.2)	0.0 (0.2)	0.1 (0.4)	0.5 (1.4)	1.0 (2.6)	1.3 (2.8)	0.8 (1.7)	1.2 (2.7)	3.0 (4.6)
2 Babbage 2	9.5 (10.9)	91.8 (17.2)	0.2 (0.7)	0.1 (0.6)	0.1 (0.7)	0.0 (0.3)	0.1 (0.8)	0.2 (0.5)	0.1 (0.6)	2.5 (5.4)	0.7 (1.9)	0.3 (0.7)	0.1 (0.4)	0.4 (1.8)
3 Firth	2.3 (3.8)	0.0 (0.0)	77.1 (11.2)	9.9 (10.4)	0.2 (1.0)	2.8 (5.5)	0.4 (1.3)	0.4 (1.0)	2.2 (4.4)	1.0 (2.5)	2.0 (3.4)	3.8 (7.4)	3.7 (7.8)	3.9 (8.3)
4 Kongakut	0.1 (0.5)	0.0 (0.0)	5.4 (8.2)	43.8 (17.4)	7.0 (10.5)	22.0 (17.0)	1.6 (3.4)	1.1 (3.1)	3.4 (6.4)	1.2 (3.3)	2.1 (4.2)	0.9 (3.0)	4.2 (11.7)	0.1 (0.8)
5 Egaksrak	0.1 (0.4)	0.0 (0.0)	0.2 (0.4)	3.2 (4.7)	50.9 (17.8)	4.6 (6.3)	7.1 (8.9)	10.1 (12.2)	1.3 (2.8)	0.9 (2.5)	2.3 (3.5)	3.4 (5.1)	1.2 (3.7)	0.0 (0.2)
6 Aichilik	0.0 (0.0)	0.0 (0.0)	1.9 (4.8)	20.9 (15.0)	5.6 (10.3)	52.3 (18.1)	2.1 (4.2)	5.7 (7.4)	1.7 (3.2)	4.3 (8.6)	1.1 (2.5)	2.0 (6.0)	0.8 (2.6)	0.0 (0.0)
7 Hulahula 1	0.0 (0.0)	0.0 (0.0)	1.1 (2.8)	1.6 (3.6)	12.2 (14.4)	3.3 (5.6)	66.6 (14.2)	4.8 (9.9)	4.7 (8.7)	0.0 (0.0)	2.5 (5.4)	0.4 (1.4)	1.8 (3.7)	0.0 (0.1)
8 Hulahula 2	0.0 (0.0)	0.0 (0.1)	0.4 (0.9)	4.5 (1.2)	15.0 (13.5)	4.0 (6.0)	6.6 (6.9)	72.4 (15.3)	0.4 (1.2)	1.5 (2.8)	0.2 (0.8)	0.7 (1.4)	0.2 (0.5)	0.0 (0.0)
9 canning	0.0 (0.7)	0.0 (0.0)	1.3 (3.0)	8.1 (8.4)	1.6 (3.4)	2.5 (4.7)	12.0 (10.6)	0.1 (0.3)	73.4 (15.3)	1.0 (3.4)	35.1 (21.5)	0.2 (0.5)	1.9 (4.4)	5.9 (9.2)
10 Kavik	0.4 (1.4)	1.1 (3.8)	1.9 (3.0)	1.8 (3.1)	0.9 (2.6)	4.3 (5.4)	0.2 (0.7)	3.0 (4.4)	3.6 (4.6)	81.5 (12.2)	4.1 (5.7)	0.4 (1.1)	0.2 (0.6)	0.2 (0.1)
11 Ivishak	0.2 (0.9)	0.0 (0.1)	1.1 (2.7)	2.0 (3.9)	3.3 (6.8)	0.8 (2.0)	1.9 (4.0)	0.2 (0.5)	6.0 (8.3)	3.9 (8.2)	40.0 (19.7)	3.8 (6.3)	4.3 (7.0)	3.9 (8.5)
12 Ribdon	0.8 (1.6)	0.0 (0.0)	2.8 (4.3)	1.5 (4.0)	1.1 (3.9)	1.2 (3.0)	0.1 (0.3)	1.2 (2.4)	0.2 (0.6)	0.7 (2.0)	3.8 (5.4)	69.7 (15.6)	6.2 (8.9)	0.2 (1.4)
13 Lupine	0.8 (2.2)	0.0 (0.0)	2.9 (4.6)	6.1 (7.0)	1.8 (3.5)	2.1 (3.9)	1.9 (3.3)	0.6 (1.5)	0.8 (2.2)	0.0 (0.0)	1.4 (2.8)	13.5 (11.0)	73.7 (14.3)	0.2 (1.1)
14 Anaktuvuk	1.3 (2.6)	0.0 (0.0)	1.7 (2.5)	0.2 (1.0)	0.0 (0.3)	0.1 (0.4)	0.1 (0.5)	0.1 (0.3)	1.7 (3.4)	0.4 (2.0)	3.2 (4.8)	0.3 (0.9)	0.5 (1.8)	82.0 (13.4)

Appendix G.- Estimated composition (with standard error) of the June 1987 sample of Arctic char (N = 207) taken **from** near the **Endicott** causeway. Estimates are listed in descending order, and those below the dotted line contribute less than 1 %. Two sites **from** the **Babbage** River, two sites from the **Hulahula** River, and three sites **from** the **Sagavanirktok** River (listed below as subpopulations) were summed to give estimates of the contributions **from** ten major drainages to the Beaufort Sea.

Population	Estimate	SE	68% Confidence Interval		95% Confidence Interval	
Sagavanirktok	0.6117	0.1563	0.4554	0.7680	0.3053	0.9180
Canning	0.2578	0.1616	0.0962	0.4194	-0.0589	0.5746
Anaktuvuk	0.1130	0.0740	0.0390	0.1870	-0.0320	0.2580
Kongakut	0.0121	0.1166	-0.1045	0.1287	-0.2164	0.2406

Hulahula	0.0050	0.0805	-0.0755	0.0855	-0.1528	0.1627
Egaksrak	0.0004	0.0696	-0.0692	0.0700	-0.1360	0.1368
Babbage	0.0000	0.0359	-0.0359	0.0359	-0.0704	0.0704
Firth	0.0000	0.0606	-0.0606	0.0606	-0.1188	0.1188
Aichilik	0.0000	0.0502	-0.0502	0.0502	-0.0984	0.0984
Kavik	0.0000	0.0271	-0.0271	0.0271	-0.0531	0.0531

Subpopulations						

Babbage						
Site #1	0.0000	0.0356	-0.0356	0.0356	-0.0698	0.0698
Site #2	0.0000	0.0065	-0.0065	0.0065	-0.0127	0.0127
Hulahula						
Site #1	0.0050	0.0802	-0.0752	0.0852	-0.1522	0.1622
Site #2	0.0000	0.0042	-0.0042	0.0042	-0.0082	0.0082
Sagavanirktok						
Ivishak	0.1924	0.1305	0.0619	0.3229	-0.0634	0.4482
Lupine	0.2390	0.0961	0.1429	0.3351	0.0506	0.4273
Ribdon	0.1803	0.0776	0.1027	0.2579	0.0282	0.3324

Appendix H.- Estimated composition (with standard error) of the July 1987 sample of Arctic char (N = 126) taken from near the **Endicott** causeway. Estimates are listed in descending order, and those below the dotted line contribute less than 1%. Two sites from the **Babbage** River, two sites from the **Hulahula** River, and three sites from the **Sagavanirktok** River (listed as **subpopulations**) were summed to give estimates of the contributions from ten major drainages to the Beaufort Sea.

Population	Estimate	SE	68% Confidence Interval		95% Confidence Interval	
canning	0.3811	0.1843,	0.1968	0.5654	0.0199	0.7423
Sagavanirktok	0.3057	0.2023	0.1034	0.5080	-0.0908	0.7023
Firth	0.1209	0.1600	-0.0391	0.2809	-0.1927	0.4345
Babbage	0.1054	0.0769	0.0285	0.1823	-0.0453	0.2561
Hulahula	0.0305	0.0564	-0.0259	0.0869	-0.0800	0.1411
Aichilik	0.0285	0.0827	-0.0542	0.1112	-0.1336	0.1906
Anaktuvuk	0.0247	0.0804	-0.0557	0.1051	-0.1329	0.1822
<hr style="border-top: 1px dashed black;"/>						
Kavik	<i>0.0032</i>	<i>0.0530</i>	<i>-0.0498</i>	<i>0.0562</i>	<i>-0.1007</i>	<i>0.1070</i>
Kongakut	0.0000	0.1116	-0.1116	0.1116	-0.2187	0.2187
Egaksrak	0.0000	0.0423	-0.0423	0.0423	-0.0829	0.0829
<hr/>						
Subpopulations						
<hr/>						
Babbage						
Site #1	0.1054	0.0767	0.0287	0.1821	-0.0449	0.2557
Site #2	0.0000	0.0120	-0.0120	0.0120	-0.0235	0.0235
Hulahula						
Site #1	0.0001	0.0555	-0.0554	0.0556	-0.1086	0.1089
Site #2	0.0304	0.0285	0.0019	0.0589	-0.0255	0.0863
Sagavanirktok						
Ivishak	0.0136	0.1453	-0.1317	0.1589	-0.2712	0.2983
Lupine	0.1916	0.1275	0.0641	0.3191	-0.0583	0.4415
Ribdon	0.1006	0.0857	0.0149	0.1863	-0.0674	0.2686
<hr/>						

Appendix I.- Estimated composition (with standard error) of the August, 1987 sample of Arctic char (N = 166) taken from near the Endicott causeway. Estimates are listed in descending order, and those below the dotted line contribute less than 1%. Two sites from the Babbage River, two sites from the Hulahula River, and three sites from the Sagavanirktok River (listed as subpopulations) were summed to give estimates of the contributions from ten major drainages to the Beaufort Sea.

Population	Estimate	SE	68% Confidence Interval		95% Confidence Interval	
Sagavanirktok	0.7683	0.1769	0.5914	0.9452	0.4216	1.1151
Hulahula	0.0889	0.0888	0.0001	0.1777	-0.0852	0.2629
Firth	0.0725	0.1149	-0.0424	0.1874	-0.1527	0.2977
Egaksrak	0.0440	0.0765	-0.0325	0.1205	-0.1060	0.1939
Anaktuvuk	0.0263	0.0406	-0.0144	0.0669	-0.0533	0.1058

canning	0.0001	0.1283	-0.1282	0.1284	-0.2514	0.2516
Kongakut	0.0000	0.0974	-0.0974	0.0974	-0.1909	0.1909
Babbage	0.0000	0.0514	-0.0514	0.0514	-0.1007	0.1007
Aichilik	0.0000	0.0425	-0.0425	0.0425	-0.0833	0.0833
Kavik	0.0000	0.0512	-0.0512	0.0512	-0.1004	0.1004

Subpopulations						

Babbage						
Site #1	0.0000	0.0469	-0.0469	0.0469	-0.0919	0.0919
Site #2	0.0000	0.0190	-0.0190	0.0190	-0.0372	0.0372
Hulahula						
Site #1	0.0889	0.0893	-0.0004	0.1782	-0.0861	0.2639
Site #2	0.0000	0.0173	-0.0173	0.0173	-0.0339	0.0339
Sagavanirktok						
Ivishak	0.4336	0.1419	0.2917	0.5755	0.1555	0.7118
Lupine	0.2345	0.0976	0.1369	0.3321	0.0432	0.4258
Ribdon	0.1001	0.0725	0.0277	0.1727	-0.0419	0.2423
