Report of the Workshop on Redfish Stock Structure (WKREDS)

22–23 January 2009

ICES Headquarters, Copenhagen

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Executive Summary

Stock structure of *Sebastes mentella* in the Irminger Sea and adjacent areas was reviewed and synthesized to determine the most parsimonious view of stock structure that is consistent with all information available. ICES currently provides advice for *S. mentella* fisheries as two distinct management units: 1) a demersal unit on the continental shelf and 2) a pelagic unit in the Irminger Sea and adjacent areas. However, the current advisory units are an interim procedure until a comprehensive review of stock identification information could be provided.

The workshop began by defining all *a priori* hypotheses, then reviewing case studies related to population structure in the context of those hypotheses. Case studies were reviewed within the scientific disciplines of geographic distribution (e.g., fishing grounds, survey data of early life stage, juveniles and adults), genetic variation (e.g., allozymes, mitochondrial DNA, nuclear DNA), phenotypic variation (e.g., life history traits, morphology, fatty acid composition) and connectivity (e.g., larval dispersal, natural tags and artificial tags) to form a general conclusion about stock structure from the perspective of that discipline. An interdisciplinary evaluation was formed by synthesizing information from each discipline to develop a holistic perspective on biological stocks. Each of the *a priori* hypotheses was tested using the most objective information available. Recommendations for practical management units considered geographic delineations that most accurately reflect the consensus on biological stock structure.

Based primarily on genetic information (i.e., microsatellites), and supported by other information on stock structure, WKREDS concludes that there are three biological stocks of *S. mentella* in the Irminger Sea and adjacent waters:

1) a 'Deep Pelagic' stock (NAFO 1-2, ICES Vb XII XIV >500m),
2) a 'Shallow Pelagic' stock (NAFO 1-2, ICES Vb XII XIV <500m), and
3) an 'Icelandic Slope' stock (ICES Va XIV).

Although biological stocks of *S. mentella* are partially defined by depth, WKREDS recognizes that definition of management units by depth and the associated fishery monitoring by depth would be impractical. Therefore, three management units are recommended that are based on geographic proxies for biological stocks that minimize mixed-stock catches:

1) a 'Deep Pelagic' management unit in the northeast Irminger Sea (defined by the spatial distribution of the deep, pelagic fishery (see section 6),
2) a 'Shallow Pelagic' management unit in NAFO areas 1 and 2, ICES areas Vb, XII, XIV (outside of the deep,pelagic area), and
3) an 'Icelandic Slope' management unit that is north and east of the existing 'redfish line.'

1　Opening of the meeting

The Study Group on Redfish Stock Structure (WKREDS) met at ICES Headquarters 22–23 January 2009 to review all reported material on the stock identity of the various redfish units (*Sebastes mentella*) in the Irminger Sea and adjacent waters and identify the most likely definition of biological stocks of *S. mentella* and suggest practical management units. WKREDS was also asked to respond to a request by NEAFC. *"NEAFC requests ICES to provide information concerning the timing and areas of larval extrusion of Sebastes mentella in the Irminger Sea in the light of the need to ensure recovery of this stock in ICES Sub-areas V,XII, XIV and NAFO Divisions 1F and 2 GHJ."* Information on timing and areas of larval extrusion are provided in section 4.1 (geographic distribution).

Given that WKREDS met for only two days, much of the work was completed by correspondence. The agenda and methodological approach were developed before the meeting, and many workshop members contributed case study reviews by correspondence prior to the meeting. During the meeting, case study reviews were discussed, and a workshop consensus was developed on each agenda item. After the meeting, workshop members continued to work by correspondence to draft the report.

Thirteen participants attended the workshop:

Steve Cadrin, chair	USA
Yuri Bakay	Russia
Matthias Bernreuther	Germany
Konstantin Drevetnyak	Russia
Einar Hjorleifsson	Iceland
Torild Johansen	Norway
Kristjan Kristinsson	Iceland
Stefano Mariani	Ireland
Sergey Melnikov	Russia
Cristophe Pampoulie	Iceland
Jakúp Reinert	Faroe Islands
Thorsteinn Sigurdsson	Iceland
Christoph Stransky	Germany

Five other participants made substantial contributions by correspondence:

Lisa Kerr	USA
Kjell Nedreaas	Norway
Fran Saborido-Rey	Spain
David Secor	USA
Christopher Zimmermann	Germany

WKREDS acknowledges the substantial scientific progress made by previous initiatives to address the issue of stock structure of redfish in the Irminger Sea and adjacent areas, including the Study Group on Redfish Stocks, the EU Redfish Project, the Faroese Redfish Project, and the Study Group on Stock Identity and Management Units of Redfish. Much of the information reviewed here was produced by those efforts.

2   Introduction

Introduction

Resource assessment and fishery management require precise definition of the 'stock' being harvested, monitored and managed. Many populations are spatially structured, with discrete subpopulations that are self-sustaining, that is they are somewhat isolated from other subpopulations of the species, and their population dynamics are determined more from within the subpopulation than from mixing with other subpopulations. Accordingly, stock identification involves a comprehensive evaluation of geographic variation and connectivity among putative stocks.

Geographically isolated stocks often exhibit measurable differences from other stocks. Subpopulations that have been reproductively isolated from other stocks develop significantly different genetic compositions over time. Genetic differences can also be expressed through phenotypic traits (i.e., characteristics that are influenced by both genetics and the environment). Therefore, even partially isolated populations can have significantly different phenotypic characters, some of which determine a stock's productivity (e.g., reproductive dynamics, growth, and mortality).

Connectivity can be evaluated using natural and artificial tags. Individuals inhabiting different environments will incorporate natural tags, such as parasites that may be unique to the area or chemical compositions that reflect chemistry of their surroundings. Conventional and electronic tagging is also valuable for documenting movements, connectivity and habitats.

The Study Group on Redfish Stock Structure (WKREDS) was formed to review all reported material on the stock identity of the various redfish units (*Sebastes mentella*) in the Irminger Sea and adjacent waters, identify the most likely definition of biological stocks of *S. mentella*, and suggest practical management units. This report describes the Workshop's review of the documented stock identity studies, interdisciplinary synthesis on the most likely stock structure of *S. mentella* that conforms to all available information and recommendations for the most appropriate management units.

General Biology

Several aspects the life history of *S. mentella* and general characteristics of the genus *Sebastes* influence population structure and should be considered in the determination of biological stocks. *Sebastes* species are widely distributed in the North Pacific, North Atlantic and southern hemisphere. Throughout their range, *Sebastes* species are adapted to a diversity of ecological niches, with overlapping spatial distributions of different species that have little or no morphological differences (Johns and Avise 1998, Alesandrini and Bernardi 1999). For some species of *Sebastes*, divergence of behavioral groups into depth-defined habitats has led to reproductive isolation (e.g., Hyde et al. 2008). Sympatric diversity of the genus *Sebastes* is a commonly used example of adaptive radiation, a rapid evolutionary radiation characterized by an increase in the morphological and ecological diversity of a single, rapidly diversifying lineage (Schluter 2000).

Unlike most finfishes, *Sebastes* species reproduce by vivipary, in which the eggs are fertilized, develop and hatch internally. In addition to spatial and temporal isolating mechanisms involved in formation of discrete subpopulations, mate recognition, courtship behavior and mate choice are additional mechanisms of reproductive isolation that facilitate relatively rapid divergence (Johns and Avise 1998). However, unlike most live-bearers, species of *Sebastes* produce many, small larvae that are extruded soon after they hatch from eggs and disperse widely as zooplankton. Relatively strict reproductive constraints and extensive larval dispersal allow adaptive radiation into a diversity of ecological niches (Rocha-Olivares 2004). The typical long life span of *Sebastes* species also tends to promote adaptation to diverse habitats (Mangel et al. 2007). *S. mentella* exhibits all of these traits that tend to facilitate divergence within populations.

History of research on *Sebastes mentella* stock structure

The chronological advancement of research on *S. mentella* is parallel with fishery development. The fishery traditionally targeted mixed redfish species on the continental slopes of Iceland, Greenland, and the Faroe Islands, and a pelagic fishery developed in the Irminger Sea in the early 1980s (Sigurdsson, et al. 2006). Icelandic researchers considered that the pelagic fishery targeted a separate stock than the traditional demersal fisheries, and the pelagic stock (referred to as 'oceanic' redfish) can be discriminated from the 'deep-sea' stock on the basis of darker, patchy skin color, heavy parasite infestations and associated muscle spots, as well as smaller size at maturity (Magnússon and Magnússon 1995). In the mid-1990s, the fishery expanded geographically and vertically to depths greater than 500m (Sigurdsson, et al. 2006) and the relationships between the traditional demersal resource, the shallow pelagic resource and the newly developed pelagic, deep-sea fishery were unknown.

In 1998, the ICES Study Group on Redfish Stocks met to coordinate future research on redfish stocks, including the acoustic survey in the Irminger Sea and adjacent areas, but recognized that stock identification was a critical issue for surveying *S. mentella* resources and managing the redfish fisheries (SGRS 1998). Information on morphology, parasites and early genetic analyses were reviewed, but the Study Group concluded that the evidence for one or two pelagic stocks was not conclusive. The workshop provided recommendations for research on stock identification, including further work on genetics, morphometrics, and parasitology as well as a manual for phenotyping.

Beginning in 2000, a four-year research project was funded within the European Commission's Fifth Framework Programme to study population structure, reproductive strategies and demography of redfish in the Irminger Sea and adjacent waters (ICES V, XII and XIV; NAFO 1), hereafter referred to as the 'EU Redfish Project' (Anon. 2004; www.redfish.de). The main workpackage of the project was stock identification. The project involved collaborative sampling efforts, and the report compiled studies on genetics, morphometrics, reproduction and maturation, otolith shape, otolith chemistry and growth. A related initiative was funded by the Faroe Islands, which included analysis of genetics, morphometrics, otolith chemistry, and fatty acids (Joensen 2002). The consensus summary statements from all partners was that morphometric and otolith analyses did not indicate stock structure in the Irminger Sea and adjacent areas, but genetics revealed weak, significant differences between demersal, 'oceanic' (<500m) and 'deep-sea pelagic' components (Anon. 2004). However, the research partners disagreed on the cause of genetic differences. Some partners interpreted genetic differences as an indication of reproductive isolation among three distinct subpopulations of *S. mentella* in the Irminger Sea and adjacent areas. Other partners maintained a one-stock hypothesis, and interpreted genetic results as an artifact of age-related effects, misrepresentative sampling, or selection, because the genetic differences appeared to contradict other life history patterns.

The one-stock hypothesis is elaborated by Saborido-Rey et al. (2004), who reviewed the existing knowledge on ecology of *S. mentella* in the Irminger Sea and adjacent waters to determine population structure. Their conclusion was based on deductive inference of a continuous distribution of larvae in the Irminger Sea, a common nursery area on the Greenland Shelf, and a succession of ontogenetic stages that suggest movement from nursery areas, to shallow areas, then to deep pelagic habitats. The authors refute genetic differences among groups, because they may result from genetic drift, selection or temporal variation (i.e., age dependency).

As the EU Redfish Project was in the final stages of documenting final results, the ICES Study Group on Stock Identity and Management Units of Redfishes met to review all stock identification material, identify most likely biological stocks and suggest practical management units (SGSIMUR 2005). Information from the EU and Faroese Redfish projects as well as spatial analyses of fishery and survey data were reviewed. The Study Group concluded that there is population structure of *S. mentella*, but the nature of the structure (i.e., reproductively isolated groups or demographic groups) is not clear. Research recommendations were that microsatellite analyses were the most reliable approach to stock identification, sampling should be based on locations rather than 'phenotypes,' and temporal stability of all geographic differences should be evaluated (SGSIMUR 2005).

In 2007, the ICES Stock Identification Methods Working Group (SIMWG) was asked to liaise with the North-Western Working Group on the stock identification issues related to redfish. SIMWG reviewed a document on "Population structure of *S. mentella* in the North Atlantic with regard to international Norwegian waters in the Norwegian Sea: Spatial and temporal dimensions" and requested further details on how microsatellites were analyzed, the source of DNA for archived samples, and a table with pair-wise comparisons among collections (SIMWG 2007). The requested analyses were subsequently provided to SIMWG, and in 2008, SIMWG concluded that there are at least three different stocks of *Sebastes mentella*: 1) Western Icelandic shelf, 2) Deep Irminger Sea and Western Faroe, 3) all other localities between the shallow Irminger Sea off Newfoundland to Norwegian waters (SIMWG 2008). SIMWG sug-

gested that a workshop should be held, involving all redfish experts and stock identification experts to consider all evidence for stock structure of *S. mentella* in the Irminger Sea and vicinity.

ICES currently defines advisory units for *S. mentella* as an interim procedure until a comprehensive review of stock identification information is available (Figures 2.1 and 2.2):

- A demersal unit on the continental shelf in ICES Divisions Va, Vb, and XIV. In 2008, ICES concluded that the status of this stock is uncertain and advised "that a management plan be developed and implemented which takes into account the uncertainties in science and the properties of the fisheries. ICES suggests that catches of *S. mentella* are set no higher than 10 000 t as a starting point for the adaptive part of the management plan." Total catch in 2007 was 17 600t (ICES 2008)

- A pelagic unit in the Irminger Sea and adjacent areas (V, XII, and XIV), including pelagic redfish in the NAFO Convention Area. The management advice in 2008 for this stock was "ICES advises that a management plan be developed and implemented which takes into account the uncertainties in science and the properties of the fisheries. ICES suggests that catches of *S. mentella* are set at 20 000 t as a starting point for the adaptive part of the management plan" (ICES 2008). Annual catches have been greater than 60 000 t since 1992.

A group of experts on redfish biology and stock identification methods were invited to the Workshop on Redfish Stock Structure to consider new information on genetic stock structure in the context of existing information on population structure.
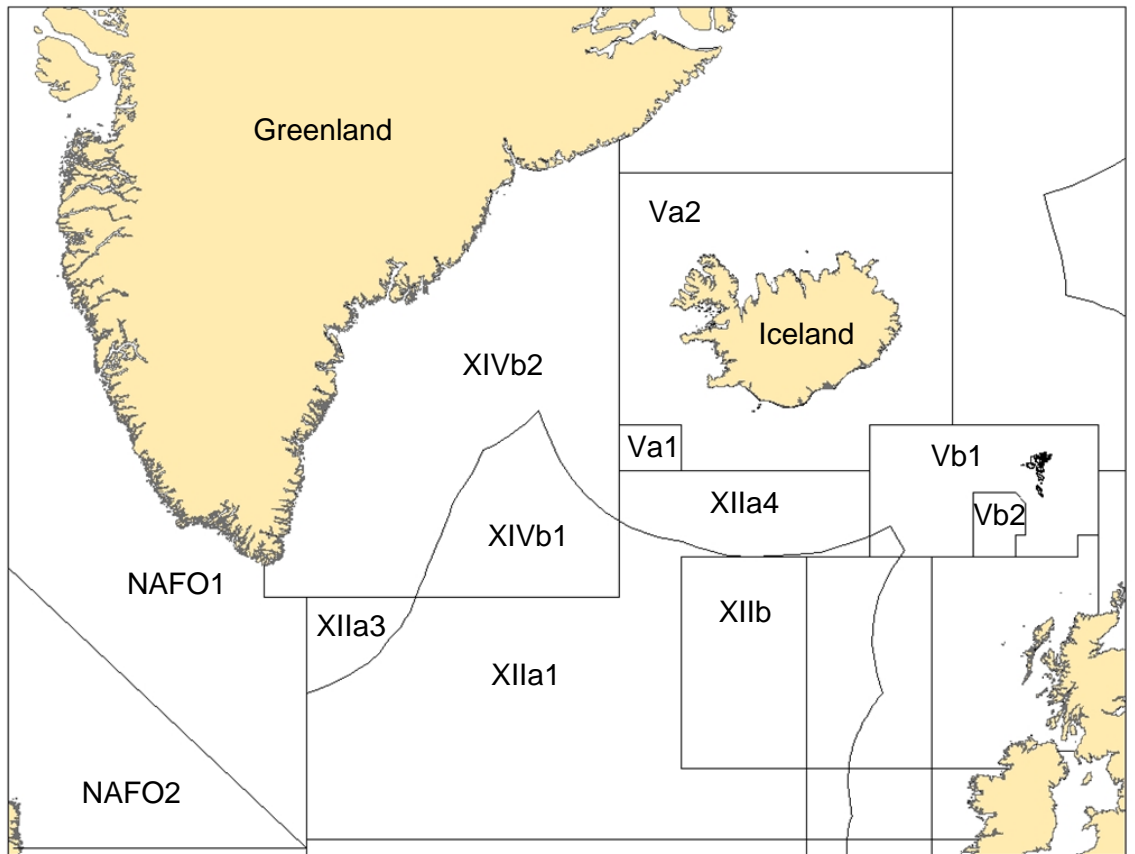
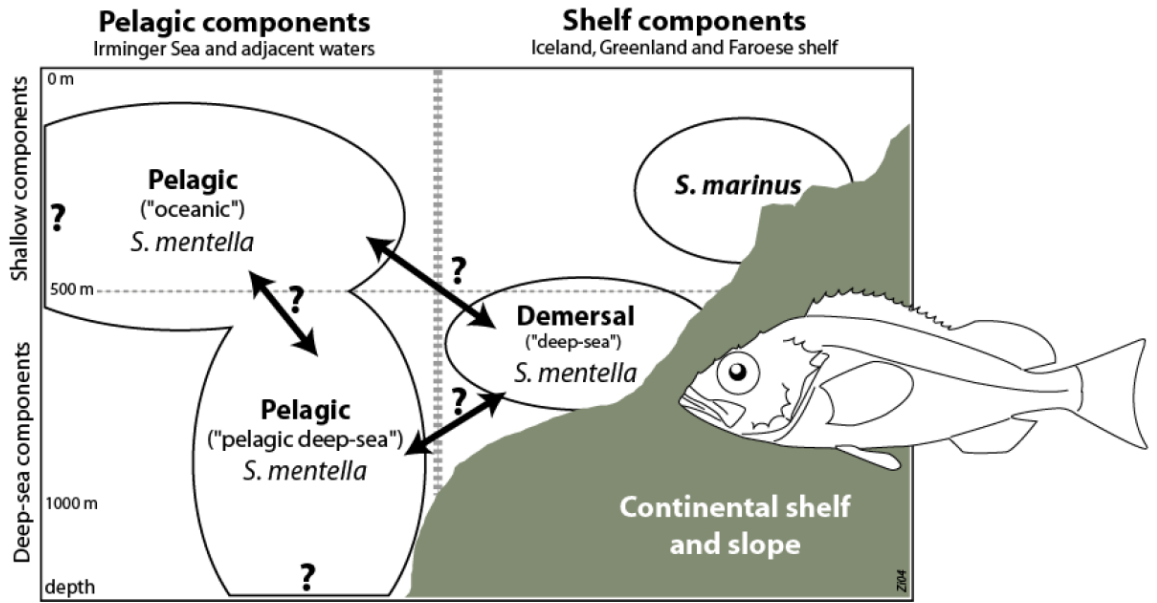**Figure 2.1. ICES and NAFO areas comprising *S. mentella* resources being considered as ICES advisory units.**

Figure 2.2. Possible relationship between redfish occurrences in the Irminger Sea and adjacent waters (from ICES 2008).

3   Methodological Approach

The workshop conducted its review of all information available on the stock structure of *S. mentella* in stages. At each stage, the workshop developed a consensus summary statement. All information available on each topic was reviewed and all perspectives were considered. Some sources of information could be validly interpreted in different ways. Therefore, the consensus statement on some issues was simply that there was no single valid interpretation. Final conclusions and recommendations were based on information that was not equivocal, and are robust to subjective interpretations of some information.

The procedural first step was to define all *a priori* hypotheses. Hypotheses were formed according to previous reviews and advisory decisions. Hypotheses were posed as one, two and three stock scenarios, with some variations within each scenario:

- Single-Population Hypothesis
  - o all *S. mentella* resources in ICES Divisions V, VI, XII, XIV and NAFO subareas 1-2 comprise a single, self-sustaining population.
- Two-Stock Hypotheses
  - o Current ICES advisory units
    - ▪ 'Demersal' unit on the continental shelf in ICES Divisions Va, Vb, and XIV
    - ▪ 'Pelagic' unit in the Irminger Sea and adjacent areas (V, VI, XII, and XIV and NAFO subareas 1-2)
  - o Depth-defined stocks
    - ▪ 'Shallow:' Irminger Sea and adjacent waters, <500m, southwest of the 'redfish line'
    - ▪ 'Deep:' Irminger Sea and adjacent waters, including pelagic >500m and demersal groups.
  - o 'Phenotypes' (as defined by Magnússon and Magnússon 1995, SGRS 1998 and SGSIMUR 2005)
    - ▪ 'Oceanic'
    - ▪ 'Deep-Sea'
- Three-Stock Hypothesis
  - o 'Slope' (possibly including separate demersal components):
    - ▪ Icelandic shelf, northeast of the 'redfish line'
    - ▪ Greenlandic shelf
    - ▪ Faroese shelf
  - o 'Shallow Pelagic:' Irminger Sea and adjacent waters, <500m, southwest of the 'redfish line'
  - o 'Deep Pelagic:' Irminger Sea and adjacent waters, >500m, southwest of 'redfish line'

Once *a priori* stock structure hypotheses were defined, case studies related to population structure of *S. mentella* in the Irminger Sea and adjacent areas were reviewed individually. Case studies published in the primary literature since 1995 (when the deep-sea resource was discovered) were prioritized. Five criteria were used to form a consensus interpretation of the results from each case study:

- Was stock identification an explicit objective of the study?
- Did the samples accurately represent the hypothetical stocks?

- Was sample size adequate to detect a meaningful difference between groups (or to generalize movements among groups)?
- Were differences between hypothetical stocks statistically tested (or were movements among groups quantified)?
- Was the analytical methodology sound (i.e., adequate to produce reliable results)? The critiques and protocols described in the SIMWG publication (Cadrin et al. 2005) served as a guide.

Workshop participants reviewed case studies using these criteria before the workshop, and presented their reviews at the workshop for discussion and a consensus review. All case studies in a discipline were considered to develop a summary of all available information within each discipline and a general conclusion about stock structure from the perspective of that discipline.

After the multidisciplinary review was complete, each perception of stock structure was considered for an interdisciplinary evaluation. Conclusions on geographic distribution, geographic variation, and connectivity were integrated for a holistic perspective on biological stocks. The final stage of evaluating biological stock structure involved consideration of each of the *a priori* hypotheses, identification of information that rigorously tested the hypotheses, and evaluation of whether the information could be used to reject hypotheses. The testing of hypotheses was based on the most objective information available (i.e., information that was not subject to equivocal interpretations and multiple scientific opinions). Conclusions about biological stocks were based on the the most robust and parsimonious view of stock structure that was consistent with the best scientific information available.

Recommendations for practical management units considered geographic delineations that most accurately reflect the consensus on biological stock structure. Definition of recommended management units accounted for the practical aspects and limitations of monitoring fisheries and the resource. Therefore, recommended management units were geographic proxies for biological stocks that were partly defined by depth.

4 Information on stock identity of *Sebastes mentella* in the Irminger Sea area

4.1 Geographic Distribution

Spatial patterns of abundance offer a basic indication of stock structure, contribute to our understanding of isolating mechanisms or connectivity in a population, and should be the first point of reference for identifying stock structure (Begg 2005). The geographic range of *S. mentella* extends across the North Atlantic, from the Grand Bank to the Barents Sea (Figure 4.1.1). The species' distribution is essentially continuous throughout its range on continental shelves or in pelagic waters near continental shelves to 1000m deep (Garabana Barro 2005, Bakay and Melnikov 2008).

The EU Redfish Project included a workpackage to investigate reproductive cycles of *S. mentella* through histological analysis of fishery samples (Anon. 2004). Spatial analysis of spawning fish (i.e., with developing gonads) in fishery catches suggests three different, but overlapping distributions of spawning fish: 1) on the Icelandic Slope, 2) in the deep, northeast Irminger Sea and 3) the shallow, southwest Irminger Sea (Figure 4.1.2). Although spawning areas can indicate separate or continuous spawning groups, the viviparous reproductive strategy of *S. mentella* complicates any inference of reproductive mixing. Spawning areas are where larvae are extruded, but the seasonality of gonad development indicates that copulation occurs approximately six months earlier (Anon. 2004), and males and females have different distributions during larval extrusion (Magnússon and Magnússon 1995) , suggesting that the copulation takes place in a different area than extrusion.

Distribution of early life history stages can reflect separate spawning groups, larval dispersal and connectivity among spawning groups (Hare 2005). *S. mentella* release their larvae from April to May (Saborido-Rey et al. 2004, Anon. 2004). Distribution of *S. mentella* larvae in the Irminger Sea varies among years, with a relatively continuous distribution in some years, and discontinuous northeast, southwest concentrations in other years (Figure 4.1.3).

Fishing patterns reflect geographic and depth distribution of the resource. Sigurðusson et al. (2006) provide an overview of the development of the pelagic *S. mentella* fishery, including locations, depth, season and size composition of catches. The review is based on fishery samples from national reports for fleets fishing in ICES areas Va, XII, XIV, NAFO1F, NAFO 2JH. In 1981, after exploratory surveys, a commercial fishery began on pre-spawning and spawning schools west of the Reykjanes Ridge (Figure 4.1.4a) from early April to mid-May at depths of 80-150m at night and 150-250m during day. In 1994, the fishery expanded to the southwest in the NEAFC area (Figure 4.1.4b), to depths of 600m and a longer fishing season (March to December). Since 1996, the fishery extended even further southwest in relatively shallow water (150-350m), eventually expanding into the NAFO area (Figure 4.1.4c). NWWG routinely updates spatial analyses of fishing effort by location (Figure 4.1.5), depth (Figure 4.1.6) and season (Figure 4.1.7).

Spatial analysis of survey data show that the shift in the fishery to the southwest since 1996 (Sigurðusson et al. 2006) reflects a similar change in the distribution of the resource and is coincident with environmental changes (SGSIMUR 2005). Subsequent to SGSIMUR, spatial distributions of *S. mentella* in the Irminger Sea were routinely updated by the SGRS (Figure 4.1.8).

A synthesis of geographic distributions of *S. mentella* in the Irminger Sea and adjacent waters for successive ontogenetic stages is provided by Saborido-Rey et al. (2004) and Melnikov (2007). Shelf, deep-sea and shallow pelagic fisheries catch *S. mentella* with developing gonads in separate, but overlapping areas of the Icelandic Shelf and Irminger Sea (Figure 4.1.2). Larvae are distributed in the Irminger Sea, in more or less continuous concentrations (Figure 4.1.3). Juveniles and adults are caught on the Greenlandic Shelf (Figure 4.1.9). Adults are distributed across continental shelves and in the Irminger Sea, where size distributions are larger in deep habitats (>500m) than in shallow habitats. When the fishery expanded to deep waters of the Irminger Sea (i.e., >500m), the average size of fish in deep water was 7cm larger (Sigurðusson et al. 2006). Size distributions of fish caught in the deep, northeast fishery are still generally larger than those in the shallow, southwest fishery (as indicated by fishery samples, Figure 4.1.10, and survey samples, Figure 4.1.11). Size distributions in the deep Irminger Sea are also bimodal is some years, suggesting recruitment from other areas. There are no reliable age data for *S. mentella* to track yearclasses from nursery grounds to adult habitats.

Reviews by Saborido-Rey et al. (2004) and Melnikov (2007) concluded that there is one stock of *S. mentella* in the Irminger Sea and adjacent areas based on spatial distribution of larvae, juveniles, and adults. However, several alternative inferences of movement and connectivity between ontogenetic stages can be deduced from spatial distributions. For example, Rikhter (1996) examined the same distributional data of larvae, juveniles and adults to conclude that there is strong evidence of two *S. mentella* populations in the Irminger Sea. Although, distributional data offers valuable exploratory information for developing stock structure hypotheses, it cannot be used to rigorously test alternative hypotheses.
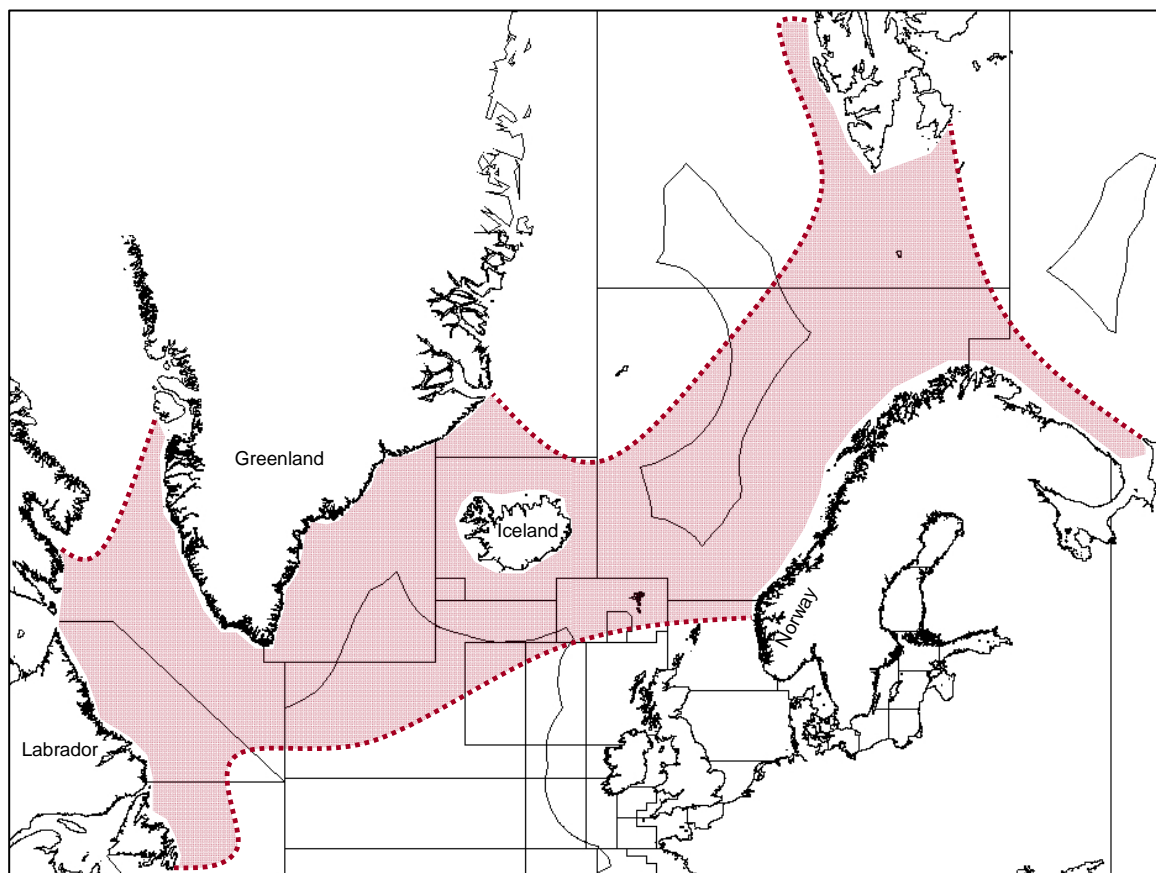
Figure 4.1.1. Geographic range of *Sebastes mentella*.

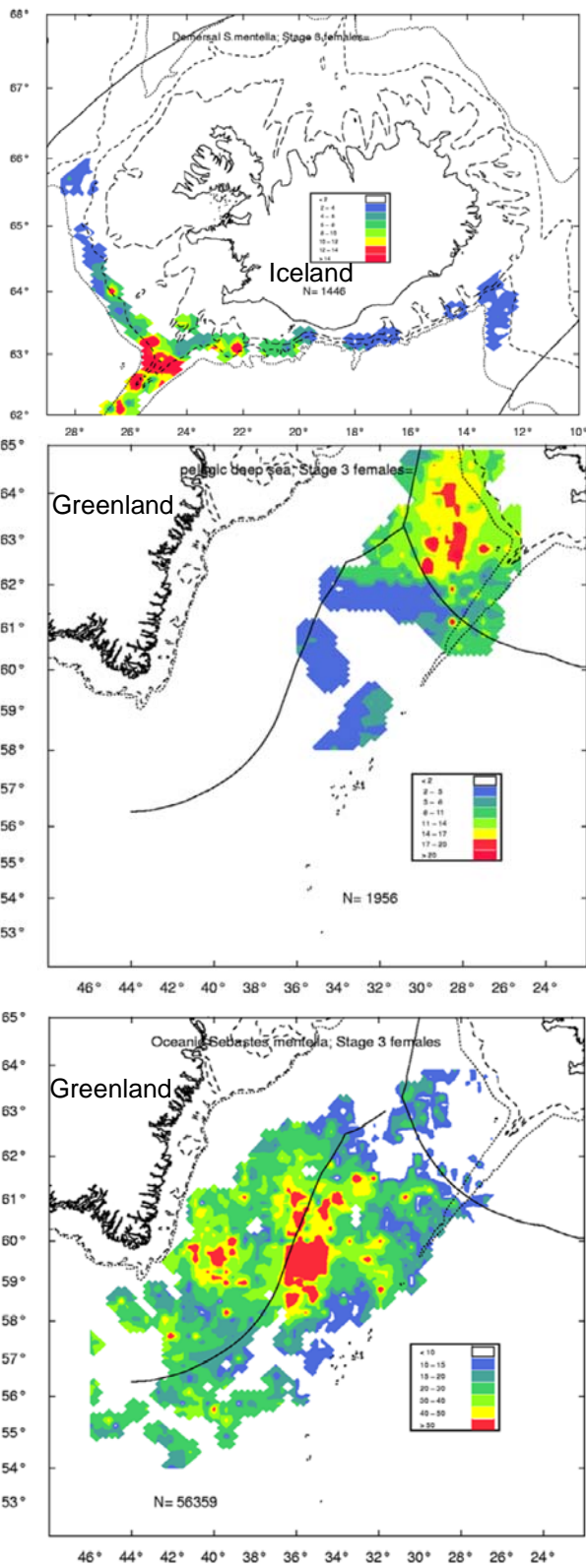**Figure 4.1.2.** Distribution of spawning female *S. mentella* (maturity stages 3a-c) in Icelandic waters (upper panel), pelagic, deep sea (middle panel) and oceanic (lower panel; from Anon. 2004).
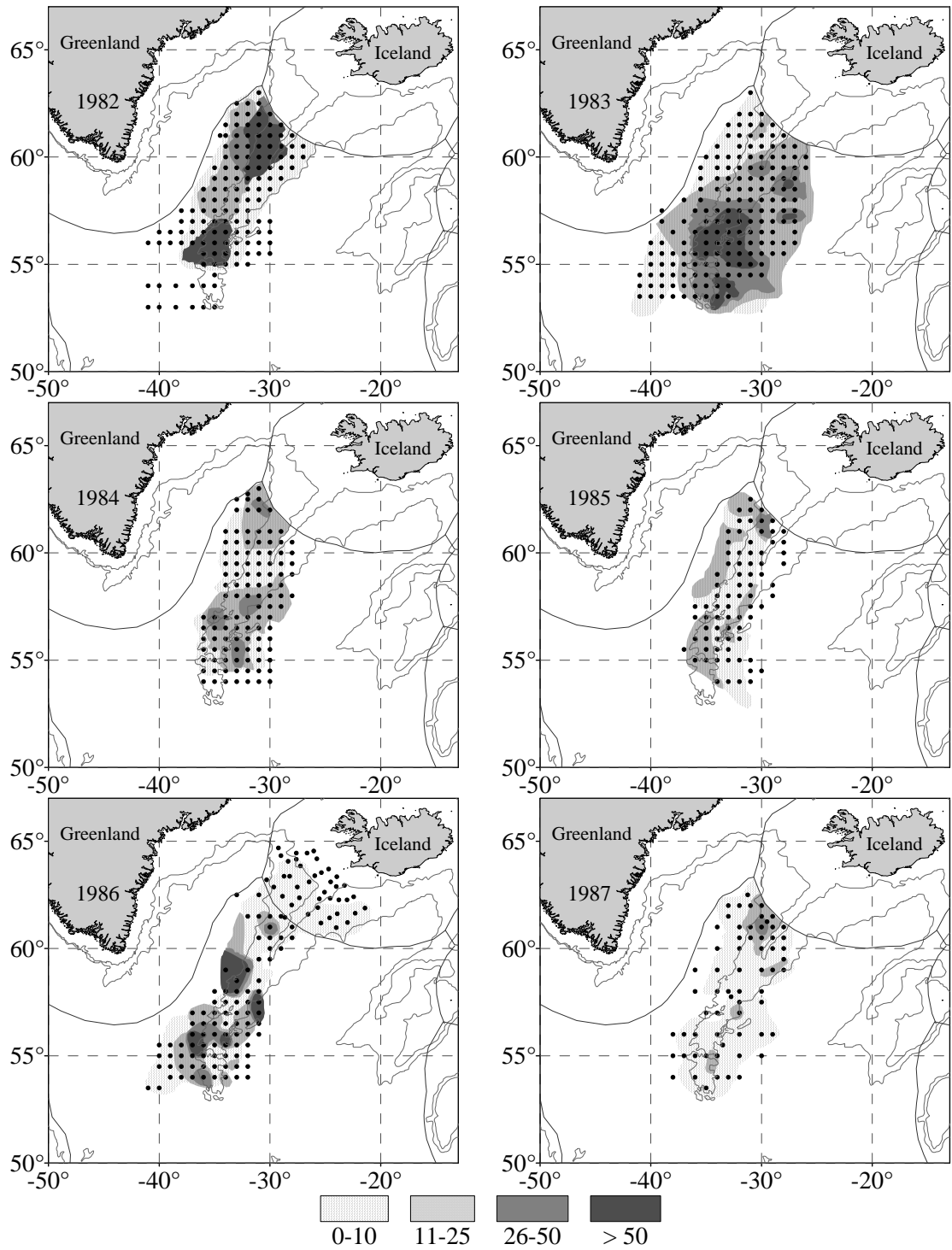
Figure 4.1.3a. Distribution of *S. mentella* larvae from Russian ichthyoplankton surveys 1982-1987 (n/m²)
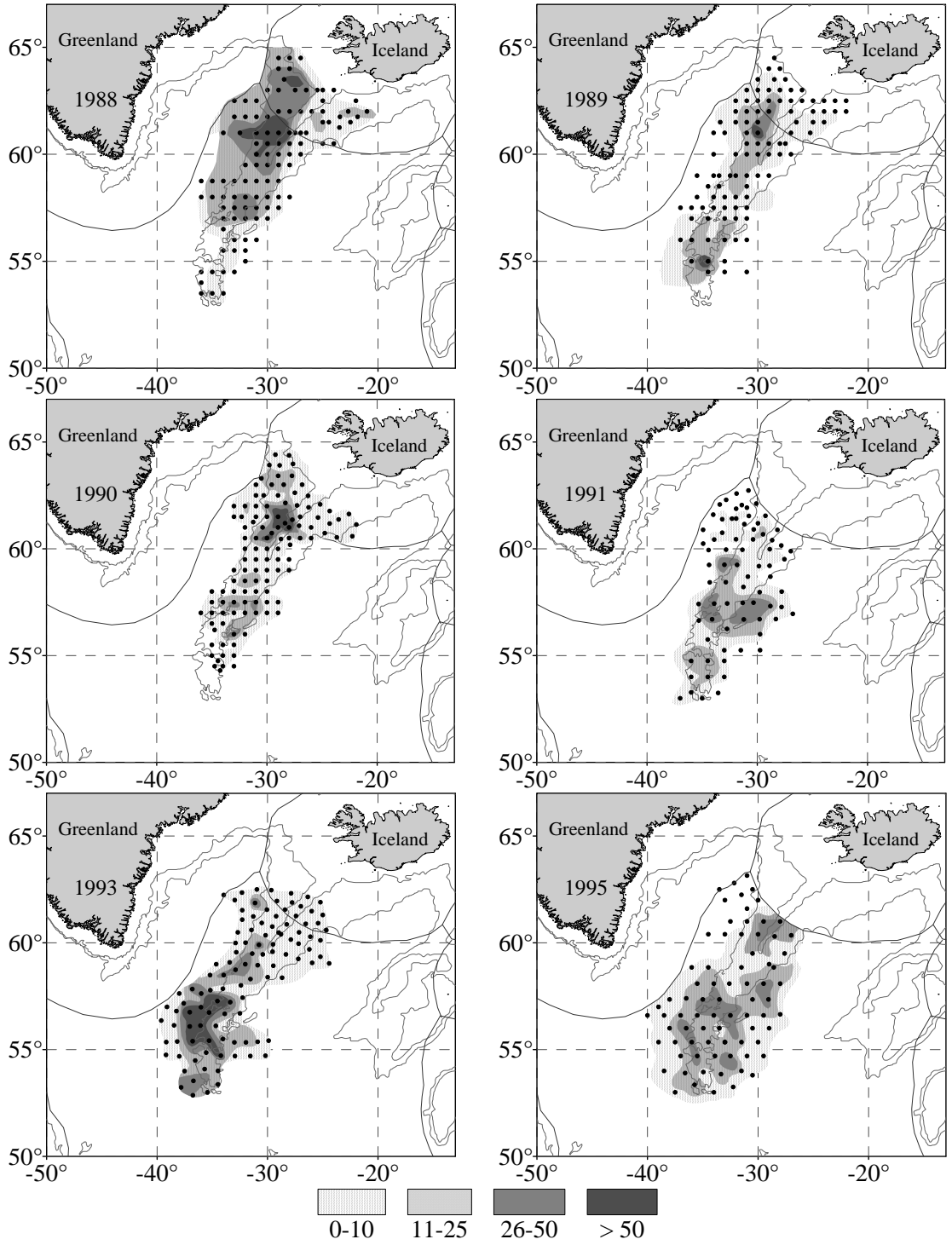
Figure 4.1.3b. Distribution of *S. mentella* larvae from Russian ichthyoplankton surveys 1988-1995 (n/m²).
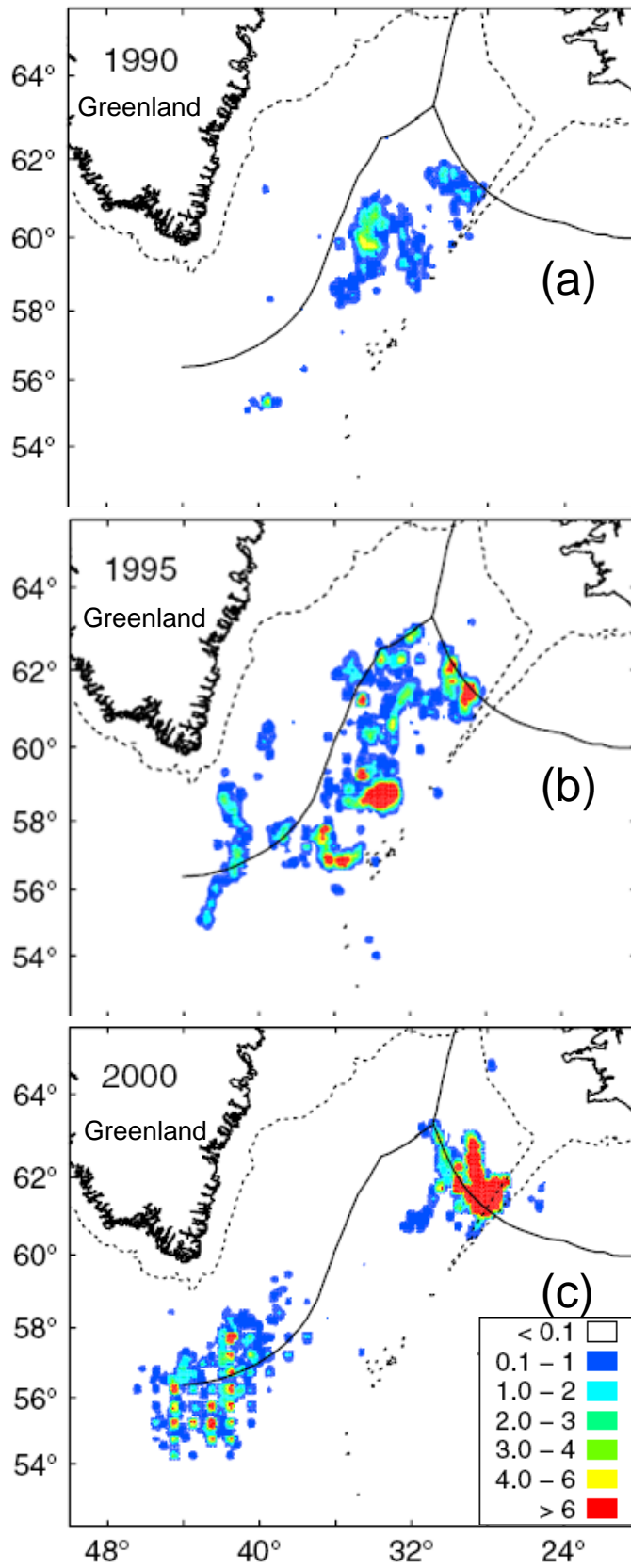
Figure 4.1.4. Fishing areas and total catch of pelagic redfish (*S. mentella*) in the Irminger Sea and adjacent waters, in 1990 (a), 1995 (b), and 2000 (c). Data are from Germany (1995), Norway (1990, 1995), the Faroe Islands (1995), and Iceland (1990, 1995). The scale given is tonnes per square nautical mile. Modified from Sigurðusson et al. (2006).
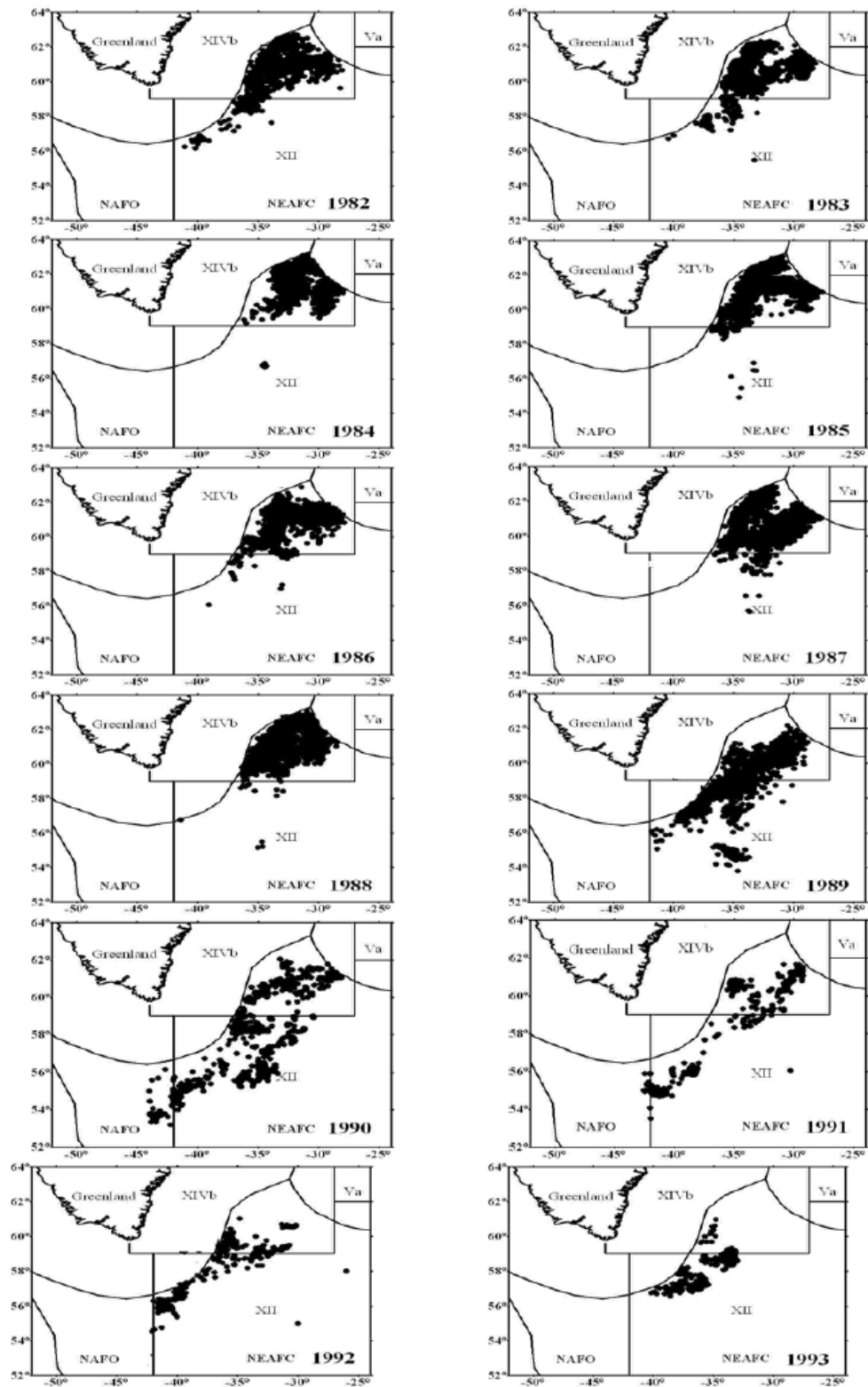
Figure 4.1.5a. Location of the Russian fleet during fishery for S. mentella in the Irminger Sea in 1982-1993 (from NWWG 2008).
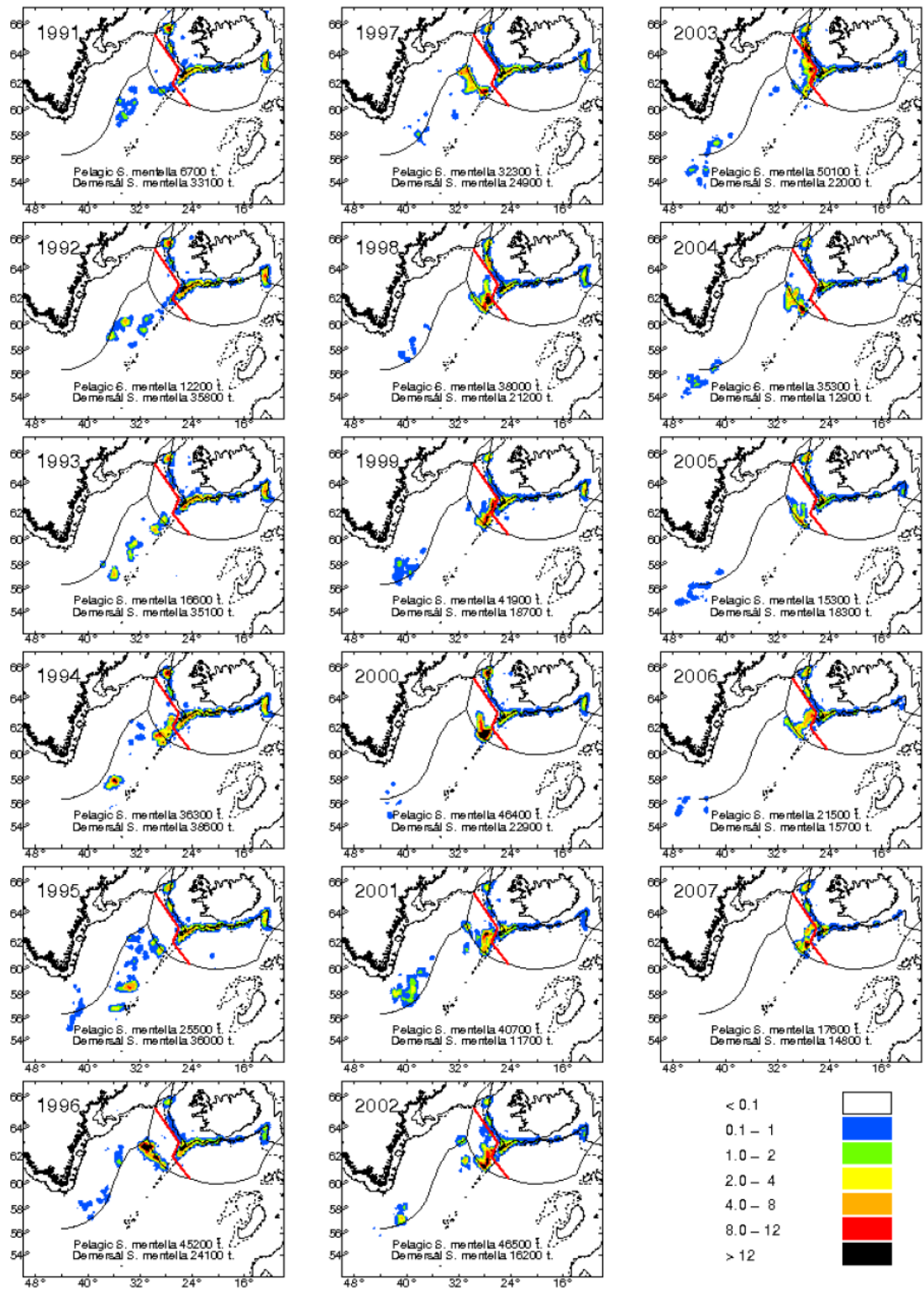
Figure 4.1.5b. Geographical distribution of the Icelandic catches of *S. mentella*. The colour scale indicates catches (tonnes per square nautical mile; from NWWG 2008).
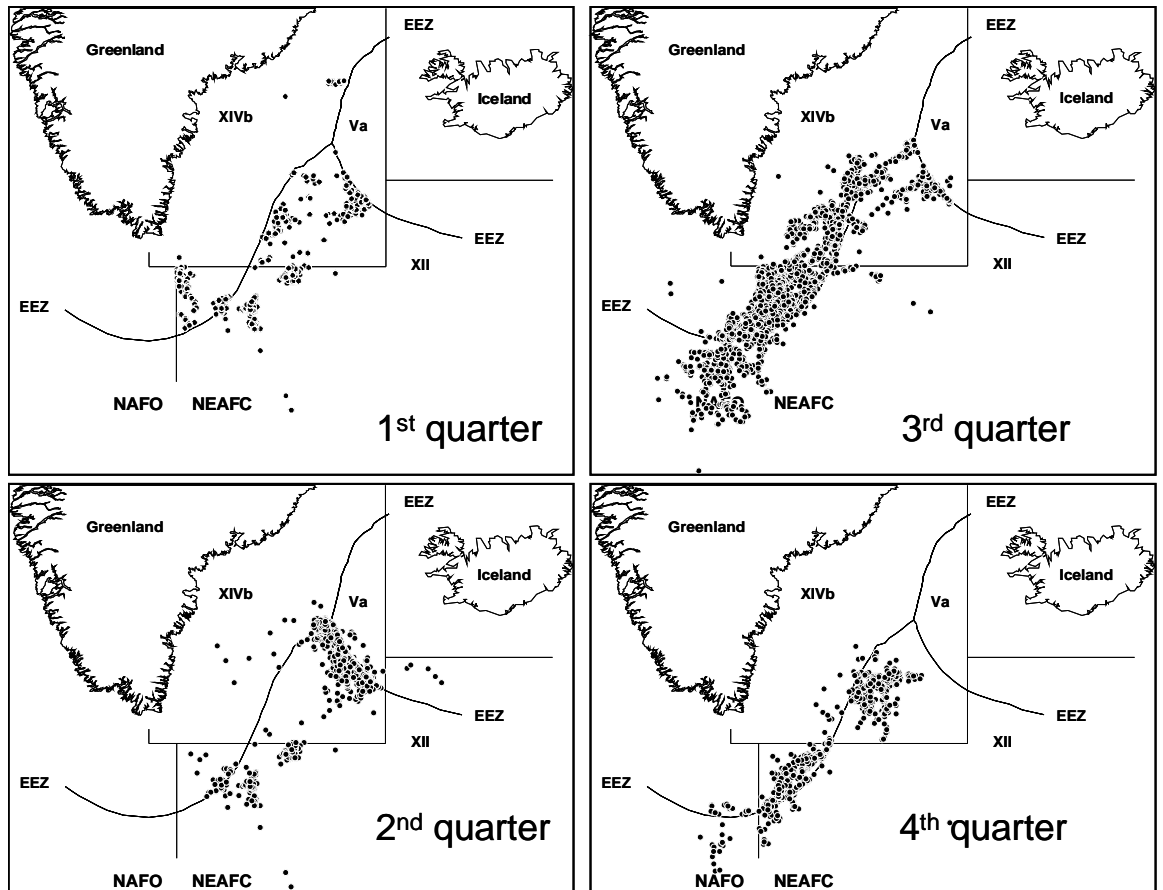
Figure 4.1.5c. Effort distribution of the German fleet fishing for pelagic *S. mentella*, 1995-2006, by quarter.
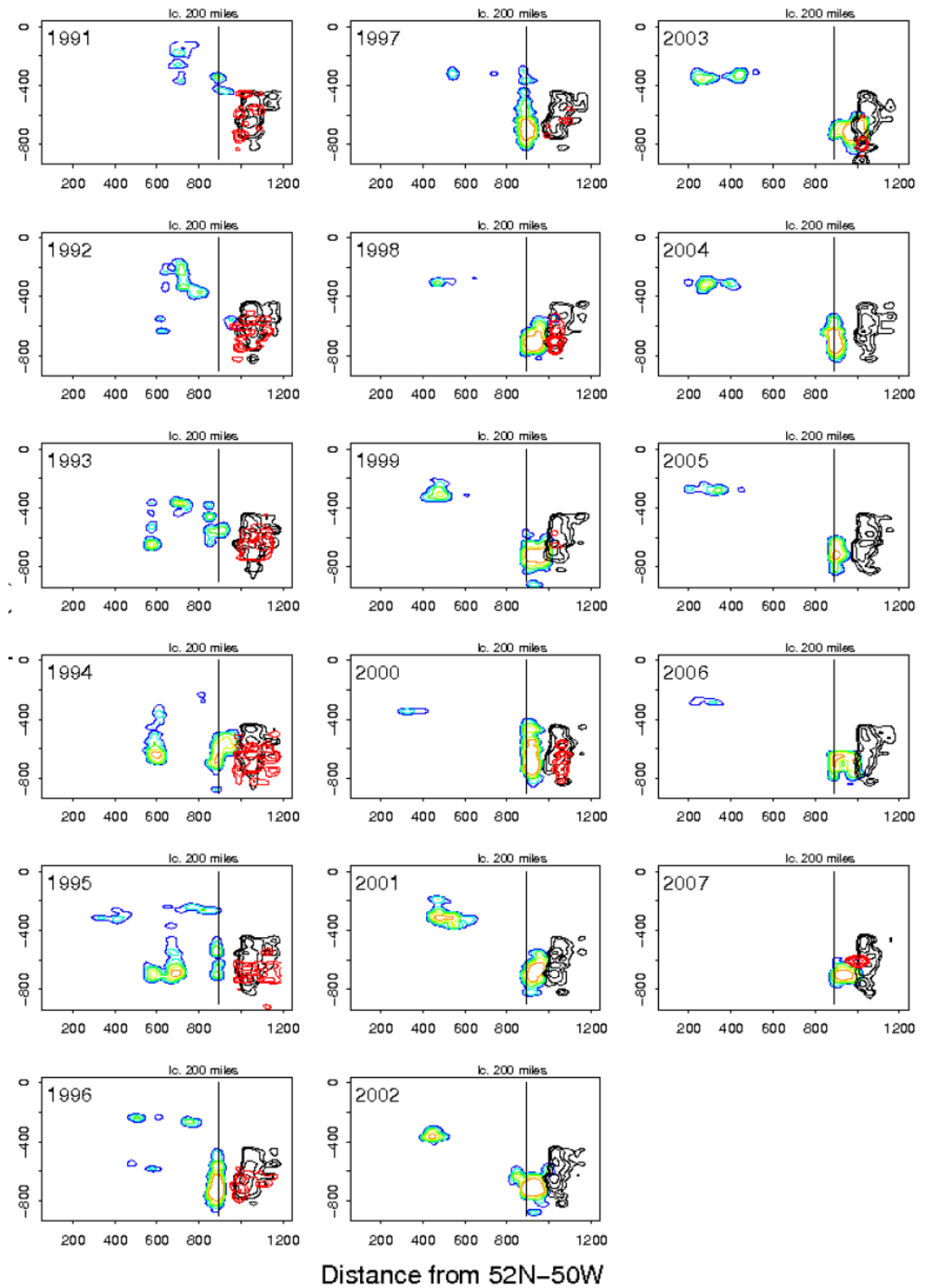
Figure 4.1.6. Distance-depth plot for Icelandic *S. mentella* catches, where distance (in NM) from a fixed position (52°N 50°W) is given. The coloured contours represent the fishery catches of pelagic *S. mentella*, the black contours indicate bottom trawl catches of demersal *S. mentella*, and the red contours represent catches of demersal *S. mentella* taken with pelagic trawls (from NWWG 2008).
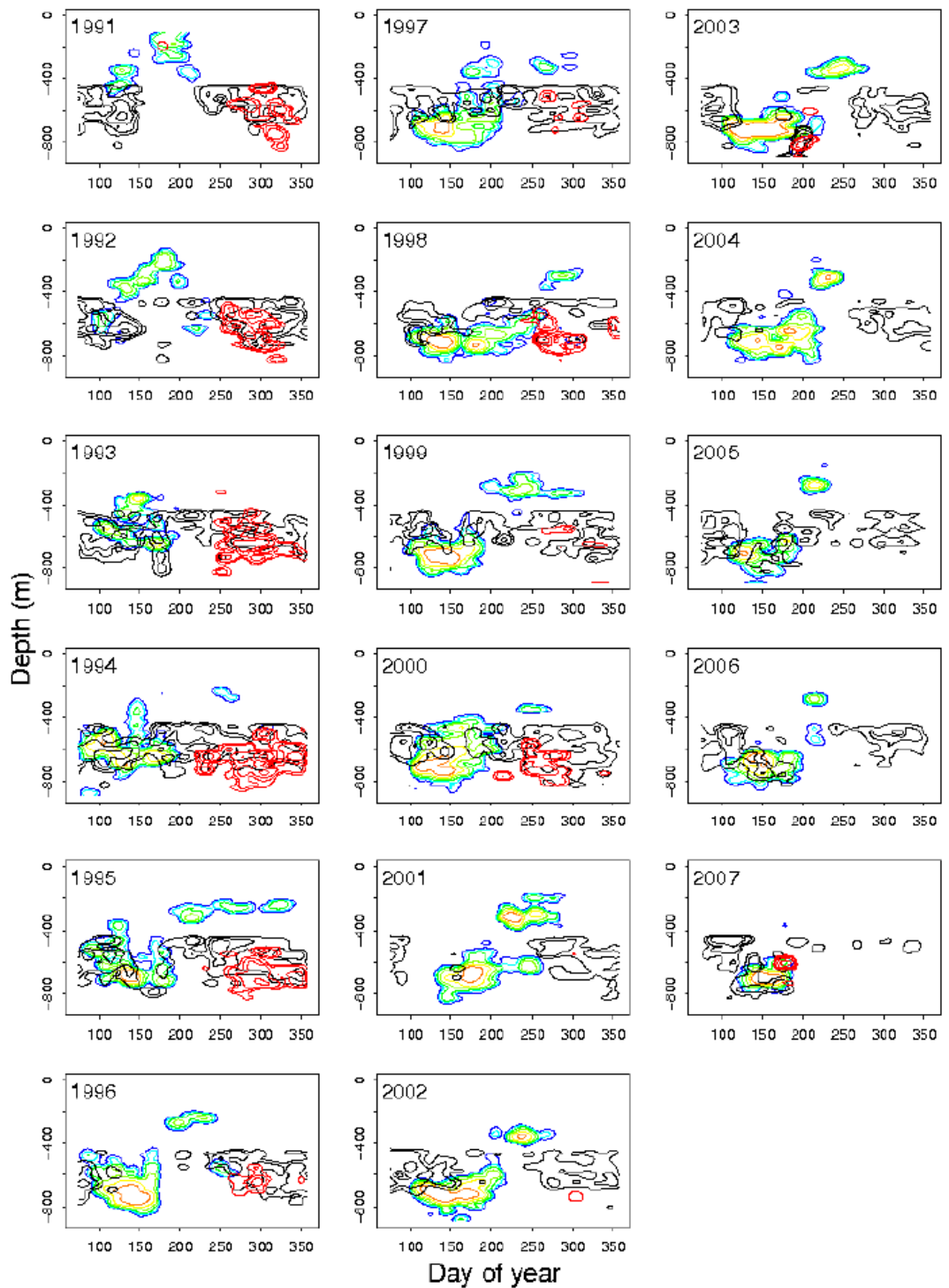
Figure 4.1.7. Depth-time plot for Icelandic *S. mentella* catches, where the y-axis is depth, the x-axis is day of the year. The coloured contours represent the fishery catches of pelagic *S. mentella*, the black contours indicate bottom trawl catches of demersal S. *mentella*, and the red contours represent catches of demersal S. mentella taken with pelagic trawls (from NWWG 2008).
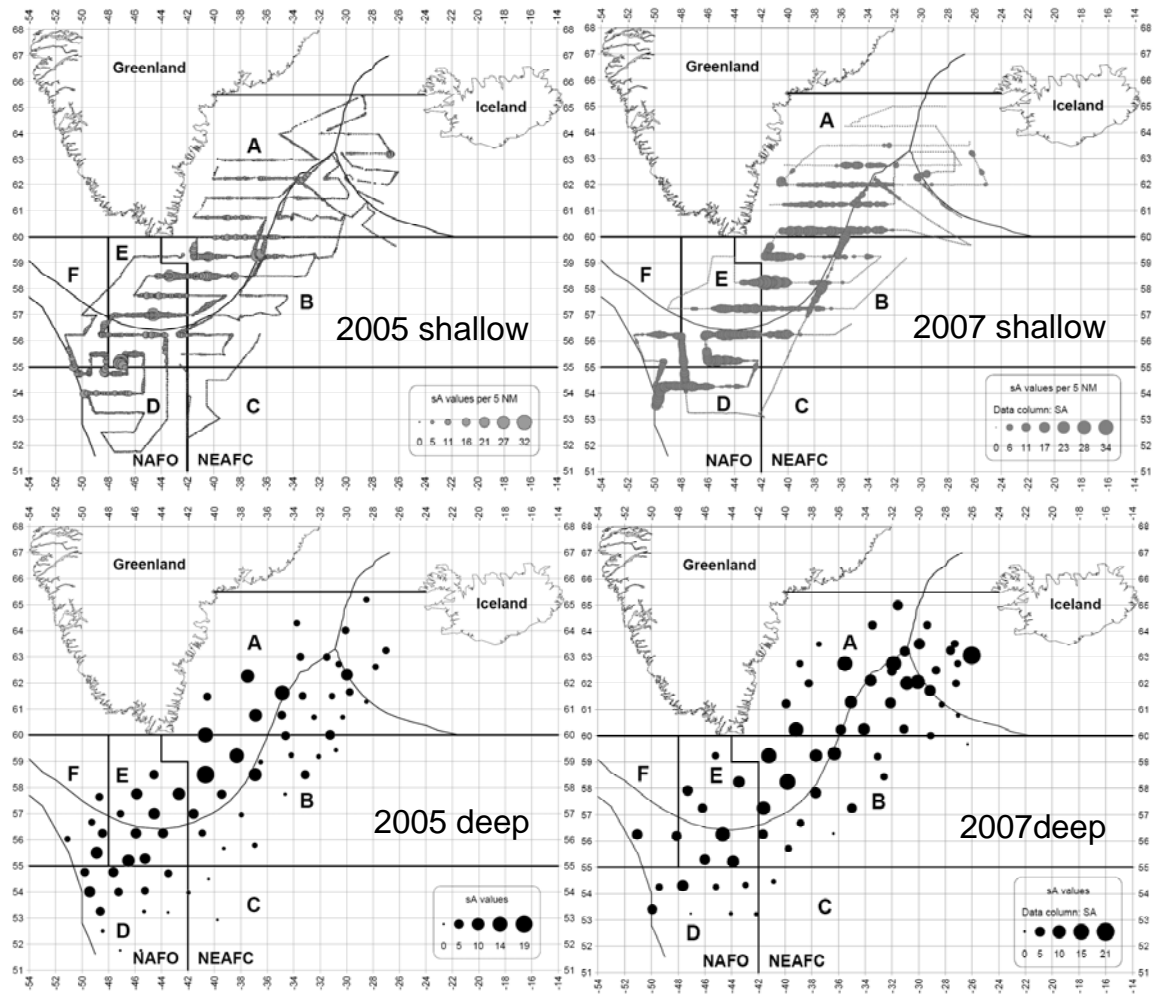
Figure 4.1.8. Redfish acoustic survey indices of abundance shallower than the deep-scattering layer (upper panels; average sA values by 5 NM sailed distance) and trawl estimates within and deeper than the deep-scattering layer (lower panles; sA values calculated by the trawl method) from the joint international redfish survey in June/July 2005 (left panels; from SGRS 2005) and 2007 (right panels; from SGRS 2007).
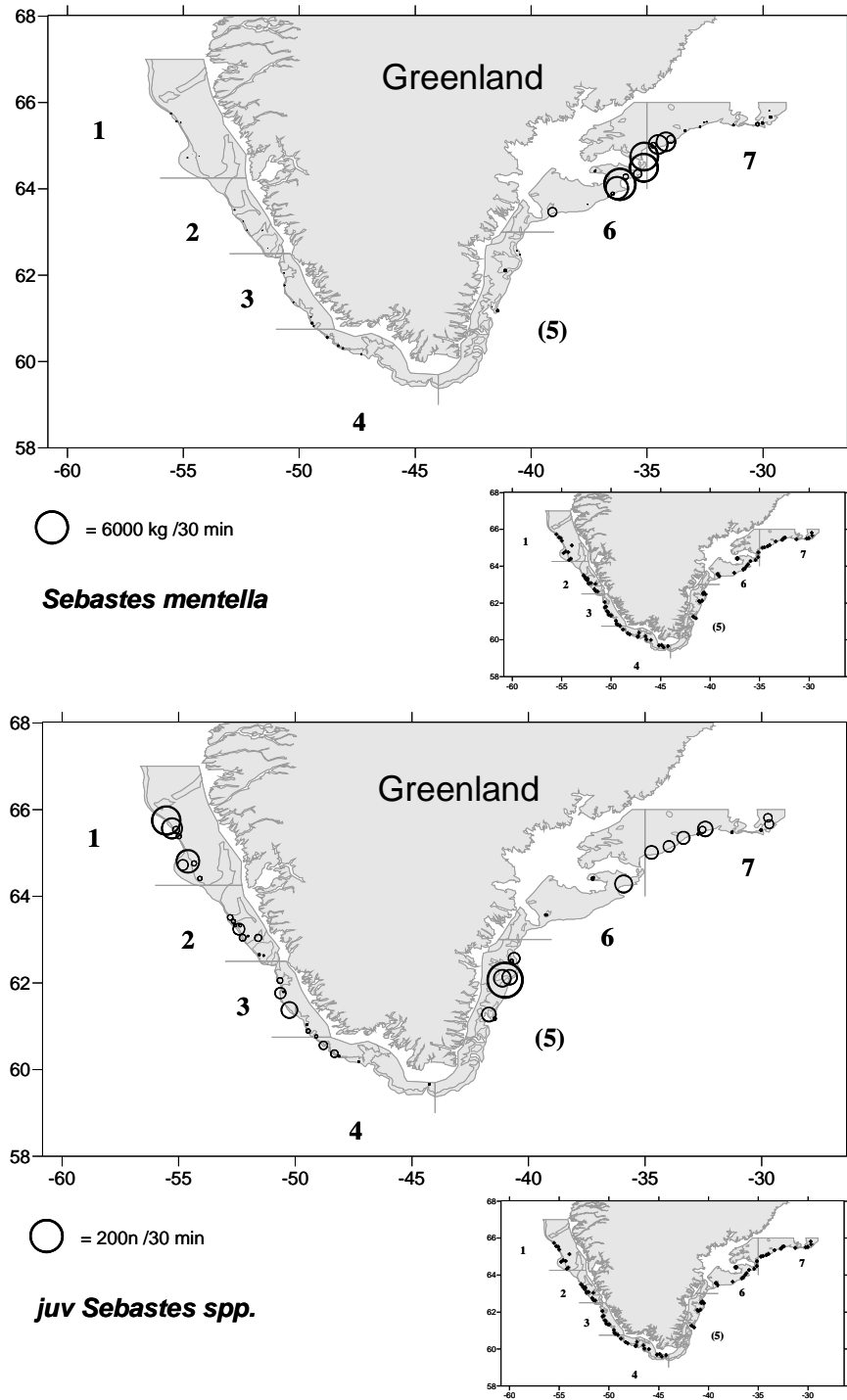
Figure 4.1.9. Stratification scheme of the German groundfish survey, positions of hauls carried out in 2007 (small panels) and normalised catches of *S. mentella* (≥17 cm, upper panel), and combined *S. mentella* and *S. marinus* juveniles (<17cm lower panel).
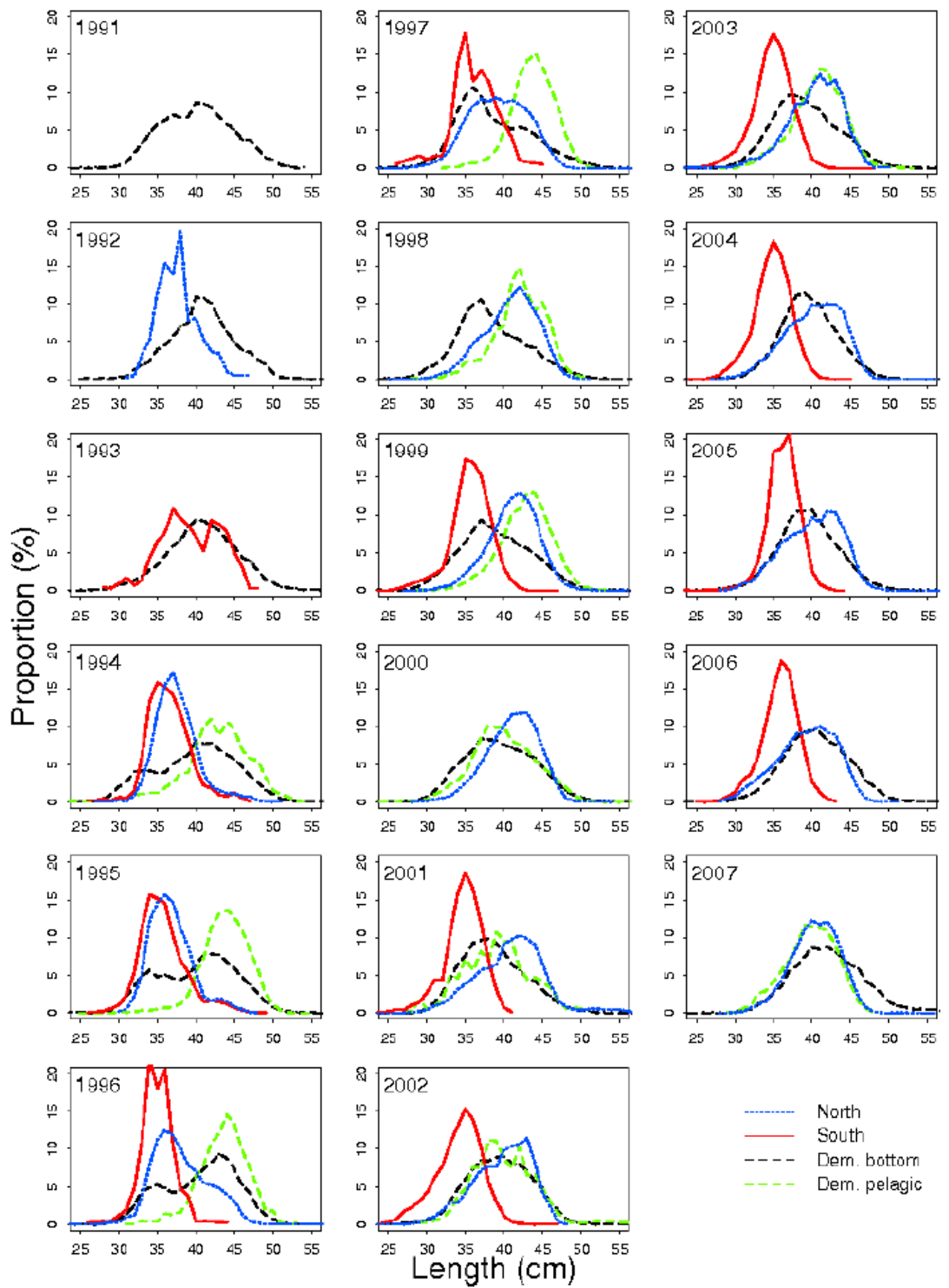
Figure 4.1.10. Length distributions from different Icelandic *S. mentella* fisheries. The blue lines represent the fishery on pelagic *S. mentella* in the northeastern area, the red lines the pelagic fishery in the southwestern area, the black lines indicate bottom trawl catches of demersal *S. mentella*, and the green lines represent catches of demersal *S. mentella* taken with pelagic trawls (from NWWG 2008).
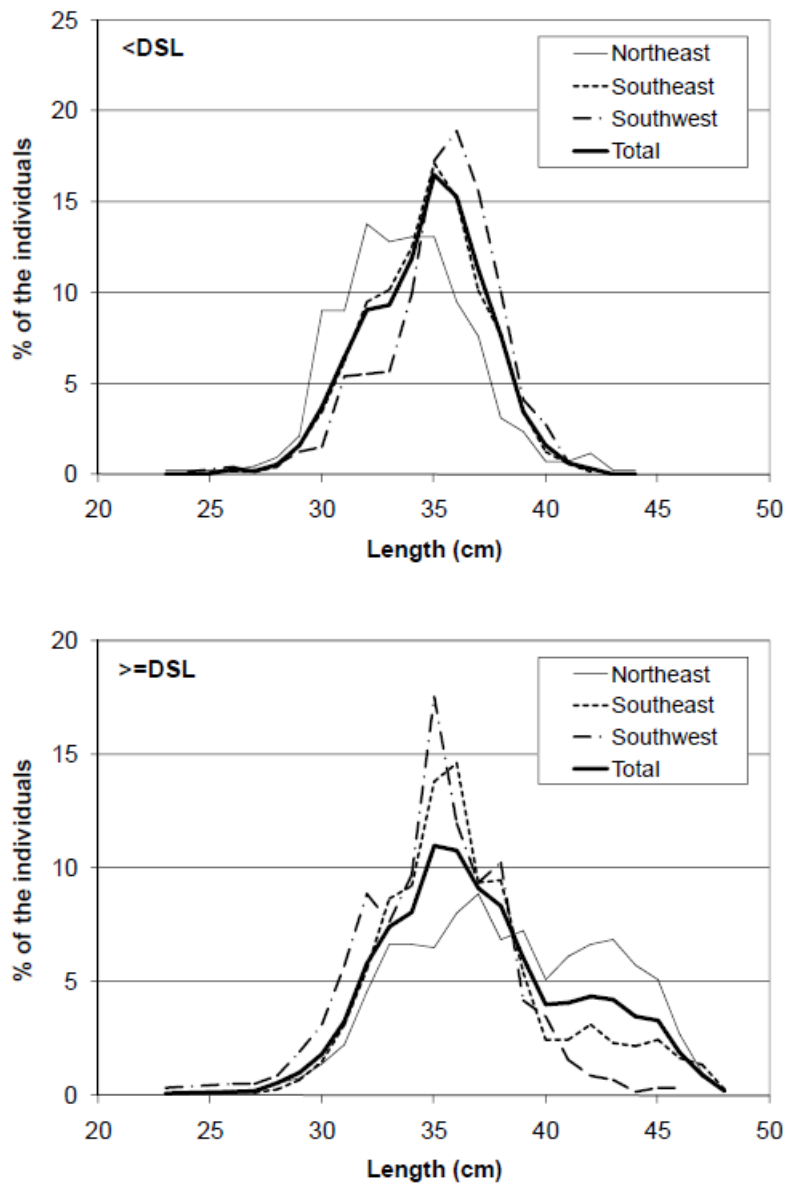
Figure 4.1.11. Length distribution of redfish in the trawls, grouped by geographical areas and combined areas (total), from fish caught shallower than the deep-scattering layer (upper panel) and within and deeper than the deep-scattering layer (lower panel; from SGRS 2007).

4.2   Geographic variation

4.2.1   Genetic Variation

Among the suite of approaches for stock identification, genetic analyses are the most rigorous to test for reproductive isolation among population components (Begg and Waldman 1999). The history of applying genetic methods to stock identification involves early development of allozyme markers, then mitochondrial DNA (mtDNA) characters, and most recently a series of nuclear DNA (nDNA) markers, each with increasing sensitivity to detect genetic differences that reflect reproductive isolation.

One of the primary reasons that WKREDS was formed was to reconcile recent information on genetic differences within *S. mentella* with all information on stock structure, including previous genetic research, life history patterns, phenotypic variation and connectivity. Earlier research on genetic variation of *S. mentella* provided weak or equivocal evidence for genetic structure or weak differences among locations. However, a common scenario in the investigation of stock structure of marine resources is that early studies reveal little variation among areas, but as more sensitive molecular markers are developed and applied to the resource, new and stronger differences are found among groups that were previously perceived to be genetically similar (Wirgin and Waldman 2005).

Over the last decade, several molecular genetic markers have been used in studies of *S. mentella* and other redfish species. These markers vary remarkably in terms of function, response to natural selection, mutational features, mode of inheritance and analytical/statistical properties. Therefore, the unique perspective of each type of genetic was considered in the synthesis of information from different studies. Furthermore, the sampling design and the type of statistical analyses conducted also play a significant role in determining results.

Allozymes

Allozymes, alternative protein expressions of a genetic locus (or gene), were the first genetic markers used to study population structure (Koljonen and Wilmot 2005). Before the discovery of the deep-sea resource, no geographic variation was detected in allozymes of *S. mentella* sampled in shallow waters (<500m). Dushchenko (1986) found polymorphism in the malic enzyme (MEP), but allozyme frequencies were not different among six shallow locations in the Irminger Sea. Similarly, in their study of genetic differences among *Sebastes* species, Nedreas and Naevedal (1991) and Nedreas et al. (1994) found genetic uniformity among shallow samples from off West Greenland, East Greenland, the Irminger Sea, the Faroe Islands and off Norway and Svalbard. However, soon after the deep-sea fishery began, preliminary information indicated a difference in allozyme frequencies between the 'oceanic' and 'deep-sea' phenotypes, with some allozymes that were unique to deep-sea specimens, and large-scale regional differences between samples from Canadian waters, the Irminger Sea and off Norway (SGRS 1998).

Johansen et al. (2000) and Johansen (2003) found significantly different allozyme frequencies among *S. mentella* sampled in the Irminger Sea, on the Flemish Cap and off southern Canada. Johansen and Sevigny (2003) determined that the source of regional variation was hybridization of *S. mentella* and *S. fasciatus* where their distributions overlap (i.e., on the Flemish Cap and in Canadian waters). Johansen et al. (2000) and Johansen (2003) also found significant differences between 'oceanic' and 'deep-

sea' phenotypes in the Irminger Sea, with only minor differences between the 'deep-sea' type and those from the Icelandic Slope. However, these studies compared each locus separately and had limited power of detecting differences. Allozyme differences were at the polymorphic MEP and IDHP (isocitrate dehydrogenase) loci and were supported by haemoglobin analyses. They concluded that the *S. mentella* in the Irminger Sea is composed of two different stock units. Note that the comparisons were not based on depth-structured samples, and many of the 'deep-sea' specimens were sampled above the deep-scattering layer (270-500m).

Subsequent investigations by Novikov et al. (2006) and Melnikov et al. (2007) also showed differences in frequency of the MEP allozyme between 'oceanic' and 'deep-sea' phenotypes. The Faroese Redfish project found differences in allozyme frequencies between samples from shallow samples (the southwest Irminger Sea, the western Icelandic shelf, north and east of the Faroes, and off Norway) and deep samples (the northeast Irminger Sea, the eastern Icelandic slope, and southwest of the Faroe Islands; Joensen 2002, SGSIMUR 2005).

The most recent study of *S. mentella* allozymes was by Danielsdottir et al. (2008), who sampled nearly two thousand specimens, tested a large number of allozymic loci (33, 13 of which were polymorphic), and analyzed all loci simultaneously to test for differences between 'oceanic' and 'deep-sea' phenotypes. Although nearly all of the 'deep-sea' samples (95%) were collected from deeper than 500m, and nearly all 'oceanic' samples (93%) were collected from shallow water (<500m), comparisons were not depth-based, and some sample locations had a mix of both phenotypes. Allozyme differences were persistent over the three-year sampling period. This study suggests the existence of two pelagic stocks on the southwest Icelandic slope and the central Irminger Sea. This conclusion is supported by significant heterozygote deficiency at all loci in pooled samples, significant differences in allele frequency between samples classified as belonging to the deep-sea and oceanic phenotypes, and clustering of the samples from different phenotypes (Figure 4.2.1.1).

Given that substantial differences in allelic frequencies are only observed in a minority of loci (mainly MEP), an alternative interpretation for the pattern observed between 'oceanic' and 'deep-sea' phenotypes is that the allozyme frequencies are influenced by different selective pressures above and below the deep-scattering layer. Such a scenario would not rule out exchange of genes between the shallow and the deep pelagic populations, but it would indicate the existence of some degree of local adaptation. Adaptive differences between shallow and deep populations could affect fitness and demographic dynamics of these populations, which should be considered in the fishery management process. Saborido-Rey et al. (2004) and Melnikov et al. (2007) contend that the pattern of divergence at the MEP enzyme locus reflects a shift of allelic frequencies resulting from selective forces that act after larger, older fish move into the deeper zone. Unfortunately, age determination is unreliable, particularly from deep samples (Stransky et al. 2004b, 2004c), and the ontogenetic movement hypothesis is not rigorously tested. Assuming that most spawning would be achieved by the larger, older fish in the deep layer, there is no reasonable explanation for the maintenance of high frequencies in the juveniles of the alleles that are selected against after the movement to the deeper layer. Thus, variation at the MEP locus between 'oceanic' and 'deep-sea' phenotypes is more parsimoniously explained as the result of adaptation to different environments by two diverging populations.

Mitochondrial DNA

In contrast to allozymes, that are the protein expressions of DNA, molecular methods can directly reveal DNA structure and polymorphisms. Mitochondria contain a small amount of DNA. Mitochondrial DNA (mtDNA), which is maternally inherited, is much simpler in form. Alternative sequences of mtDNA (i.e., haplotypes) are easier to analyze than nuclear DNA (Magoulas 2005). One corollary of the simplicity of mtDNA is that its mutation rates are relatively constant, and mtDNA divergence can be used as a 'molecular clock' to indicate the duration of reproductive isolation between two populations.

Sundt and Johansen (1998) found a low level of mtDNA variation among *Sebastes* species in the North Atlantic, suggesting a recent evolutionary divergence. As a component of the EU Redfish Project, Schmidt (2005) also found a low level of genetic differentiation in mtDNA among North Atlantic *Sebastes* species. A phylogenetic analysis revealed a pattern and levels of divergence similar to those normally observed within the same species, which suggests that speciation rate in this group is rapid (Figure 4.2.1.2). Analysis of molecular variance indicated that most of the genetic variation occurred between species, but there was also significant variation among samples within species. Haplotype frequencies differed between the samples of the 'deep-sea' phenotype and other samples of *S. mentella*, because one haplotype was frequent in 'deep-sea' samples and only occurred in two other *S. mentella* samples. Ingimarsdóttir (2008) also found differences in mtDNA haplotype frequencies among 'oceanic,' 'deep-sea,' and demersal samples of *S. mentella*, and estimated that the subgroups in the Irminger sea diverged approximately 4 000 years ago.

Nuclear DNA

Several aspects of nuclear DNA (nDNA) are commonly used to study population structure, and each has different sensitivities and interpretations. When little is known about the genome of a species (i.e., DNA sequences have not been indentified), Random Amplified Polymorphic DNA (RAPD) can be used to explore patterns of variability, because RAPD primers recognize simple nucleotide sequences that should arise frequently in any DNA (Smith 2005). Johansen et al. (1997) and Johansen and Dahle (2004) found significant differences in allele frequencies of four RAPD primers among all samples of *S. mentella* from the Gulf of St. Lawrence, Norway and the Irminger Sea ('oceanic' and 'deep-sea'). However, RAPD is a technique that produces results that may not be repeatable, and is no longer considered to be a reliable approach for testing population structure hypotheses.

Amplified Fragment Length Polymorphism (AFLP) is another type of nDNA character that can be used for stock identification. Similar to RAPD, AFLP can be applied to species without prior information about its genome, but it uses fragment lengths between arbitrary restriction sites to measure genetic variation (Liu 2005). Schmidt (2005) found genetic patterns among *S. mentella* sampled from the Irminger Sea, Greenland and Iceland, but the significant differences between all samples indicated that AFLP markers may be too variable to detect biological meaningful patterns of genetic structure among subpopulations of *S. mentella*. Similar to RAPD, AFLP results are not always repeatable among laboratories, and AFLP characters are inherited as dominant markers (Liu 2005). Therefore, both RAPD and AFLP are considered to be more exploratory than confirmatory for stock identification studies.

Microsatellites are segments of nDNA consisting of tandem nucleotide repeats. Microsatellites are generally non-coding, so they are not subjected to selection and have a rapid mutation rate, because all microsatellite mutations are non-lethal. Both of these characteristics make them the most effective character for studying population structure (Wirgin and Waldman 2005). A series of increasingly rigorous analyses of microsatellite characters indicate a general pattern of population structure of *S. mentella* that involves three distinct genetic groups located in 1) the deep Irminger Sea, 2) shallow pelagic habitats and 3) demersal habitats:

- The Faroese Redfish project found differences in microsatellite frequencies between three geographically overlapping, but genetically distinct groups: 1) shallow (<500m) samples from the southwest Irminger Sea, the northern and eastern Faroese Shelf and the Norwegian coast, 2) deep (>500m) samples from the northeast Irminger Sea, the eastern Icelandic Slope and the southwest Faroese Slope, and 3) the western Icelandic Shelf and southwest Faroese Shelf (Figure 4.2.1.3; Joensen 2002, SGSIMUR 2005). Analyses of these samples were later refined by Stefánsson et al. (unpublished, below).

- Roques et al. (2002) used microsatellite characters to demonstrate the presence of hybridisation between *S. mentella* and *S. fasciatus* in the Gulf of Saint Lawrence, which appears to represent a unique evolutionarily significant unit. They concluded that there are three distinct populations of *S. mentella*: 1) in the area of hybridization with *S. fasciatus* off southern Canada, 2) in a 'panoceanic' area from Labrador to the Faroe Islands, and 3) in the Barents Sea. However, all 'panoceanic' samples in the Irminger Sea and adjacent areas were from shallow habitats (<500m).

- Using eight highly variable microsatellite loci, Schmidt (2005) found weak but significant genetic structure in *S. mentella*. Significant genetic differences were found between three groups of samples: 1) on the Flemish Cap, 2) in the deep (>500m), central Irminger Sea, and 3) in shallow (<500m) samples off Greenland, off Iceland, and in southern Irminger Sea (Figure 4.2.1.4).

- Pampoulie & Danielsdottir (2008) used nine microsatellite loci to distinguish all the Atlantic species of *Sebastes*, but analyses also indicate that the 'oceanic' and 'deep-sea' phenotypes are genetically distinct, with considerable misclassification of genotype using 'phenotyping.'

- Although the comparisons tested by Pampoulie & Danielsdottir (2008) were primarily based on phenotypic identification, the data were regrouped by depth by Stefánsson et al. (2009). The revised and expanded analysis of nearly two thousand specimens shows that populations below and above the 550 m depth boundary are well differentiated based on microsatellite variation (Figure 4.2.1.5). The analyses also suggest that the shallow and deep pelagic subpopulations may represent incipient species that were allopatric (i.e., geographically separate) during the Pleistocene glaciation but secondarily came in contact to form their current sympatric (i.e., overlapping) distribution.

- A spatially expanded analysis rigorously tests for genetic differences between shallow (<550m) and deep (>550m) *S. mentella* in the Irminger Sea (Stefánsson et al. unpublished; details in SIMWG 2007 and 2008). The analyses show temporally stable differences between deep and shallow pelagic samples, providing evidence that fish inhabiting waters deeper than 550m are genetically distinct from the shallower ones. Analyses of shallow

samples are similar to that reported by Roques et al (2002), with the addition of genetically distinct deep samples and samples on the Icelandic slope. Geographic distributions of the three genetically distinct clusters are shown in Figure 4.2.1.6 and the proportion of each group by depth is shown in Figure 4.2.1.7.

Synthesis of all genetic information suggests that *S. mentella* from Newfoundland and the Gulf of Saint Lawrence (NAFO areas 3 and 4) are genetically distinct from *S. mentella* in the rest of the North Atlantic because of strong evidence of adaptive local hybridization with *S. fasciatus*. A 'panoceanic,' shallow (<500m) subpopulation of *S. mentella* extends from Labrador to at least the coast of Norway, perhaps to the Barents Sea (Roques et al. 2002 found one Norwegian sample was significantly differentiated from the panoceanic group, but Stefansson et al. unpublished did not). *S. mentella* in the deep Irminger Sea (> 500 m) and *S. mentella* on the Icelandic slope are also distinct subpopulations.

This perception of genetic structure in the Irminger Sea and adjacent waters contrasts with the previously posed single-stock hypothesis (Saborido-Rey et al. 2004, Melnikov 2007). The revised view of stock structure results from more extensive genetic testing, the use of neutral and powerful markers, refinement of analyses by depth (rather than by phenotype), and robust statistical approaches. The hypothesis that fish move to deeper habitats as they age is refuted by the substantial differences between deep and shallow pelagic samples in microsatellite allelic frequencies (which are not vulnerable to selection, and have been tested for temporal stability). Saborido-Rey et al. (2004) suggest that genetic differences may result from genetic drift or a 'sweepstakes' effect (i.e., each year class is genetically distinct because it is produced from a small, randomly selected portion of the adult population), both of which imply genetic population structure and reproductive isolation, therefore refuting the assumption of panmixia. The revised perception of genetic structure explains some of the previously observed patterns in genetic analyses. For example, the lack of correlation between genetic distance and geographic distance (e.g., Roques et al. 2002) probably results from depth-based differences among locations that are geographically close.

Based primarily on microsatellite information, but also supported by results from analyses of allozyme, AFLP and RAPD characters, WKREDS concludes that there are four genetic stocks of *S. mentella* (three in the area of concern, the Irminger Sea and adjacent waters):

1. 'Western' (NAFO 3+) – This stock extends south and west of the Flemish Cap
2. 'Shallow Pelagic' (NAFO 1-2, ICES Vb XII XIV <500m) – This stock extends from Greenland and the Irminger Sea to the coast of Norway, perhaps to the Barents Sea (ICES I-II). The stock primarily consists of *S. mentella* in pelagic habitats (though demersal habitats east of the Faroe Islands appear to be part of this stock).
3. 'Deep Pelagic' (NAFO 1-2, ICES Vb XII XIV >500m) – This stock also primarily consists of *S. mentella* in pelagic habitats, but includes demersal habitats west of the Faroe Islands. Note that this genetic stock does not necessarily equate to the 'deep-sea' phenotype.
4. 'Icelandic Slope' (ICES Va XIV) – The northwest Faroese Slope may be part of this stock.

Note that juveniles on the Greenland Shelf are most likely from the 'shallow pelagic,' 'deep pelagic,' and 'Icelandic Slope' stocks.
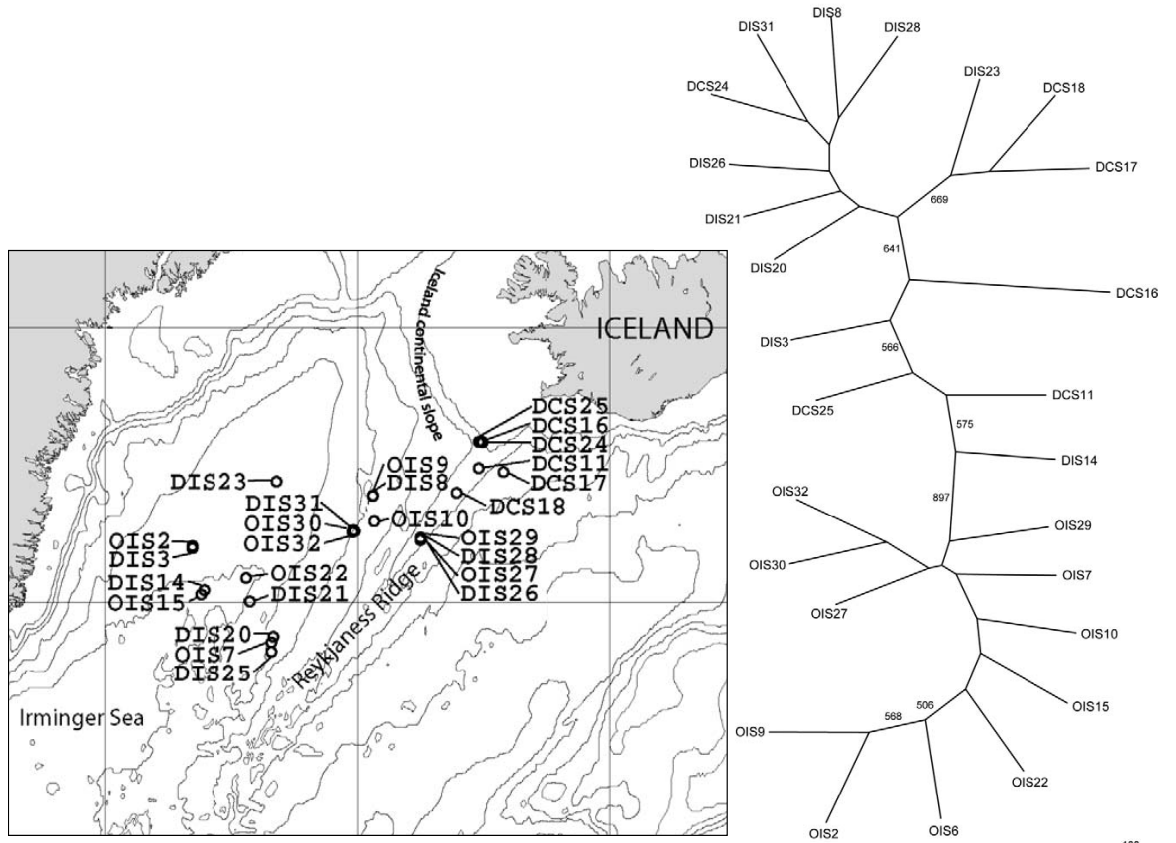
Figure 4.2.1.1. Sample locations (left panel) and sample codes, with the first letter indicating the 'deep-sea' (D) or 'oceanic' (O) phenotype, and the second and third letters indicate sample location (IS: Irminger Sea; CS: Icelandic Slope). Consensus neighbor-joining dendrogram (right panel) showing the relationship among the 26 samples. Nei's genetic distance between samples based on eight allozyme loci was used to construct the dendrogram (from Daníelsdóttir et al. 2008).
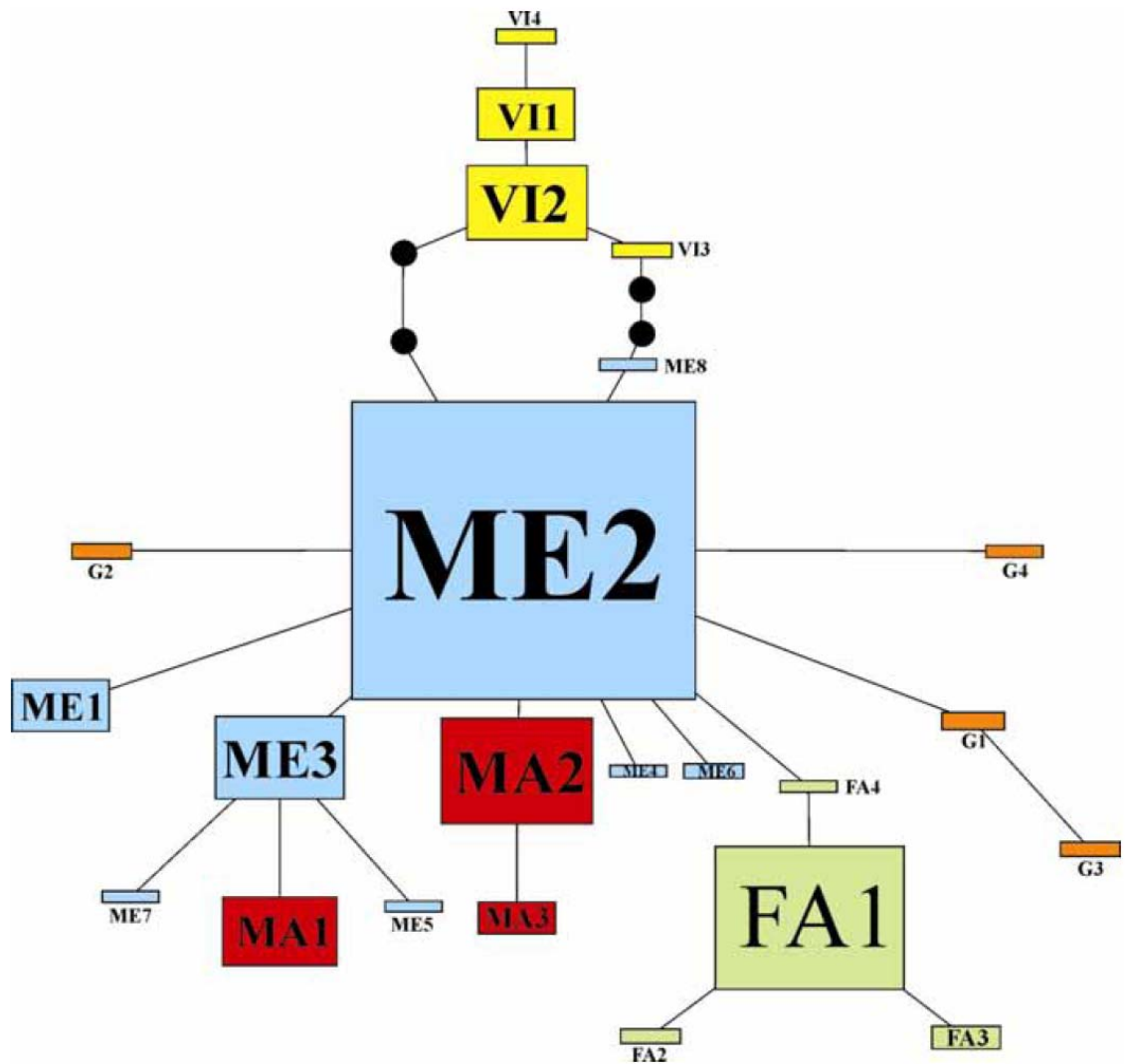
Figure 4.2.1.2. Statistical parsimony network showing the genealogical relationships of the ND3 haplotypes of the North Atlantic *Sebastes* species. Each rectangle represents one haplotype. Haplotypes are designated by name (ME: *S. mentella*; MA: *S. marinus*; G: "giant" *S. marinus*; FA: *S. fasciatus*; VI: *S.viviparus*; ALUT: *S. alutus*; CAP: *S. capensis*; HEL: *Helicolenus dactylopterus*). Each line represents a single mutational step connecting two haplotypes and small black circles represent hypothetical (not detected) haplotypes. The size of the rectangles corresponds to the haplotype frequency (from Schmidt 2005).
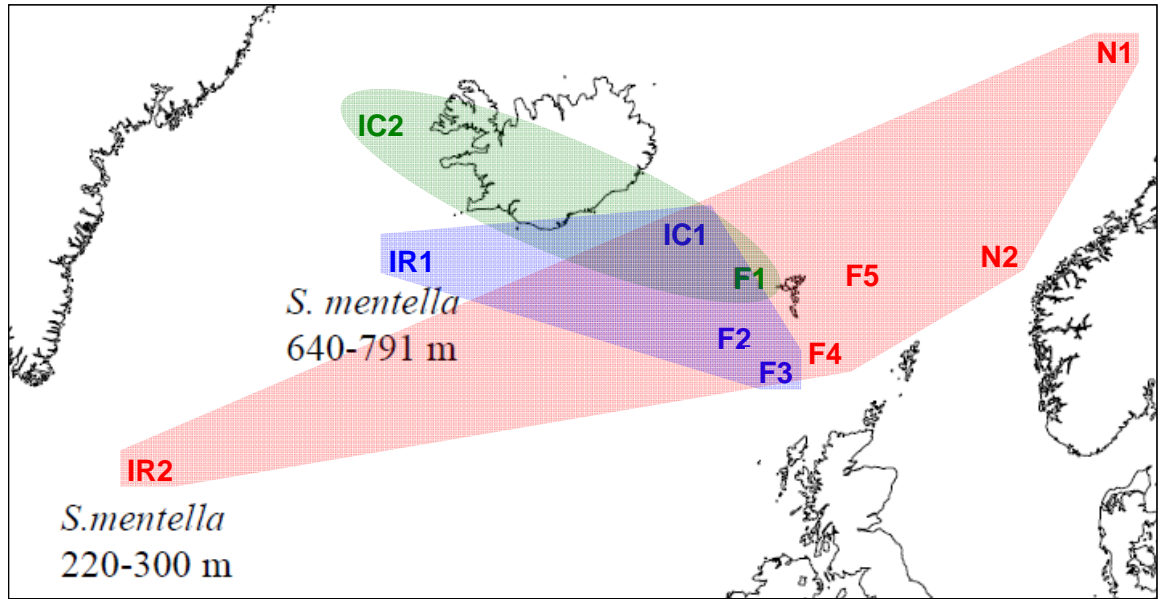
Figure 4.2.1.3. Eleven locations where *S. mentella* were sampled for the Faroese Redfish Project. Colors indicate three genetically distinct clusters detected by analysis of microsatellites (modified from SGSIMUR 2005). Samples were collected in shallow (IR2, F4, F5, N1 and N2, depth < 540m) and deep (depth > 580m) waters, as well as on continental shelf of Iceland and Faroe island (depth > 500m).
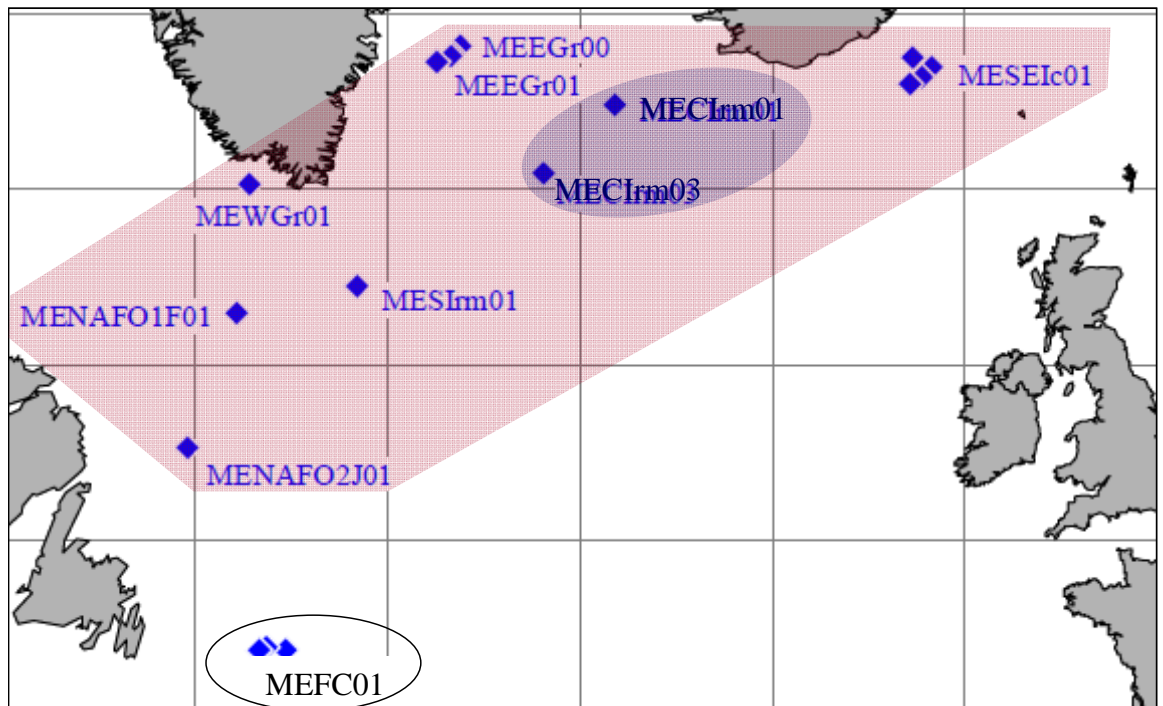
Figure 4.2.1.4. Sampling locations for the microsatellite analysis of *S. mentella*. Colors, ellipses and the polygon indicate three genetically similar clusters (modified from Schmidt 2005).
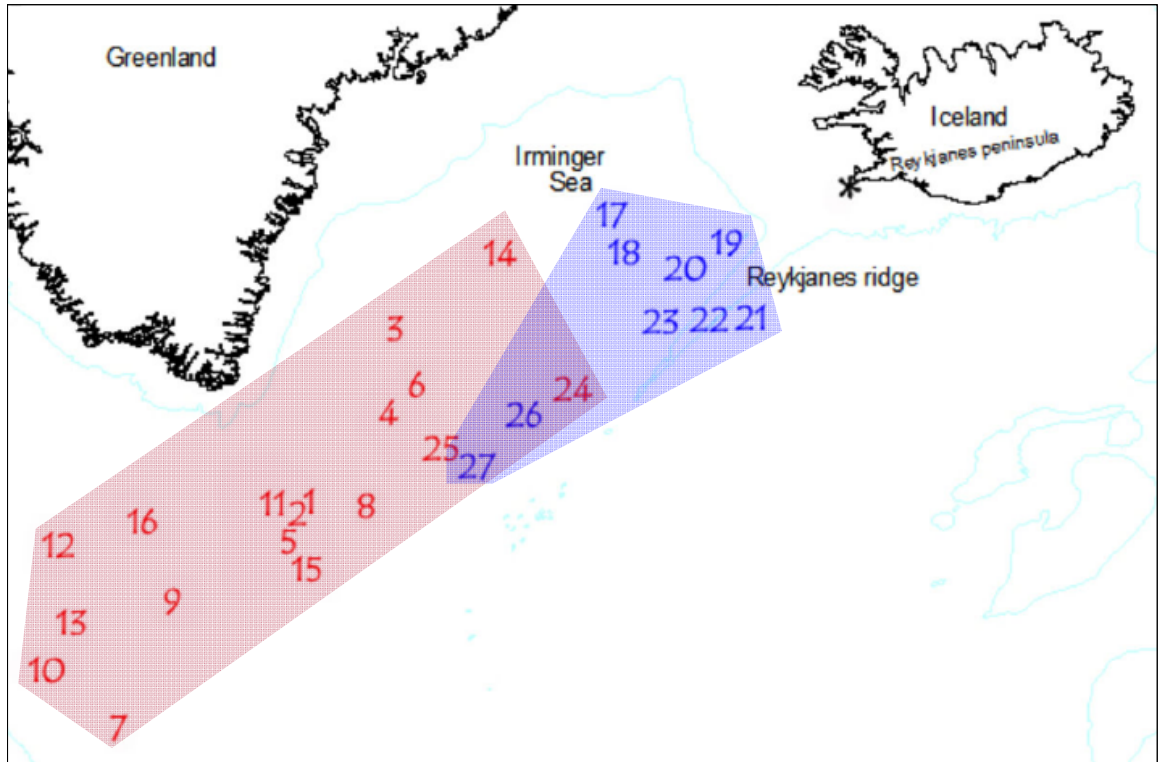
Figure 4.2.1.5. Sample locations of *S. mentella* from the shallow (red, depth < 500m) and deep (blue, depth > 500m) mesopelagic-zones of the Irminger Sea collected for microsatellite loci analyses. Microsatellite analyses revealed the presence of two genetically distinct clusters represented by shaded areas: red = shallow mesopelagic-zone and blue = deep mesopelagic-zone. The asterisk shows the location of the centre of circle (south-west tip of the Reykjanes peninsula, Iceland; 63°82N, 811 22°77W), which was used for calculations of distance (modified from Stefánsson et al. 2009).
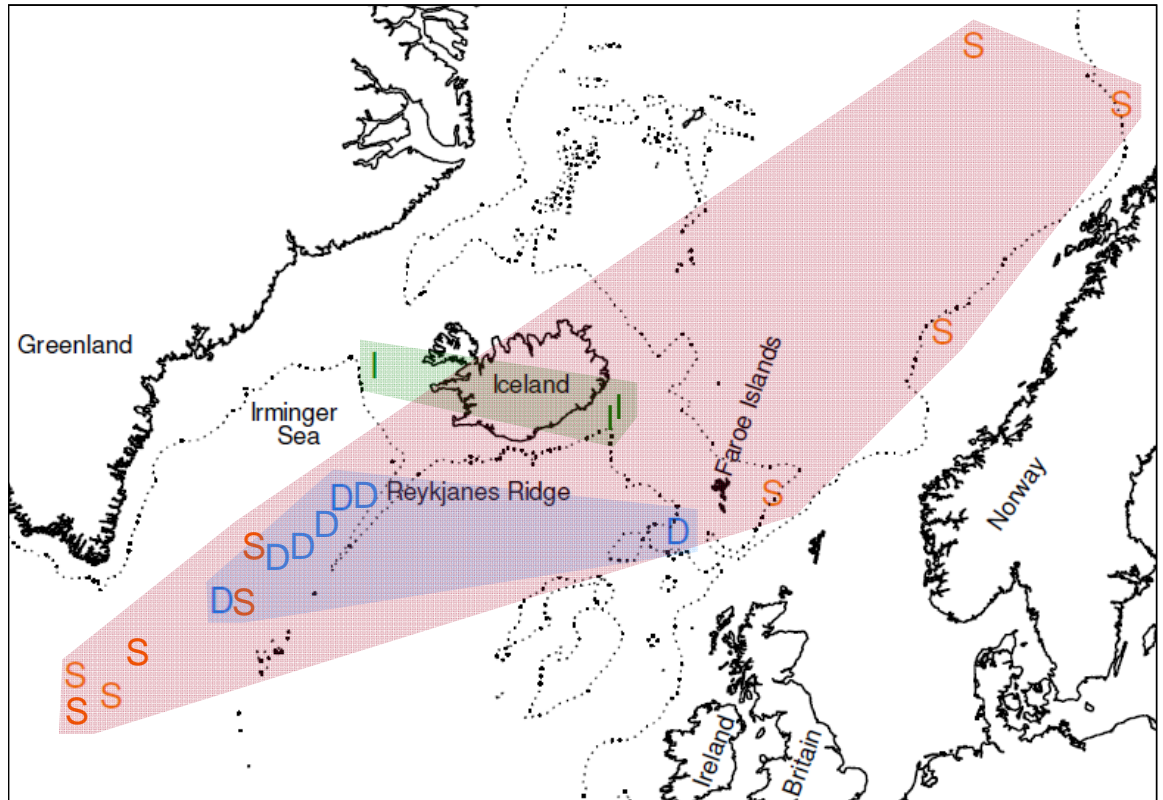
Figure 4.2.1.6. Samples location of *S. mentella* **and clustering of groups according to microsatellites loci as interpreted from Bayesian based cluster analysis (modified from Stefánsson et al. unpublished). Different clusters are represented in different shaded areas and by letters: D: 'deep pelagic' (blue, depth > 500m), I: 'Icelandic Slope' (green, depth < 500m) and S: 'shallow pelagic' (red, depth < 500m).**
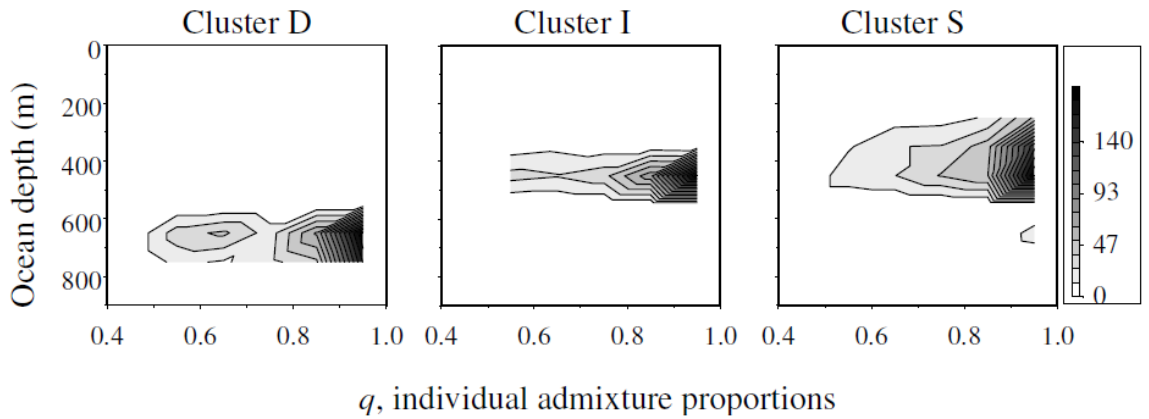
Figure 4.2.1.7. Contour plots representing the proportional distribution of samples (*q***) by depth (m) and cluster (D: 'deep pealgic'; I: 'Icelandic Slope'; S: 'shallow pelagic'). Only values that were ≥ 0.5 were plotted for each cluster. Scale bar represents number of individuals (from Stefánsson et al. unpublished).**

4.2.2   Phenotypic variation

Geographic variation in phenotypic characters (measurable traits that are influenced by both genetics and environmental factors) is valuable for stock identification, because maintenance of phenotypic differences among groups indicates limited mixing, and adaptive differences may have a genetic basis. Investigation of phenotypic variation can be used to define putative genetic stocks (for confirmation using genetic techniques). If phenotypic differences are indicative of distinct biological stocks and they are temporally stable, they can offer a practical measure for stock discrimination or stock composition analysis.

The study of phenotypic variation has played a large role in the investigation of *S. mentella* population structure. Soon after the discovery of the deep-sea resource, phenotypic differences between 'oceanic' and 'deep-sea' forms were recognized (Magnússon and Magnússon 1995). Several phenotypic characters have been used to study stock structure of *S. mentella*, including life history traits (e.g., size distributions, size at maturity), morphology (e.g., body form, meristics, otolith shape) and fatty acid composition.

Phenotypic variation can be particularly valuable for stock identification when it is associated with life history characteristics and vital rates (e.g., growth, reproduction, mortality) that are also critically important for population dynamics, stock assessment and fishery management (Begg 2005). There are some indications of different ontogenetic rates among the genetic stocks of *S. mentella* identified in Section 4.1.1. As discussed in section 4.1 and illustrated in Figures 4.1.10 and 4.1.11, size distributions are relatively smaller in the shallow, southwest Irminger Sea than in the deep, northeast area, and this relative difference has persisted over time. However, age determination is not reliable for *S. mentella* (Stransky et al. 2005b, 2005c), so the cause of different size distributions (i.e., growth differences, mortality differences, movement patterns) is difficult to interpret. Pelagic phenotypes have been partially identified based on size-at-maturity, with the 'deep-sea' types having larger size at maturity than the 'oceanic' type (Magnússon and Magnússon 1995, SGRS 1998). Melnikov (2007) used length distributions, maturity stages and distribution of various life stages to infer that fast growing and early maturing individuals of each year-class recruit to the pelagic areas of the Irminger Sea, whereas slow growing and late maturing individuals recruit to the deepwater habitat along the slopes of East-Greenland, along the Iceland-Greenland Ridge to the slopes west and south of Iceland (the deep-sea *S. mentella* stock). However, these interpretations of ontogenetic movements are based on deduction and are not consistent with the genetic differences between shallow and deep pelagic samples.

Geographic differences in morphology can also indicate subpopulations that have limited mixing and morphological patterns can reflect life history differences and possibly adaptations to different environments (Cadrin 2000). Several studies have investigated patterns of morphology for *S. mentella*. Nagel et al. (1991) found that *S. mentella* on the Reykjanes Ridge had more vertebrae than those collected in other areas (off east and west Greenland, the Irminger Sea, off Norway and in the Barents Sea). Rikther (1996) also found significantly greater number of vertebrae, anal fin rays and pectoral fin rays in *S. mentella* sampled from the Icelandic Slope than from those from the Irminger Sea. Significant differences in meristic features usually indicates environmental difference during early life stages (Waldman 2005). Reinert and Lastein (1992) found morphometric differences between samples from the Irminger Sea, the Faroes and off Norway, with some morphometric heterogeneity within Faroe

samples, but not among Irminger Sea samples (which were all collected from shallow depths).

After the discovery of the deep Irminger Sea resources of *S. mentella*, pelagic phenotypes were defined primarily on the basis of color ('deep-sea' types are redder, and 'oceanic' types are more grayish red), body shape ('deep-sea' are more stout), as well as size at maturity and parasites (Magnússon and Magnússon 1995, SGRS 1998). Pelagic phenotypes were secondarily identified on the basis of general appearance ('deep-sea' are brighter, and 'oceanic' are less 'clean'), color pattern ('oceanic' have black and red spots), filets ('oceanic' filets have dark spots), and morphometry ('oceanic' have narrower head; Figure 4.2.2.1; SGRS 1998).

Garabana Barro (2005) attempted to use morphometric analysis to quantify the differences between 'deep-sea' and 'oceanic' phenotypes, but found that morphometric variation could not accurately classify individuals to 'type.' Morphology was also compared among samples from the Flemish Cap, Faroe Islands, Greenland Shelf, Icelandic Slope, Irminger Sea, and Norwegian Sea, but all were morphometrically too similar to support accurate classification of specimens to locations. One subtle pattern of variation was that specimens from the Irminger Sea specimens were more fusiform than those from other areas. As a part of the EU Redfish Project, an identification key was developed to codify the phenotyping technique used by Icelandic researchers, but the key could not be effectively used by all of the partners in the project (Anon. 2004). A refined phenotyping key was based on preopercular spine morphology (Figure 4.2.2.2), size at maturity and parasites (SGSIMUR 2005).

Another component of the EU Redfish project was an investigation of geographic variation in otolith morphology. Stransky (2005) measured outline shape of otoliths collected from *S. mentella* throughout the North Atlantic. Otolith shape could not accurately classify specimens to specific areas (Flemish Cap, Davis Strait, West Greenland Shelf, East Greenland Shelf, Irminger Sea, Icelandic Slope, Faroe Islands, and Barents Sea), but could accurately classify specimens to three broad regions: 1) Flemish Cap and Davis Strait, 2) Greenland Shelf, Irminger Sea, Icelandic Slope, and Faroe Islands, and 3) Barents Sea. Stransky (2002) compared otolith shape among samples in the Irminger Sea by depth, but no clear clear differences between depth groups were found.

Daníelsdóttir et al. (2008) found significant differences in allelic frequency of allozyme loci between specimens classified to 'oceanic' or 'deep-sea' phenotypes based on external morphology. However, there was considerable misclassification between phenotypes and genotypes. Stefánsson et al. (2009) found significant differences in meristics and morphometry between specimens of 'oceanic' or 'deep-sea' classified according to genotypes within the Irminger Sea. However, statistical analyses suggest that these differences could not be used alone for stock identification. In addition to difficulties applying a standardized classification, phenotyping has limited utility for stock identification, because the two types have overlapping geographic and depth distributions (Table 4.2.2.1, Figure 4.2.2.3; Kristinsson and Sigurdsson 2007).

A relatively new approach stock identification is the investigation of fatty acid composition. Fatty acids are phenotypic characters in that they reflect both genetic composition and the environment, with some specific fatty acids concentrations more heritable than others (Grahl-Nielsen 2005). As a part of the Faroese Redfish project, Joensen and Grahl-Nielsen (2004) measured fatty acid profiles in heart tissue of *S. mentella* from eleven areas in the North Atlantic from Norway to the Irminger Sea.

Significant differences were found among four stocks: 1) the shallow Irminger Sea, 2) the deep Irminger Sea, southeast Icelandic Slope and southwest Faroese Slope, 3) the western Icelandic Shelf, and 4) north and northeast Faroe Islands and Norway (Figure 4.2.2.4). Stocks identified through fatty acid profiles are similar to those identified from microsatellite DNA analysis, supporting the conclusions drawn from genetic analysis. Fatty acid profiles, however, must be viewed cautiously in the context of stock identification, as they may be influenced by environmental factors such as diet or temperature (Joensen 2002).

In summary, geographic variation in life history is apparent from size distributions and size-at-maturity, but precise evaluation of growth or maturity is difficult without reliable age determination. Subtle morphological differences exist between 'oceanic' and 'deep-sea' forms, and the phenotypes appear to have a genetic basis. Geographic patterns of fatty acid profiles are similar to those from genetic analysis. Although interpretation of phenotypic traits is somewhat subjective (i.e., can be validly interpreted in several ways), all information on phenotypic variability is consistent with the genetic stocks identified in Section 4.2.1.

Table 4.2.2.1. Distribution of Icelandic catch by depth (m), proportion of 'oceanic' type redfish, standard deviation of the mean proportion, reported catch (t) of 'oceanic' and 'deep-sea' redfish (only when depth is reported). Data based on samples from the commercial fishery and from the log-books. The catches as well as the samples are divided according to the areas (N: north; S: south) shown in Figure 4.2.2.3.

Area	Year	Depth	Depth range	st.dev	prop. oceanic	Catch ocean	Catch deep	not classified
N	1995	200	200_400	6.91	95.11	1784	92	0
N	1995	400	400_600	22.17	76.52	2212	679	0
N	1995	600	600_800	29.86	50.91	1499	1446	0
N	1996	0	0_200	NA	NA	NA	NA	2
N	1996	200	200_400	NA	100.00	428	0	0
N	1996	400	400_600	21.99	67.36	3727	1806	0
N	1996	600	600_800	23.63	33.05	16583	33597	0
N	1996	600	600_800	NA	NA	NA	NA	2177
N	1997	0	0_200	NA	NA	NA	NA	174
N	1997	200	200_400	NA	80.98	1197	281	0
N	1997	400	400_600	33.50	42.34	1745	2377	0
N	1997	600	600_800	30.72	27.00	8837	23898	0
N	1997	800	800_1000	30.62	28.19	189	481	0
N	1998	200	200_400	NA	NA	NA	NA	21
N	1998	400	400_600	10.39	15.48	499	2722	0
N	1998	600	600_800	8.35	7.42	3186	39744	0
N	1998	800	800_1000	NA	0.00	0	475	0
N	1999	400	400_600	NA	5.14	60	1103	0
N	1999	600	600_800	6.14	5.57	1960	33221	0
N	1999	800	800_1000	7.97	9.92	169	1538	0
N	2000	200	200_400	NA	NA	NA	NA	42
N	2000	400	400_600	6.83	4.50	503	10672	0
N	2000	600	600_800	5.78	5.68	1858	30868	0
N	2000	800	800_1000	3.59	2.95	18	606	0
N	2001	200	200_400	NA	NA	NA	NA	155
N	2001	400	400_600	1.43	1.06	21	1999	0
N	2001	600	600_800	6.96	4.01	1033	24733	0
N	2001	800	800_1000	11.70	14.36	113	674	0
N	2002	400	400_600	NA	NA	NA	NA	911
N	2002	600	600_800	5.53	3.97	1474	35694	0
N	2002	800	800_1000	NA	NA	NA	NA	0
N	2003	400	400_600	52.24	30.16	206	478	0
N	2003	600	600_800	15.45	5.26	2165	38976	0
N	2003	800	800_1000	NA	NA	NA	NA	1496
N	2004	200	200_400	NA	83.12	430	1	0
N	2004	400	400_600	19.08	11.47	2509	1938	0
N	2004	600	600_800	4.20	3.59	10102	27158	0
N	2004	800	800_1000	1.38	9.51	600	571	0

Table 4.2.2.1. continued.

Area	Year	Depth	Depth range	st.dev	prop. oceanic	Catch ocean	Catch deep	not classified
S	1995	200	200_400	3.27	97.95	4913	103	0
S	1995	400	400_600	NA	100.00	3184	0	0
S	1995	600	600_800	26.47	55.69	10383	8261	0
S	1995	600	600_800	NA	NA	NA	NA	74
S	1996	200	200_400	NA	NA	NA	NA	3411
S	1996	400	400_600	2.55	98.57	1155	17	0
S	1997	200	200_400	19.88	85.94	1413	231	0
S	1997	400	400_600	NA	NA	NA	NA	453
S	1998	200	200_400	NA	NA	NA	NA	1838
S	1998	400	400_600	NA	NA	NA	NA	11
S	1998	600	600_800	NA	NA	NA	NA	23
S	1999	0	0_200	NA	NA	NA	NA	34
S	1999	200	200_400	1.47	99.22	5663	44	0
S	1999	400	400_600	26.99	86.30	113	18	0
S	2000	200	200_400	NA	NA	NA	NA	664
S	2001	0	0_200	NA	100.00	618	0	0
S	2001	200	200_400	15.37	91.08	11908	1166	0
S	2001	400	400_600	NA	NA	NA	NA	50
S	2001	600	600_800	NA	NA	NA	NA	2
S	2002	200	200_400	0.00	100.00	5093	0	0
S	2002	400	400_600	NA	NA	NA	NA	280
S	2003	200	200_400	0.00	100.00	4988	0	0
S	2003	400	400_600	NA	100.00	90	0	0
S	2004	200	200_400	NA	91.17	4271	414	0
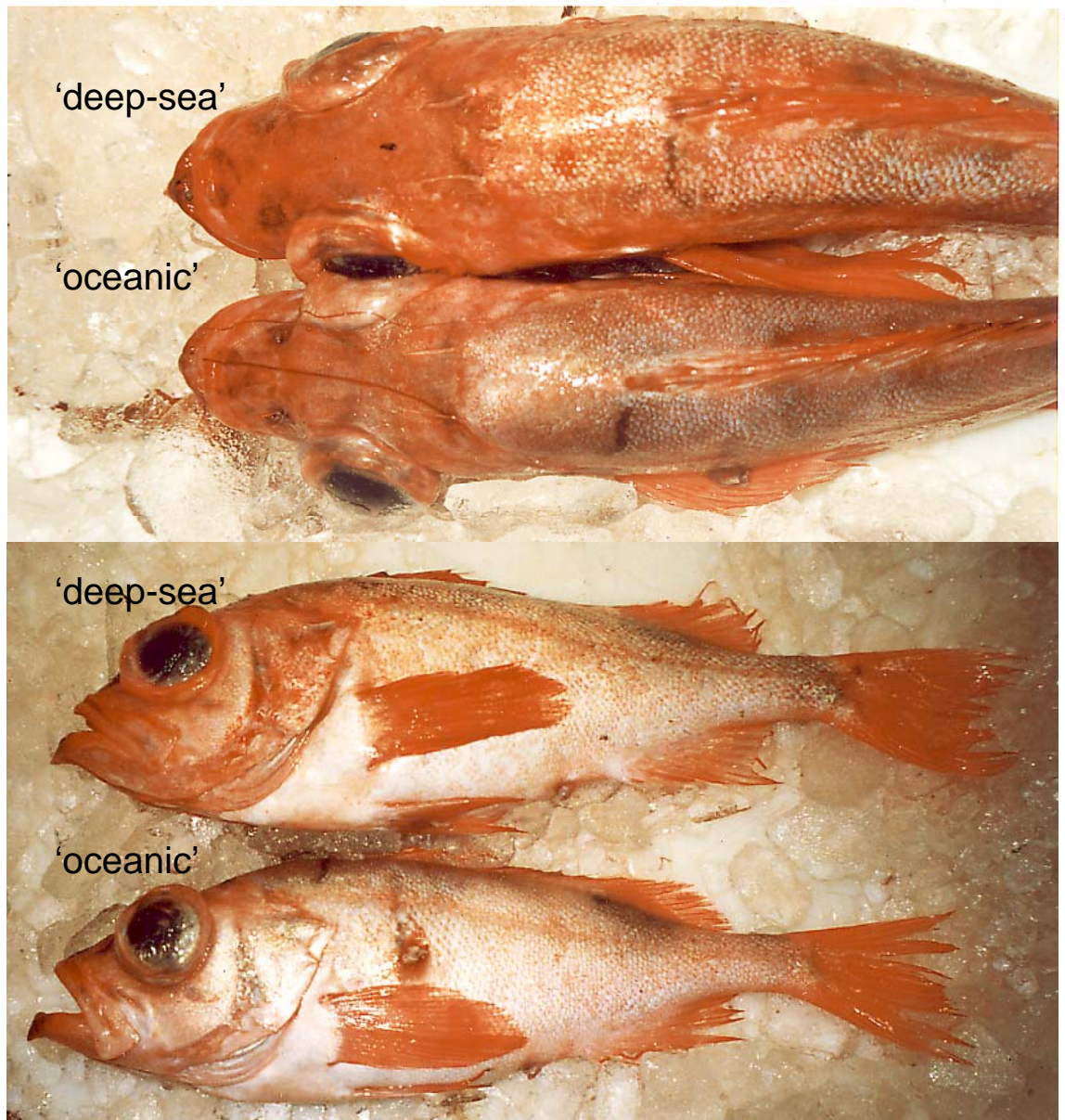
Figure 4.2.2.1. General morphology of 'deep-sea' and 'oceanic' phenotypes in the Irminger Sea (photos from T. Johansen).
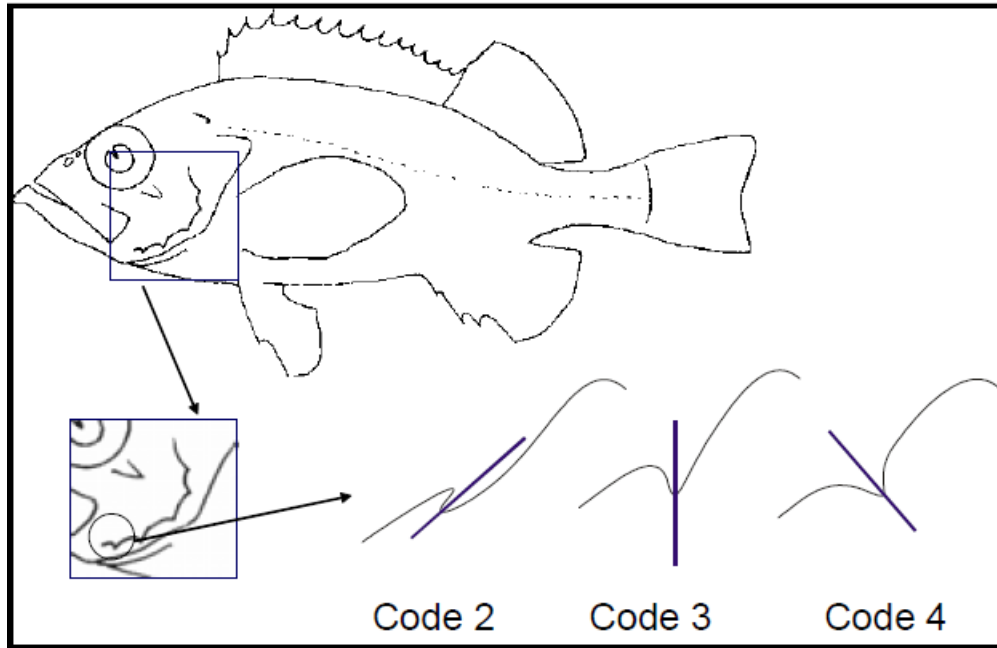
Figure 4.2.2.2. Morphological characters associated with the preopercular spine (the position of third and fifth preopercular spines) used to identify 'deep-sea' (code 2) and 'oceanic' (code 4) phenotypes of *S. mentella* (from Garabana Barro 2004).
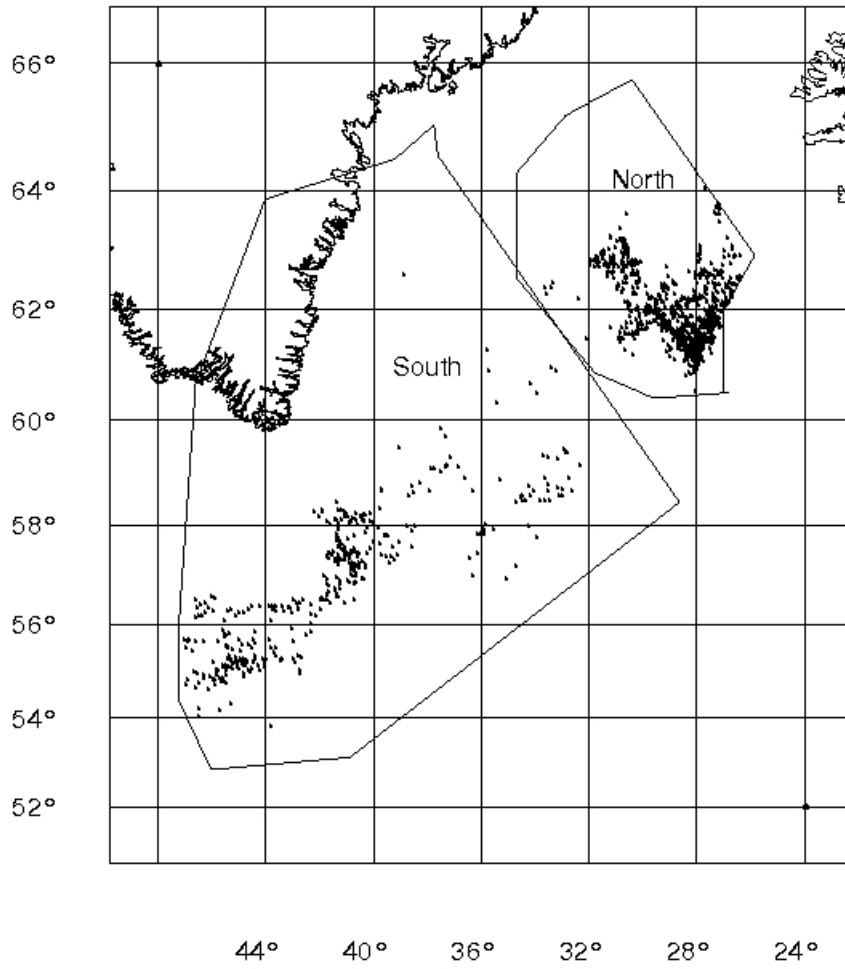
Figure 4.2.2.3. Division of areas between south an north (used in classification of 'deep-sea' and 'oceanic' types in Table 4.2.2.1). The points indicate geographical positions of available samples of pelagic S. mentella from the commercial catches of the Icelandic fleet 1994-2006.
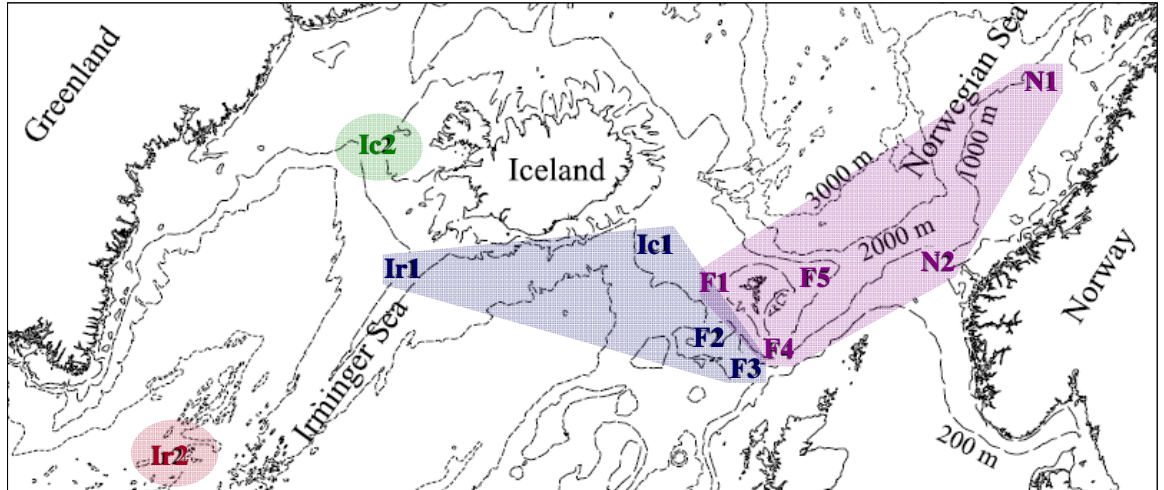
Figure 4.2.2.4. Locations where *S. mentella* were sampled for fatty acid analysis. Colors indicate statistical cluster (modified from Joensen and Grahl-Nielsen 2003). Samples were collected in shallow (IR2, F4, F5, N1 and N2, depth < 540m) and deep (depth > 580m) waters, as well as on continental shelf of Iceland and Faroe Islands (depth > 500m).

4.3   Connectivity

The degree of isolation or mixing of subpopulations is an important aspect of defining stock structure. Connectivity can be evaluated by modeling dispersal of early life stages, mark-recapture analysis of artificial tags or examination of natural tags (e.g., otolith chemistry, parasite infestation). Mixing of groups can involve two distinct patterns that have different influence on population structure and reproductive dynamics: 1) 'overlap' is a pattern in which individuals from reproductively isolated subpopulations share the same habitats in some seasons, but have isolating mechanisms (e.g., separate areas or seasons for reproduction), and 2) 'diffusion' or reproductive mixing, which allows gene flow and correspondence in reproductive dynamics among groups.

Connectivity among geographic groups of *S. mentella* has been studied using several approaches. Rikhter (1996) inferred larval drift of *S. mentella* from distribution of larvae, surface currents and distribution of age-0 demersal stages. He concluded that there are two different stocks in the area of the Irminger Sea: 1) a coastal stock, inhabiting the Iceland and eastern Greenland shelf slopes and 2) a pelagic stock, which occurs in the open sea. The significant differences in number of vertebrae and fin rays found by Rikhter (1996), may also indicate different larval environments, because those features are typically determined during early life stages (Waldman 2005). Saborido-Rey et al. (2004) reviewed previous investigations of *S. mentella* larval drift in the Irminger Sea and adjacent areas and conclude that larvae drift from the central and eastern Irminger Sea towards the Greenlandic Shelf (Figure 4.3.1).

A traditional approach to stock identification and connectivity is the use of parasites as biological tags, and the approach has been revived through advanced methodology (MacKenzie and Abaunza 2005). Patterns of parasite infestation have played a large role in the study of *S. mentella* stock structure. Pelagic phenotypes are partially defined by the prevalence of the parasitic copepod *Sphyrion lumpi*. Unfortunately, there are conflicting patterns of *S. lumpi* infestation (SGRS 1998). Some researchers found increasing infection rates with depth (Magnússon et al. 1995, Magnússon and Magnússon 1995), but others found decreasing infection with depth (Del Rio 1996 and Sarralde et al. 1997).

Parasites and pigmented patches have been used as indicators of population structure of *Sebastes mentella* in the Irminger Sea and adjacent waters by a long series of Russian investigations (1983-2008). Infestation rate of *Sphyrion lumpi* and the entire parasite fauna was similar in all the areas of the pelagic Irminger Sea and adjacent waters (Bakay 1988, 2000, 2001). Parasite fauna above (0-500 m) and below (501-1000 m) the deep-scattering layer were also similar (Bakay and Melnikov 2002, 2008). No geographical variability and considerable year-to-year differences were found in the occurrence of pigment patches on the skin (Bogovski and Bakay 1989). Bakay and Melnikov (2008) interpreted the predominance of pigment patches in individuals at depths greater than 500m and the decrease in occurrence of pigment patches on the skin and muscular melanosis of individuals longer than 40cm and to be a consequence of age-dependent changes and ontogenetic movement to deeper pelagic habitats. Bakay and Melnikov (2008) concluded that the *Sebastes mentella* resource in all depths of the Irminger Sea and adjacent Labrador waters is single stock. However, this interpretation of movement from shallow to deep pelagic environments is refuted by recent genetic evidence of reproductively isolated groups.

By contrast, parasite fauna are distinctly different for pelagic and demersal *S. mentella* in the Reykjanes Ridge area (Melnikov et al. 2005, Melnikov and Bakay 2006). Pelagic

S. mentella are frequently infected by *Sphyrion lumpi*, but those on the Icelandic Slope are not. Conversely, pelagic *Sebastes mentella* do not have some parasites that are found on the slope, such as *Microcotyle sebastis* (Monogenea), and some rarer parasites: *Spinitectus oviflagellis* (Nematoda), *Echinorhynchus gadi, Corynosoma strumosum, Acanthocephalus* sp. (Acanthocephala). The infestation rate of the nematod *Anisakis simplex* is also significantly different between pelagic and demersal *Sebastes mentella.*

Similarity in parasite faunas of *Sebastes mentella* from different areas of the southeastern slope of Greenland and the pelagic Irminger Sea suggests that redfish concentrations in these regions are closely related. A shift in composition of parasite fauna suggests that maturating specimens of redfish migrate from shallow habitats on the slope to the Irminger Sea and to deep waters of the Greenland slope. Am ontogenetic change in parasite fauna of fish in the Irminger Sea occurs as a result of fish moving from the continental shelf, which is the indigenous area of myxosporidians, to a pelagic environment where they feed on copepods, meso- and bathypelagic fish and young squids. The decrease in the composition of trematodes, nematodes and acanthocephalans is accounted for by a shift in diet away from near-bottom crustaceans. The presence of the copepod *Sphyrion lumpi* indirectly suggests a movement of maturating specimens of *Sebastes mentella* from the slope to pelagic waters during summer (Melnikov et al. 2005).

A more recent approach to using natural tags for stock identification is otolith chemistry. As otoliths grow, they incorporate the chemical signature of the fish's environment, so that each growth zone is an archive of the fish's environmental history (Campana 2005). Stransky et al. (2005a) used otolith microchemistry to investigate connectivity between redfish habitats on the East Greenland Shelf and in the Irminger Sea. The study confirmed that elemental signatures in cores of otoliths collected from E. Greenland cores were temporally stable. Similar elemental concentrations (Li, Sr, Mg, Ba, and Cu) were found between redfish otoliths collected in the Irminger Sea and East Greenland. The lack of clear spatial differences in otolith chemistry could indicate either common natal origin of adults or a lack of variation in elemental chemistry across large expanses of the ocean in this region.

Tagging has a long history in fishery research and the study of movement patterns (Thorsteinsson 2002). A particular challenge in tagging redfish is the barotraumas associated with bringing fish to the surface. Sigurðusson et al (2006) solved this dilemma using an innovative *in situ* tagging device. Although the objective of the tagging project was to demonstrate effectiveness of in situ tagging technology, there were some tag releases and a few long-term recaptures that offer valuable insights into movement patterns. Sample sizes were low and not designed to represent a management unit or biological stock, but the 49 recaptured tags include several movements from deep, pelagic environments to demersal habitats on the Icelandic Slope (Figure 4.3.2, Table 4.3.1). These movements document distributional overlap between the two groups and perhaps connectivity. The recapture information was updated during the WKREDS meeting, because a tag was returned to Icelandic Researchers from the Russian fishery. Data storage tags were also deployed, but none have been recaptured to date.

Information from larval drift, parasites, otolith chemistry and tagging suggest that subpopulations of *S. mentella* mix during early life stages, as larvae and juveniles, then adults recruit to different habitat groups that have overlapping distributions. Synthesis of information on connectivity and genetic composition indicates that overlapping adult distributions do not involve reproductive mixing.

Table 4.3.1. Results of tagging experiments, updated from Sigurðusson et al (2006).

|	Release Information					Recapture Information						Depth
				Depth	Length				Depth	Distance		Change
Recap.	Lat.	Lon.	Date	(m)	(cm)	Date	Lat.	Lon.	(m)	(NM).	Days	(m)
1	63.08	-23.80	22.10.2003	504	43	28.10.2003	63.10	-23.80		0.7	6	
2	63.11	-23.67	23.10.2003	521	37	10.2.2004	62.93	-24.43	531	23.5	110	-10
3	63.11	-23.67	23.10.2003	506	37	17.8.2005	63.08	-20.83	466	76.9	664	40
4	63.11	-23.67	23.10.2003	503	35	26.8.2004	63.15	-23.42	482	7.1	308	21
5	63.11	-23.67	23.10.2003	507	38	28.9.2004	63.00	-24.18	458	15.6	341	49
6	63.11	-23.67	23.10.2003	507	39	26.6.2005	63.98	-11.72	350	323.1	612	157
7	63.11	-23.71	23.10.2003	505	36	10.4.2004	63.00	-24.13	503	13.1	170	2
8	63.03	-24.01	24.10.2003	503	43	16.8.2004	63.30	-12.17		320.9	297	
9	63.09	-23.77	24.10.2003	502	37	16.8.2004	63.47	-12.33		309	297	
10	63.09	-23.77	24.10.2003	502	39	11.4.2004	63.00	-24.00	549	8.2	170	-47
11	63.11	-23.68	25.10.2003	510	42	22.6.2006	64.03	-13.23	302	284.1	971	208
12	63.11	-23.68	25.10.2003	500	42	19.2.2004	63.08	-23.83	512	4.4	117	-12
13	63.11	-23.68	25.10.2003	503	39	21.1.2004	63.02	-23.95	521	9.3	88	-18
14	63.03	-23.98	8.6.2004	495	36	28.1.2005	62.98	-25.00	512	27.8	234	-17
15	63.03	-24.02	10.6.2004	500	39	31.3.2005	63.50	-26.10	513	63	294	-13
16	63.03	-24.02	10.6.2004	497	36	18.2.2006	62.85	-24.59	549	18.9	618	-52
17	63.03	-24.02	10.6.2004	500	42	28.11.2004	63.05	-23.98	494	1.8	171	6
18	63.02	-24.04	10.6.2004	510	41	7.10.2004	65.82	-27.35	567	188.3	119	-57
19	63.02	-24.04	10.6.2004	495	38	15.3.2006	62.93	-24.27	604	8.2	643	-109
20	63.02	-24.04	10.6.2004	510	37	15.11.2006	62.75	-24.58	670	22.1	888	-160
21	62.98	-24.20	12.6.2004	505	36	16.10.2004	63.17	-23.40	458	24.6	126	47
22	62.98	-24.20	12.6.2004	535	38	17.8.2005	63.17	-23.43	439	23.8	431	96
23	61.29	-28.22	14.6.2004	764	42	23.6.2004	61.50	-28.32	778	13	9	-14
24	61.29	-28.22	14.6.2004	720	37	17.6.2004	61.35	-28.25	622	3.8	3	98
25	61.38	-28.33	14.6.2004	710	42	17.6.2004	61.38	-28.43	741	3	3	-31
26	61.26	-28.16	15.6.2004	750	37	23.6.2004	61.53	-28.27	778	16.5	8	-28
27	61.36	-28.42	15.6.2004	720	38	19.6.2004	61.38	-28.28	741	4.2	4	-21
28	61.36	-28.42	15.6.2004	720	39	19.6.2004	61.28	-28.13	778	9.6	4	-58
29	61.40	-28.47	16.6.2004	680	43	27.5.2008	61.85	-28.78	686	28.3	1441	-6
30	61.32	-28.24	16.6.2004	670	40	29.6.2004	61.90	-28.57	778	36.2	13	-108
31	61.31	-28.20	17.6.2004	740	40	26.6.2004	61.60	-28.32		17.8	9	
32	61.38	-28.31	18.6.2004	744	42	19.6.2004	61.40	-28.30	732	1.5	1	12
33	61.35	-28.21	19.6.2004	740	40	28.4.2005	61.77	-29.07	687	35.1	313	53
34	61.35	-28.21	19.6.2004	740	39	19.4.2006	61.42	-28.55		10.6	669	
35	61.52	-28.42	19.6.2004	740	41	21.6.2004	61.35	-28.23	622	11.2	2	118
36	61.37	-28.21	20.6.2004	700		6.11.2004	65.87	-27.28	549	271.1	139	151
37	61.37	-28.21	20.6.2004	700	41	1.7.2004	62.08	-28.53	641	44	11	59
38	63.03	-24.02	22.10.2003	504		30.1.2006	65.87	-27.23	549	189.6	831	-45
39	63.03	-24.02	22.10.2003	506	38	27.2.2005	62.93	-25.17	586	31.8	494	-80
40	62.38	-28.55	15.6.2005	640	42	25.5.2006	62.67	-26.95	750	47.4	344	-110
41	62.38	-28.80	18.6.2005	686	42	3.5.2006	61.35	-28.42	741	62.9	319	-55
42	62.48	-28.98	20.6.2005	739	39	23.5.2007	61.75	-27.60	732	58.7	702	7
43	62.45	-28.57	20.6.2005	707	40	9.6.2007	62.88	-27.27	659	44.3	719	48
44	62.57	-28.93	21.6.2005	690	42	1.6.2006	61.20	-28.10	675	85.3	345	15
45	62.68	-28.67	22.6.2005	807	42	17.6.2007	63.15	-26.45	659	66.7	725	148
46	62.22	-31.07	27.8.2006	651	40	24.4.2008	61.20	-28.08	600	104.5	606	51
47	62.38	-31.03	28.8.2006	690	42	15.5.2008	61.71	-29.15	600	66.6	626	90
48	64.38	-27.72	17.7.2008	661		20.10.2008	65.90	-27.05		92.5	95	
49	64.18	-27.47	11.6.2005	697	43	7.2.2006	64.02	-26.87	659	18.6	241	38
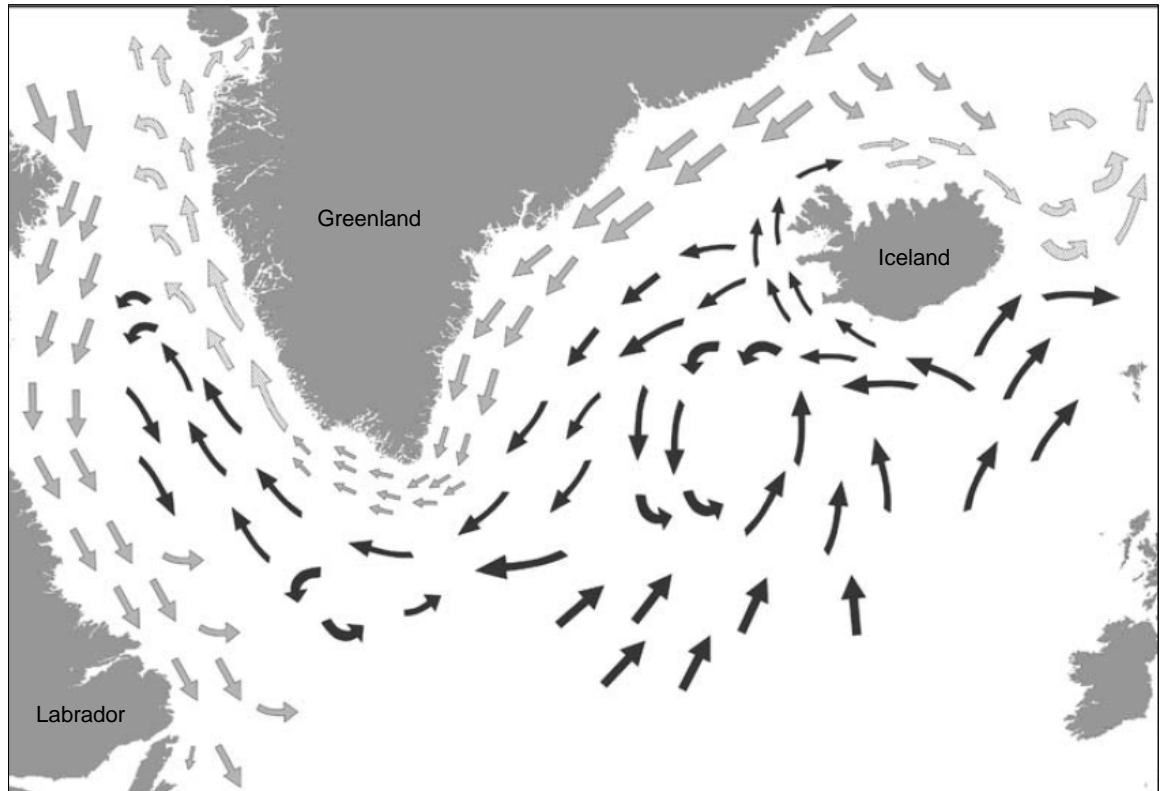
Figure 4.3.1. General trends of ocean currents in the Northwest Atlantic. Grey arrows represents cold, Labrador and Irminger currents. Dark arrows are the North Atlantic current and their branches (from SGRS 1998).
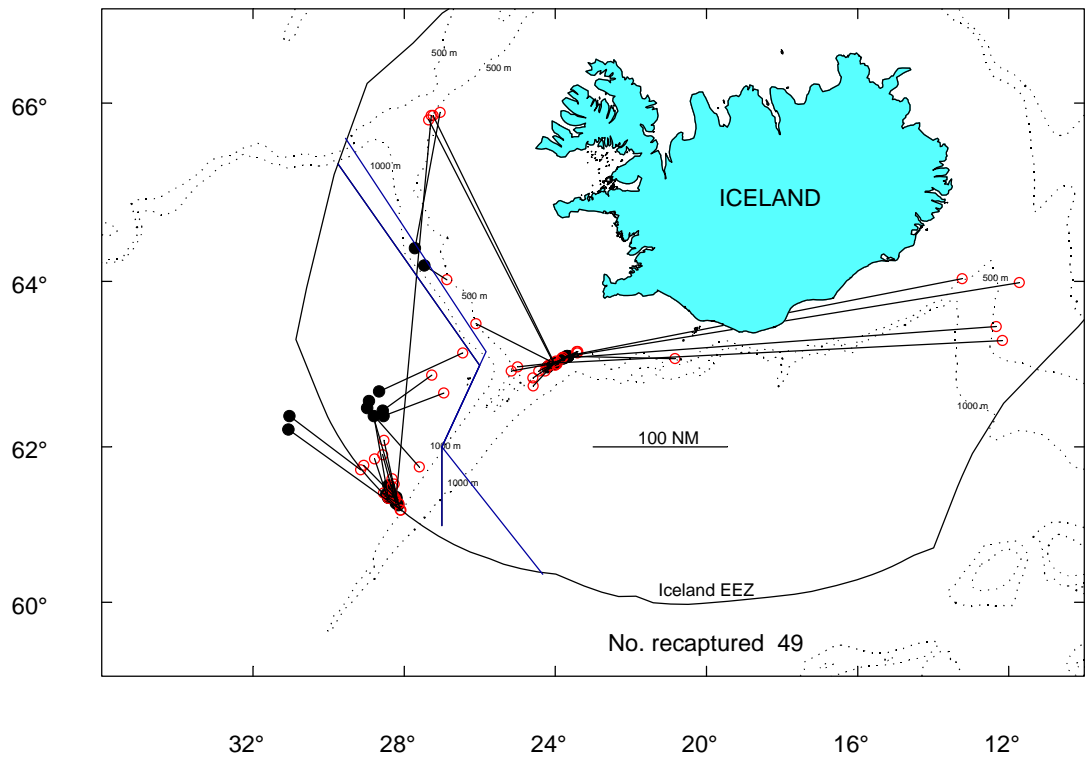
Figure 4.3.2. Results of tagging experiments, updated from Sigurðusson et al (2006). Black dots indicate the tagging site and red, open cirles indicates the recapture site. The line for different management units are shown as blue lines.

5   Biological Stocks

A synthesis of all available information was used to test each of the *a priori* stock structure hypotheses.

- The single-population hypothesis was rejected on the basis of significant differences in microsatellite allelic frequencies among deep Irminger Sea, shallow Irminger Sea and Icelandic Slope samples, as well as significant differences in allozymes and fatty acid profiles among the same three groups, and distinct parasitological differences between Icelandic Slope and pelagic specimens.

- Several two-stock hypotheses were tested.
    o The current management unit hypothesis (one pelagic stock and one demersal stock) was rejected on the basis of significant differences in microsatellite allelic frequencies between deep and shallow Irminger Sea samples, as well as significant differences in allozymes and fatty acid profiles.
    o The two depth-defined stocks (one stock <500m and one stock >500m) was rejected on the basis of significant differences in microsatellite allelic frequencies between continental slope and pelagic samples, as well as significant differences in allozymes, fatty acid profiles and parasite fauna.
    o The two phenotype hypothesis ('oceanic' and 'deep-sea') was similarly rejected on the basis of significant differences in microsatellite allelic frequencies between continental slope and pelagic samples, as well as significant differences in allozymes, fatty acid profiles and parasite fauna.

- One *a priori* three-stock hypothesis (slope, shallow and deep pelagic stocks) was not entirely consistent with all data, because heterogeneity within continental slope samples from Iceland and the Faroe Islands was indicated by microsatellites and fatty acids. However, this heterogeneity was recognized in the *a priori* evaluation as a possible alternative hypothesis. The alternative three-stock hypothesis was consistent with all information on stock structure:

Based primarily on microsatellite information, supported by analyses of allozymes, fatty acids, as well as some parasite patterns, WKREDS concludes that there are four biological stocks in the entire geographic range of *S. mentella*, and three stocks in the area of concern, the Irminger Sea and adjacent waters:

1) 'Western' (NAFO 3+)

2) 'Deep Pelagic' (NAFO 1-2, ICES Vb XII XIV >500m)
- Primarily pelagic habitats, but includes demersal habitats west of the Faroe Islands
- Not to be confused with the 'deep-sea' phenotype

3) 'Shallow Pelagic' (NAFO 1-2, ICES Vb XII XIV <500m)
- Extends to ICES I-II
- Primarily pelagic habitats, but includes demersal habitats east of the Faroe Islands

4) Icelandic Slope (ICES Va XIV)

Note that juveniles on the Greenland Shelf are most likely from the 'shallow pelagic,' 'deep pelagic,' and 'Icelandic Shelf/Slope' stocks. This consensus perception of biological stock structure is based primarily on genetic patterns among adult samples. Other stock identification information (e.g., overlapping distributions of life stages, growth and maturity patterns, generally similar morphometry and parasite patterns) cannot be used to rigorously reject any hypothesis, because several alternative interpretations of those data are equally valid. The consensus view of biological stock structure cannot be rejected by any information available. On the contrary, many of the phenotypic patterns can be interpreted as a reflection of this biological stock structure (e.g., subtle morphological differences among areas, different size distributions by depth, different size-at-maturity, and 'phenotypes').

6   Recommended Management Units

Although biological stocks of *S. mentella* are partially defined by depth, WKREDS recognizes that definition of management units by depth and the associated fishery monitoring by depth would be impractical. Depth-based differences in genetic stocks can be viewed as geographically separated units (Figure 6.1). Therefore, WKREDS recommends three management units that are based on geographic proxies for biological stocks that minimize mixed-stock catches. Using the approach developed by SGSIMUR (2005), boundaries of recommended management units are based on spatial patterns of the recent fishery to minimize mixed-stock catches (Figure 6.2).

A. The 'Deep Pelagic' Management Unit: the northeast Irminger Sea (Figure 6.2). The coordinates of the recommended boundary are in Table 6.1.

B. The 'Shallow Pelagic' Management Unit: NAFO areas 1 and 2, ICES areas Vb, XII, XIV outside of the 'deep pelagic' management unit area defined in Figure 6.2. This area will include some mixed-stock catches of the 'deep pelagic' stock southwest of the Faroe Islands.

C. The 'Icelandic Slope' Management Unit: North and east of the existing 'redfish line' (Figure 6.2). This area will include some of the 'deep pelagic' stock that occasionally extends inside the boundary.

Spatial and seasonal patterns in the pelagic fishery have been relatively stable since 1996 (Sigurðusson et al. 2006, NWWG 2008). Spatial analysis of pelagic fishery catch and effort by depth, inside and outside the recommended 'deep pelagic' management unit boundaries indicate that the boundaries effectively delineate the deep, pelagic fishery from the shallow, pelagic fishery, with a small portion of mixed-stock catches (Table 6.2, Figures 6.3 and 6.4).

These recommended managment units are illustrated in Figure 6.5. Given the overlapping distributions of the associated biological stocks, mixed-stock catches in Irminger Sea should be monitored for stock composition. Surveys should be stratified by depth (i.e., <500 m and >500 m), and used to collect genetic samples to serve as baselines for genetic stock composition.

Table 6.1. Coordinates of the recommended boundary of the 'deep pelagic' management unit.

BOUNDARY POINT	LAT	LON	LAT	LON
1	645700	-283000	64.95000	-28.50
2	630000	-253300	63.00000	-25.55
3	615500	-264500	61.91667	-26.75
4	610000	-263000	61.00000	-26.50
5	590000	-300000	59.00000	-30.00
6	590000	-340000	59.00000	-34.00
7	613000	-340000	61.50000	-34.00
8	625000	-360000	62.83333	-36.00
9 same as 1	645700	-283000	64.95000	-28.50

Table. 6.2. Reported catch in the northeast Irminger Sea inside and outside the recommended management unit boundary for the 'deep pelagic' stock.

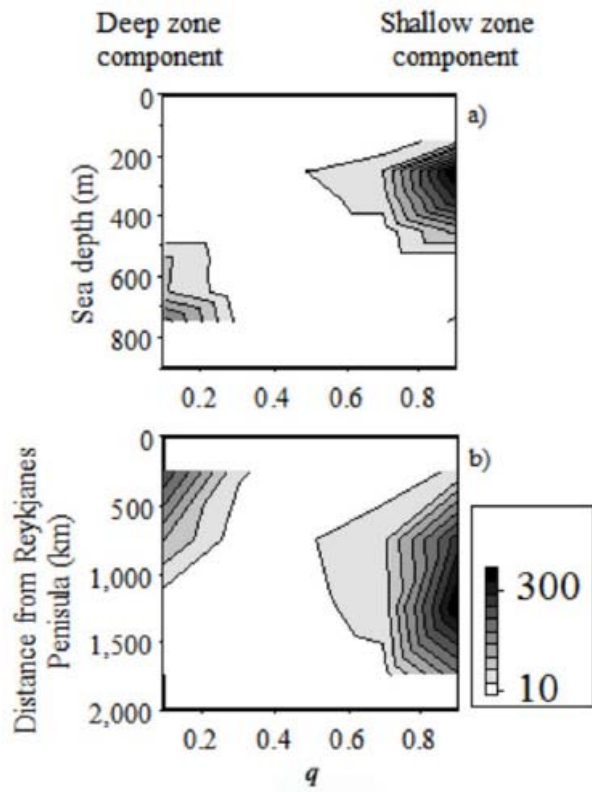| Year	outsite box tonnes	inside box tonnes	Total catch
1996	13087	57288	70376
1997	19014	63770	82784
1998	22512	63469	85981
1999	23113	56382	79494
2000	19384	77401	96785
2001	29868	69770	99639
2002	24635	78669	103304
2003	40825	77259	118084
2004	18661	65020	83682
2005	20056	33027	53083
2006	7691	48156	55848
2007	30	17534	17564
Sum catch	238877	707746	946622

Figure 6.1. Contour plots representing the proportional distribution of samples (q) by a) depth (m) and b) distance (km) from the south-west tip of the Reykjanes Peninsula. A q value of zero represents a pure 'deep pelagic' sample, whereas a q value of 1 represents a pure 'shallow pelagic' sample.
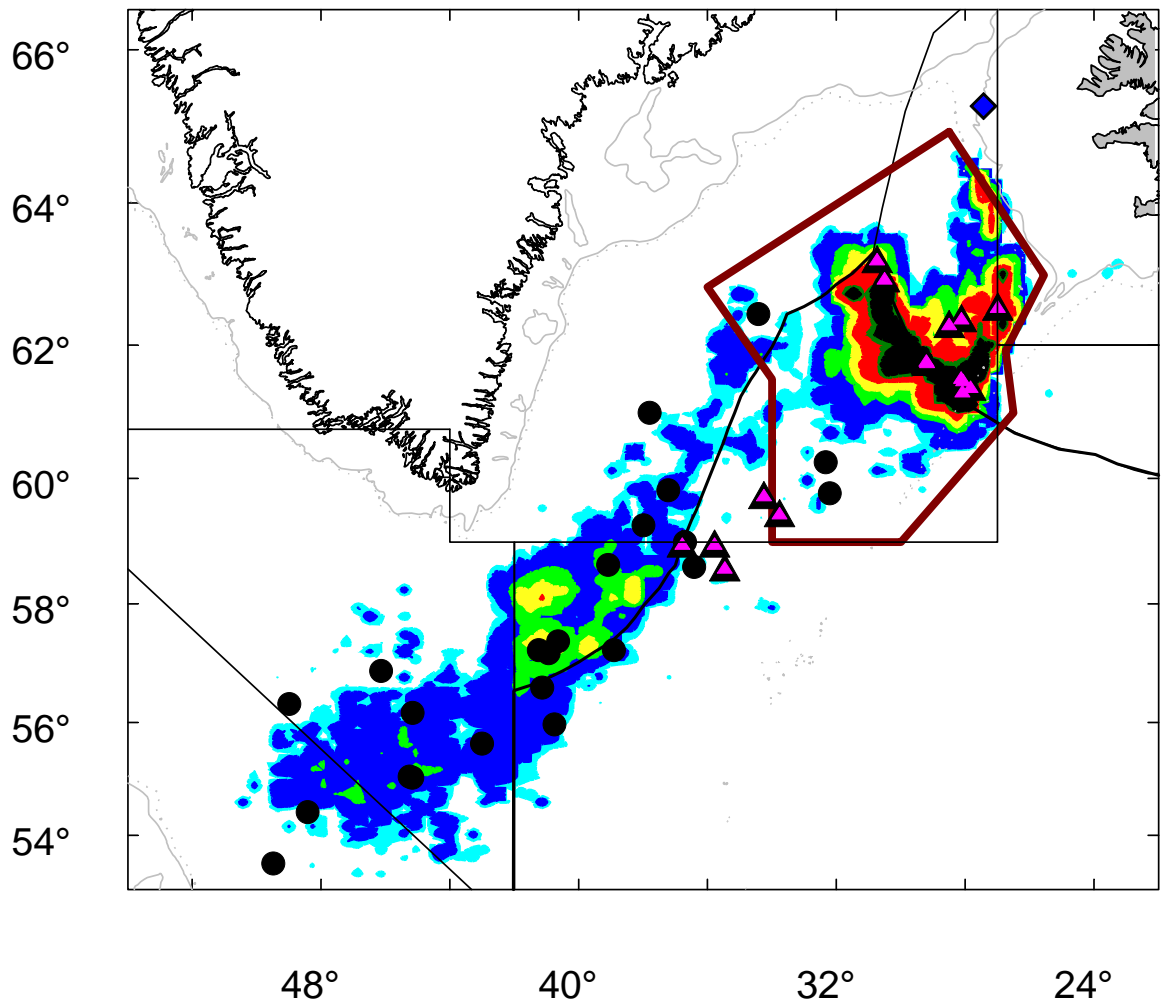
Figure 6.2. Recommended management unit boundaries (red polygon), with fishing distribution and genetic sample locations. Fishery data are from Iceland, Russia, Germany, Norway, Faroe Island and Greenland (1996-2007). Black circles: 'shallow pelagic' genotype; pink triangles: 'deep pelagic' genotype; blue dimonds = 'Icelandic Slope' genotype. The box with black thick lines indicates the suggested box for the 'deep pelagic' management unit and the red line indicates the "redfish line" used by Icelandic authorities in 2003. Depth contour on the maps are 500, 1000 and 200 m.
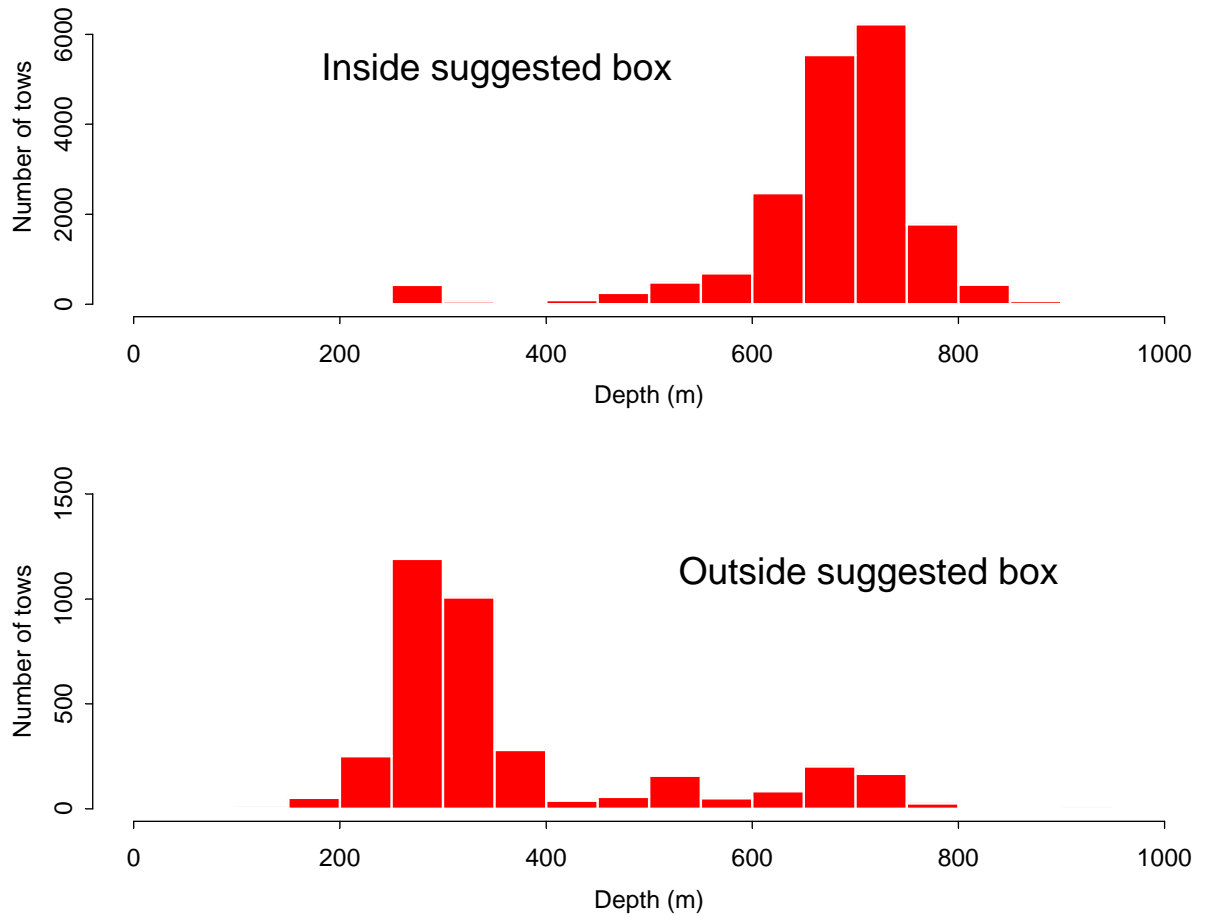
Figure 6.3. Distribution of number of tows made by the fishery, by depth. Upper panel shows the distribution of tows inside the recommended 'deep pelagic' management unit boundary, and the lower panel shows number of tows outside the box. Fishery data are from Iceland, Russia, Germany, Norway, Faroe Island and Greenland (1996-2007).
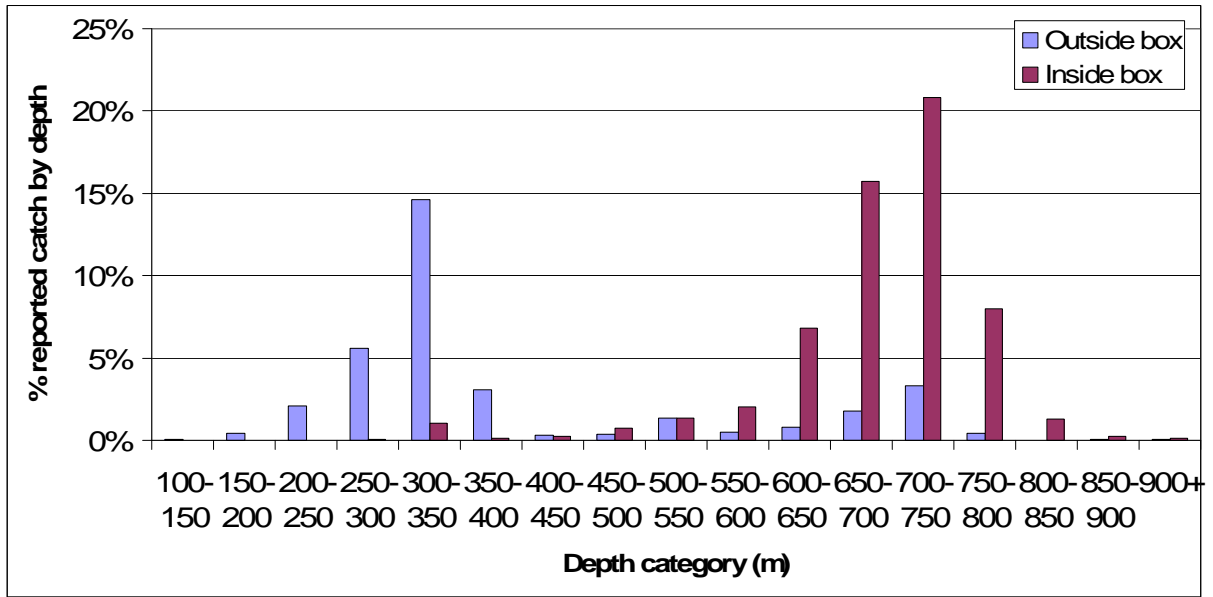
Figure 6.4. Distribution of catches by depth, 1996-2007, inside and outside the recommended 'deep pelagic' management unit boundary. Data where depth is not reported are excluded.
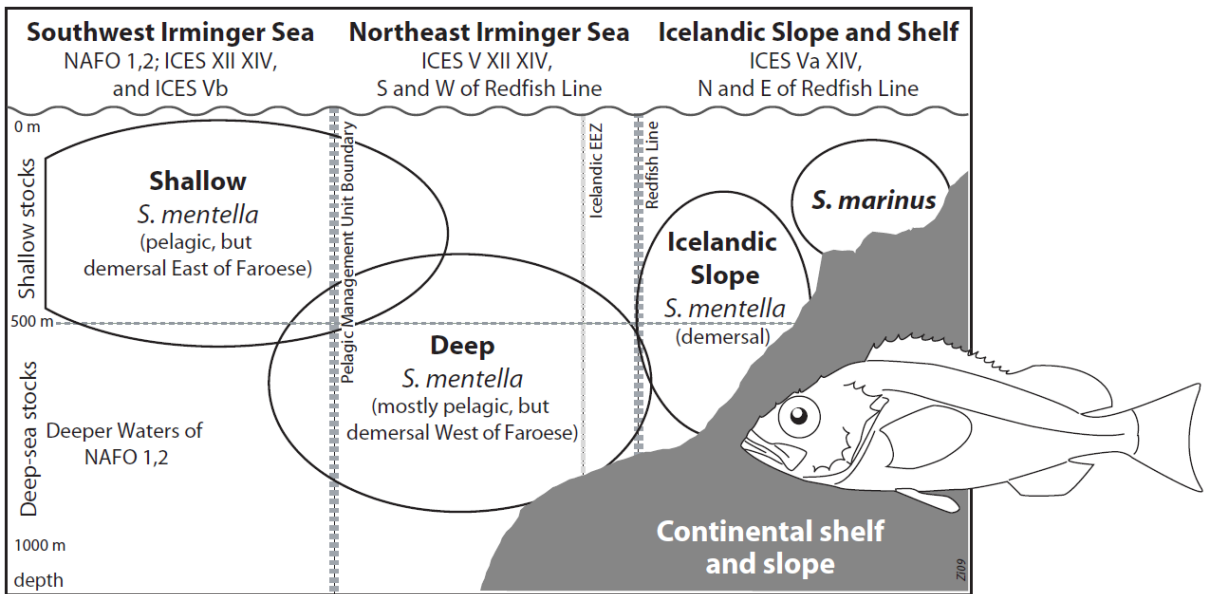

Figure 6.5. Biological stocks and recommended management units of redfish in the Irminger Sea and adjacent waters.

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Annex 2: Agenda

Workshop on Redfish Stock Structure (WKREDS)

Chair: Steve Cadrin, USA

ICES Headquarters, Copenhagen

10:00 22 January to 18:00 23 January, 2009

Thursday, 22 January 2009

1. Opening

2. Adoption of agenda and timetable

3. Introductions

4. Background Information - Define stock structure hypotheses and putative boundaries to provide context in which to review information.

5. Term of Reference a) Review all reported material on the stock identity of the various redfish units (Sebastes mentella) in the Irminger Sea and adjacent waters.

    5.1. Develop Process for technical reviews

    5.2. Technical Reviews

Friday, 23 January 2009

6. Term of reference b) identify the most likely definition of biological stocks of S. mentella and suggest practical management units.

    6.1. Interdisciplinary analysis of biological stocks, integrating conclusions on geographic distribution, geographic variation, and connectivity for a holistic perspective on biological stocks.

    6.2. Spatial definition of biological stocks

    6.3. Definition of practical management units:

        6.3.1.   Definition by fishery data (spatial, seasonal?, fishing technology?)

        6.3.2.   Definition by survey data (spatial, seasonal?, survey technology?)

7. Develop WKREDS Report

    7.1. Draft consensus recommendation to ACOM and NWWG on management units

    7.2. Draft WKREDS report (due 6 February 2009)

Annex 3: Recommendations

RECOMMENDATION	FOR FOLLOW UP BY:
1. Sebastes mentella in the Inrminger Sea and adjacent areas should be managed as three units that reflect biological stocks: 1) the 'Deep' management unit in the northeast Irminger Sea, 2) the 'Shallow' management unit (NAFO areas 1 and 2, ICES areas Vb, XII, XIV), and 3) the 'Icelandic Slope' management unit (north and east of the existing 'redfish line').	ADGRS
2. Mixed-stock catches in Irminger Sea should be monitored for stock composition.	NWWG
3. Surveys should be stratified by depth (i.e., <500 m and >500 m), and used to collect genetic samples to serve as baselines for genetic stock composition.	PGRS
4. Collaboration among national institutes and universities should continue to refine the perception of stock structure, similar to the sample sharing and partnerships developed by the EU REDFISH project and the Faroese Redfish Project.	SciCom, SIMWG
5.All developmental stages should be sampled to define spatial ditributions (e.g., mating areas, larvae in both Irminger Sea and Norwegian Sea, post-settlement, juveniles on Greenland and Norwegian nursery grounds, etc.)	PGRS
6. Further work on age determination and validation is needed.	NWWG
7. *In situ* tagging should continue, particularly with archival tags.	NWWG, SIMWG
8. Further exploration is needed on the relationship between 'deep' and 'shallow' genetic stocks and 'oceanic' and 'deep sea' phenotypes, respectively. Adaptive characters should be studied to help interpret ecology and divergence of genetic groups.	SIMWG

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"ВСЕРОССИЙСКИЙ НАУЧНО-
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№ _____   от _10·02·2009_

Dr Gerd Hubold
General Secretary ICES
H.C.Andersens Blvd. 44-46
DK 1553 Copenhagen V
Denmark

Cc: Mike Sissenwine, ACOM Chair
Hans Lassen, Head of Advisory Programme

Subject:
Meeting of the ICES Study Group
on Redfish Stock Structure (WKREDS)

Dear Dr G. Hubold,

I refer to the meeting of the ICES Study on Redfish Stock Structure (WKREDS) (Chair: Steve Cadrin, USA), that met on 22-23 January 2009. By this letter as a delegate to ICES from the Russian Federation, I want to express my disappointment by the Study Group having failed to reach consensus among experts in developing scientific recommendations required by its ToRs.

The Russian members of this Group strongly disagreed with the approach taken at the meeting where, in fact, primarily genetic data were used as a basis of recommendations having implications for the overall management regime of pelagic redfish *Sebastes mentella* in the Irminger Sea and adjacent waters. We believe that this contradicts the principle of holistic scientific assessment.

For this reason the Russian scientists requested to include their special comment (attached) in the Group's report, highlighting the need and importance of applying other study methods for stock identification, such as analysis of biology and ecology of the species, morphometry, composition and shape of otoliths, before any "biological stocks" or "management units" for redfish, or any other species, could be conclusively and definitively decided and proposed to managers. But that was rejected.

This situation could hardly be acceptable to the Russian Federation and we would appreciate, if you give due consideration to this matter and take appropriate action to rectify the situation, so that the view of Russian science could rightly be represented in the advice given by ICES to NEAFC.

Sincerely yours,

Vasily Sokolov
Research Director, VNIRO
Russian Delegate to ICES

Special comment (Russian Federation)

Three Russian members of WKREDS presented the following view: "On the basis of results of researches of population structure of *S. mentella* in the Irminger Sea and adjacent waters including analyses of biological data, identifying all stages of the life cycle, functional role of various areas within the distribution range, specific features of reproduction, using parasites and pigment patches as natural marks, Russian researchers came to a conclusion about the existence of a single, self-sustaining population in this area. Division of *S. mentella* into several "biological stocks" in the Irminger Sea and adjacent waters, as suggested by WKREDS, based mainly on genetic results is likely to be biologically groundless.

Taking into account existing evidence of a single stock of *S. mentella* in the Irminger Sea and adjacent areas, and disagreement between WKREDS members concerning the number of "biological stocks" we suggest to keep current management units for *S. mentella* unchanged.

Before deciding what management units and how many of them there should be, it is necessary to clarify main biological questions related to *S. mentella*, i.e., to determine the areas of overlapping geographical distribution of possible biological stocks, to create a model of life-history and migrations of *S. mentella* in order to determine criteria which can be used for the definition of management units."