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DISCRIMINATION OF HERRING POPULATIONS IN A NORTHERN NORWEGIAN FJORD: GENETIC AND BIOLOGICAL ASPECTS

by

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ABSTRACT

From a trawl survey in a fjord system in northern Norway, it has been possible to separate catches of herring into two distinct groups characterized by different number of vertebrae (VS). Low-vertebral herring (VS = 52-55) belong to a local stock of spring-spawning fjord stock called the Balsfjord herring. High-vertebral herring (VS = 56-60) belong to an immigrating population of Atlanto- Scandian herring spawned off the Norwegian coast. The separation between the stocks was verified by genetic analysis of herring samples using enzyme electrophoresis. The Balsfjord herring is characterized by a very high frequency (0.93) of a rare allele (designated 110) at the LDH-2 locus which is expressed in white muscle tissue.

In comparison, this allele is usually not found (frequency < 0.01) in samples of Atlanto-Scandian herring. The discrimination between the two stocks in Balsfjord was, however, evident from the biological data obtained (age distribution, VS, mean length and length distributions) as well as the genetic characters investigated. In addition, the Balsfjord herring, especially at mature stage, seem to be distributed at 60-200 m depth and was caught by using bottom trawl. The Atlanto-Scandian herring, mainly 2 or 3 years old, was found in the upper water layer (0-60 m). The genetic data indicate very limited or no gene flow between the two herring stocks in Balsfjord. This fjord system, therefore, offers unique possibility to study interaction and isolating mechanisms with regards to marine fish stocks.

INTRODUCTION

The herring, Clupea harengus L., is a species widely distributed in the north Atlantic and a large number of subunits or stocks are believed to exist. This subdivision or population structure is mainly based on knowledge of discrete spawning sites, life history parameters (growth characteristics; age distribution; size at maturity) and meristic characters (number of vertebrae VS; number of keeled scales; otolith features). For details see Parrish and Saville (1965).

Population studies on herring in Norwegian waters using genetic characteristics, were initiated nearly twenty years ago (Nævdal; 1969). This work has continued and recently the methods of enzyme electrophoresis (Harris and Hopkinson, 1976) have permitted more detailed investigations. During the last eight years mass screening of herring samples from the Norwegian coast have provided genetic data on thousands of individual herring. Local stocks of fjord herring have been described earlier (Aasen, 1951), but new genetic information clearly demonstrated a number of locally distributed herring stocks in several fjord systems (Jørstad and Nævdal, 1981; Jørstad and Nævdal, 1983).

The different stocks of herring seem to be localized in fjords which have a limited exchange with oceanic and coastal waters. Very little genetic variation was, however, observed for the coastal or oceanic herring called Atlanto-Scandian herring which is in agreement with similar work on oceanic herring stocks (Anderson et al. 1981; Kornfield et al. 1982; Grant, 1984)

With respect to the different Norwegian fjord stocks of herring, the genetics of the population in Balsfjord in northern Norway were surprising. For several enzyme loci, alleles were found at very high frequencies which were very rare in Atlanto-Scandian herring. The existance of nearly diagnostic loci for differentiation between Atlanto-Scandian herring and the local stock suggested that several important studies on herring stocks could be initiated in this area. It was not until this year, however, that the University of Tromsø carried out a cruise in Balsfjord where sampling and studies of herring were of major interest.

MATERIAL AND METHODS

Sampling

Herring samples were collected during a trawl survey in Balsfjord, Sørfjord and Stålvikbotn with R/V "Johan Ruud" from February 20-28, 1986. The sampling gear consisted of a bottom shrimp trawl and a pelagic midwater trawl. All tows were about 30 minutes in duration with a towing speed of 2 nautical miles per hour. Sampling area, trawl stations and haul type are shown in Fig. 1.

From each trawl haul a random subsample of 100 herring were measured for total length to the nearest 0.5 cm below. The weight was determined and grouped into 5 g intervals. Sex and maturity stages were identified for 50 herring from each subsample. Otoliths and scales were taken from 30 herring for age estimation and growth zone examination.

These fish were also frozen for vertebrae counts on land. The methods used for data collection are described in Anon (1984).

Backcalculation of growth

To describe the mean individual growth of herring yearclasses, fish lengths were backcalculated based on otolith zone radia. If the otolith radia and the fish lengths are linearly correlated, a method of backcalcuating fish lengths from these can be applied. The method of backcalculation of fish lengths from growth markings in scales, otoliths or other hard skeletal parts was introduced by Lea (1910). A description of the method, based on otoliths, are outlined by Gjøsæter (1984) and the following equation was applied:

$$L(n) = a + \frac{L(c) - a}{R(c)} * R(n)$$

where L(n) is estimated length corresponding to measured otolith radius R(n) of winter-ring number n. L(c) and R(c) are the fish length and otolith radius measured at capture, and is the intercept of the L-axis for R=0, estimated by the straight line drawn through a plot of otolith radius versus fish length (Gjøsæter, 1984).

For the back-calculation presented in this paper only the six inner otolith growth zones were used.

The parameters in the von Bertalaffy growthmodel were estimated by fitting the backcalculated growth data to the model.

Electrophoresis

To investigate genetic variation within the area, individual samples of white muscle were frozen for examination in the labo-

ratory. These samples were analysed by horizontal starch gel electrophoresis and selective staining of the following polymorphic enzymes: Phosphoglucometase (PGM), phosphoglucose isomerase (PGI), isocitrate dehydrogenase (IDH), lactate dehydrogenase (LDH) and maleate dehydrogenase (MDH). In this paper we present the results obtained for the LDH-2 locus which have earlier been shown to discriminate between herring stocks (Jørstad and Nævdal, 1983). A detailed picture of this enzyme polymorphism is shown in Fig. 5 where the three alleles and the different genotypes controlling the banding pattern on the gel are given.

In the statistical treatment of the data we used the G-test (Sokal and Rohlf, 1969) to test for deviation from Hardy-Weinberg's equilibrium. In some cases we applied the test described by Christiansen et al. (1977) which facilitates detection of an excess or deficiency of heterozygotes. The G-test was also used when analysing within-group homogeneity and in pairwise tests between different samples.

RESULTS

Distribution of herring within the area

In addition to Balsfjord (Fig. 1), herring was found in the two adjacent fjords Stålvikbotn and Sørfjord. During the trawl survey both bottom and pelagic trawls were used, and sampling data are summarized in Table 1. A total of 19 catches were taken, 13 of which were bottom trawl catches (depths from 60 to 180 m). The pelagic trawl hauls were carried out at 20 to 45 m. As can be seen from Table 1, the catches in kgs varied from very small quantities up to about one metric ton. The mean length of the herring in the different catches varied from about 14 cm up to above 30 cm. In the pelagic trawl stations the herring was seen in dense shoals, as shown in Fig. 6 A. On the other hand, at the bottom trawl stations, the herring was located very near the bottom (Fig. 6B and C).

Growth characteristics and vertebrae counts

The length frequency distributions of the sampled herring by fjord and by subarea are shown in Fig. 2 (Balsfjord) and Fig. 3 (Sørfjord and Stålvikbotn). Figure 4 (A, B and C) shows the results from the vertebrae counts. In Balsfjord the vertebrae counts give a bimodal distribution with one peak between 54-55 VS and one peak about 57 VS. The herring in Balsfjord were split into low-vertebral herring (VS=52-55) and high-vertebral herring (VS=56-60).

The proportion of males to females in the investigated material were found to be 1:3 for low-vertebral herring and 1:2 for high-vertebral herring.

The bulk majority of low-vertebral herring were mature fish in stages 3 and 4 (see Anon., 1984), while high-vertebral herring were immature in stages 1 and 2.

For low-vertebral herring the weight/length relation was described by a regression line in the following form:

$$\log W = -5.75 + 3.23(\log L), \text{ with corr.} = 0.985$$

$$W = 0.00318 * L^{3.23}$$

For back-calculation of growth from otolith radia, a plot of otolith radia versus fish length gave a linear relation with intercept on the L-axis (for R=0) close to zero. The following regression model was found:

$$\log L = 1.651 + 1.034 (\log R)$$

Backcalculation of growth was conducted for both low- and high-vertebral herring and the results are presented in Table 2. From the table it can be seen that the growth of the two herring groups is very similar in the first years of life. At the age of 4 the high-vertebral herring seems to grow faster.

Table 3 gives mean length by age of herring caught in Balsfjord. By computer fitting this data to the von Bertlanffy growth equation, the following growth parameters where found for the fjord herring:

$$L(max) = 32 \text{ cm}, \; k = 0.30 \text{ and } t(0) \; 0 - 0.40$$

Genetic variation in herring samples

The LDH-2 polymorphism in white muscle of herring was first reported by Odense et al. (1966), and Nævdal (1970) has described the alleles found in herring populations along the Norwegian coast. In contrast with earlier work, we have used starch gel and the enzyme banding pattern, indicating the different alleles and genotypes, as given in Fig. 5. Three alleles have been found in Norwegian herring populations, one (70) which moves slower and another (110) which moves faster than the most common allele (100). Most interesting is the distribution of the fast moving allele 110, which is almost exclusively found in fjord herring populations (Jørstad and Nævdal, 1981). The highest frequency of this allele was observed in a 0-group sample taken in Balsfjord. The sample was, however, clearly a mixture of herring from different population units, as indicated by a large excess of homozygotes for this locus.

In this study, more than 900 individuals from 11 trawl stations were frozen and later analysed by electrophoresis. Herring from three fjords (Balsfjord, Stålvikbotn, Sørfjord) were represented. The results obtained for the LDH-2 locus are given in Table 4 which shows the genotype distributions and allele frequencies in the samples from different stations. As seen, the frequency of LDH-2 (110) varied from 0 and to 0.963 for the sample taken at St. 293.

Four of the samples (St. 270, 274, 293 and 304), all taken by bottom trawl in Balsfjord, have high frequencies (>0.85) of

LDH-2(110) which agree with earlier estimates for the herring in this fjord. In contrast, the samples from Sørfjord and Stålviksbotn have very low frequencies of this allele, 0.021 and 0 respectively. In addition, these samples have a relatively higher frequency (0.03) of the slower allele (70) which are in accordance with the distribution of LDH-2 alleles normally found in samples of Atlanto-Scandian herring.

When considering the total material analysed, it was obvious that the distribution of genotypes deviates significantly from the values expected from Hardy-Weinberg's equilibrium. The observed number of LDH-2 (100/110) was 64 whereas the expected figure was 445, giving an enormous deficiency of heterozygotes ($d = 25.4$, $p < 0.001$, Christiansen et al. 1976; $G = 818$, $p > 0.001$, G-test).

When performing tests for H.W. proportions in the samples from the different trawl stations, three samples (St. 281, 323 and 324) taken in Balsfjord, have a significant deficiency of heterozygotes. The other samples, where the frequency of LDH-2(100) was absent or very low or occurs at very high values, were in agreement with H.W.'s expectations.

Obviously, the material analysed consists of herring from two herring stocks which were very divergent genetically. Based on the frequency of LDH-2(110), the samples were grouped into Balsfjord herring (St. 270, 274, 293 and 304) and Atlanto-Scandian herring (St. 278, 302, 353 and 385). For both groups of herring, the distribution of genotypes were in agreement with expected values estimated from Hardy-Weinberg's equilibrium.

Comparisons between genetic and biological data

The genetic data demonstrated that the herring samples were highly heterogeneous. The samples taken in Stålevikbotn and Sørfjord have both a very low frequency for LDH-2(110) and these samples consist of young, immature herring, mainly 2-3 years

o . Mean length of these herring sample was about 18-20 cm (Table 5). The mean vertebrae count for the samples was about 57 which nicely agree with values earlier estimated for Atlanto-Scandian herring. Thus both the genetic information and the biological parametres support evidence that this herring was offspring from the Atlanto-Scandian herring spawned along the Norwegian coast.

For the samples taken in Balsfjord the situation was very different. Here, for the samples taken with pelagic trawl (St. 278, 302), the mean length of herring was 18.2 cm, mean VS was 57.1 and the analyses of LDH-2 demonstrated a very low frequency of allele 110. Clearly, these herring also belonged to the Atlanto-Scandian herring stock. Several samples (St. 270, 274, 304 and 293) taken with bottom trawl at relatively deep water consisted of the Balsfjord herring characterized by a very high frequency of LDH-2(110) (>0.83). These samples was dominated by older herring (5-12 years) and with a mean VS of 54.5 and mean length of 27.2 cm. These observations are in accordance with the earlier results on the Balsfjord herring (Jørstad and Nævdal, 1983).

Three of the samples from Balsfjord (St. 281, 323 and 324) have intermediate frequencies for LDH-2(110) (0.484, 0.653 and 0.811 respectively). All these have an excess of homozygotes as seen in test for H.W. equilibrium and, conclusively, are a mixture of individuals from the two different stocks - Atlanto-Scandian herring and Balsfjord herring. Mean length, VS and age distribution were also intermediate for these samples compared to pure samples from the different stocks (Table 5).

Details for three sampling stations are shown in Fig. 6-8 where St. 278 represents a sample of Atlanto-Scandian herring, St. 274 consists of Balsfjord herring and St. 281 consists of a mixture of herring from both stocks.

The echograms (Fig. 6) demonstrated that the Balsfjord herring is found on the bottom, meanwhile Atlantic-Scandian herring occur pelagic. On the echogram from St. 281 the major fraction of herring is localized on the bottom, but one can clearly see herring also occuring higher up in the water column. For the samples taken at these stations the information about mean length (Table 5), vertebrae count distributions (Fig. 7), and age distributions (Fig. 8) verified the existance of pure herring stocks as well as mixture of the two stocks.

The sample taken at St. 281 was also examined in more details. Fig. 9 shows the enzyme pattern obtained in starch gel electrophoreses of 30 individual samples of white muscle. Each individual was classified as either Balsfjord herring or Atlanto-Scandian herring based on enzyme pattern and LDH-2 genotype. The genotype classification was, in addition, compared to the biological information, shown in Table 6. Obviously, there was a nice agreement between stock classification (by genotype), vertebrae counts, age distributions and mean length.

DISCUSSION

The data reported here, confirm and extend the earlier observations on the genetically unique herring stock in the Balsfjord area. The genetic characteristics of this population suggest that it is the most divergent population of herring reported in the north Atlantic. This conclusion seems to be valid also with regards to populations in Norwegian waters (Jørstad and Nævdal, 1983) as well as elsewhere (Anderson et al. 1981; Kornfield et al. 1982; Grant 1984).

The trawl survey with "J. Ruud" in February this year, provided new information about the spatial distribution of the Balsfjord herring and permitted a close comparison of genetic and biological parameters for a large number of samples. In addition to the genetic pecularities detected, the Balsfjord herring stock

differed in the biological characters estimated such as growth parameters and mean vertebrae number (VS). Preliminary observations (Pedersen, unpublished), also indicate discrete spawning sites of the Balsfjord herring in shallow waters on the bottom of the fjord.

Several of the samples analyzed consisted of a mixture of Balsfjord herring and young Atlanto-Scandian herring occurring pelagically in the upper water layer. Similar observations have been reported, (Jørstad and Nævdal, 1981) especially for the 0-group herring. On the cruise with "J. Ruud" this year, it was clearly demonstrated that in most cases the two herring stocks were distributed at different depth in the fjord. It is therefore possible that the Atlanto-Scandian herring found at bottom trawl stations have been caught when the trawl was lifted to the vessel when terminating the haul.

On the other hand, offspring from the large Atlanto-Scandian herring stock are usually distributed in all fjords in northern part of Norway when large yearclasses occur. This means that immature herring from this stock are normally found also in the Balsfjord area. The existance of the Balsfjord herring with its reported genetic characteristics, suggest that the immigrating herring which do not belong to the fjord stock are leaving the fjord system before maturation. In this way, herring from other stocks will not contribute to the local gene pool. For this reason, further studies on the dynamics and interaction between herring stocks should be continued in this area.

The Balsfjord herring stock must also be recognized as a specific genetic resource demanding separate stock management and concervation (FAO, 1981). All kinds of human activity, including fishing effort, stock enhancement programmes, and pollution should be carefully evaluated with regards to preservation of this unique herring stock.

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Table 1. Catch in kgs and mean length of herring for each trawl station. BT = bottom trawl; PT = pelagic trawl. Each trawl haul lasted for 30 minutes. "J. Ruud" February 1986.

TRAWL NUMBER	DATE	TIME LOCAL	GEAR	DEPTH HAUL (m)	CATCH (kg)	MEAN LENGTH/ STD (cm)
270	20/2	05.10	BT	174	30	29.9/1.9
273	20/2	06.09	BT	180	5	29.8/2.9
274	20/2	10.26	BT	180	65	30.1/2.1
278	21/2	01.30	PT	35	15	17.8/1.3
279	21/2	05.03	PT	75	4	17.7/1.5
281	21/2	10.44	BT	70	1000	21.1/3.8
293	21/2	15.41	BT	108	190	26.4/2.8
301	22/2	00.07	BT	73	10	25.6/2.9
302	22/2	02.00	PT	45	6	17.1/2.3
304	22/2	12.51	BT	60	500	24.0/2.4
323	23/2	08.42	BT	120	45	23.6/4.7
324	23/2	10.37	BT	136	15	26.7/3.4
337	23/2	20.36	PT	20	4.5	17.5/2.5
340	24/2	05.03	PT	0	0.2	14.6/2.2
353	25/2	09.03	BT	60	150	18.5/3.7
367	26/2	02.19	BT	60	10	20.1/3.9
385	28/2	08.45	BT	150	200	19.7/1.5
388	28/2	16.22	BT	58	2	20.1/2.6
390	28/2	22.05	PT	35	60	26.7/7.0

Table 2. Backcalculated mean length for all the measured otolith annuli by low and high-vertebral herring.

	LOW-VERTEBRAL			HIGH-VERTEBRAL		
YEAR	N	MEAN LENGTH (mm)	STD	N	MEAN LENGTH (mm)	STD
1	156	114.2	19.2	158	112.2	18.9
2	155	162.8	21.9	148	160.4	21.4
3	140	197.0	23.8	59	203.8	33.5
4	108	225.7	63.6	19	243.0	32.0
5	58	232.9	28.3	14	256.7	30.7
6	12	234.0	28.7	5	266.0	34.4

Table 3. Mean length at different age estimated for pooled samples of herring in Balsfjorden.

AGE	N	MEAN-LENGTH	STD
2	21	162.7	11.8
3	34	190.6	17.8
4	12	230.0	15.5
5	31	249.0	17.6
6	25	258.8	21.9
7	17	283.2	20.8
8	42	288.9	27.9
9	27	294.1	17.0
10	2	302.5	3.5
11	4	302.5	5.0
12	10	314.0	11.3

Table 4. Genotype distribution and allele frequencies for the LDH-2 locus in samples of herring at different trawl stations, "Johan Ruud", February 1986.

Station	N	Genotype distribution						Allele frequencies		
		70/70	70/100	70/110	100/100	100/110	110/110	70	100	110
270	95	0	0	0	3	15	77	0	.111	.889
274	50	0	0	0	1	3	46	0	.050	.950
278	96	0	6	0	89	1	0	.031	.964	.005
281	95	0	6	0	39	8	42	.032	.484	.484
293	95	0	0	0	0	7	88	0	.037	.963
302	96	0	12	0	84	0	0	.063	.938	0
304	25	0	0	0	0	7	18	0	.140	.860
323	95	0	2	0	26	10	57	.011	.337	.653
324	95	0	1	1	11	11	71	.011	.179	.811
353	96	0	5	0	88	2	1	.026	.953	.021
385	94	0	6	0	88	0	0	.032	.968	0

Table 5. Comparisons between biological characteristics in different trawl samples of herring and allele frequencies at the LDH-2 locus. Each sample was classified to herring stock based on the allele frequencies. 1: Atlanto-Scandian herring; 2: Balsfjord herring.

Station no.	Fjord/ area		Gear	Depth (m)	N	Mean length (mm)	N	Vertebrae no.	Age	LDH-2			Herring stock
										70	100	110	
270	Bals	III	BT	174	95	299.3/19.9	(30)	54,8/1.0	(3-12)	0	0.111	0.889	2
273	-	III	BT	180	16	298.1/28.6		-	(5-12)				
274	-	III	BT	180	50	301.3/20.7	(30)	54.5/1.2	(5-12)	0	0.05	0.95	2
278	-	II	PT	35	98	177.7/12.8	(30)	57.2/0.8	(2-3)	0.031	0.964	0.05	1
279	_	II	BT	70	100	118.7/15.3							
281	-	I	BT	70	100	211.2/37.9	(30)	56.1/1.1	(2-6)	0.032	0.484	0.484	1+2
293	-	II	BT	108	95	263.5/27.6	(30)	54.6/0.8	(5-9)	0	0.037	0.963	2
301	-	I	BT	73	100	256.3/28.6		-	-				
302	-	I	PT	45	100	170.8/22.5	(30)	57.2/0.7	(2-3)	0.063	0.938	0	1
304	-	I	BT	60	100	240.4/24.2	(25)	54.1/0.8	(5-11)	0	0.14	0.86	2
323	-	V	BT	120	99	236.1/47.1	(30)	54.2/1.4	(3-12)	0.011	0.337	0.653	1+2
324	-	IV	BT	136	100	266.9/33.9	(30)	54.3/1.2	(3-12)	0.011	0.179	0.811	1+2
337	-	V	PT	20	75	175.0/24.6		-	-				
340	-	VI	PT	0	8	146.3/21.9		57.0/0	(1-3)				
353	STÅL		BT	60	100	184.6/37.4	(30)	56.7/1.3	(2-5)	0.020	0.953	0.021	1
367	-		BT	60	73	200.8/39.6			(4-12)				
385	SØR	I	BT	150	96	197.1/14.7	(30)	57.1/1.1	(2-3)	0.032	0.968	0	1
388	-	III	BT	58	63	201.0/25.9	(30)	57.3/0.9	(3-5)				
390	-	III	BT	35	100	267.4/70.5	(30)	57.1/0.7	(3-11)				

Table 6. Individual classification of 30 herring from trawl station 281. The banding pattern of LDH-2 allozymes and alleles envolved are shown in Fig. 10, and the electrophoretic analyses of the herring individuals are shown in Fig. 11. Identification to herring stocks (1= Atlanto-Scandian herring; 2= Balsfjord herring) are based and the genotype classification.

Fish no.	Length (mm)	Weight (g)	Vertebrae no.	Age (oth.)	Genotype LDH-2	Herring stock
1	265	130	56	5	110/110	2
2	270	143	56		110/110	2
3	240	85	55	5	110/110	2
4	160	22	57	2	100/100	1
5	205	56	58		100/100	1
6	250	90	55		110/110	2
7	180	33	57	3	70/100	1
8	260	116	55	5	110/110	2
9	265	118	55	6	100/110	2
10	170	25	57	3	100/100	1
11	190	35	58	3	100/100	1
12	170	27	57	3	70/100	1
13	250	99	55	5	110/110	2
14	250	105	55	5	110/110	2
15	180	34	57	3	100/100	1
16	250	109	55	4	110/110	2
17	180	31	57	3	100/100	1
18	215	52	57	3	100/100	1
19	165	26	57	2	70/100	1
20	265	119	55	5	100/110	2
21	165	24	56	3	100/100	1
22	265	120	57	5	100/110	2
23	265	117	55	5	110/110	2
24	175	28	57	3	100/100	1
25	240	81	54	4	110/110	2
26	200	42	58	3	100/100	1
27	260	123	55	5	110/110	2
28	170	28	55	3	110/110	2
29	250	100	56	5	110/110	2
30	270	146	56	5	110/110	2

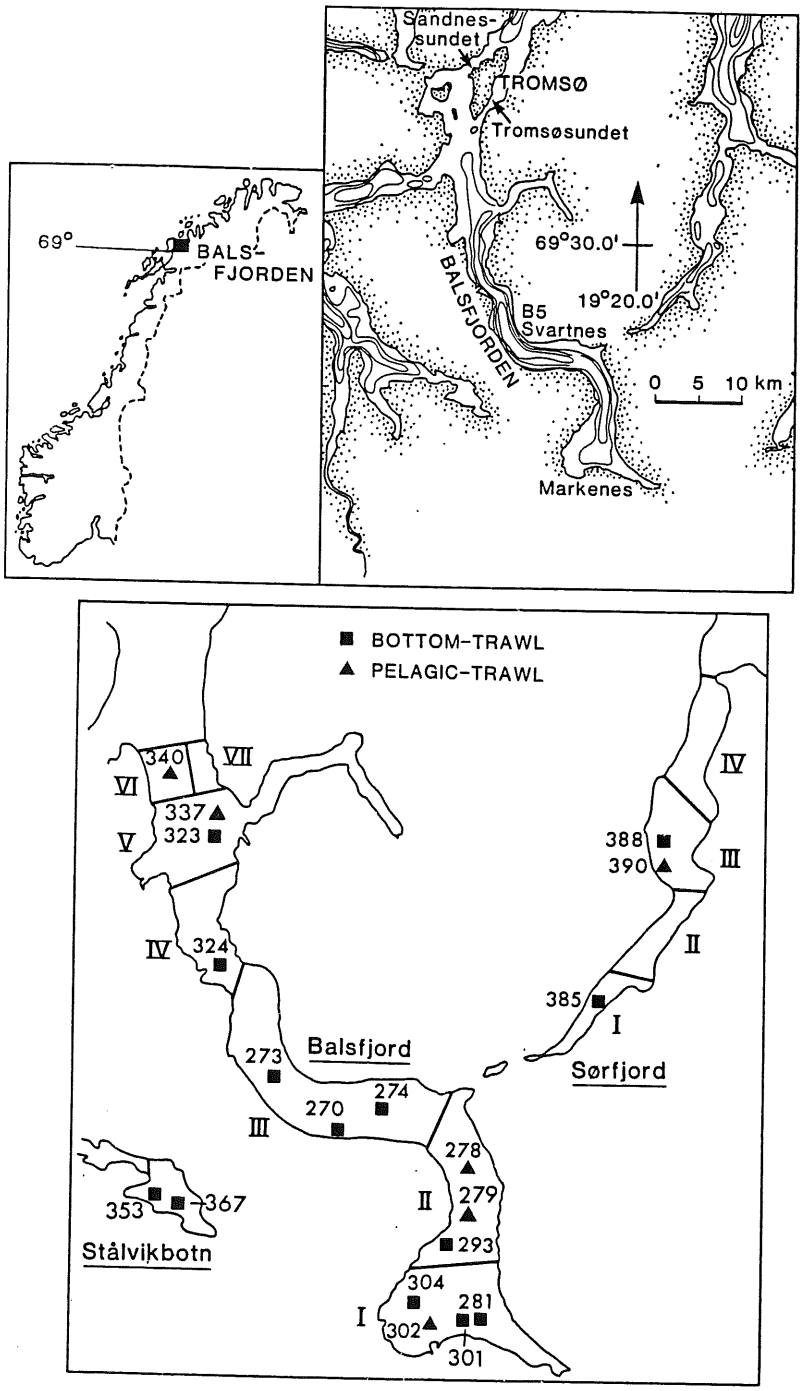

Fig. 1. Area of investigation and trawl stations during the cruise with "Johan Ruud", February 20-28, 1986.

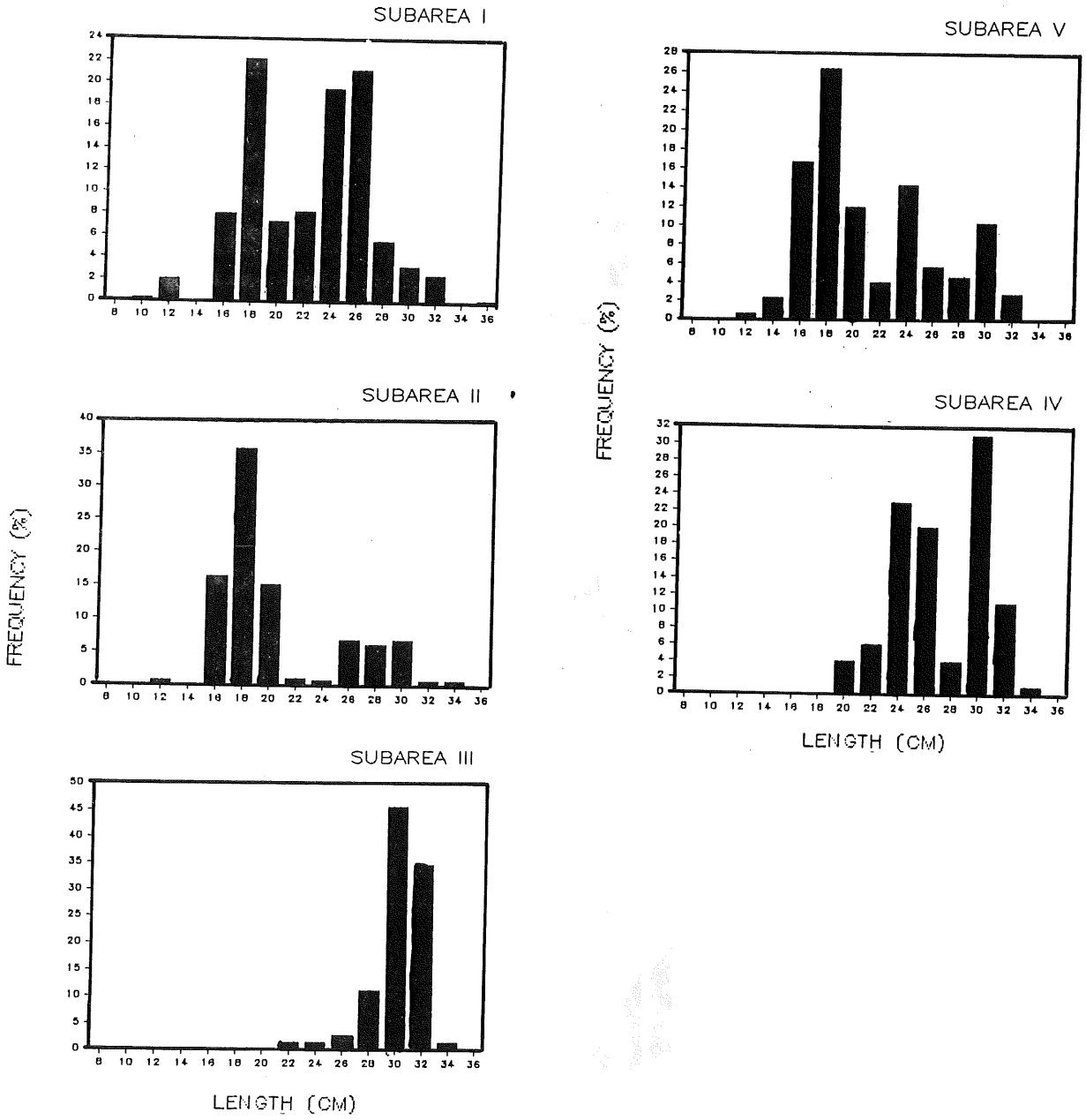

Fig. 2. Length distributions of herring in different area (I-V) in Balsfjord, February 1986. Pooled data from bottom and pelagic trawl samples.

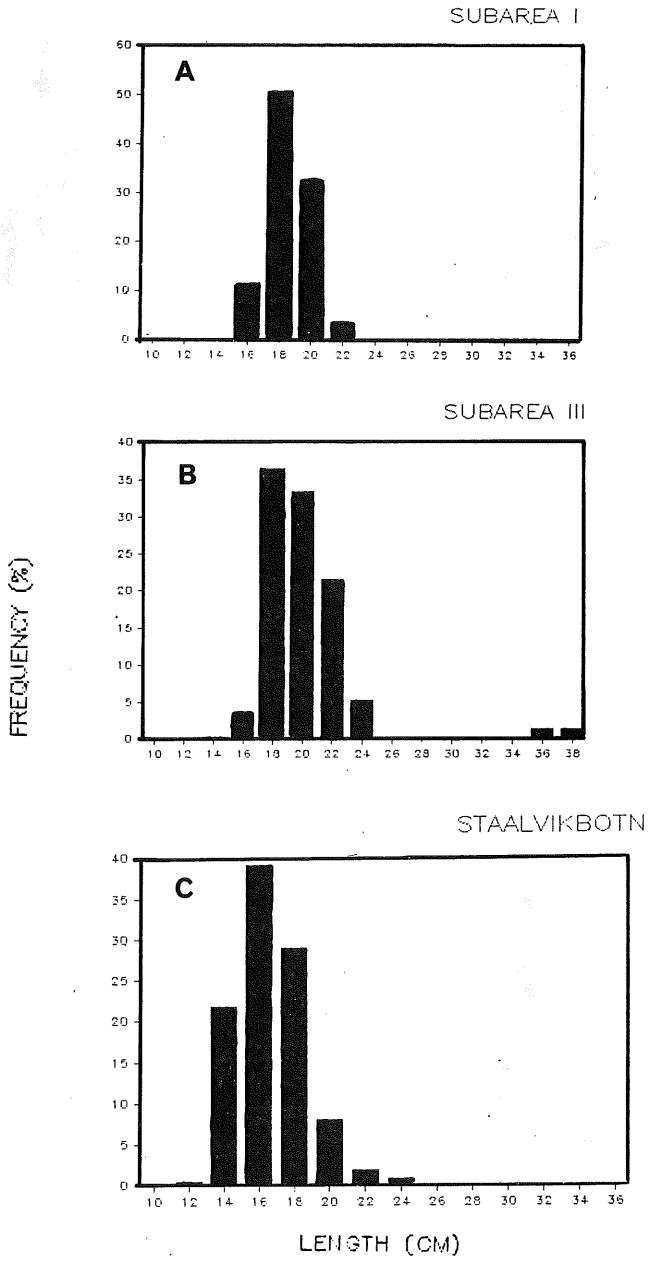

Fig. 3. Length distributions of herring in Sørfjorden (A and B) and Stålvikbotn, February 1986.

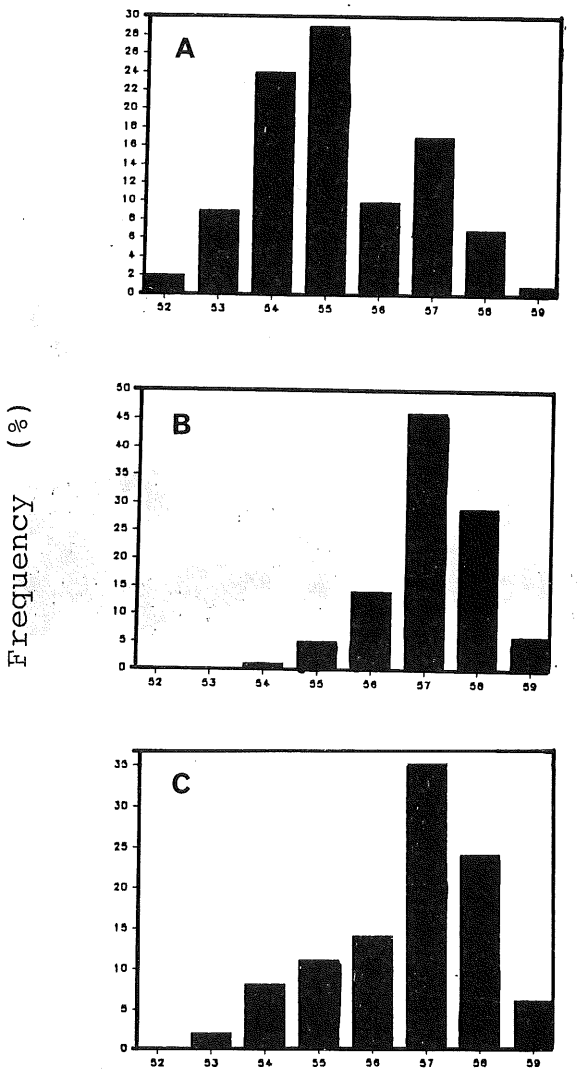

Fig. 4. Distribution of vertebrae counts in pooled samples of herring from Balsfjord (A, n=248), Sørfjorden (B, n=107) and Stålvikbotn (C, n=60), February 1986.

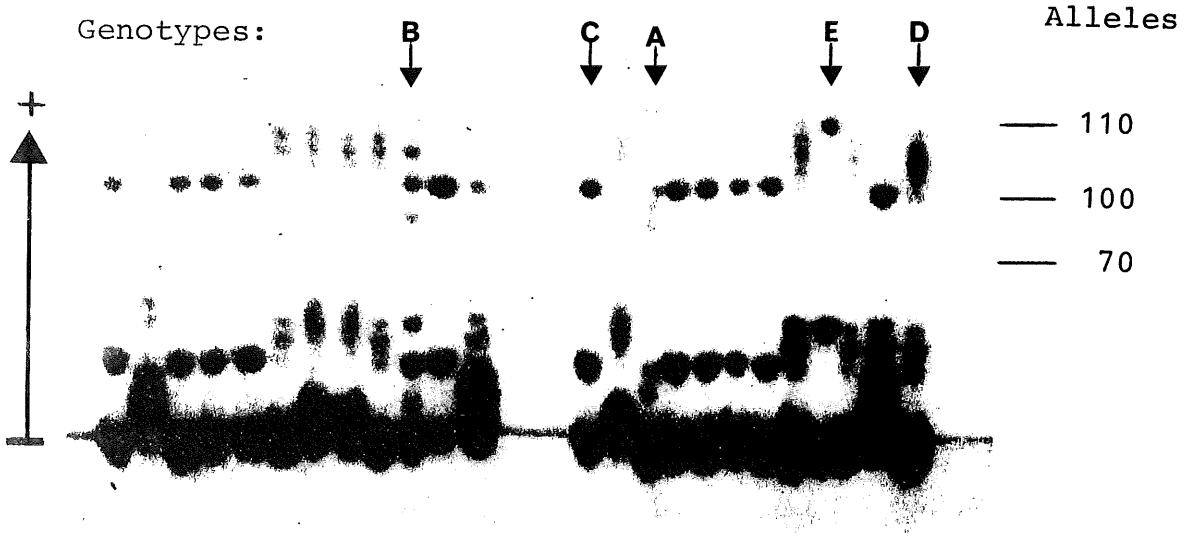

Fig. 5. The LDH-2 polymorphism.
Enzyme banding pattern after starch gel electrophoresis of white muscle samples from individual herring. The LDH-2 alleles which control the banding pattern are given and the different LDH-2 genotypes are indicated:

A: Genotype 70/100
B: Genotype 70/110
C: Genotype 100/100
D: Genotype 100/110
E: Genotype 110/110

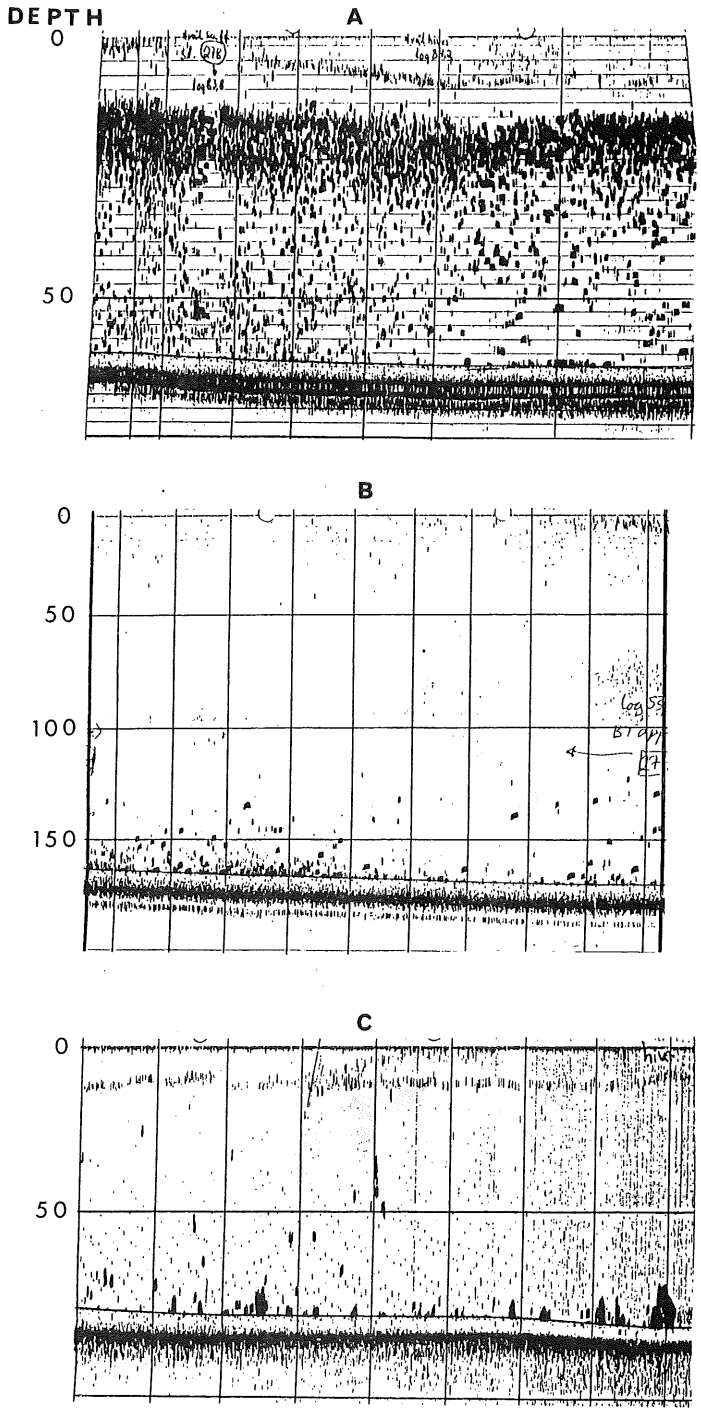

Fig. 6. Eckogram showing the distribution of herring at three trawl stations in Balsfjord. The allele frequencies for the LDH-2 locus are also given.

		70	100	110
A:	St. 278, PT - 35 m	0.031	0.964	0.005
B:	St. 274, BT - 180 m		0.050	0.950
C:	St. 281, BT - 70 m	0.032	0.484	0.484

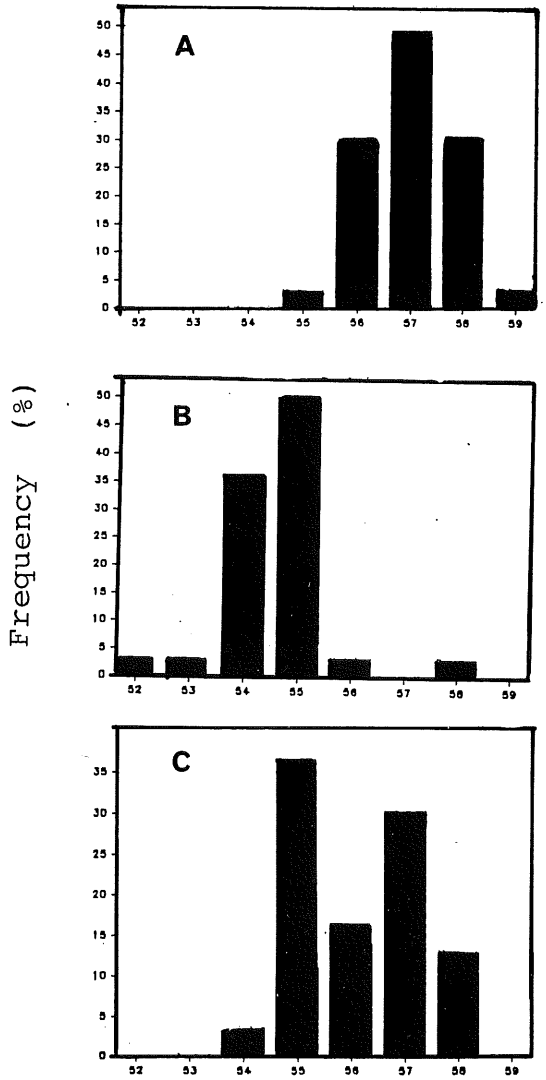

Fig. 7. Distribution of vertebrae counts and in three trawl samples of herring in Balsfjord. The allele frequencies for the LDH-2 locus are also given.

		70	100	110
A:	St. 278, PT - 35 m	0.031	0.964	0.005
B:	St. 274, BT - 180 m		0.050	0.950
C:	St. 281, BT - 70 m	0.032	0.484	0.484

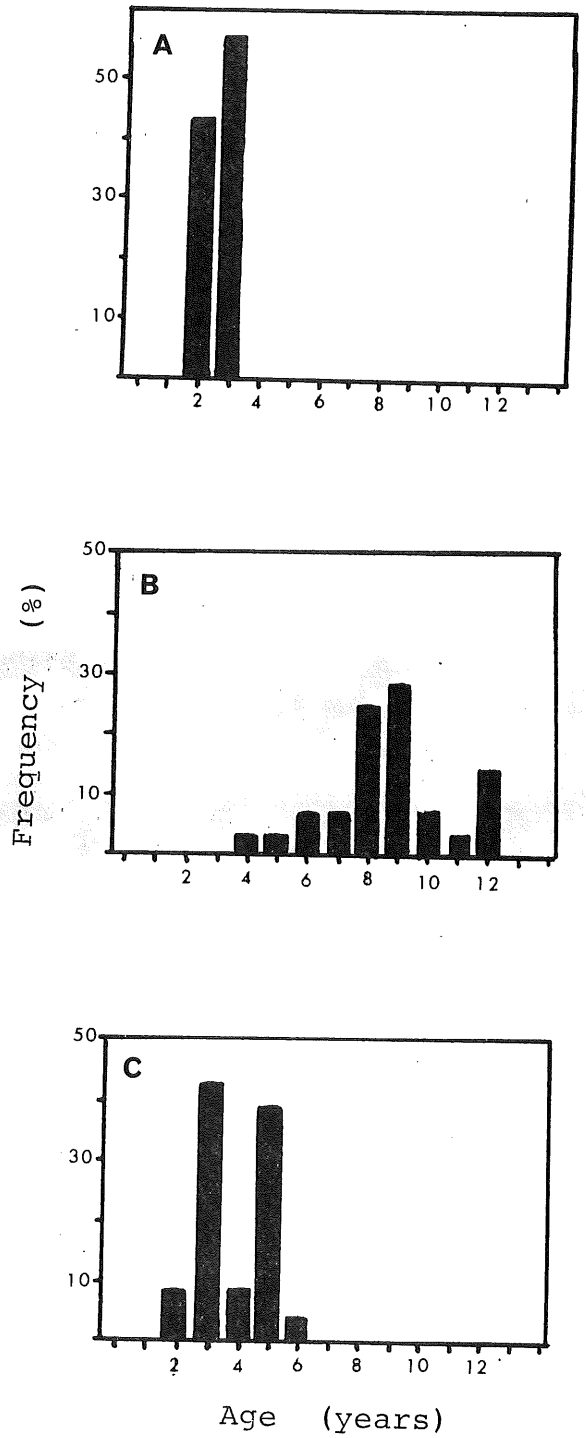

Fig. 8. Age distributions in three trawl samples of herring in Balsfjord. Allele frequencies at the LDH-2 locus are also given.

		70	100	110
A:	St. 278, PT - 35 m	0.031	0.964	0.005
B:	St. 274, BT - 180 m		0.050	0.950
C:	St. 281, BT - 70 m	0.032	0.484	0.484

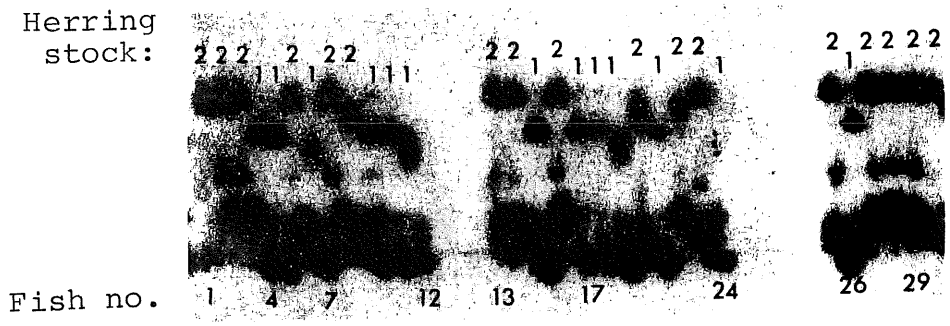

Fig. 9. Individual banding pattern of LDH-2 allozymes and classification to herring stock for 30 herrings taken at Stations 281 (see also Table 6).

1: Atlanto-Scandian herring (genotype 70/100 and 100/100)

2: Balsfjord herring (genotype 100/110 and 110/110)

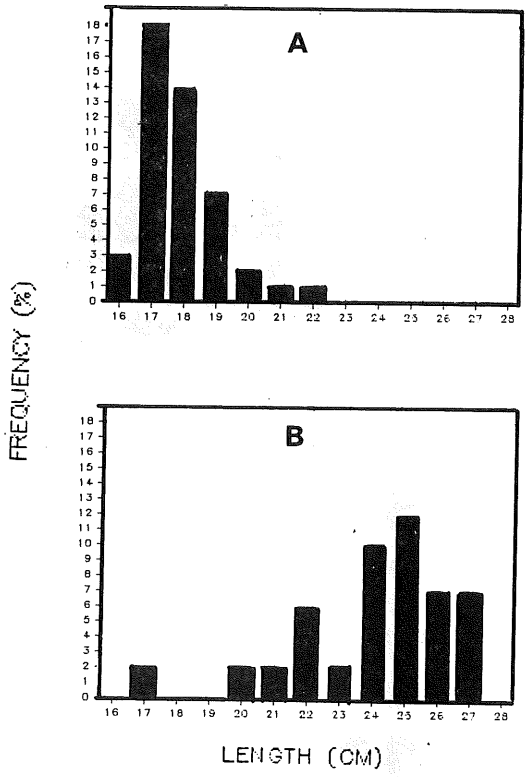

Fig. 10. Length distribution of Atlanto-Scandian herring (A) and Balsfjord herring (B) at station 281. The individual fish have been classified according to LDH-2 genotype.

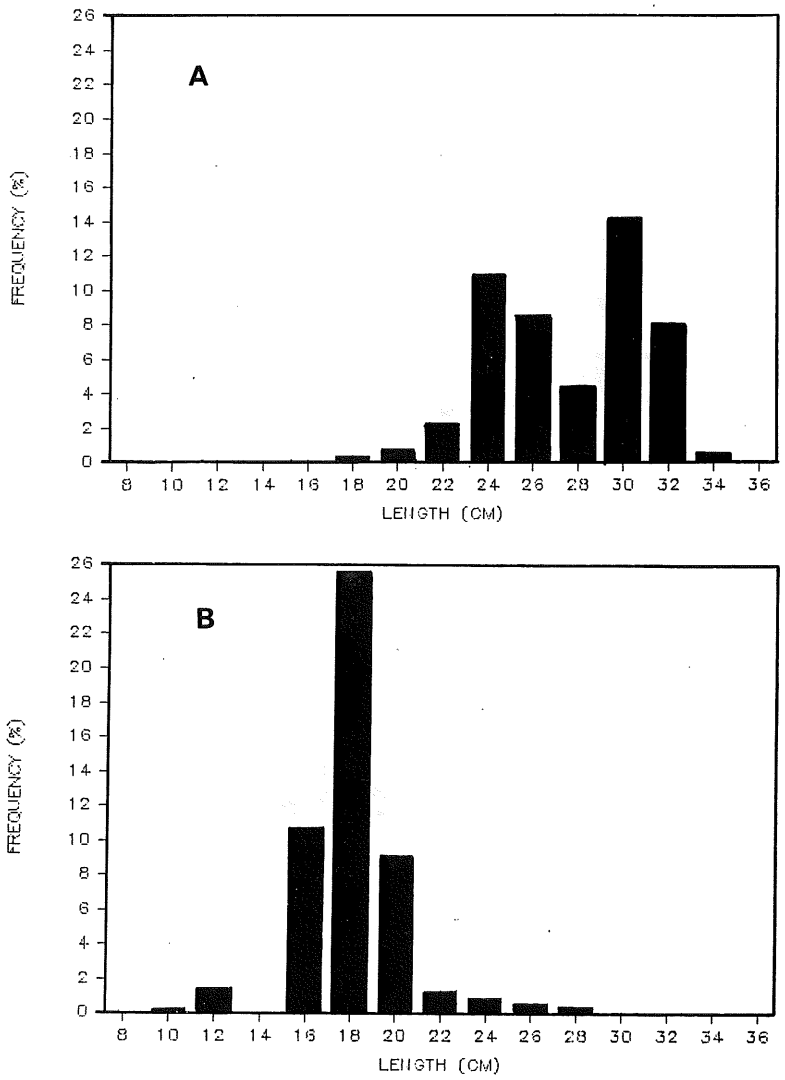

Fig. 11. Length distribution in herring stocks in Balsfjord, February 1986. All individuals were grouped into Balsfjord herring (shown in A) and Atlanto-Scandian herring (shown in B) based on genotype classification. The total material consists of 1115 individuals.