# Analysis of population and genetic characteristics of redfish of the Irminger Sea

by

Novikov G.G., Stroganov A.N., Afanasjev K.I.

Faculty of biology, Moscow State University, Vorobjovy Gory, 119899
Moscow, Russia

Shibanov V.N., Melnikov S.P.

Knipovich Polar Research Institute of Marine Fisheries and Oceanography (PINRO)
6, Knipovich Street, 183763, Murmansk, Russia

**ABSTRACT**

Redfish *Sebastes mentella*, inhabiting the Irminger Sea pelagial and adjacent waters, is the object of analysis.

The aim of the paper is to analyze redfish genetic parameters using electrophoresis to study a distribution of allele frequencies of marker enzymatic loci used for this species. Standardized enzymatic systems used for population and genetic analyses performed for redfish both in Russia and abroad have been studied, i.e. NADP - dependent malate dehydrogenase (malic enzyme) (MEP-2), NAD - dependent malate dehydrogenase (MDH), glucose-6-phosphate isomerase (PGI), isocitrate dehydrogenase (IDH), lactate dehydrogenase (LDG), phosphoglucomutase (PGM), superoxide dismutase (SOD) and fluorescense esterases (ESTD).

When collecting samples for genetic analysis, the redfish "oceanic" or "deep-sea" types were preliminarily not identified by morphologic features.

Based on the analysis performed, a conclusion was drawn that the Irminger Sea pelagial is inhabited by genetically integral self-sustaining population of redfish. Due to implementation of strategy of extending the area of redfish distribution and increase in efficiency of energy exchange, a somewhat proportion of it, while increasing in length with age, adapts larger depths; in this case, a minor priority (due to any not revealed reasons) obtain the specimens, the genome of which a dominating allele of locus MEP-2* is available in. However, with an increase in age, under an influence of natural loss and enhanced mortality of specimens homozygotic by alternative allele, the abundance of a deep-sea grouping reduces, and contribution of these specimens to a single reproductive potential of the redfish population decreases

even more, that does not result in intensification of formation processes and isolation of reproductively isolated groupings affected by environmental factors.

## INTRODUCTION

Redfish (*Sebastes mentella* Travin) is widely distributed in the North Atlantic region, having adapted different depths from the surface to deep and near-bottom waters. Vast area of its distribution and habitation in different depths pre-determined peculiarities of the life cycle and ecological subdivision of the species.

In the second half of the 20th century a number of hypotheses was suggested regarding the morpho-ecological and population and genetic structure of redfish from the North Atlantic areas, based on different methods for isolating or integrating local groupingss: from groupings related to specific areas to those inhabiting different depth ranges. (Yanulov, 1962; Surkova 1962; Dushchenko 1986; Rikhter 1996; Johansen et al. 1996, 1997). A number of papers aimed at substantiating a possibility to isolate two reproductively isolated groupings in the Irminger Sea pelagial, using different methods (from morphometric to molecular-genetic), and, as a consequence, two commercial stocks of redfish also, i.e. "oceanic" and "deep-sea", is of specific interest (Magnusson, J. 1977, 1983; Magnusson J., Magnusson J.V. 1995; Danielsdottir A., Gislason D. 2001).

To analyze genetic parameters of redfish from the Irminger Sea, electrophoresis was used to study distribution of allele frequencies of marker enzymatic loci applied for this species.

## MATERIALS AND METHODS

Samples of redfish (white muscles) for genetic analyses were collected by PINRO specialists in the course of trawl-acoustic surveys carried out in the Irminger Sea areas (limited by positions 55°- 62°N, 28°- 46°W) during 1999 and 2000. The samples were selected from catches taken by a mid-water trawl from 130 to 1060 m. In specific depths, samples were taken vertically from 100 to 300 m depth (Tables 1 and 2).

When collecting samples for genetic analyses, the "oceanic" and "deep-sea" types of redfish were not identified by morphological features.

Samples taken in different sites of the distribution area were examined by means of electrophoresis in starch gel. Standardized enzymatic systems used for the population and genetic analyses performed for redfish both in Russia and abroad have been studied, i.e. NADP dependent malate dehydrogenase (malic enzyme) (MEP-2), NAD - dependent malate dehydrogenase (MDH), glucose-6-phosphate isomerase (PGI), isocitrate dehydrogenase (IDH), lactate dehydrogenase (LDG), phosphoglucomutase (PGM), superoxide dismutase (SOD) and fluorescense esterases (ESTD).

Prior to processing, samples of tissue were stored frozen at − 18°C. The tissue pieces were homogenized before electrophoresis. The samples were centrifuged, and transparent supernatant was used. Following the electrophoresis, proteins were stained with Cumassi-R-250, and standard methods for histological and chemical analysis

were applied to reveal localization of enzymatic systems. Inventory of processed data on redfish is given in Tables 1 and 2.

**RESULTS AND DISCUSSION**

The analysis for eight protein systems has shown that in all the redfish samples examined the malic enzyme (Table 8), NAD dependent malate dehydrogenase, glucose-6-phosphate isomerase and isocitrate dehydrogenase (Tables 3, 4 and 5) are represented by 2-allele systems; phosphoglucomutase (Table 6) – by a 3-allele system, and lactate dehydrogenase, superoxide dismutase and fluorescense esterases are monomorphic (Table 7).

In this case, a level of polymorphism has occurred to be fairly low. And only values for frequencies of the malic enzyme locus alleles allow to reliably describe a status of the redfish population in the Irminger Sea. It should be necessary to note that the absolute values for frequencies, alleles "60" and "100" of MEP-2* locus (Table 8), obtained in our experiments, are similar to those being known from earlier papers both by foreign and Russian researchers (Dushchenko 1986; Johansen et al. 1996, 1997).

Analysis for frequency distribution of MEP-2* locus alleles from the samples examined (1999, 2000) allows to suggest that most probably a mosaic disatribution of samples with different frequencies in different depths of the Irminger Sea is available (Table 8, Fig.1). Thus, the frequency of "100" allele of MEP-2* locus in redfish from the samples taken within 250-400 m depths may constitute both 0,400 and 0,750, and in the samples from 600-800 m – it makes up both 0,850 and 0,383 (Fig.1). Such significant dispersion of frequencies may to a certain degree give evidence both of occasional variation in a proportion of different alleles within the samples and of specific displacement of different length-age groups within a yearly migration cycle (feeding – fertilization – extrusion of larva) and during the entire period of ontogenesis of the species also. Analysis of the data on length-age parameters of redfish, obtained in parallel by PINRO specialists, allows to approach the processes occurring within the population of redfish in the Irminger Sea more attentively. Thus, the examined samples for 2000 showed a prevalence in a proportion of adult age groups in large depths (Fig.2). Phenomenon of localization of adult age groups in large depths is sufficiently well known for different deep-sea species (Savvatimsky 1992). As for the redfish, a preference of large depths while increasing in length with age (Fig.3) may be explained both by a transition to larger-size food objects (squid, fish) and by more favorable conditions in deep waters: variation in the strength of water currents and reduction in the current velocity (Stepanov 1983), that are typical of deep-water and near-bottom layers, can be expedient for redfish from an energetic point of view. The analysis for frequency dynamics of heterozygotes and homozygotes between the samples taken in 290 - 340 m and 590-790 m depths (by the data for 2000) has shown a relative stability of heterozygosity among these samples, obtained from different depths (total heterozygosity for the samples taken in 290-340 m is 0,41 and 0,31 – in 590-790 m). In this case, a significant reduction in a proportion of homozygotes by alternative allele (from 0,40 in 290-340 m to 0,18 in 590-790 m depths) was marked against the background of the heterozygosity stability, that gives evidence of a relatively short life duration of fish homozygous by alternative allele. Thus, in the reproductively integral redfish population studied there

are probably specimens which are more resistant to the environmental factors effect and demonstrate higher rate of survival just during a transition to the deeper-sea way of life at later stages of ontogenesis.

**CONCLUSION**

Summarizing the results obtained, one may conclude that according to the data for 1999-2000 a genetically integral self-sustaining population of redfish inhabits the pelagial of the Irminger Sea. A major contribution to the reproduction of this population is made by specimens inhabiting the depths from 200 to 600 m. Due to implementation of strategy of extending the area of redfish distribution and increase in efficiency of energy exchange, a somewhat proportion of it, while increasing in length with age, adapts larger depths; in this case, a minor priority (due to some reasons) is obtained by the specimens, the genome of which a dominating allele of locus MEP-2* is available in. However, with an increase in age, under an influence of natural loss and enhanced mortality of specimens, homozygotic by alternative allele, the abundance of a deep-sea grouping reduces, and contribution of these specimens to a single reproductive potential of the redfish population decreases even more, that does not result in intensification of formation processes and isolation of reproductively isolated groupings affected by environmental factors.

**REFERENCES**

DANIELSDOTTIR, A., GISLASON, D. 2001. Genetic differentiation of pelagic and deep-sea *Sebastes mentella* in the Irminger Sea based on microsatellite markers. NWWG, Faroe Islands, 24 April – 3 May 2001. 15 pp.

DUSHCHENKO, V.V. 1986. Polymorphism of NADF –dependent malate dehydrogenase in *Sebastes mentella* Travin (Scorpaenidae) in the Irminger Sea. – In: Voprosy ikhtiologii. Vol.26(3):522-524.

JOHANSEN, T., DANIELSDOTTIR, A.K., KRISTINSSON, K., PETERSEN, P.H., NEVDAL, G. 1996. Studies on the relationship between deep-sea and Oceanic *Sebastes mentella* in the Irminger Sea by the use of haemoglobin And allozyme analyses. ICES C.M. 1996/G:27.

JOHANSEN, T., DANIELDOTTIR, A.K., MELAND, K., NEVDAL, G. 1997. Studies on the relationship between deep-sea and oceanic *Sebastes mentella* In the Irminger Sea by the use of haemoglobin, allozyme analyses and RAPD. ICES C.M. 1997/HH:13.

MAGNUSSON, J. 1977. Pelagic redfish in the Irminger Sea. Distribution and abundance. ICES C.M. 1977/H:43.

MAGNUSSON, J. 1983. The Irminger Sea – oceanic stock redfish. "Spawning" and "spawning area". ICES C.M. 1983/G:56.

MAGNUSSON, J., MAGNUSSON, J,V. 1995. Oceanic redfish (*Sebastes mentella*) in the Irminger Sea and adjacent waters. Sci. MAR., 59(3-4):241-254.

RIKHTER, V.A. 1996. On population structure of beaked redfish (*Sebastes mentella* Travin) in the Irminger Sea as related to larval drift. NAFO Sci. Coun. Studies., N 27:49-56.

SAVVATIMSKY, P.I. 1992. Roughead grenadier (*Macrourus berglax* L.) – potential object of trawl and long-line fishery in the North Atlantic. – In: Selected papers of PINRO. – Murmansk, 1992. P.45-67 (in Russian).

STEPANOV, V.N. 1983. Oceanic sphere. – Moscow, MYSL Press, 270 pp. (in Russian).

SURKOVA, E.N. 1962. Structural peculiarities of scale in redfish of the Northwest Atlantic. – In: Soviet fisheries investigations in the Northwestern Atlantic Ocean. – Moscow, VNIRO, P. 313-318 (in Russian).

YANULOV, K.P. 1962. On groupings of redfish (*Sebastes mentella* Travin) in the Labrador-Newfoundland area. – In: Soviet fisheries investigations in the Northwestern Atlantic Ocean. – Moscow, VNIRO, P.295-296 (in Russian).

**TABLE 1. Inventory of processed data on redfish (survey for 1999)**

| No.of sam-ple | Characteristic of sample | No. of indiv.in sample | No.of enzyme systems examined | Total number of samples analyzed. |
|---|---|---|---|---|
| 1 | 23.06 1999<br>59°30'N  37°08'W<br>Depth - 490-700 м | 20 | 8 | 160 |
| 2 | 23.06 1999<br>59°30'N 37°31'W<br>Depth - 235-420 м | 20 | 8 | 160 |
| 3 | 25.06 1999<br>58°45'N 37°13'W<br> Depth - 475-810 м | 30 | 8 | 240 |
| 4 | 25.06 1999<br>58°45'N  36°51'W<br>Depth -  200-360 м | 30 | 8 | 240 |
| 5 | 26.06 1999<br>58°47'N  31°01'W<br>Depth  520-1060м | 20 | 8 | 160 |
| 6 | 27.06 1999<br>58°00'N  33°52'W<br>Depth - 545-800 м | 20 | 8 | 160 |
| 7 | 27.06 1999<br>58°00'N  34°18'W<br>Depth - 260-427 м | 10 | 8 | 80 |
| 8 | 28.06 1999<br>57°57'N  36°41'W<br> Depth -190-290 м | 30 | 8 | 240 |
| 9 |  28.06 1999<br> 58°01'N 36°39'W<br> Depth - 340-540 м | 20 | 8 | 160 |
| 10 | 28.06 1999<br> 57°57'N  36°44'W<br> Depth - 550-805 м | 30 | 8 | 240 |
| 11 | 02.07 1999<br>56°41'N  40°28'W<br> Depth - 500-810 м | 30 | 8 | 240 |
| 12 |  02.07 1999<br> 56°20'N  40°32'W<br> Depth - 220-250 м | 30 | 8 | 240 |
| 13 | 04.07 1999<br>55°21'N  45°53'W<br>Depth - 450-810 м | 20 | 8 | 160 |
| 14 | 04.07 1999<br>55°20'N  46°11'W<br> Depth - 130-350 м | 30 | 8 | 240 |
| 15 | 10.07 1999<br>56°41'N 32°01'W<br>Depth -  525-680 м | 30 | 8 | 240 |
|  | TOTAL | 370 |  | 2960 |

**TABLE 2. Inventory of processed data on redfish (survey for 2000)**

| No.of samp-le | Characteristic of sample | No.of indiv.in sample N | No.of enzyme systems analyzed | Total number of samples examined |
|---|---|---|---|---|
| 1 | 03.06.2000<br>61°30'-61°50'N 28°10'-29°10'W<br>Depth - 740-840 м | 10 | 8 | 80 |
| 2 | 04-06.2000<br>61°20'-61°50'N 28°10'-29°10'W<br>Depth - 705-770 м | 10 | 8 | 80 |
| 3 | 06.06.2000<br>61°30'-61°50'N 28°20'-29°10'W<br>Depth - 640-740 м | 10 | 8 | 80 |
| 4 | 07.06.2000<br>61°20'-61°50'N 28°10'-29°10'W<br>Depth - 760-780 м | 10 | 8 | 80 |
| 5 | 08.06.2000<br>61°20'-61°40'N 28°10'-28°20'W<br>Depth - 740-760 м | 10 | 8 | 80 |
| 6 | 09.06.2000<br>61°30'-61°40'N 28°10'-29°10'W<br>Depth - 760-770 м | 10 | 4 | 40 |
| 7 | 09-10.06.2000<br>61°20'-61°40'N 28°10'-29°10'W<br>Depth - 760 м | 10 | 4 | 40 |
| 8 | 12.06.2000<br>61°40'N 29°10'W<br>Depth - 780-800 м | 10 | 4 | 40 |
| 9 | 21.06.2000<br>61°20'-61°30'N 28°10'-28°20'W<br>Depth - 650-720 м | 10 | 4 | 40 |
| 10 | 26.06.2000<br>61°30'N 28°20'W<br>Depth - 720-750 м | 10 | 4 | 40 |
| 11 | 10-11..07.2000<br>61°14'N 28°10'W<br>Depth - 580-600 м | 10 | 4 | 40 |
| 12 | 20-21.07.2000<br>61°10'-61°30'N 28°10'-28°20'W<br>Depth - 540-750 м | 10 | 4 | 40 |
| 13 | 03.08.2000<br>57°40'N 41°56'W<br>Depth - 240-345 м | 10 | 4 | 40 |
| 14 | 07.08.2000<br>57°40'N 41°59'W<br>Depth - 300-340 м | 10 | 4 | 40 |
| 15 | 16.08.2000<br>57°32'N 41°54'W<br>Depth - 300-340 м | 10 | 4 | 40 |
| 16 | 12.09.2000<br>56°09'N 41°39'W<br>Depth - 270-350 м | 10 | 4 | 40 |
| 17 | 28.09.2000 | 10 | 4 | 40 |

| | | | | |
|---|---|---|---|---|
| | 58°09'N  38°59'W<br>Depth - 320-360 м | | | |
| 18 | 30.09.2000<br>58°02'  39°00'W<br>Depth 320-350 м | 10 | 4 | 40 |
| 19 | 06-07.10.2000<br>57°37'N  39°30'W<br>Depth -  320м | 10 | 4 | 40 |
| 20 | 09.10.2000<br>57°56'N  39°26'W<br>Depth - 280-340 м | 10 | 4 | 40 |
| | TOTAL | 200 | | 1000 |

**TABLE 3. Allele frequencies of MDH locus in redfish samples**.

| Samples | | Alleles of MDH locus | |
|---|---|---|---|
| No. | Mean depth of trawling | 20 | 100 |
| 1999 | | | |
| 1 | 595м | - | 1,000 |
| 2 | 328м | - | 1,000 |
| 3 | 643м | 0,017 | 0,983 |
| 4 | 280м | - | 1,000 |
| 5 | 790м | 0,025 | 0,975 |
| 6 | 672м | - | 1,000 |
| 7 | 344м | - | 1,000 |
| 8 | 240м | - | 1,000 |
| 9 | 440м | - | 1,000 |
| 10 | 678м | 0,017 | 0,983 |
| 11 | 675м | - | 1,000 |
| 12 | 660м | - | 1,000 |
| 13 | 630м | - | 1,000 |
| 14 | 240м | - | 1,000 |
| 15 | 603м | 0,017 | 0,983 |
| 2000 | | | |
| 1 | 790м | - | 1,000 |
| 2 | 730м | 0,050 | 0,950 |
| 3 | 690м | - | 1,000 |
| 4 | 770м | - | 1,000 |
| 5 | 750 м | 0,050 | 0,950 |
| 6 | 765 м | - | 1,000 |
| 7 | 760м | 0,050 | 0,950 |
| 8 | 790м | - | 1,000 |
| 9 | 685м | 0,050 | 0,950 |
| 10 | 735м | 0,100 | 0,900 |
| 11 | 590м | - | 1,000 |
| 12 | 645м | - | 1,000 |
| 13 | 290м | - | 1,000 |
| 14 | 320м | - | 1,000 |
| 15 | 320м | - | 1,000 |
| 16 | 310м | - | 1,000 |
| 17 | 340м | - | 1,000 |
| 18 | 335м | - | 1,000 |
| 19 | 320м | - | 1,000 |
| 20 | 310м | - | 1,000 |

**TABLE 4. Allele frequencies of PGI locus in redfish samples**.

| No. | Samples Mean depth of trawling | Alleles of PGI locus 100 | 120 |
|-----|--------------------------------|------|------|
| | Samples | Alleles of PGI locus | |
| 1999 | | | |
| 1 | 595м | 1,000 | - |
| 2 | 328м | 1,000 | - |
| 3 | 643м | 1,000 | - |
| 4 | 280м | 1,000 | - |
| 5 | 790м | 1,000 | - |
| 6 | 672м | 1,000 | - |
| 7 | 344м | 1,000 | - |
| 8 | 240м | 1,000 | - |
| 9 | 440м | 1,000 | - |
| 10 | 678м | 1,000 | - |
| 11 | 675м | 0,983 | 0,017 |
| 12 | 660м | 1,000 | - |
| 13 | 630м | 1,000 | - |
| 14 | 240м | 1,000 | - |
| 15 | 603м | 1,000 | - |
| 2000 | | | |
| 1 | 790м | 1,000 | - |
| 2 | 730м | 1,000 | - |
| 3 | 690м | 1,000 | - |
| 4 | 770м | 1,000 | - |
| 5 | 750м | 1,000 | - |
| 6 | 765м | 1,000 | - |
| 7 | 760м | 1,000 | - |
| 8 | 790м | 0,950 | 0,050 |
| 9 | 685м | 1,000 | - |
| 10 | 735м | 1,000 | - |
| 11 | 590м | 1,000 | - |
| 12 | 645м | 1,000 | - |
| 13 | 290м | 1,000 | - |
| 14 | 320м | 1,000 | - |
| 15 | 320м | 1,000 | - |
| 16 | 310м | 1,000 | - |
| 17 | 340м | 1,000 | - |
| 18 | 335м | 1,000 | - |
| 19 | 320м | 1,000 | - |
| 20 | 310м | 1,000 | - |

**TABLE 5. Allele frequencies of IDH locus in redfish samples.**

| Samples | | Alleles of IDH locus | |
|---|---|---|---|
| No. | Mean depth of trawling | 100 | 120 |
| 1999 | | | |
| 1 | 595м | 1,000 | - |
| 2 | 328м | 1,000 | - |
| 3 | 643м | 1,000 | - |
| 4 | 280м | 1,000 | - |
| 5 | 790м | 1,000 | - |
| 6 | 672м | 1,000 | - |
| 7 | 344м | 0,950 | 0,050 |
| 8 | 240м | 1,000 | - |
| 9 | 440м | 1,000 | - |
| 10 | 678м | 1,000 | - |
| 11 | 675м | 1,000 | - |
| 12 | 660м | 1,000 | - |
| 13 | 630м | 1,000 | - |
| 14 | 240м | 1,000 | - |
| 15 | 603м | 1,000 | - |
| 2000 | | | |
| 1 | 790м | 1,000 | - |
| 2 | 730м | 1,000 | - |
| 3 | 690м | 1,000 | - |
| 4 | 770м | 1,000 | - |
| 5 | 750м | 1,000 | - |
| 6 | 765м | 1,000 | - |
| 7 | 760м | 1,000 | - |
| 8 | 790м | 1,000 | - |
| 9 | 685м | 1,000 | - |
| 10 | 735м | 1,000 | - |
| 11 | 590м | 1,000 | - |
| 12 | 645м | 1,000 | - |
| 13 | 290м | 1,000 | - |
| 14 | 320м | 1,000 | - |
| 15 | 320м | 1,000 | - |
| 16 | 310м | 1,000 | - |
| 17 | 340м | 1,000 | - |
| 18 | 335м | 1,000 | - |
| 19 | 320м | 1,000 | - |
| 20 | 310м | 1,000 | - |

**TABLE 6. Allele frequencies of PGM locus in redfish samples**.

| Samples | | Alleles of PGM locus | | |
|---|---|---|---|---|
| No. | Mean depth of trawling | 70 | 100 | 120 |
| 1999 | | | | |
| 1 | 595м | 0,400 | 0,600 | - |
| 2 | 328м | - | 1,000 | - |
| 3 | 643м | - | 1,000 | - |
| 4 | 280м | - | 1,000 | - |
| 5 | 790м | - | 1,000 | - |
| 6 | 672м | - | 1,000 | - |
| 7 | 344м | 0,050 | 0,950 | - |
| 8 | 240м | - | 1,000 | - |
| 9 | 440м | - | 1,000 | - |
| 10 | 678м | 0,017 | 0,983 | - |
| 11 | 675м | - | 1,000 | - |
| 12 | 660м | - | 1,000 | - |
| 13 | 630м | - | 1,000 | - |
| 14 | 240м | - | 1,000 | - |
| 15 | 603м | - | 0,983 | - |
| 2000 | | | | |
| 1 | 790м | - | 1,000 | - |
| 2 | 730м | - | 1,000 | - |
| 3 | 690м | - | 1,000 | - |
| 4 | 770м | - | 1,000 | - |
| 5 | 750м | - | 1,000 | - |

**TABLE 7. Allele frequencies of SOD, LDH, ESTD loci in redfish samples**.

| Samples | | SOD | LDH | ESTD |
|---|---|---|---|---|
| No. | Mean depth of trawling | 100 | 100 | 100 |
| 1999 | | | | |
| 1 | 595м | 1,000 | 1,000 | 1,000 |
| 2 | 328м | 1,000 | 1,000 | 1,000 |
| 3 | 643м | 1,000 | 1,000 | 1,000 |
| 4 | 280м | 1,000 | 1,000 | 1,000 |
| 5 | 790м | 1,000 | 1,000 | 1,000 |
| 6 | 672м | 1,000 | 1,000 | 1,000 |
| 7 | 344м | 1,000 | 1,000 | 1,000 |
| 8 | 240м | 1,000 | 1,000 | 1,000 |
| 9 | 440м | 1,000 | 1,000 | 1,000 |
| 10 | 678м | 1,000 | 1,000 | 1,000 |
| 11 | 675м | 1,000 | 1,000 | 1,000 |
| 12 | 660м | 1,000 | 1,000 | 1,000 |
| 13 | 630м | 1,000 | 1,000 | 1,000 |
| 14 | 240м | 1,000 | 1,000 | 1,000 |
| 15 | 603м | 1,000 | 1,000 | 1,000 |
| 2000 | | | | |
| 1 | 790м | - | 1,000 | - |
| 2 | 730м | - | 1,000 | - |
| 3 | 690м | - | 1,000 | - |
| 4 | 770м | - | 1,000 | - |
| 5 | 750м | - | 1,000 | - |

**TABLE 8. Allele frequences of MEP-2 locus in redfish samples.**

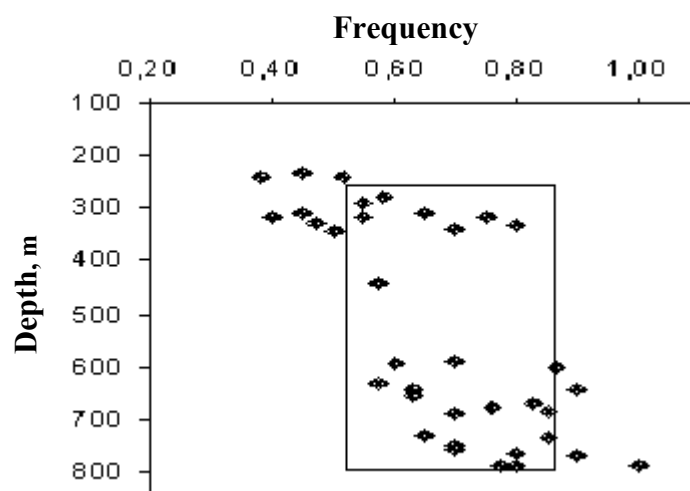| Samples | | Alleles of MEP-2 locus | |
|---|---|---|---|
| No. | Mean depth of trawling | 60 | 100 |
| 1999 | | | |
| 1 | 595м | 0,617 | 0,383 |
| 2 | 328м | 0,482 | 0,518 |
| 3 | 643м | 0,417 | 0,583 |
| 4 | 280м | 0,525 | 0,475 |
| 5 | 790м | 0,500 | 0,500 |
| 6 | 672м | 0,425 | 0,575 |
| 7 | 344м | 0,400 | 0,600 |
| 8 | 240м | 0,133 | 0,867 |
| 9 | 440м | 0,425 | 0,575 |
| 10 | 678м | 0,367 | 0,633 |
| 11 | 675м | 0,550 | 0,450 |
| 12 | 660м | 0,175 | 0,825 |
| 13 | 630м | 0,367 | 0,633 |
| 14 | 240м | 0,241 | 0,759 |
| 15 | 603м | 0,225 | 0,775 |
| 2000 | | | |
| 1 | 790м | 0,200 | 0,800 |
| 2 | 730м | 0,350 | 0,650 |
| 3 | 690м | 0,300 | 0,700 |
| 4 | 770м | 0,100 | 0,900 |
| 5 | 750м | 0,300 | 0,700 |
| 6 | 765м | 0,200 | 0,800 |
| 7 | 760м | 0,300 | 0,700 |
| 8 | 790м | - | 1,000 |
| 9 | 685м | 0,150 | 0,850 |
| 10 | 735м | 0,150 | 0,850 |
| 11 | 590м | 0,300 | 0,700 |
| 12 | 645м | 0,100 | 0,900 |
| 13 | 290м | 0,450 | 0,550 |
| 14 | 320м | 0,600 | 0,400 |
| 15 | 320м | 0,250 | 0,750 |
| 16 | 310м | 0,350 | 0,650 |
| 17 | 340м | 0,300 | 0,700 |
| 18 | 335м | 0,200 | 0,800 |
| 19 | 320м | 0,450 | 0,550 |
| 20 | 310м | 0,550 | 0,450 |

Fig.1. Allele frequencies of MEP-2*100 in redfish samples from different depths (1999, 2000).
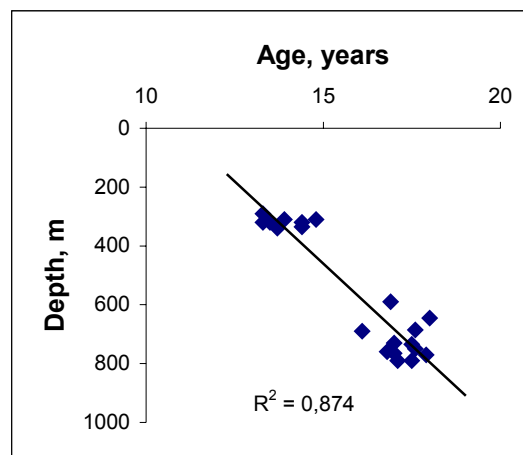


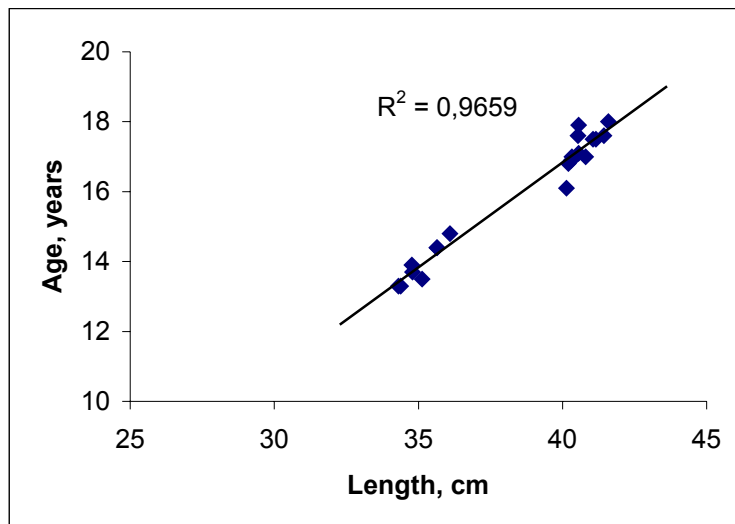Fig.2. Distribution of different-age-samples taken in different depth in the Irminger Sea pelagial, 2000.

Fig.3. Length-age characteristic of redfish, 2000.