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Description of the methods used for estimating the abundance of *Sebastes fasciatus* and S. *mentella* in Units 1 and 2

Description des méthodes utilisées pour estimer l'abondance de *Sebastes fasciatus* et de S. *mentella* dans les unités 1 et 2

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Abstract

Efforts have been made to assess the situation of *Sebastes fasciatus* and *S. mentella* in Units 1 and 2. Because no visual distinction is possible between those two redfish species, methods have been developed to estimate indices of abundance of each species from the historic databases. The discrimination criteria used, coming mainly from the Redfish Multidisciplinary Research program 1995-99, were anal fin ray counts (AFC) and the analysis of the malate dehydrogenase (MDH). These characters have been used to split the redfish sp. into species or genotypes. The main method use AFC to evaluate the number of each species caught by tow. A correction was calculated at different depth intervals to reflect the difference in depth distribution for the two species. Proportions of species abundance by depth zone have been calculated from MDH analysis and applied for sets when no discrimination criterion had been recorded. Another method using AFC-length keys subsequently converted into species using MDH was also elaborated. Those methods have been used to analyze different surveys in Units 1 and 2.

The estimates of *S. fasciatus* abundance can be different depending of the method used. These gaps are more important for years when no discrimination character were recorded. In Unit 1, *S. fasciatus* was dominant at lower depth zone and *S. mentella* in deep water, the mixing zone being mainly between 183-274 m. Each species showed different length frequencies, *S. fasciatus* is generally smaller then *S. mentella.* Because of this, the AFC-length key method was found appropriate to separate species. In Unit 1, the Cod Sentinel summer survey, the GEAC survey and the survey in 4T showed decreasing trends in the last years or low historic abundance for both species. Only the Cod Sentinel fall survey showed stable but low level indices of abundance from 1995 to 2002. In Unit 2, little information was available. Like in Unit 1, *S. fasciatus* dominates in shallow areas (less than 366 m). Moreover, a survey covering only division 4V showed indices of abundance at a low level in the last years.

The discrimination by AFC recorded at each tow and corrected to genotype is simple to perform and could give good estimates of species composition. In years with no criteria of separation recorded, genotype proportions by depth or AFC-length keys could give acceptable estimates of the two species, but should be interpreted with caution because fluctuations of abundance due to mortality, recruitment and/or switch in depth preference could have affected the results of these methods. However, abundance of *S. fasciatus* evaluated by whatever methods show the same trend, so both methods were found useful to get general trends of the redfish species.

Résumé

On tente d'évaluer l'état des stocks de *Sebastes fasciatus* et de *S. mentella* des unités 1 et 2. Comme il est impossible d'identifier à vue ces deux espèces de sébaste, on a élaboré des méthodes pour estimer les indices d'abondance de chacune fondées sur des données historiques. Les critères de discrimination utilisés, provenant principalement du Programme zonal multidisciplinaire de recherche sur le sébaste de 1995-1999, sont le nombre de rayons de la nageoire anale et le patron électrophorétique en malate déshydrogénase (MDH). Ces caractères ont permis de classer les spécimens selon l'espèce ou le génotype. La méthode principale fait appel au nombre de rayons de la nageoire anale pour évaluer le nombre d'individus de chaque espèce capturés par trait. On a calculé un facteur de correction pour différents intervalles de profondeur, qui reflète la différence dans la distribution des deux espèces selon la profondeur. L'abondance de chaque espèce selon la strate de profondeur a été établie d'après une analyse de la MDH, puis elle a été appliquée aux traits pour lesquels aucun critère de discrimination n'avait été consigné. On a aussi mis au point une autre méthode fondée sur des clés du nombre de rayons de la nageoire anale selon la longueur, permettant d'identifier l'espèce d'après la MDH. Ces méthodes ont servi à analyser les données de divers relevés réalisés dans les unités 1 et 2.

Les estimations de l'abondance de *S. fasciatus* diffèrent selon la méthode utilisée. Ces écarts sont plus marqués pendant les années pour lesquelles aucun caractère de discrimination n'a été consigné. Dans l'unité 1, *S. fasciatus* était l'espèce la plus abondante dans la zone moins profonde alors que *S. mentella* l'était en eau profonde, la zone de mélange des deux espèces se situant principalement entre 183 et 274 m. Les deux espèces montraient des fréquences de longueur différentes, *S. fasciatus* étant généralement plus petit que *S. mentella*; la clé du nombre de rayons de la nageoire anale selon la longueur s'est donc révélée appropriée pour les distinguer. Dans l'unité 1, le relevé d'été de la morue par pêche sentinelle, le relevé effectué par le GEAC et le relevé effectué dans 4T ont révélé des tendances à la baisse des deux espèces durant les dernières années ou une faible abondance historique. Seul le relevé d'automne de la morue par pêche sentinelle a donné des indices d'abondance stable mais faible de 1995 à 2002. Peu d'information est disponible pour l'unité 2. Comme dans l'unité 1, *S. fasciatus* y est l'espèce dominante en eau peu profonde (moins de 366 m de profondeur). Qui plus est, un relevé ne couvrant que la division 4V a donné des indices d'abondance faible dans cette unité durant les dernières années.

Il est facile de distinguer les deux espèces selon le nombre de rayons de la nageoire anale consigné pour les spécimens capturés dans chaque trait et corrigé selon le génotype, ce qui pourrait permettre d'obtenir de bonnes estimations de la composition des prises selon l'espèce. Dans le cas des années pour lesquelles aucun critère de discrimination n'a été consigné, les proportions des génotypes selon la profondeur ou les clés du nombre de rayons de la nageoire anale selon la longueur pourraient donner des estimations acceptables de l'abondance des deux espèces, mais ces estimations devraient être interprétées avec prudence car les fluctuations de l'abondance imputables à la mortalité, au recrutement et/ou à un changement de profondeur fréquentée peuvent avoir influer sur les résultats obtenus à l'aide de ces méthodes. Toutefois, l'abondance de *S. fasciatus*, qu'elle soit évaluée à l'aide de l'une ou l'autre de ces méthodes, montre la même tendance; elles se révéleront donc utiles pour établir les tendances générales de l'abondance de ces deux espèces.

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Introduction

Three species of redfish are known to inhabit the Northwest Atlantic: the acadian redfish, *Sebastes fasciatus*, the deep-water redfish, *S. mentella* and the golden redfish, *S. marinus.* Except at Flemish cap, *S. marinus* occurs only sporadically (Ni and McKone 1983). Visual distinction between *S. mentella* and *S. fasciatus* is nearly impossible and there is even confusion with *S. marinus*. Futhermore, hybridisation and subsequent introgression (incorporation of genes of one species into the gene pool of another) occur between *S. fasciatus* and *S. mentella* in units 1 and 2 (Rubec *et al.* 1991; Roque *et al.* 2001). Due to this taxonomic difficulty, the redfish in the Northwest Atlantic is currently managed as one "species" although various morphologic and biochemical characters that could be use to separate redfish sp. have been recorded by DFO since the 1980s.

Unit 1 represents a relatively new management unit. Redfish in the Gulf of St. Lawrence were previously managed as NAFO Div. 4RST only. In 1993, 3Pn4Vn (Jan. to May), were included with 4RST to constitute the Unit 1 stock (Atkinson and Power 1991). Unit 2 was also implemented in 1993. Subdivisions 3Pn4Vn (June to December), were included with 3Ps4Vs4Wfgj to constitute the Unit 2 stock.

To provide to the Committee on the Status of Endangered Wildlife in Canada (COSEWIC) information on the status of the redfish species and to improve our understanding on redfish population dynamics, efforts have been made to develop methods to separate redfish species using the historic databases. These methods are described in this document and are used to compute the abundance of *S. fasciatus* and *S. mentella.* The results presented in this paper are complementary to those of Morin *et al.* (2004) which presents redfish population indices, including Units 1 and 2, in the species-at-risk context for all the Northwest Atlantic stocks in Canadian waters. The present document also includes other analyses done on different surveys conducted in Units 1 and 2 that were not included in Morin *et al.* (2004).

Criteria of species identification

Various criteria have been used to distinguish the two main species of redfish, *S. fasciatus* and *S. mentella*. Since no difference in color and general shape are observed between them, other criteria have been studied to separate them. Three characters have been commonly recorded in DFO surveys: the anal fin ray counts (AFC), the insertion of extrinsic gas bladder muscle (GBM) and the malate dehydrogenase locus (MDH) (see Sévigny et al. 2003 for a review).

Anal fin ray counts

The anal fin ray counts is usually 8 or higher for *S. mentella* and 7 or lower for *S. fasciatus*. AFC is the most accurate external morphological criteria to discriminate redfish species (Ni 1981; Rubec *et al.* 1991) and the best for large samples in the field (Kenchington 1986). However, Valentin (unpublished data) observed some natural variability, since a proportion (8%) of *S. fasciatus* (identified by MDH) with 8 or 9 rays and, at a lesser extent (0.7%), *S. mentella* with 7 rays have been observed in areas of allopatry. This overlap is more important in area of sympatry were hybridisation and introgression is suspected to occur as in Units 1 and 2 (Desrosiers et al. 1999; Roque et al. 2001; Valentin et al. 2002). Rubec *et al.* (1991) observed 24% of *S. fasciatus* with 8 rays or more and 12% of *S. mentella* with 7 rays or less in the Gulf of St. Lawrence. Thus, this criteria is not 100% precise and assigning all fish with 8 rays to *S. mentella* or 7 rays to *S. fasciatus* would underestimate the number of one species.

Gas bladder muscle insertion

The insertion of extrinsic gas bladder main muscle shows difference between *S. fasciatus* and *S. mentella* (Ni 1981; Kenchington 1986). The main muscle passes generally between ventral ribs 3-4 (or sometime 4-5) for *S. fasciatus*, whereas in *S. mentella* the muscle passes between ventral ribs 2-3 (Ni 1981). Unfortunately, some gas bladder muscles could form branches that get through multiple ribs. Such patterns prevent species determination (Ni 1981).

Malate dehydrogenase

Finally, the most accurate criterion is the electrophoretic patterns of the malate dehydrogenase. The variety of allozyme loci produces different protein banding patterns and could be visualise through electrophoresis coupled with histological staining. Payne and Ni (1982) and McGlade *et al.* (1983) pointed out phenotypic differences on the MDH of the liver of redfish species. Allele MDH*A^1 is the most common found in *S. mentella* while MDH*A^2 is more common in *S. fasciatus*. Thus, genotype homozygote for MDH*A^2 is typical of *S. fasciatus*, while homozygote for MDH*A^1 typical of *S. mentella*. The heterozygote genotype could be interpreted as hybrid.

Biological factors

Differences in habitat selection and biological characteristics could be useful to separate species. The two main species of redfish exhibit difference in their depth preference (Rubec *et al.* 1991). *Sebastes fasciatus* dominates the shallow zone (< 250 m in summer) whereas *S. mentella* dominates at deeper depth (> 250 m in summer) (Ni 1982; Rubec *et al.* 1991). In the Gulf of St. Lawrence, the depth of transition between the two species is 250 m in summer, but some mixtures occurred at 220-250 m (Miller and Laberge unpublished data).

Other meristic criteria

The meristic database (vertebrae, dorsal and anal fin rays) presented in Ni (1982) has been used to derive proportions of each species by depth zone based on the survey stratification for various survey series within three “stock” areas (SA2+Div. 3K, Div. 3LN, and Div. 3O). See Morin et al (2004) for the description of the methods used. This database was not used for Units 1 and 2.

Material and Methods

An important component of the data used to discriminate Units 1 and 2 redfish came mainly from the Redfish Multidisciplinary Research Program 1995-1999 (RMRP) which examine several aspects of the biology and fisheries of redfish (Gascon 2003). During this program, the criteria recorded were AFC, GBM and MDH on all fish sampled. The data used and the analyses performed will be presented for the two stocks separately.

Unit 1

Description of the data available

The different groundfish surveys used in the analyses for Unit 1 are listed in Table 1. The criterion with the largest amount of data is AFC. Some AFC have been collected in 1984 to 1987 during the summer DFO survey on the *Lady Hammond.* In 1984, AFC were not systematically sampled on all sizes and thus, these data were not considered. In 1985-87, AFC were recorded for 8-9% of all the fish measured. Since 1993, AFC have been recorded systematically on all stations during the summer DFO survey. Overall, AFC were recorded for 40-73% of the fish measured each year. Because AFC is the most abundant source of data we decided to separate species using AFC when available.

GBM data have been recorded in 1994-1997, 2001 and 2002 and MDH during the 1993-1998 period on the DFO summer survey conducted on the CCGS *Alfred Needler*. Because the MDH sampling was not conducted every year and the sample sizes are low, these data alone cannot be used to discriminate species on all surveys.

Other surveys with redfish sp. catch information exist in Unit 1, but represent only short series and/or without any criteria of species separation recorded. Those surveys are the Cod Sentinel fisheries in summer and in autumn since 1995 and the 4T surveys done by DFO Gulf region since 1971. Also, AFC have been recorded in 2001 and 2002 in the surveys conducted by GEAC (Groundfish Enterprise Allocation Council) since 1998. Finally, the winter DFO surveys done from 1978 to 1994 on the *Gadus Atlantica* which had some data of AFC and MDH were measured in 1983 and AFC in 1994 were examined.

Description of the analyses

DFO summer surveys

Description of the surveys

Summer DFO bottom trawl surveys have been conducted by the *Lady Hammond* using a Western IIA trawl from 1984 to 1989 and by the *CCGS Alfred Needler* using a URI trawl since 1990. Because of the different fishing efficiencies, length corrections had to be applied in order to merge these two series together. This length-dependant correction for *Sebastes* sp. has been calculated from a comparative study conducted in 1990 (D. Swain and H. Bourdage, pers. comm.):

$$\textbf{Corrected Abundance} = \textbf{Abundance}\left\{\exp[-0.5386+(6.0832e^{-0.1138L})]\right\}$$

Where L is fish length

For example, the URI trawl is 6.7 times more efficient than the Western IIA trawl at a length of 8 cm, but 1.6 times less efficient at a length of 39 cm. This correction was applied to the abundances of redfish by length at each tow of the *Lady Hammond* survey. The ratio of corrected and not corrected total numbers of all genotypes was applied to the numbers for each species at each tow. The abundance by length was corrected at each length interval for each depth zone before splitting by genotype.

For the two surveys, when 2 or less successful tows were made in a stratum, a multiplicative model (Gavaris 1980) was used to get an estimation of catch per tow (kg) for these strata. This model was applied in order to obtain a standardised area covered each year for the abundance estimations. The model use strata and year as factors influencing the mean catch per tow (Van Eeckhaute et al. 1999). The final value estimated for these strata was a weighted average of the value obtained by the multiplicative model and the mean or weight of the real tows realized in these strata. For each year, the ratio between the *Sebastes* sp. biomass corrected by the multiplicative model and not corrected biomass was applied to the abundances by genotype.

Depth preferences

To describe the depth distribution of each redfish species in the years surveyed (1993 to 1996), we plotted the 2.5, 50 and 97.5% values of sampled and occupied cumulative distribution functions (CDF) following Perry and Smith (1994). The analyses were done using the computer program Habitat developed by Pierre Gagnon (see Castonguay *et al.* 1999). AFC was the criterion of separation (≤ 7 rays, *S. fasciatus* and ≥ 8 rays, *S. mentella*) at each tow for those analyses.

Analyses on the AFC and MDH data

The proportion of genotype (of the fish for which MDH was determined) by depth zone at each year was determined for the RMRP data. Inter-annual variation was also evaluated using a chi-square test. In case of tows with no AFC data, this relation (Genotype proportions by depth [GPD]) could be used to get abundance by species.

It has been demonstrated that an overlap of AFC occurs between *S. fasciatus* and *S. mentella* (Rubec *et al.* 1991; Valentin unpublished data). In order to correct for this variability, we first evaluated the proportions of fish with "abnormal" AFC for each genotype determined by MDH (1993 to 1996). The data collected in 1997 were not used in the analysis because the sampling targeted specific lengths and thus the data was not representative of the population. In addition, inter-annual variation has been evaluated using a Chi-square test. Since depth distribution is different for the two species (Rubec *et al.* 1991), we analyzed the variability of AFC in different depth zones corresponding to stratified survey depth intervals (Table 2). The relationship (AFC correction) between depth and species could be used to convert the numbers by AFC to numbers by genotype for each tow (AFC by tow).

Total abundance

For the years when valid AFC data were available for most of the sets (1985 to 1987 and 1993 to 2002) AFC converted with the AFC correction have been used to get abundance by genotype at each tow (See Table 3 for the list of the methods used each year). For the few tows without AFC data in these years, the catch by species was obtained with the GPD. The PACES program (Bourdages 2001) was then used to estimate the abundance of the DFO surveys.

For years with no valid AFC data in any tow (1984,1988-1992), abundance by species has been estimated using AFC-length keys (see next section for a description) of the closest year (1985 for 1984, 1987 for 1988-1989 and 1993 for 1990-1992; Table 3).

The three methods to separate the genotypes (AFC by tow, GPD and AFC-keys) were applied when it was possible to compare the abundance indices of *S. fasciatus* obtained by each method.

Length frequencies and mature population

In order to get length frequencies by species and, subsequently, abundance of mature fish, we made AFC-2 cm length keys by depth interval. The total number of fish by 2 cm length classes in the depth intervals of unit 1 could be split by AFC using those keys and then transformed to numbers by genotype with the AFC correction. When no AFC data was available for some length interval, the closest interval was taken. For years with no AFC data, keys from the closest year were used. The total number of mature fish was obtained with the sum of all fish longer than the lengths at 50% of maturity (L50) in all depth zones (*S. fasciatus* = 20.4 cm; *S. mentella* = 23.8 cm, heterozygous = 22.7 cm) (Morin *et al.* 2004).

Other surveys

No species discrimination data have been recorded during the July and October Sentinel surveys conducted in the Gulf of St. Lawrence since 1995 (Morin et al. 2001). However, the GPD estimated on the *A. Needler* survey could be used to separate the catch by species at each tow to get the abundance by genotype for the summer sentinel survey. This is assuming that there is little changes in the distribution of redfish between July and August. For the October survey, since redfish undergo seasonal shift in their depth distribution (Rubec *et al.* 1991), the *A. Needler* GPD cannot be applied because of the 2 months separation. The abundance was thus estimated for redfish sp. together.

A groundfish survey has been conducted in 4T by the DFO Gulf region since 1971 in September. The redfish catches at each tow were separated by species using genotype proportions by depth of the *A. Needler* survey.

A grid survey was conducted by GEAC (Morin et al. 2001) in June/July since 1998 in Divisions and Subdivisions 4RST3Pn4Vn. The primary goal of this survey is to describe the distribution of redfish in the Gulf of St. Lawrence and the Cabot Strait. The data recorded in this survey are also used to compute an abundance index (Morin et al. 2001). AFC data of 2001 and 2002 were converted to genotype using the AFC correction of the *A. Needler* to get a table of genotype by depth interval for the GEAC survey. This table was used to separate redfish catches by tow from 1998 to 2000. In 2001 and 2002, the AFC recorded at each tow have been converted, with the AFC correction, into genotype to get catches by species.

The AFC and MDH data recorded on board the *Gadus Atlantica* in winter in 1983 and 1994 were used to separate the genotypes for all the years of the survey (1978 to 1994). Proportions by genotype (determined from MDH) for each depth zone have been calculated for 1983. Those proportions were used from 1978 to 1989. From 1990 to 1994, the genotype proportions of 1983 could not be used since an important change had been observed at the end of the 1980 : a shift for deeper water in the distribution of redfish (Castonguay *et al.* 1999). The AFC of 1994 transform to genotype by depth interval using the 1983 MDH-AFC relation was used to get the genotype proportions by depth interval. After numbers of redfish caught have been split by species for each tow using these proportions, the PACES program was used to get total abundance indices by genotype per year.

Unit 2

The data

The DFO summer survey in Unit 2 started in 1994 but no criteria of species identification has been systematically recorded. However, AFC, GBM and MDH have been recorded in 1995 to 1998 as part of the RMRP. A survey conducted in 4V since 1970 by DFO Maritimes in summer, was also analyzed although it covers partly Unit 2.

Description of the analyses

Genotype proportions by depth interval (GDP) were calculated the same way as for Unit 1 but with the Unit 2 MDH data and were used to separate species for each tow to get total abundance with the PACES program. Depth intervals are presented in Table 4. Genotype proportions by depth were also applied on the survey of 4V. To get abundance of mature population, AFC-length keys by depth intervals were estimated and were applied on the length frequencies. As for Unit 1, the AFC frequencies have then been transformed to genotype using the AFC correction for each depth interval.

The same method used in Unit 1 was applied in Unit 2 to get length frequencies by genotype and estimates of the abundance of mature fish. The L50 estimated for males and females combined are *S. fasciatus* = 22.5 cm, *S. mentella* = 23.7 cm and heterozygotes = 24.4 cm.

Results

Unit 1

DFO summer surveys

The use of the length-dependent correction has permitted to merge the two DFO series, while the multiplicative model allowed us estimating catches in incomplete strata in order to have a standard area surveyed each year (Table 5). As we can observe, the length-dependent correction had a great impact on abundance of *S. fasciatus* only in 1984 (Figure 1) and the multiplicative model causes little change particularly in the last years because only rare strata were incomplete.

The cumulative distribution functions show that *S. fasciatus* were found in shallower water (median at 250 m) than *S. mentella* (around 300 m) in the summer (Figure 2).

Little inter-annual differences were observed in the proportions of genotypes by depth zone (Table 6). Genotype proportions in depth zones under 274 m in 1993 were significantly different between years (Chi-square test, $p < 0.005$). The small sample size for depth lower then 183 m and a higher proportion of *S. mentella* encountered in depths between 183 and 274 m in 1993 could explain the divergence for these zones. After pooling the data of 1993 to 1996 together, we can see on Table 7 that *S. fasciatus* is dominant in depth zone lower than 274 m while *S. mentella* and heterozygous dominate over 274 m. In the absence of AFC, these percentages of genotypes at each depth interval (GPD) have been used to separate species for each tow.

Proportions of AFC for each genotype from the summer DFO survey in Unit 1 between 1993 and 1996 were compared between years. No significant inter-annual variation was observed (Table 8, Chi-square test, $p > 0.5$). The data were pooled for the other analyses. Around 70 % of the *S. fasciatus* had 7 rays or less and the rest had 8 rays or more (Figure 3). For *S. mentella* and heterozygous around 90 % of the fish had 8 rays or more and around 10 % had 7 rays or less. The proportion of fish with 8 rays belonging to *S. fasciatus* is more important in shallower depths (Table 9). These proportions have been used to attribute the proportions of AFC between each species (AFC correction). For example, at depth 2, 86.9% of fish with 7 rays are attributed to *S. fasciatus, 8.2% to S. mentella* and the remaining to heterozygotes.

AFC-length keys were estimated at each depth interval for the years 1985 to 1987 and 1993 to 2002. An example is showed in Table 10. In all keys *S. fasciatus* (AFC ≤ 7) were generally smaller than *S. mentella*. This corresponds to the pattern previously observed in this survey (Morin et al. 2001).

The abundance estimates of *S. fasciatus* obtained with the three methods showed small difference for the 1993 to 2002 period (Figure 4). Before 1993, higher values were observed for the AFC-length keys method then with the two other methods.

Based on this information, we concluded that AFC by tow method gives the most accurate estimate of abundance by species. However, for years with no AFC data available, we selected the AFC-length key method, which rely partially on measured character of the year survey (length) instead of proportion by genotype, which is based only on data for the years 1993 to 1996.

Other surveys

As observed in the GEAC survey in 2001-2002, *S. fasciatus* dominates in water shallower then 274 m while *S. mentella* is more frequently observed under 274 m (Table 11).

The proportion of genotype by depth zone was different in winter (Table 12). In 1983, there is a sharp distinction between depth distribution of *S. fasciatus* and *S. mentella*, the first one dominates water under 274 m, whereas the last one dominates over 274 m. Again, we observe an important proportion of fish with “abnormal” AFC, since fish with ≥8 rays have genotype of *S. fasciatus* and fish with ≤7 rays have genotype of *S. mentella* (Table 13). We observe a shift in the proportion of *S. fasciatus* by depth from 1983 to 1994 (Table 12 and 14). *Sebastes fasciatus* becomes dominant in all depth zones in 1994.

Description of survey indices

DFO summer surveys

The results on the different indices of abundance of total and mature population and distributions from the DFO summer surveys are presented and discussed in Morin *et al.* (2004).

The length frequencies from 1984 to 2002 are illustrated on Figures 5 to 7 for each genotype. For *S. fasciatus*, three year classes were present at the end of the 1980s and beginning of the 1990s. The first one is the 1980 year-class which showed a constant decline from 1984 to 1992. The two others, the 1985 and 1988 classes were abundant in 1987 and 1990-1991, but disappeared rapidly in the survey afterwards. In recent years, several year-classes were observed but in low numbers in comparison to the previous year-classes. For *S. mentella* and heterozygous fish, the same year-classes were present during the 1984 to 1992 period. However, the *S. mentella* component of the 1988 year-class was lower and questionable. This is probably due to the presence of *S. fasciatus* with 8 anal fin rays that were distributed into *S. mentella* with the discrimination method used. Also, the *S. mentella* component of 1980 year-class was slightly lower than *S. fasciatus* but they persisted in the 1990s which is not the case for S. fasciatus. Thus, in recent years the large sizes were dominated by individuals of *S. mentella* and heterozygous fish whereas the *S. fasciatus* dominated the small sizes.

Other surveys

The distribution of the catch of the 3 genotypes observed on the summer Sentinel survey are similar. The best catches were found east of Anticosti Island deeper than 200 m (Figures 8 to 10). All three genotypes showed a decreasing trend in abundance since 1996 (Figure 11). The indices of *S. mentella* were higher than *S. fasciatus* because commercial trawls are used which are more efficient in catching larger individuals. For fall sentinel, catch rate distribution and indices of abundance are fairly constant for *Sebastes* sp (Figures 12 and 13).

In the southern Gulf of St. Lawrence sampled in September on the 4T survey, redfish occurred only in the deep parts of the Laurentian Channel and the few tows with redfish showed decreasing catch rate from 1970 to 2001 (Figures 14 to 16). Three periods of higher abundance of *S. fasciatus are observed* in the early 1970, 1981-1982 and 1986-1992 (Figure 17). Since 1988, there is a strong decline for both species and in the last years, the catches remain at a low level even if a small increase is observed. No conversion factor due to a vessel change was applied to the years before 1985.

The GEAC survey showed little changes in catch rate distribution of the three genotypes in the Laurentian Channel from 1998 to 2002 (Figures 18 to 20). Catches *of S. mentella* were more important than catches of *S. fasciatus* in this survey because a commercial gear with a liner was used. Mean length frequencies by tow are presented on Figure 21 for years 2001 and 2002. It is observed that *S. fasciatus* dominates at small length classes while *S. mentella* does at large length classes.

A decrease in the distribution of the catch rates from 1978 to 1994 for the *Gadus Atlantica* winter survey was observed (Figures 22 to 24). Figure 25 shows the abundance estimated by species for this survey. Three periods of high abundance (end of 1980s, 1987 and 1990) can be observed followed by low abundance periods. Abundance indices were low in the last years of the survey. It is difficult to interpret the evolution of winter distribution and abundance because of the area surveyed varied each year due to fluctuation in the ice coverage. Also, a possible change in winter distribution of redfish in the last decade is suspected, possibly due to environmental factors. The change in abundance indices could have resulted from the more southern distribution (outside the survey area) despite of a decrease in population size.

Unit 2

The results on the different indices of abundance of total and mature population and distributions from the DFO summer surveys are presented and discussed in Morin *et al.* (2004).

Sebastes fasciatus dominates at depths less then 366 m in Unit 2 (Table 15). Moreover, an overlap occurred between AFC of both species (Table 16). The redfish with 8 anal fin rays belong in a greater proportion to *S. fasciatus* at depth les than 274 m but are mainly *S. mentella* at greater depth.

The 4V survey shows a significant decrease in catch rate in 4V in the shallow part and at a lesser extent in the deep portion (Figures 26 to 28). Also, high estimates of abundance for *S. fasciatus* in 1984 and 1987-1994 were observed. In 2002, *S. fasciatus* was at low level, while *S. mentella* and heterozygous individuals did not vary much (Figure 29).

Discussion

The objective of the project was to develop simple methods to evaluate the abundance and distribution of the two main redfish species, *S. fasciatus* and *S. mentella* in the Northwest Atlantic, particularly for Units 1 and 2. Other methods or rules to separate species have been developed in the past in the Gulf of St. Lawrence. Rubec *et al.* (1991) developed what was called the 60% rule: when 60% of the fish set have 8 rays or more, the whole catch was considered *S. mentella*, whereas 60% have 7 rays or less, it was *S. fasciatus*. Intermediate percentages were interpreted as 50% of both species. St-Pierre and de Lafontaine (1995) also used a similar approach. In Unit 1, where a lot of hybridisation occurs, 100% classification of one species seems questionable. This is more important in depths of transition of the two species (220-250 m). Moreover, the analysis of MDH of the Redfish Multidisciplinary Research Program shows that very few tows had 100% of one species.

The separation by AFC recorded at each tow and corrected to genotype is a simple method to perform and gives a good estimate of species composition when these data are available. Because redfish with ≥ 8 rays belong in different proportions to *S. fasciatus* depending on the depth, this justify the use of a correction instead of just separating species of fish with ≤ 7 rays from fish with ≥ 8 rays. Taking into account these different proportions improve the precision of the separation of the two species.

In addition, alternative methods have to be developed to evaluate the abundance of each species for the years where no separation criteria were recorded. The use of genotype proportions by depth or AFC-length keys could give an acceptable estimate. Abundance evaluated with this method is similar to the evaluation by AFC corrected for years during the reference period (1993 to 1996), but when these methods are used for years with no separation data, it may be less accurate if changes occurred. For example, the significant difference between two methods for 1990 and 1991 could be explained by the appearance of a strong recruitment that may have affected the proportions by depth interval. This recruitment is mainly due to the 1988 year class of *S. fasciatus* (Sévigny and de la Fontaine 1992). Thus, the very abundant small length classes of 1990 and 1991 were predominantly *S. fasciatus*, but the proportion used to separate species are from years when proportions may be different. The AFC-length key method estimate is believed to give a more accurate abundance of *S. mentella* and this is the approach chosen for years without AFC data. This method assigns the number by species from proportions by length classes, which may tend to vary less than proportions by depth intervals. In addition, it is based on a biological character (length) recorded for the year in question rather than only on assumptions from other years. Moreover, as we observed in 1993 on the cumulative distribution functions, depth preference could vary from year to year, changing the genotype proportions by depth especially in the transition depths of the two species. This change in depth selection was also observed in winter between 1983 and 1994. The fluctuations of abundance due to mortality, recruitment and changes in depth preference could influence genotype proportion by depth or AFC-length relationship**.** Thus, the abundance and distribution evaluated in years 1984 and 1987 to 1992 have to be taken with caution.

Also, some caution have to be raised regarding the length-dependent conversion factor to merge the two survey series of the *L. Hammond* and *A. Needler*. This correction is for redfish sp together and cannot be applied by species at each tow. Since the URI trawl is more efficient catching small fish then the Western IIA, the conversion of the *L. Hammond* catches to *A. Needler* equivalents raises the number of small fish (more *S. fasciatus*) while it decreases to a lesser extent the number of large fish (more *S.mentella*).

The results of the different surveys presented in this paper have not been included in Morin *et al.* (2004) as primary indices because of the uncertainties on the species separation, they are only partial surveys or short series. In addition, many assumptions are made on long periods (e.g. 1971 to 2001 in 4T) and cannot take into account the variability of the biological criteria used to establish the discrimination factors. Moreover, the use of different gears with different length efficiency for each survey could add uncertainties. *S. mentella* and *S. fasciatus* have different length frequencies in Unit 1. Thus, the use of genotype proportions by depth with the *A. Needler* data to evaluate the abundance by species for other surveys with different gears could affect the separation of the catches by species. The information by species coming from these surveys have to be used with caution.

Abundance of *S. mentella* is believed to be a conservative estimate, since heterozygous individuals have been considered separately. Sévigny *et al.* (2000) observed a lack of difference in the size distribution of the genotypes "*S. mentella*" and "heterozygous" from MDH analysis and similar distribution in the Gulf of St. Lawrence suggesting that heterozygous individuals have more affinities with *S. mentella* then with *S. fasciatus*. All the analyses we have done (depth distribution, abundance and catch rates) show also strong similarities between those two genotypes.

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Table 1 - Surveys and details on species discrimination data for Unit 1.

Survey	1	2	3	4	5	6	7
Area	4RST	4RST	4RST	4RST	4T	3Pn4RS	4RS
Month	August	August	July	October	September	January	June
1971					X		
1972					X		
1973					X		
1974					X		
1975					X		
1976					X		
1977					X		
1978					X	X	
1979					X	X	
1980					X	X	
1981					X	X	
1982					X		
1983					X	AM	
1984	A				X	X	
1985	A				X	X	
1986	A				X	X	
1987	A				X	X	
1988	X				X	X	
1989	X				X	X	
1990		AM			X	X	
1991		AM			X	X	
1992		AM			X	X	
1993		AM			X	AM	
1994		AGM			X	AGM	
1995		AGM	X	X	X		
1996		AGM	X	X	X		
1997		AGM	X	X	X		
1998		A	X	X	X		X
1999		A	X	X	X		X
2000		A	X	X	X		X
2001		AGM	X	X	X		A
2002		AGM	X	X	X		A

X = No discrimination data, A = AFC, G = GBM, M = MDH

1) Stratified random groundfish survey in the northern Gulf done by the Quebec region with *Lady Hammond*

2) Stratified random grounsfish/shrimp survey in the northern Gulf done by the Quebec region with CCGS *Alfred Needler*

3) Sentinel stratified random groundfish survey in northern Gulf done by fishing vessels

4) Sentinel stratified random groundfish survey in northern Gulf done by fishing vessels

5) Stratified random ground fish survey in 4T done by Gulf region

6) Stratified random groundfish survey in 3Pn4RS done by Newfoundland and Quebec region

7) Grid survey for redfish in 4RST3Pn4Vn done by GEAC

Table 2. Depth intervals in Unit 1.

Interval	Depth	
	Fathoms	Meters
1	< 100	< 183
2	100-150	183-274
3	150-200	274-366
4	> 200	> 366

Table 3. Methods used to evaluate total abundance by genotype.

Survey year	Method applied
1984	AFC-Length keys of 1985 was applied
1985	AFC by tow
1986	AFC by tow
1987	AFC by tow
1988	AFC-length keys of 1987 was applied
1989	AFC-length keys of 1987 was applied
1990	AFC-length keys of 1993 was applied
1991	AFC-length keys of 1993 was applied
1992	AFC-length keys of 1993 was applied
1993	AFC by tow
1994	AFC by tow
1995	AFC by tow
1996	AFC by tow
1997	AFC by tow
1998	AFC by tow
1999	AFC by tow
2000	AFC by tow
2001	AFC by tow
2002	AFC by tow

AFC by tow: AFC transformed to genotypes by set with the AFC correction.
AFC-length key: Length frequencies by depth zone are split to genotype using length-AFC keys and then AFC-MDH relationship. (see text for details of the analysis)

Table 4. Depth intervals in Unit 2.

Interval	Depth	
	Fathoms	Meters
1	0-150	0-274
2	150-200	274-366
3	> 200	> 366

Table 5. Mean weight (kg/tow) of redfish sp during the DFO research surveys in the Gulf of St. Lawrence between 1984 to 1989. The grey scale indicates the values estimated with the multiplicative model when 0 or 1 tow was done by stratum and the framed cells when two stations were done.

		Catch (kg)/ set of 0,8 nautical miles					
Div.	Stratum	1984	1985	1986	1987	1988	1989
4R	801	66.08	75.61	110.93	98.13	63.07	187.85
	802	22.58	62.46	31.85	81.10	33.18	32.65
	809	287.05	127.88	158.87	527.93	276.17	191.41
	810	244.13	286.19	267.06	276.24	460.44	534.65
	811	182.54	91.07	193.93	172.43	186.51	401.75
	812	122.66	125.57	133.94	103.94	198.23	183.84
	813	94.92	33.16	22.56	97.55	59.53	67.28
	820	0.73	2.98	0.83	5.51	41.79	43.15
	821	1.52	0.65	2.39	2.70	19.69	6.46
	822	1.52	1.32	0.85	0.97	1.22	1.60
	823	1.92	13.97	0.98	1.04	0.54	2.01
	824	45.29	35.49	1.91	1.56	0.32	27.48
4S	803	53.55	84.65	59.63	145.35	130.12	62.31
	804	133.30	113.16	45.95	64.55	29.53	12.81
	805	51.01	31.49	72.36	38.35	53.81	40.81
	806	45.63	126.32	30.48	71.70	42.28	19.88
	807	186.65	85.92	74.43	134.23	276.73	593.40
	808	113.80	92.87	101.01	171.20	389.94	141.44
	814	74.89	247.51	90.77	64.67	73.33	49.47
	815	63.17	142.76	198.97	231.38	157.72	268.53
	816	44.72	81.55	88.39	21.39	35.18	21.36
	817	69.29	40.64	30.90	40.82	31.03	52.52
	818	167.29	132.53	132.88	111.25	158.73	51.69
	819	335.97	98.15	235.61	226.92	151.79	315.33
	827	31.93	20.15	9.00	79.74	0.51	8.91
	828	1.31	1.53	1.19	2.25	13.27	52.23
	829	3.60	19.65	1.66	1.24	2.38	8.32
	830	64.64	1.67	4.04	0.77	14.91	1.01
	831	17.82	16.37	15.15	65.60	130.45	31.44
	832	8.90	8.98	2.30	19.78	166.85	0.72
	833	0.24	0.18	0.01	0.24	1.48	0.55
4T	401	219.84	58.63	119.02	182.16	566.30	74.96
	402	153.71	118.90	91.75	147.38	346.79	328.01
	403	287.40	44.35	98.04	134.03	165.96	106.86
	404	413.04	207.13	104.82	229.77	145.63	390.80
	405	146.87	64.31	58.69	69.82	76.91	140.60
	406	154.47	64.30	56.78	40.17	33.89	84.68
	407	229.00	87.32	36.77	35.26	151.42	84.14
	408	120.99	58.58	36.49	20.46	94.95	26.61
	409	30.69	23.03	15.31	31.85	42.62	10.49
	410	75.63	56.76	90.36	30.70	42.73	35.19
	411	2.61	1.96	1.30	1.89	2.41	2.30
	412	8.16	6.13	4.07	5.74	8.24	7.20
	413	1.65	1.24	0.83	1.19	1.56	1.46
	414	11.55	8.67	5.76	53.32	1.15	10.19

Table 6. Inter-annual variation of frequencies of each genotype by depth and the Khi-square test value (* indicate that results were significant at $P < 0.005$)

Survey year	**Genotype**			
	S. fasciatus (A^2A^2)	S. mentella (A^1A^1)	Heterozygous (A^1A^2)	Khi^2 test Value
Depth 1 (< 183 m)				
1993	**5**	**7**	**1**	**40.5***
1994	35	0	1	
1995	35	1	1	
1996	37	3	1	
Depth 2 (183-274 m)				
1993	**75**	**63**	**18**	**29.0***
1994	64	15	8	
1995	65	36	16	
1996	151	44	19	
Depth 3 (274-366 m)				
1993	25	63	21	3.0
1994	25	82	18	
1995	41	107	28	
1996	59	174	56	
Depth 4 (> 366 m)				
1993	2	45	19	13.4
1994	1	31	12	
1995	8	35	9	
1996	7	40	7	

Table 7. Frequencies (%) of typical genotype (based on MDH) of redfish species by depth interval for data from DFO summer surveys 1993 to 1996 in Unit 1.

Genotype	**Depth interval (m)**			
	< 183	183-274	274-366	> 366
S. fasciatus	0.882	0.618	0.215	0.083
S. mentella	0.087	0.275	0.609	0.699
Heterozygous	0.031	0.106	0.176	0.218
N	127	574	699	216

Table 8. Inter-annual variability of anal fin ray count (AFC) for each typical genotype of redfish species (based on MDH) and the Khi-square test values (no results was significant at $p < 0.05$)

AFC	**Survey year**				Khi^2 test value
	1993	1994	1995	1996	
S. fasciatus					
6	2	0	2	1	
7	64	84	113	168	
8	32	41	32	81	13.5
9	3	0	2	4	
10	0	0	0	0	
S. mentella					
6	0	0	0	0	
7	18	3	17	27	
8	109	97	118	173	13.6
9	41	28	43	61	
10	2	0	1	0	
Heterozygous					
6	0	0	0	0	
7	9	3	5	12	
8	33	32	41	57	11.1
9	16	4	8	13	
10	0	0	0	1	

Table 9. Frequencies (%) of each typical genotype of redfish species (based on MDH) by anal fin rays count in summer surveys from 1993 to 1996 in unit 1 by depth interval and number of fish sampled (N).

AFC	Genotype			N
	S. fasciatus	***S. mentella***	**Heterozygous**	
Depth 1 (< 183 m)				
6	1.000	0.000	0.000	1
7	0.953	0.023	0.023	86
8	0.895	0.053	0.053	19
9	-	-	-	0
10	-	-	-	0
Depth 2 (183-274 m)				
6	1.000	0.000	0.000	2
7	0.869	0.082	0.050	282
8	0.424	0.428	0.148	271
9	0.098	0.706	0.196	51
10	0.000	0.000	1.000	1
Depth 3 (274-366 m)				
6	1.000	0.000	0.000	3
7	0.750	0.190	0.060	116
8	0.105	0.672	0.224	411
9	0.015	0.824	0.160	131
10	0.000	1.000	0.000	3
Depth 4 (> 366 m)				
6	-	-	-	0
7	0.303	0.515	0.182	33
8	0.043	0.743	0.214	140
9	0.050	0.700	0.250	40
10	-	-	-	0

Table 10. Example of length-AFC key (1994 at depth interval 2).

Length (cm)	AFC 6	7	8	9	10
0.5					
2.5					
4.5					
6.5					
8.5	1	3	0	0	0
10.5	3	16	4	0	0
12.5	5	47	39	9	0
14.5	6	93	48	4	0
16.5	12	188	70	3	0
18.5	5	112	30	5	0
20.5	1	27	16	1	0
22.5	0	13	8	1	0
24.5	1	13	6	0	0
26.5	0	15	13	1	0
28.5	1	21	41	5	0
30.5	1	34	34	8	0
32.5	0	18	42	13	0
34.5	1	15	48	23	1
36.5	0	9	52	21	0
38.5	0	4	42	22	0
40.5	0	4	27	12	0
42.5	0	1	14	2	0
44.5	0	0	5	3	0
46.5	0	0	2	2	0
48.5	0	0	1	0	0
50.5	0	0	0	1	0
52.5	0	0	1	0	0
54.5					

Table 11. Frequencies (%) of typical genotype of Unit 1 redfish by depth interval (based on AFC corrected) for data from GEAC surveys 2001-2002.

Genotype	**Depth interval (m)**			
	< 183	183-274	274-366	> 366
S. fasciatus	0.820	0.709	0.230	0.101
S. mentella	0.122	0.200	0.603	0.708
Heterozygous	0.058	0.091	0.166	0.191
N	59	1 330	1 363	850

Table 12. Frequencies (%) of typical genotype of Unit 1 redfish by depth interval (based on MDH) for data from the 1983 DFO winter survey. Number of fish sampled each depth zone (N) is indicated.

Genotype	Depth interval (m)			
	< 183	183-274	274-366	> 366
S. fasciatus	1	0.931	0.356	0.024
S. mentella	0	0.009	0.435	0.697
Heterozygous	0	0.060	0.209	0.279
N	98	350	306	290

Table 13. Frequencies (%) of typical genotype of Unit 1 redfish (based on MDH) by anal fin rays count in the 1983 DFO winter survey. Number of fish sampled by AFC (N) is indicated.

AFC	Genotype			**N**
	S. fasciatus	***S. mentella***	**Heterozygous**	
6	0.692	0.179	0.128	39
7	0.786	0.125	0.089	495
8	0.260	0.515	0.225	431
9	0.160	0.600	0.240	75
10	-	-	-	-

Table 14. Frequencies (%) of typical genotypes of Unit 1 redfish by depth interval (based on AFC corrected) for data from the 1994 DFO winter survey 1994. Number of fish by depth interval (N) is indicated.

Genotype	Depth interval (m)			
	< 183	183-274	274-366	> 366
S. fasciatus	0.730	0.668	0.528	0.451
S. mentella	0.165	0.212	0.317	0.374
Heterozygous	0.105	0.120	0.156	0.175
N	438	1462	1749	6160

Table 15. Frequencies (%) of typical genotype of Unit 2 redfish species by depth interval (based on MDH) for data from DFO summer survey 1995 to 1998.

Genotype	Depth interval (m)		
	0-274	274-366	> 366
S. fasciatus	0.878	0.637	0.294
S. mentella	0.097	0.291	0.550
Heterozygous	0.025	0.072	0.157

Table 16. Frequencies (%) of genotype (based on MDH) by anal fin rays count and by depth interval of Unit 2 redfish in DFO summer survey from 1995 to 1998. Number of fish by AFC (N) is indicated.

AFC	Genotype			N
	S. fasciatus (A^2A^2)	***S. mentella*** (A^1A^1)	**Heterozygous** (A^1A^2)	
Depth 1 (< 274 m)				
6	0.875	0.125	0.000	8
7	0.960	0.028	0.012	606
8	0.737	0.202	0.061	198
9	0.167	0.767	0.067	30
10	0.000	1.000	0.000	1
Depth 2 (274-366 m)				
6	0.500	0.250	0.250	4
7	0.930	0.043	0.027	370
8	0.366	0.519	0.116	268
9	0.083	0.800	0.117	60
10	0.000	0.333	0.667	3
Depth 3 (> 366 m)				
6	1.000	0.000	0.000	10
7	0.851	0.113	0.035	282
8	0.142	0.647	0.211	578
9	0.023	0.799	0.178	264
10	0.000	0.938	0.063	16

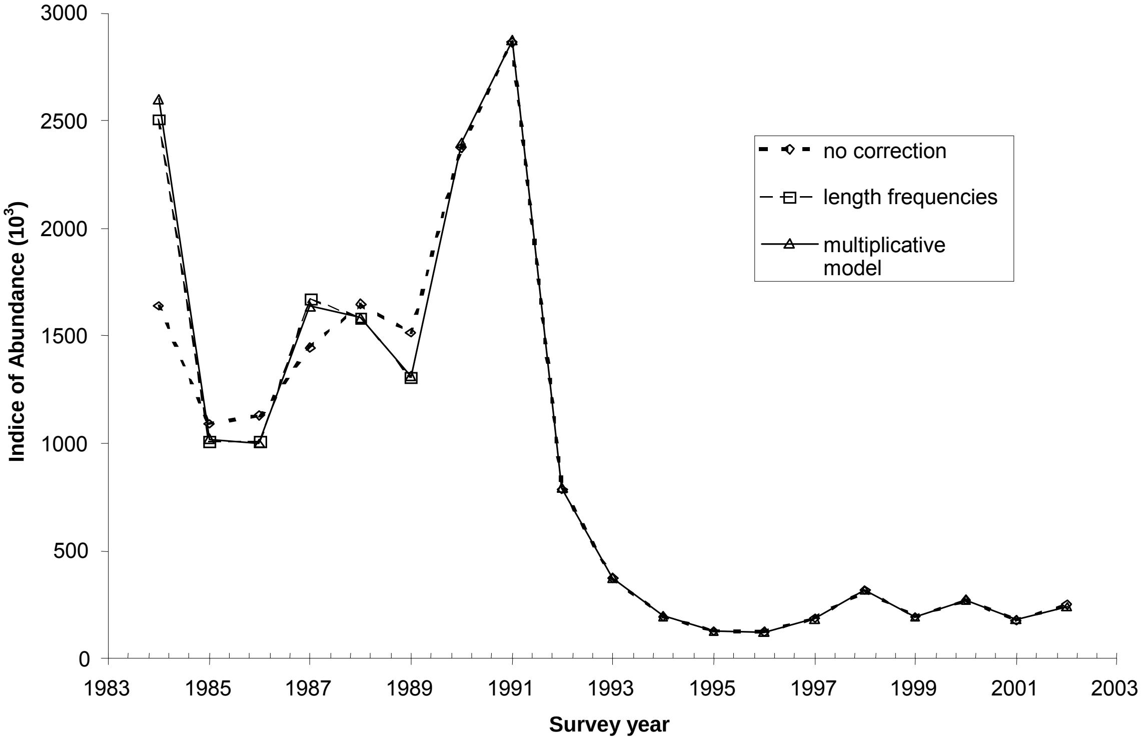


Figure 1. Comparison of indices of abundance of redfish sp. with length-dependent correction from 1984 to 1989 and multiplicative model applied all years.

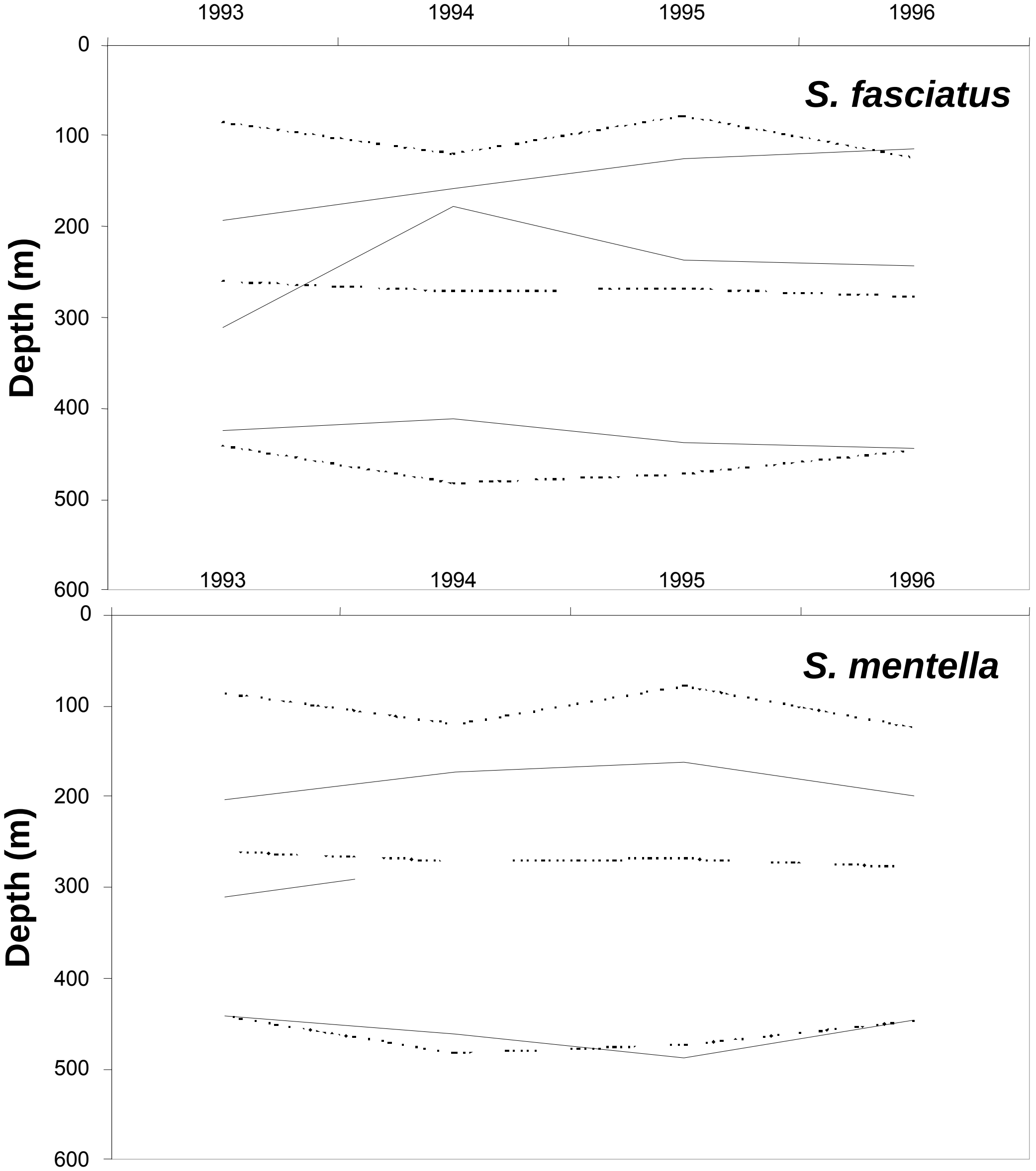


Figure 2. Cumulative distribution function of depth occupied by species separated by AFC (≤7: *S. fasciatus* ; ≥ 8: *S. mentella*). The top, middle and bottom solid lines represent the 2.5, 50 and 97.5 percentile respectively. The dashed lines represent percentile of sampled depth in the same sequence.

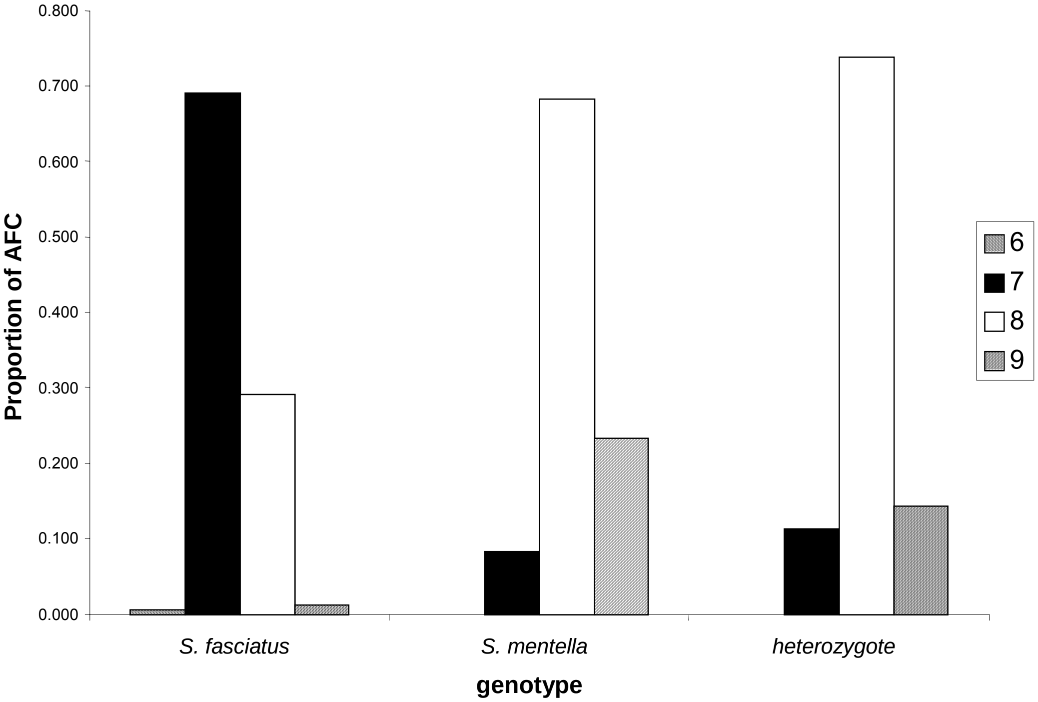


Figure 3. Anal fin rays count (AFC) by genotype (from MDH analysis) of the fish caught in summer from 1993 to 1996 in Unit 1.

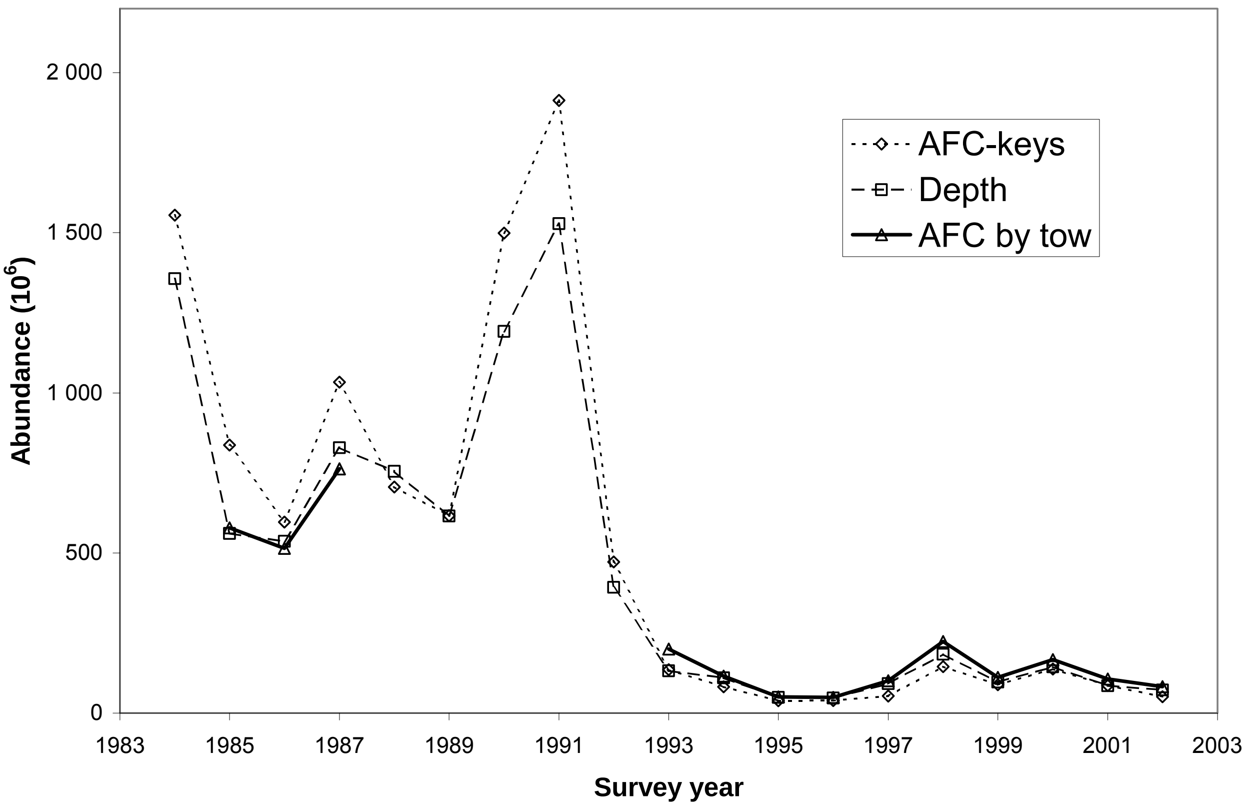


Figure 4. Comparison of different methods to estimate the abundance of *S. fasciatus* on the *L. Hammond* and *A. Needler* series.

AFC by tow: Numbers of each AFC at tow are converted into genotype using the **AFC correction** at different depth intervals from 1993 to 1996.
Depth: Separation of species by proportion of genotype by depth evaluated from the 1993 to 1996 data.
AFC-Keys: Total length frequencies by depth are converted into AFC frequencies using AFC- 2 cm length keys and then to genotypes using the **AFC correction**.

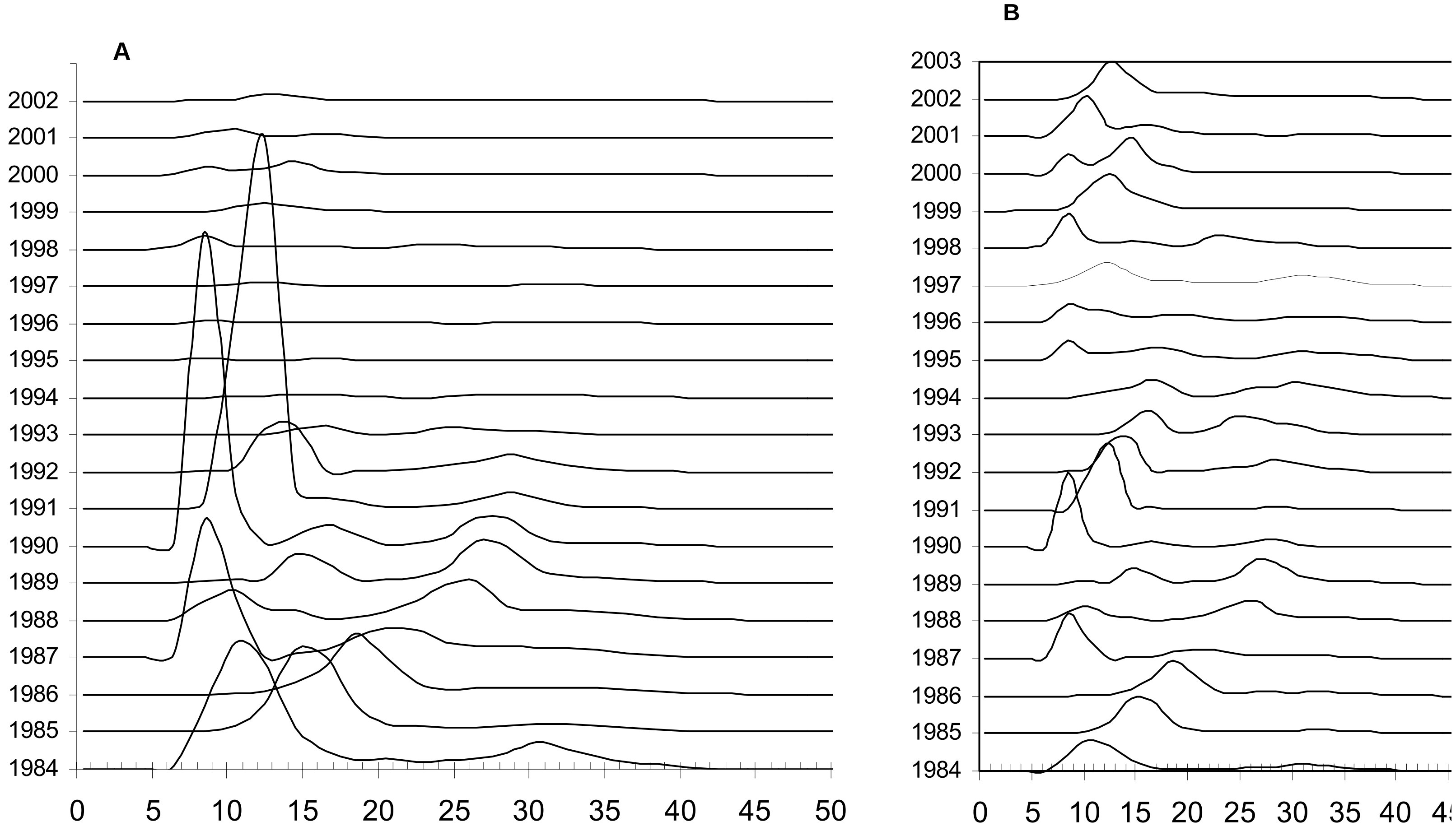


Figure 5. Length frequencies of *S. fasciatus* observed during the DFO research survey in Unit 1 from 1984 to 2002 (in number (A) and in percentage (B)).

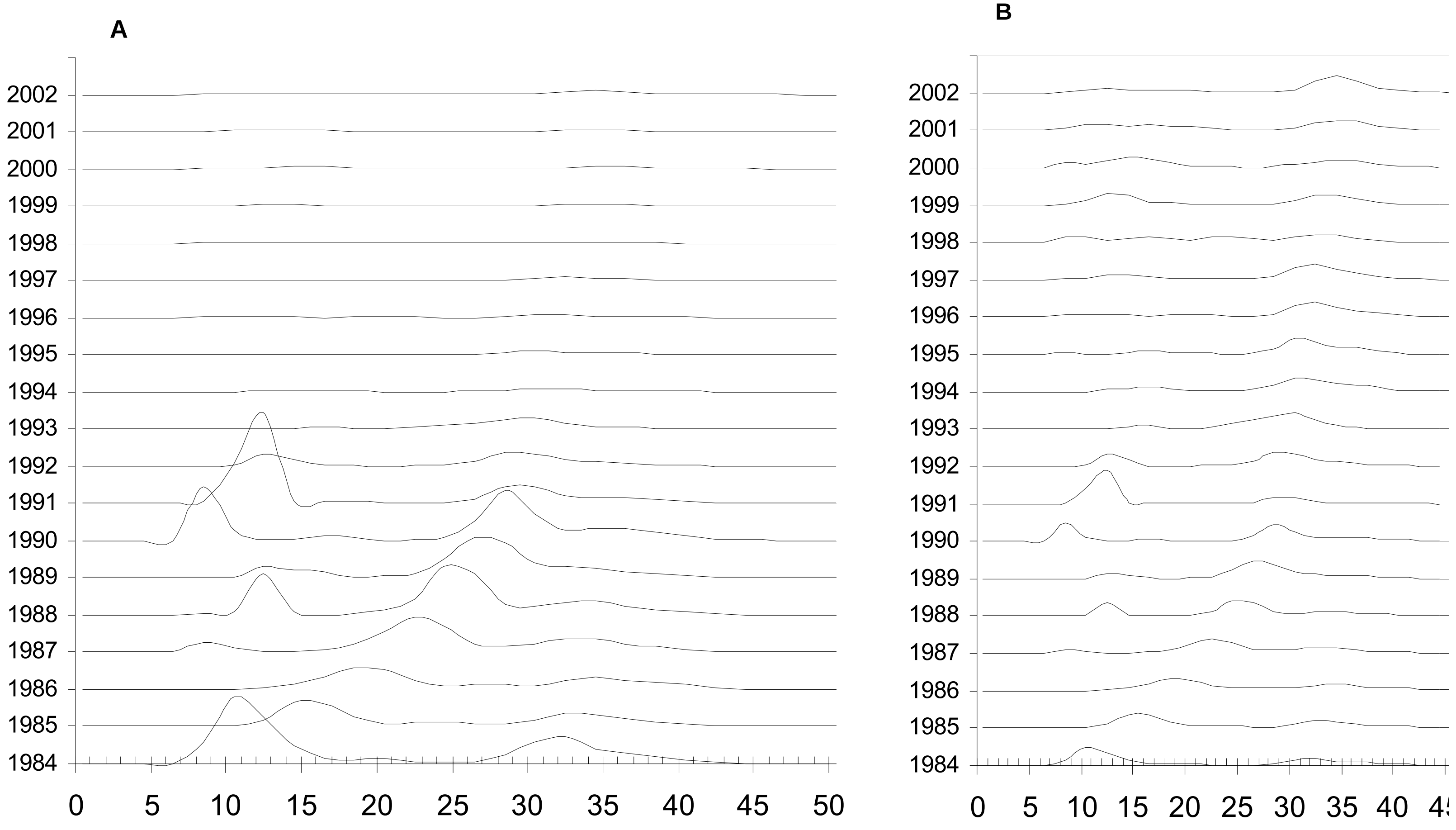


Figure 6. Length frequencies of *S. mentella* observed during the DFO research survey in Unit 1 from 1984 to 2002 (in number (A) and in percentage (B)).

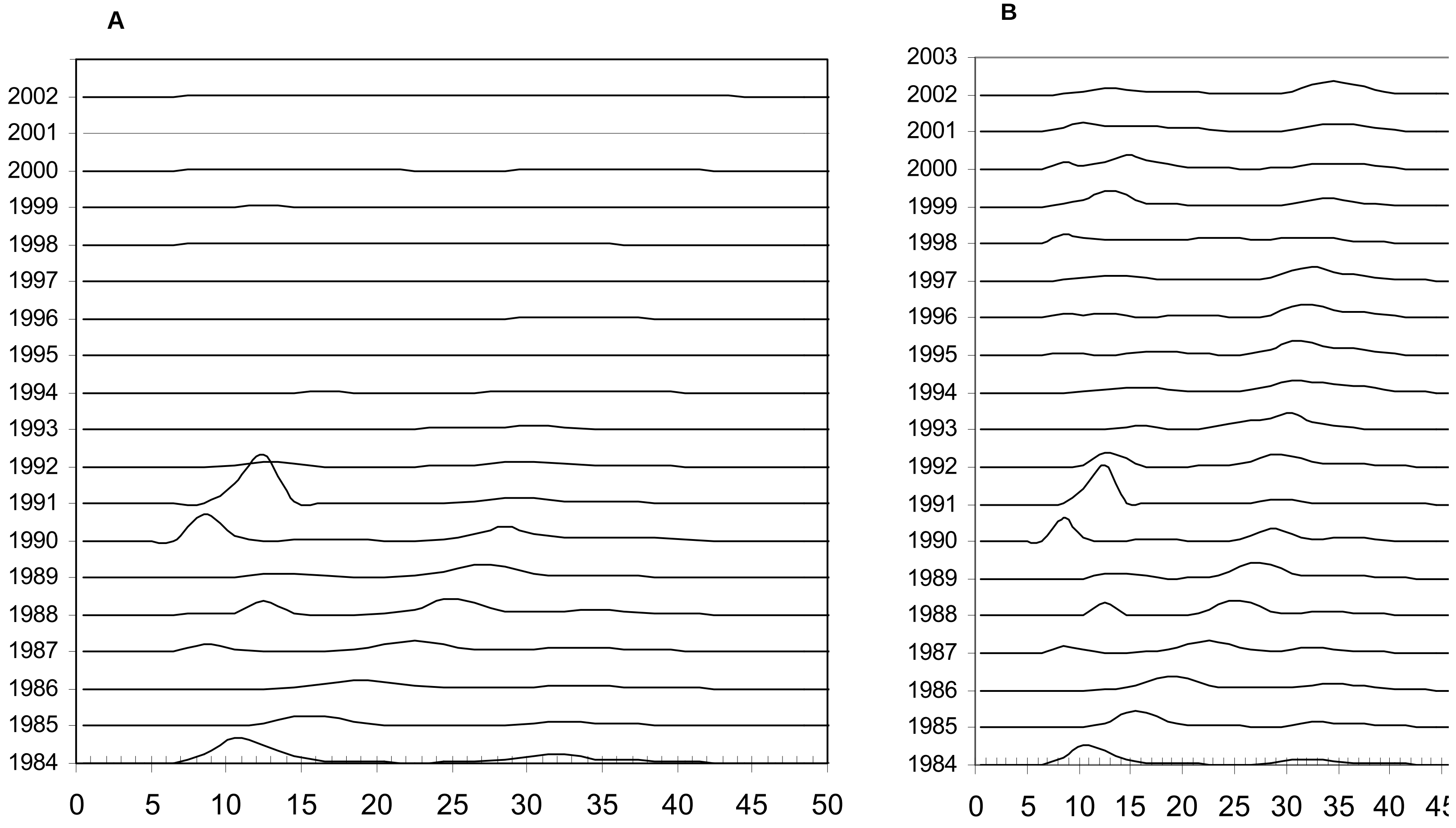
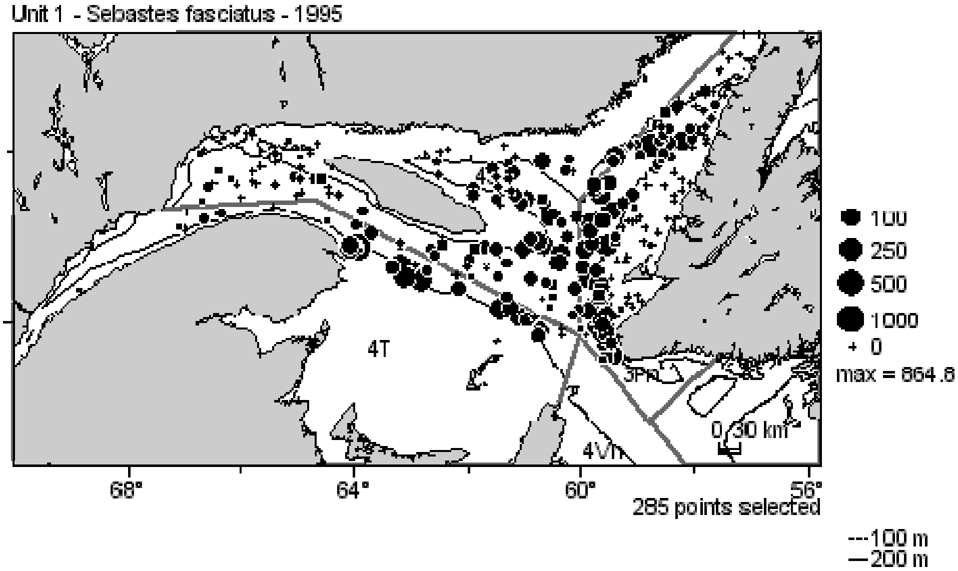


Figure 7. Length frequencies of redfish heterozygous observed during the DFO research survey in Unit 1 from 1984 to 2002 (in number (A) and in percentage (B)).



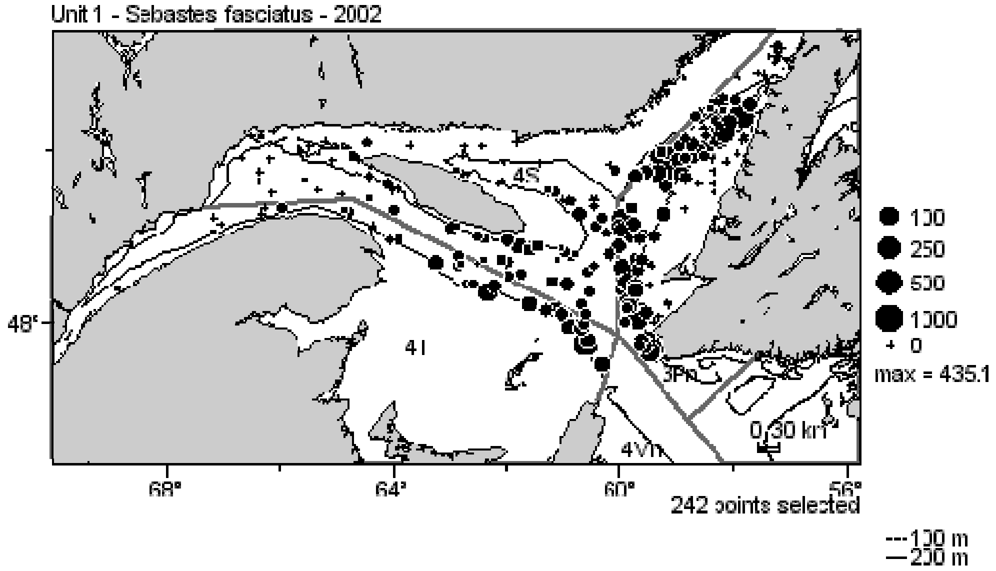


Figure 8. Distribution of *S. fasciatus* in the 1995 and 2002 Cod Sentinel surveys in summer.

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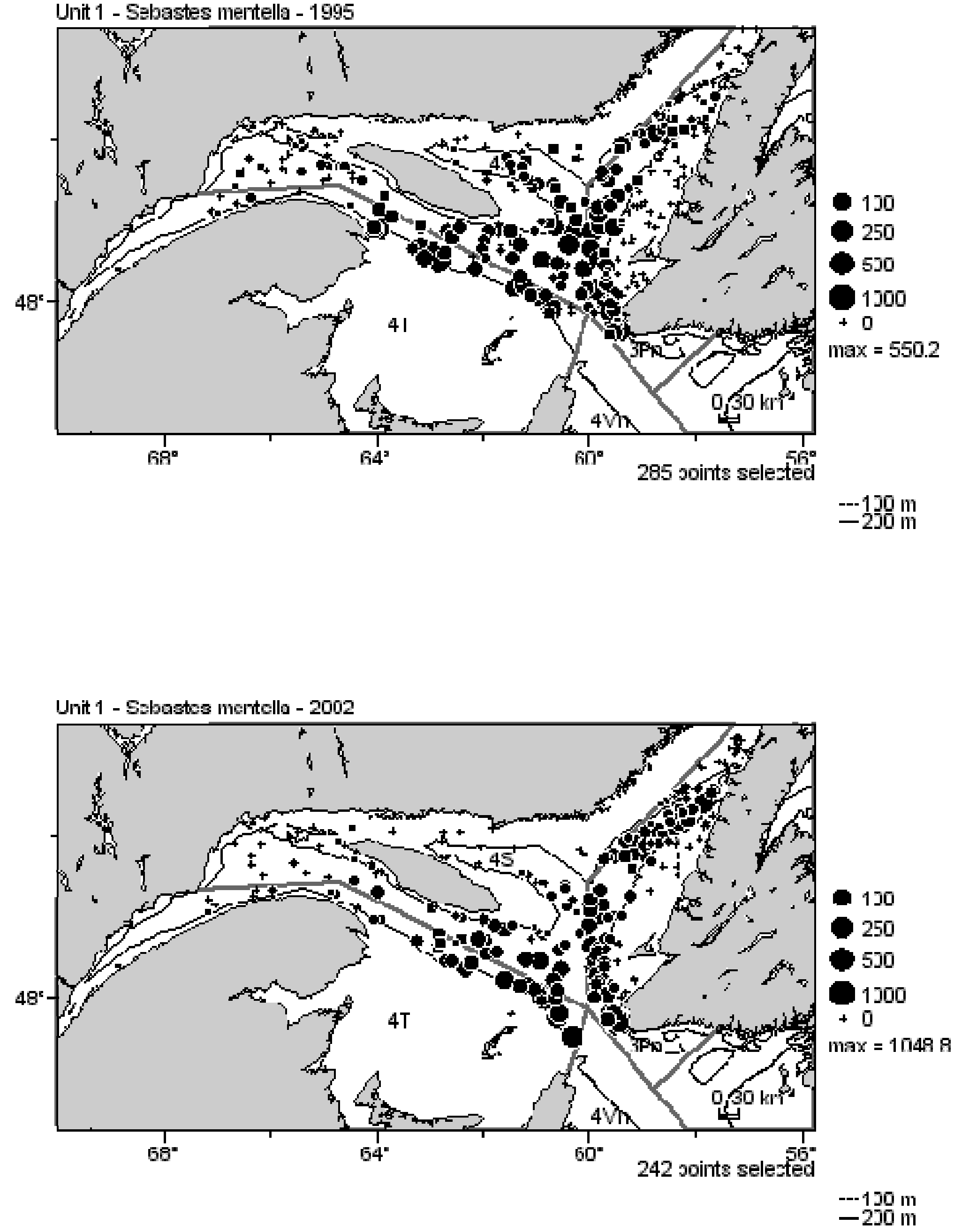


Figure 9. Distribution of *S. mentella* in the 1995 and 2002 Cod Sentinel surveys in summer.

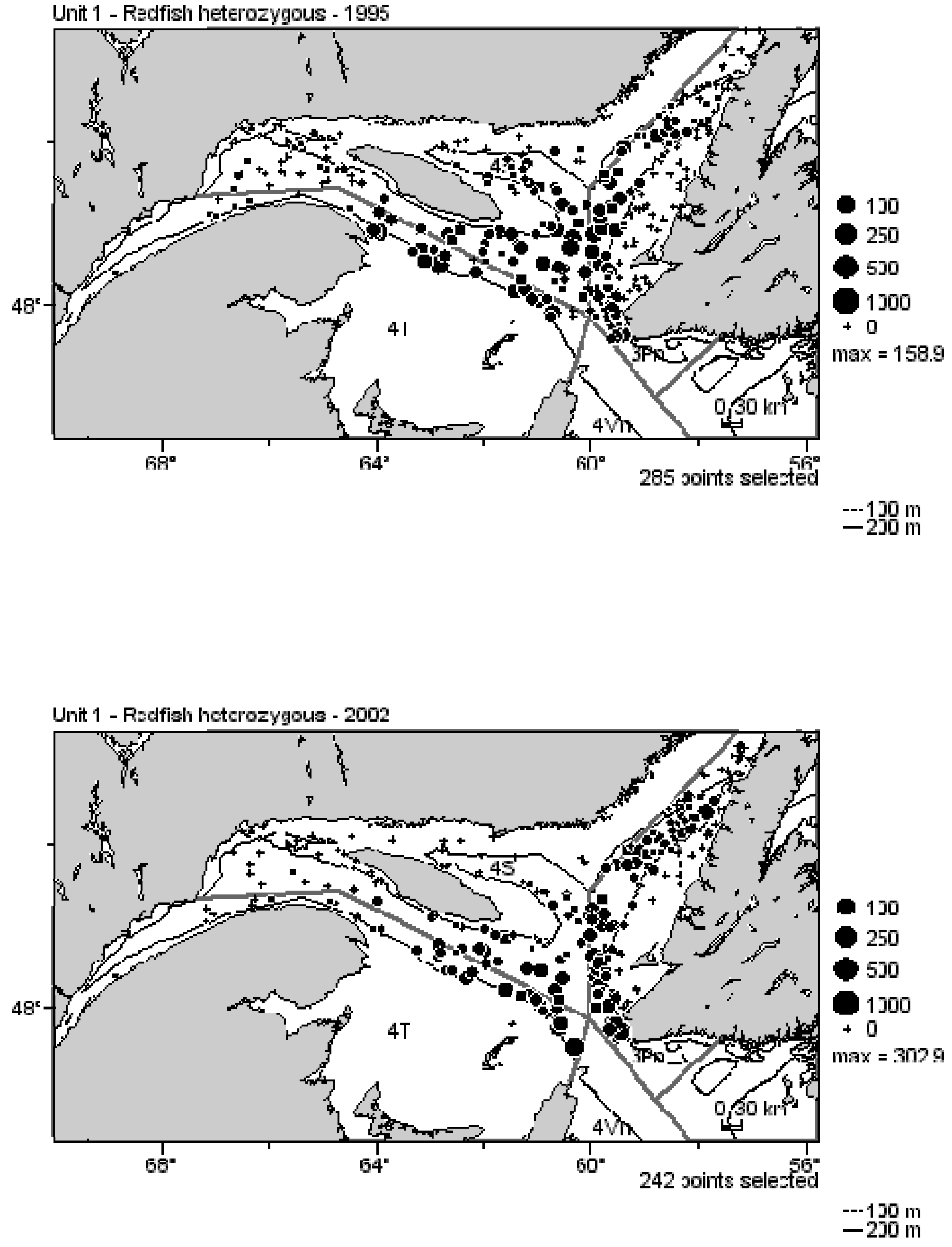


Figure 10. Distribution of redfish heterozygous individuals in the 1995 and 2002 Cod Sentinel surveys in summer.

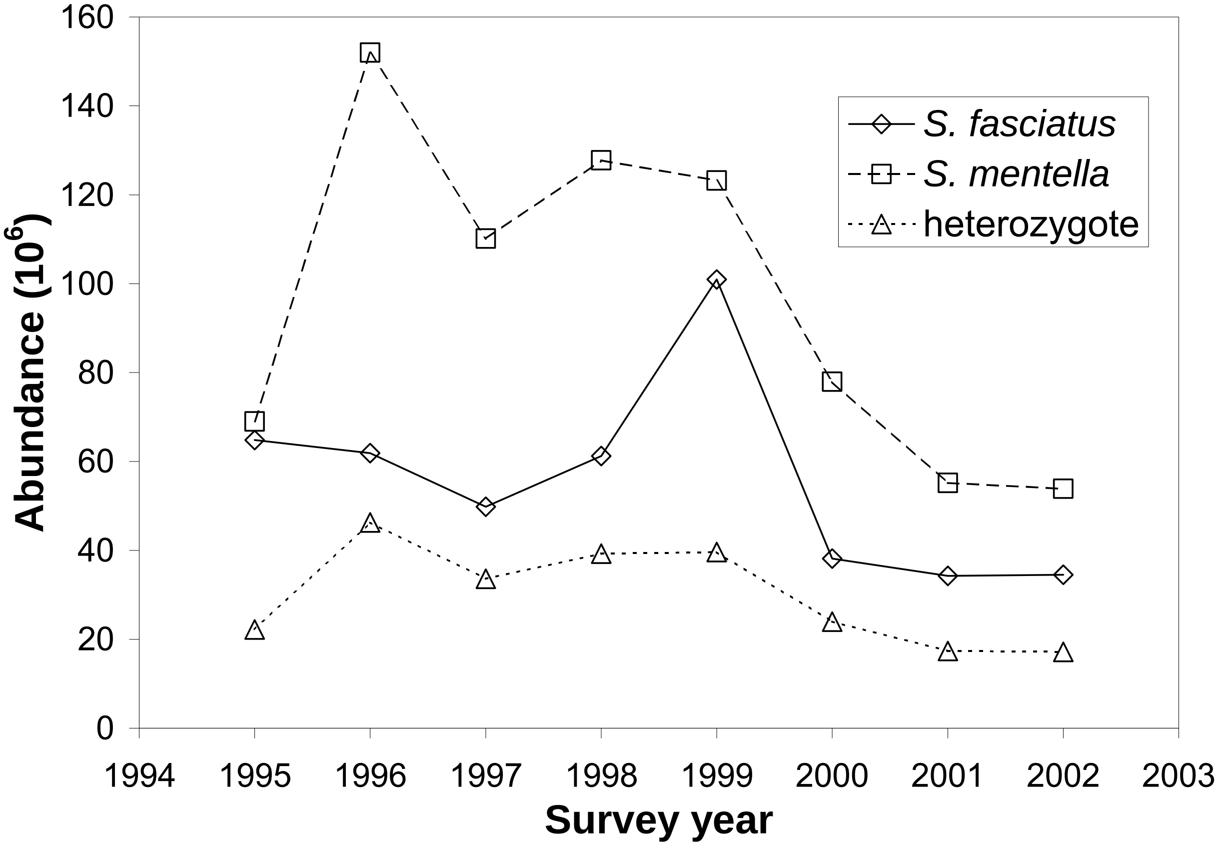
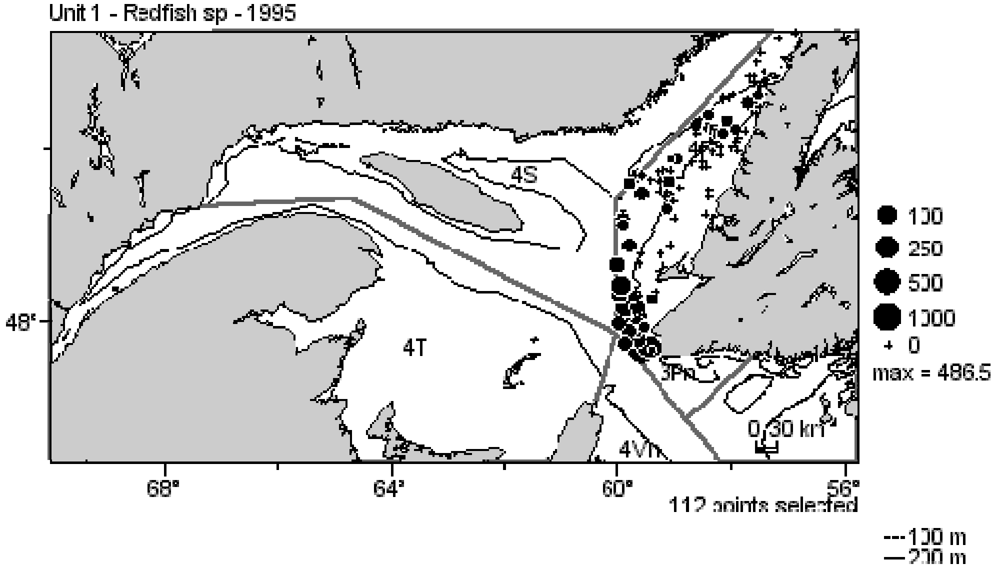


Figure 11. Indices of abundance from Cod Sentinel survey in summer. Species were separated with genotype proportions by depth calculated from *A. Needler* survey for the 1993 to 1996 period.



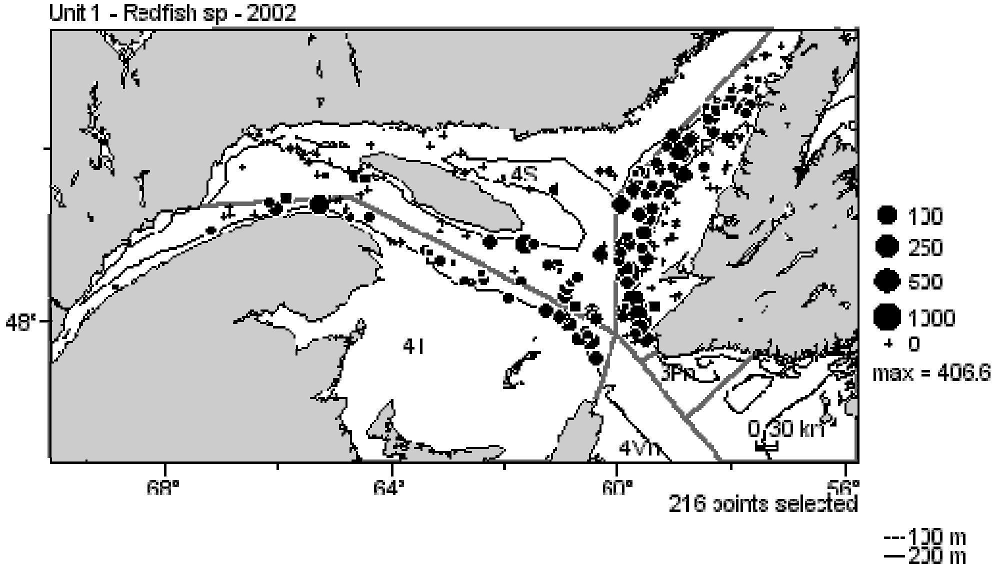


Figure 12. Distribution of redfish sp. in the 1995 and 2002 Cod Sentinel surveys in fall.

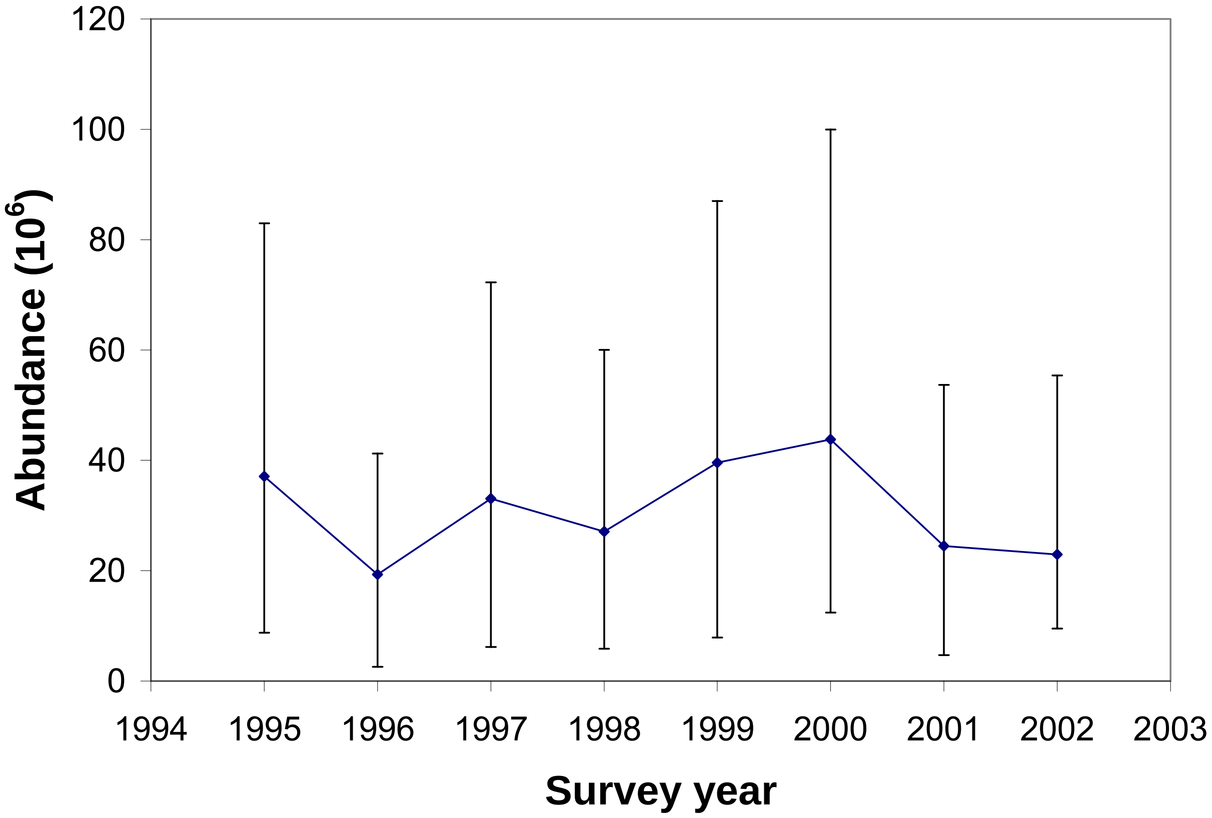


Figure 13. Indices of abundance of redfish sp. from the Cod Sentinel survey in fall with 95 % confidence intervals.

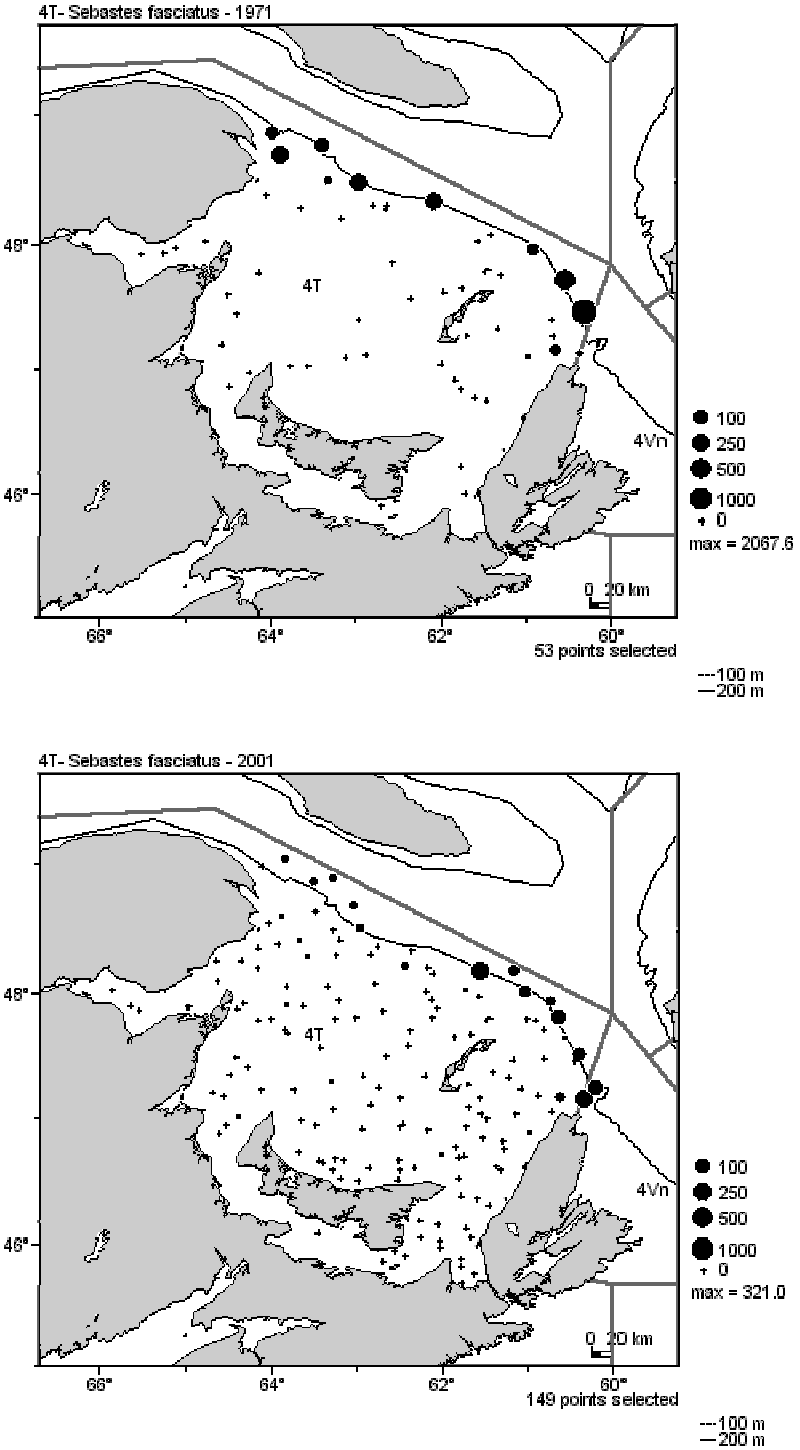


Figure 14. Distribution of *S. fasciatus* in the 1971 and 2001 surveys in 4T.

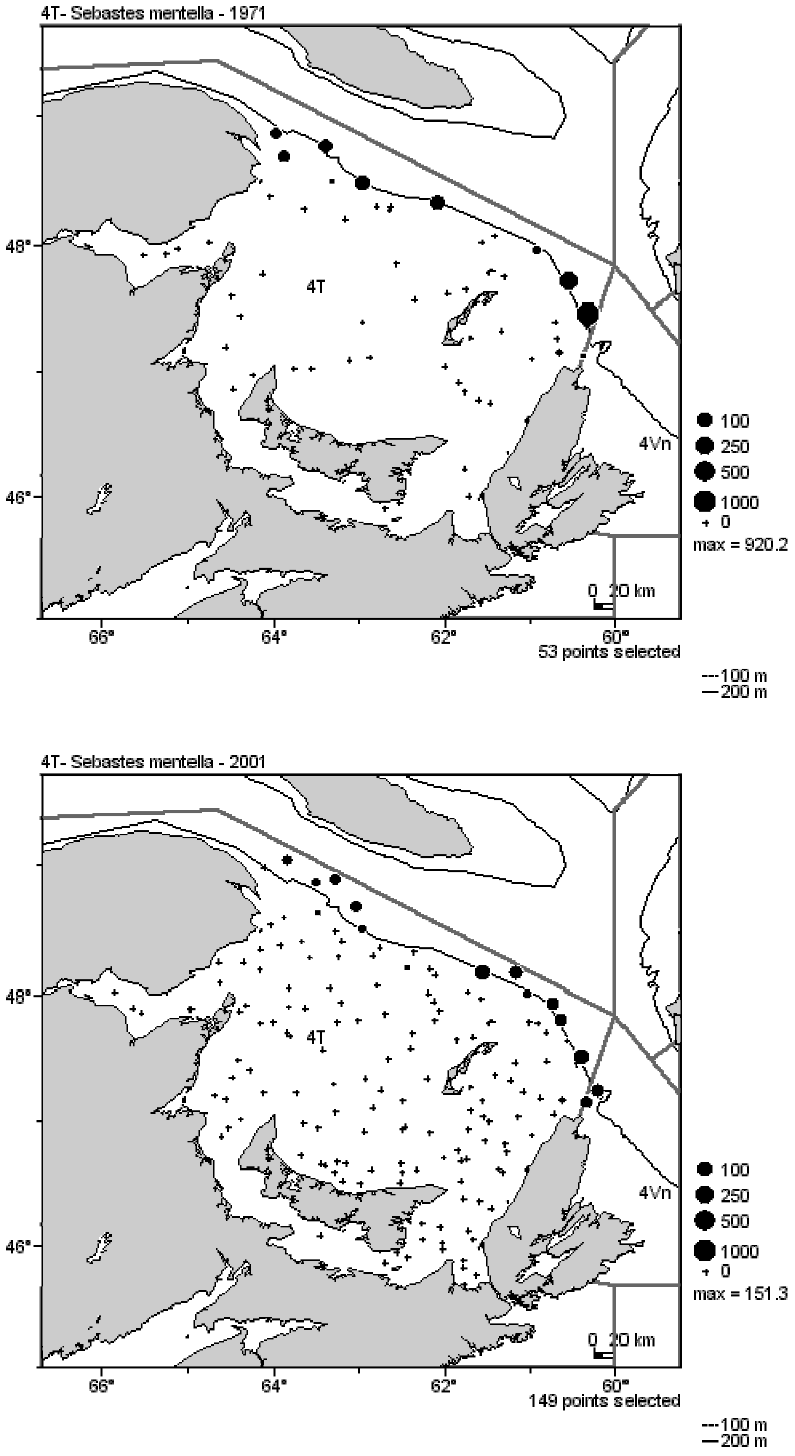


Figure 15. Distribution of *S. mentella* in the 1971 and 2001 surveys in 4T.

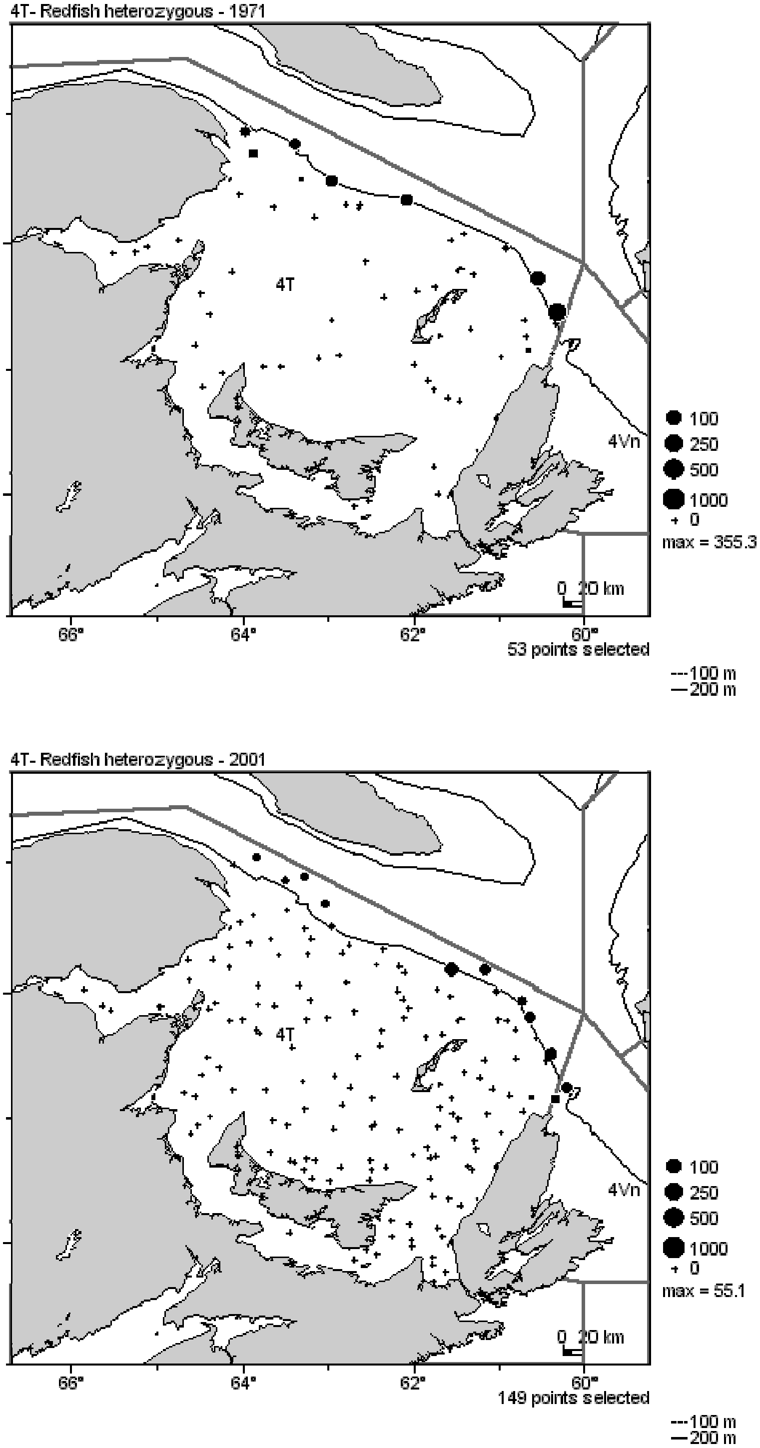


Figure 16. Distribution of redfish heterozygous individuals in the 1971 and 2001 surveys in 4T.

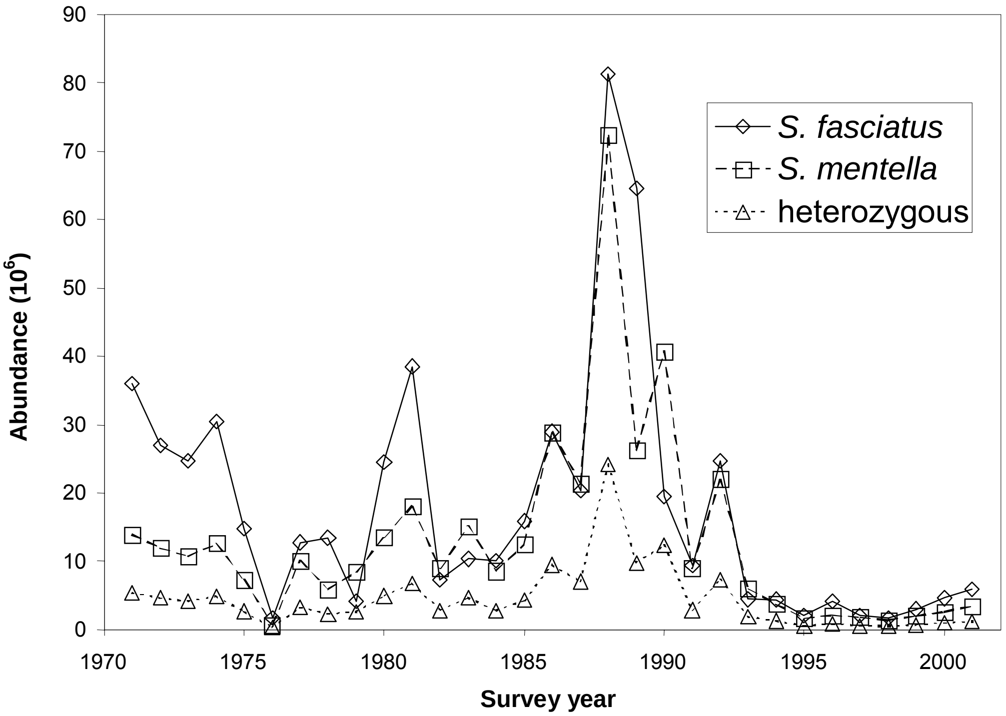


Figure 17. Indices of abundance from the 4T September survey. Species were separated with genotype proportions by depth calculated from *A. Needler* survey for the 1993 to 1996 period.

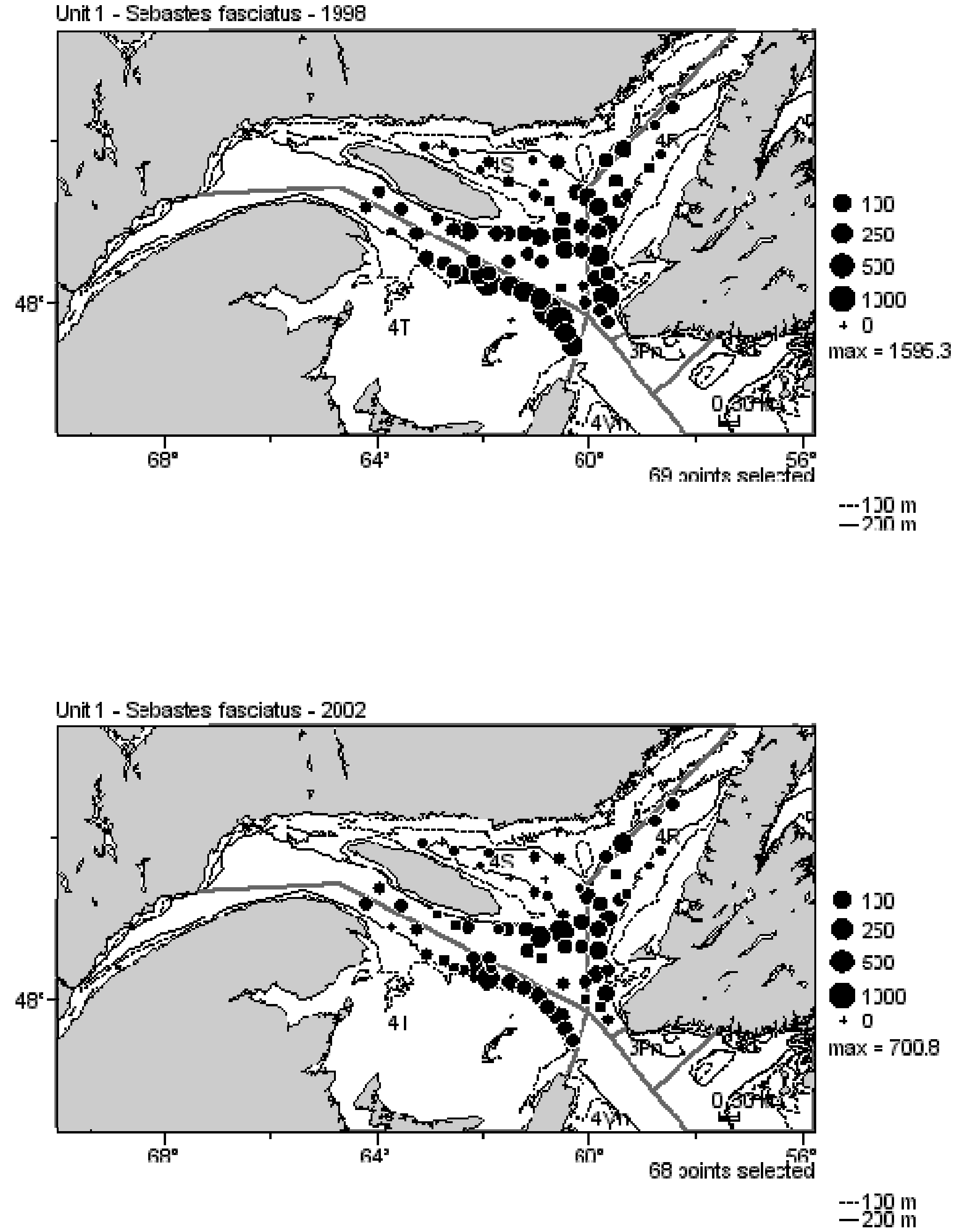
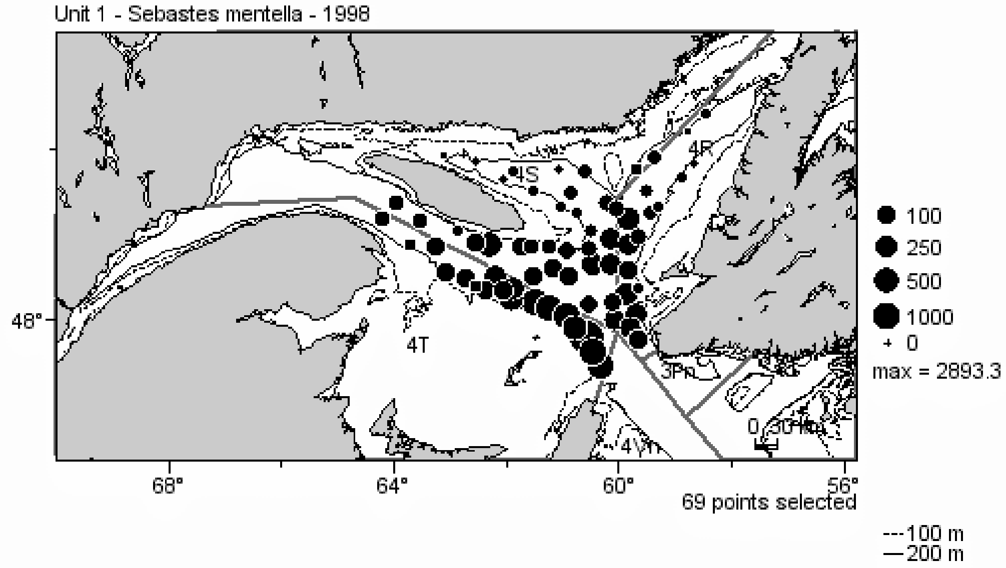


Figure 18. Distribution of *S. fasciatus* in 1998 and 2002 GEAC surveys.



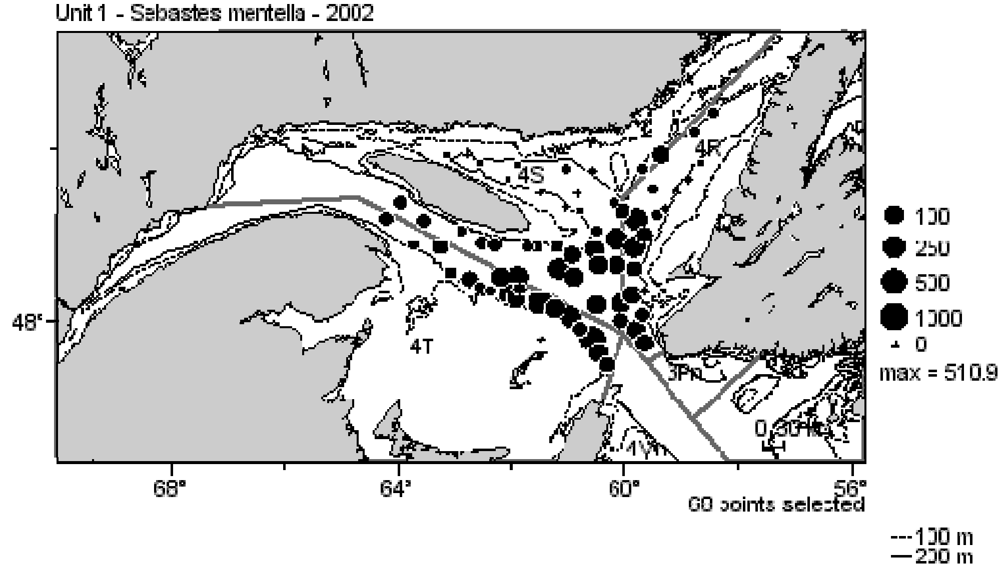
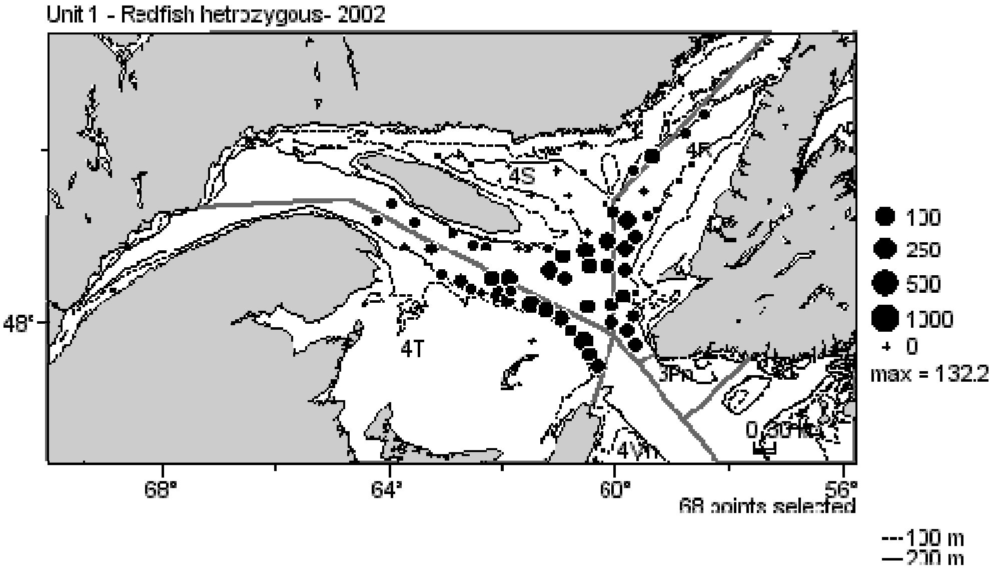


Figure 19. Distribution of *S. mentella* in 1998 and 2002 GEAC surveys.



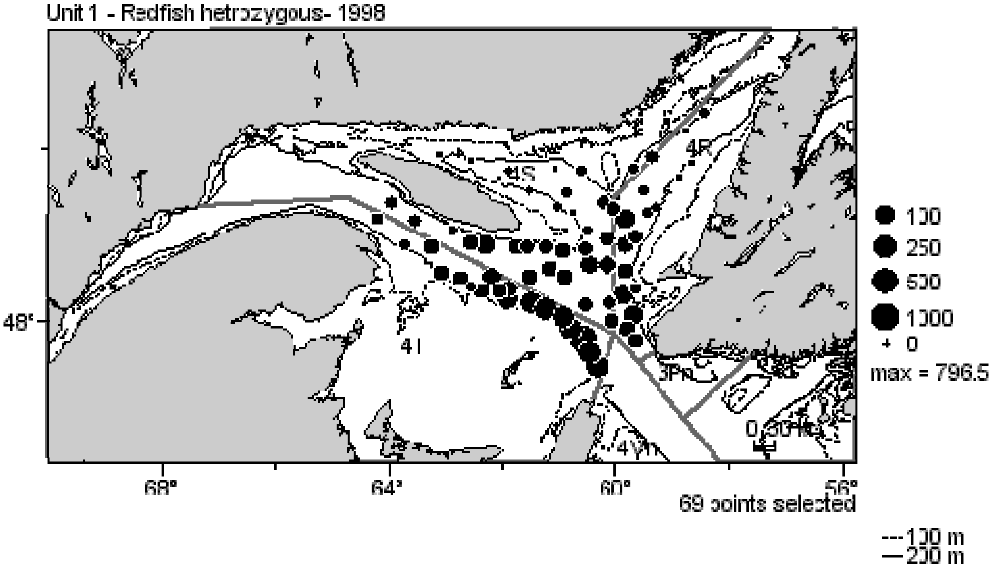
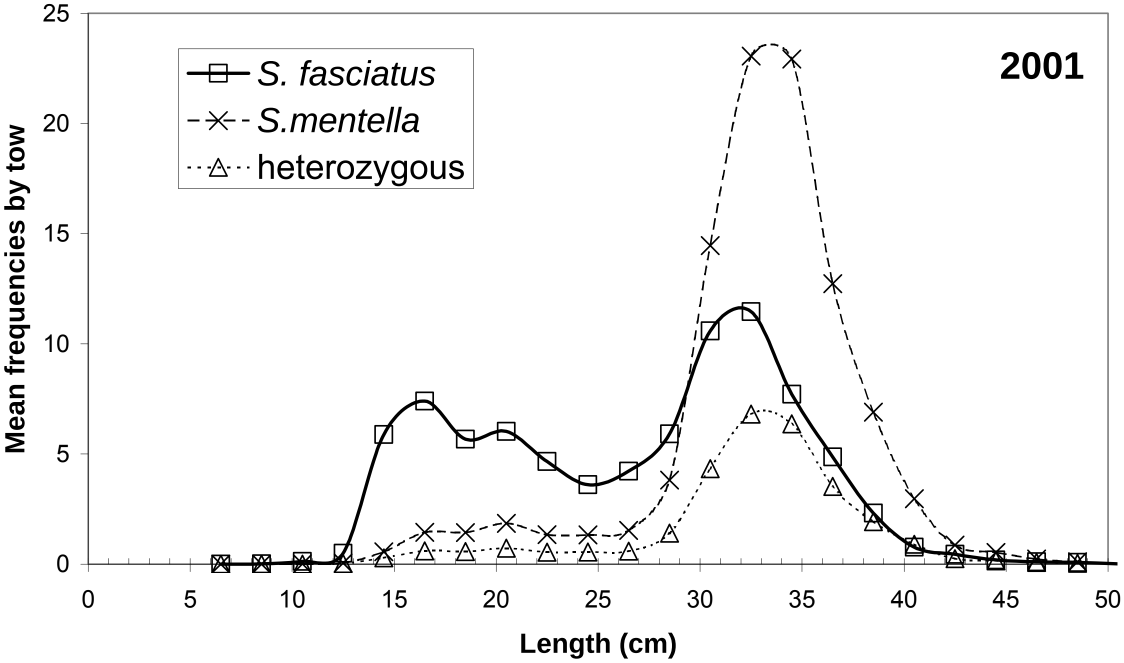


Figure 20. Distribution of redfish heterozygous individuals in 1998 and 2002 GEAC surveys.



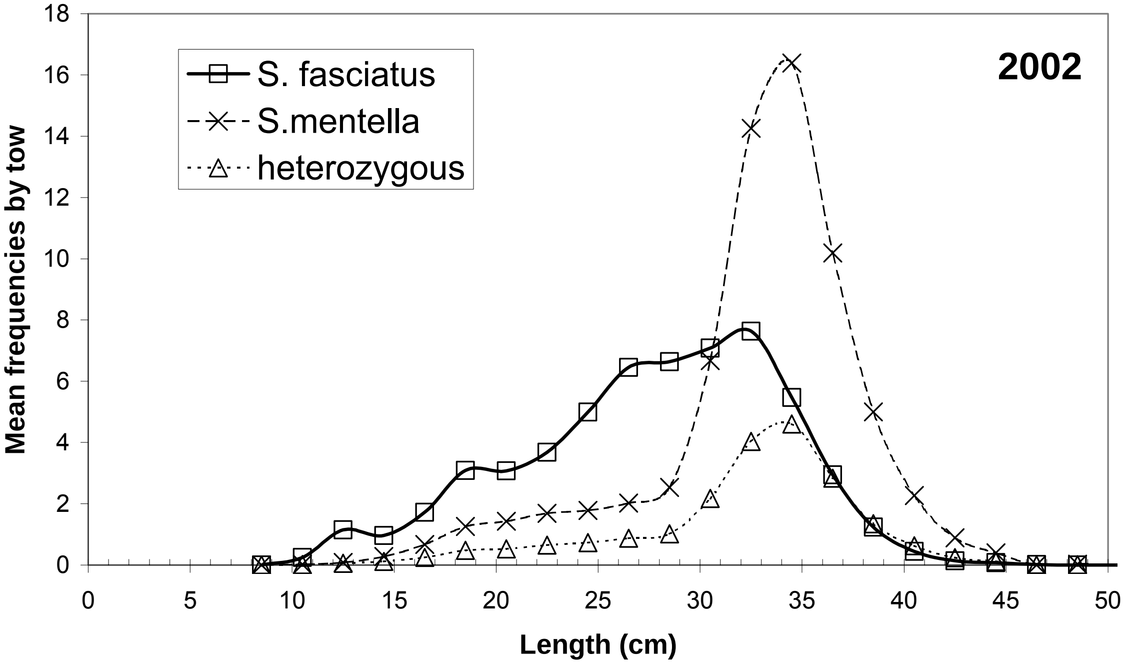


Figure 21. Length frequencies of redfish sp. in 2001 and 2002 observed on the GEAC survey.

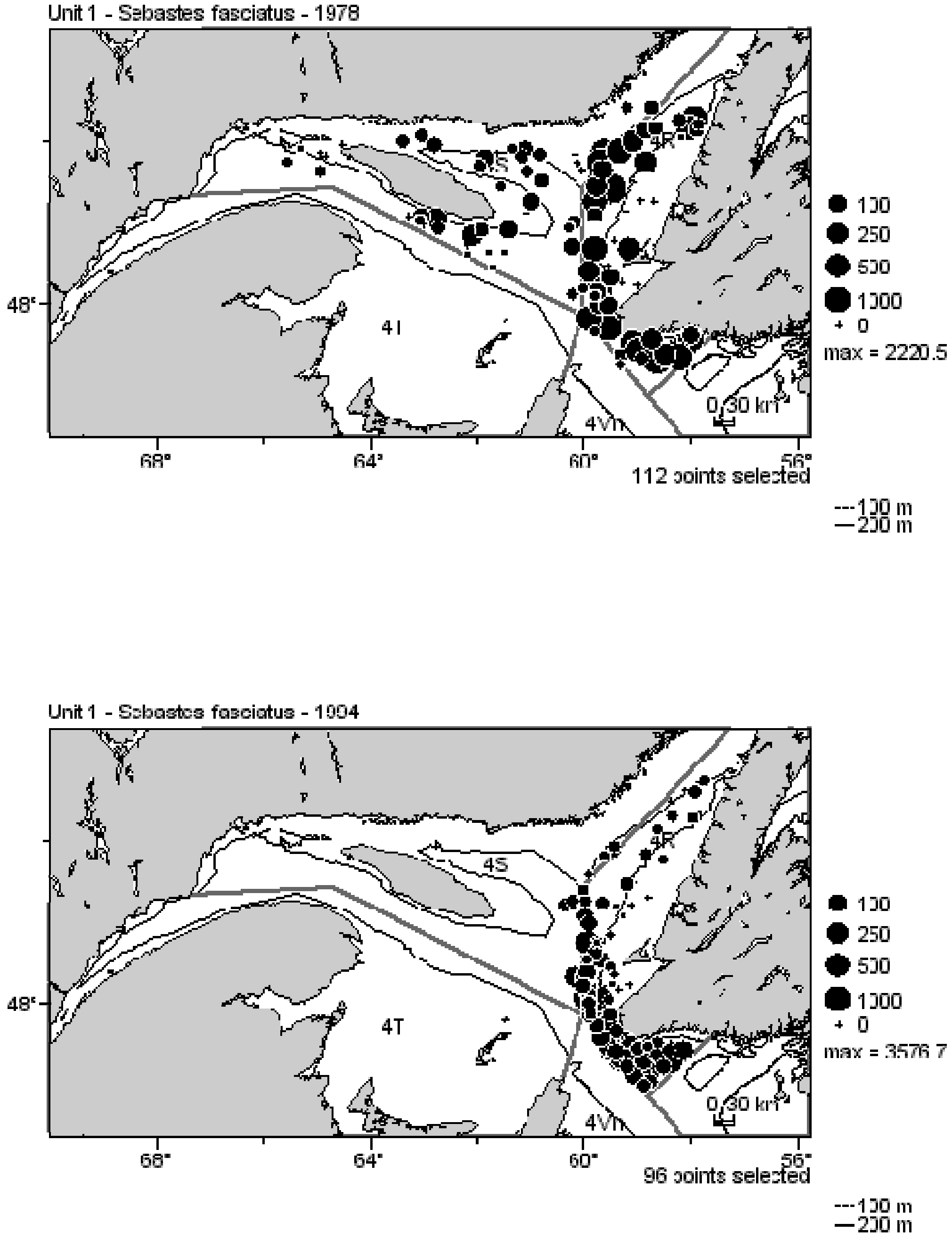


Figure 22. Distribution of *S. fasciatus* in the 1978 and 1994 surveys of *Gadus Atlantica*.

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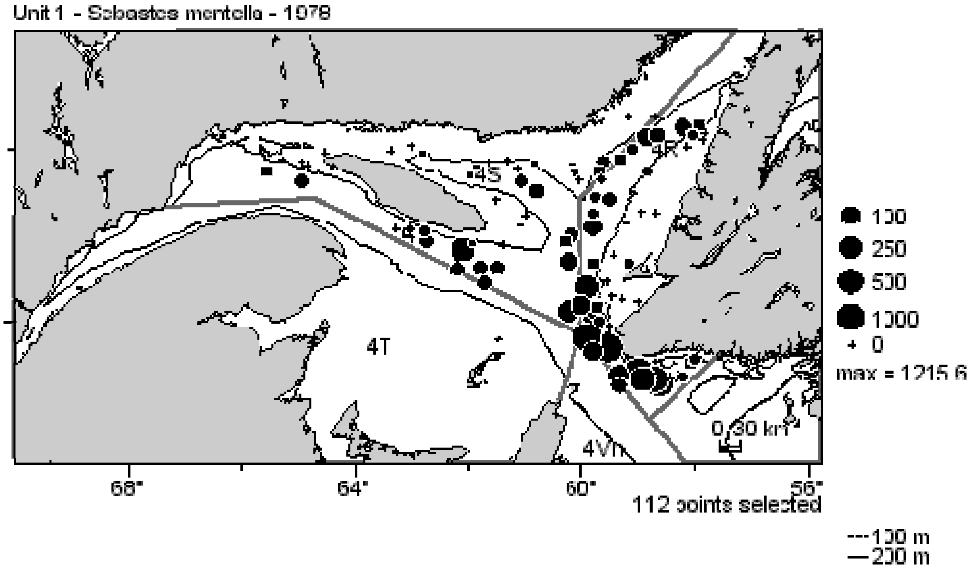

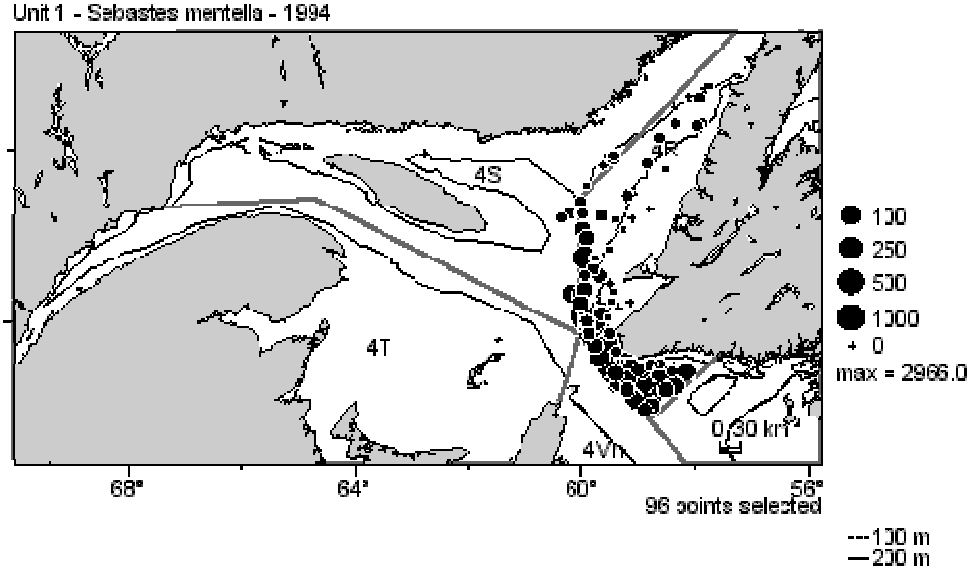

Figure 23. Distribution of *S. mentella* in the 1978 and 1994 surveys of *Gadus Atlantica*.

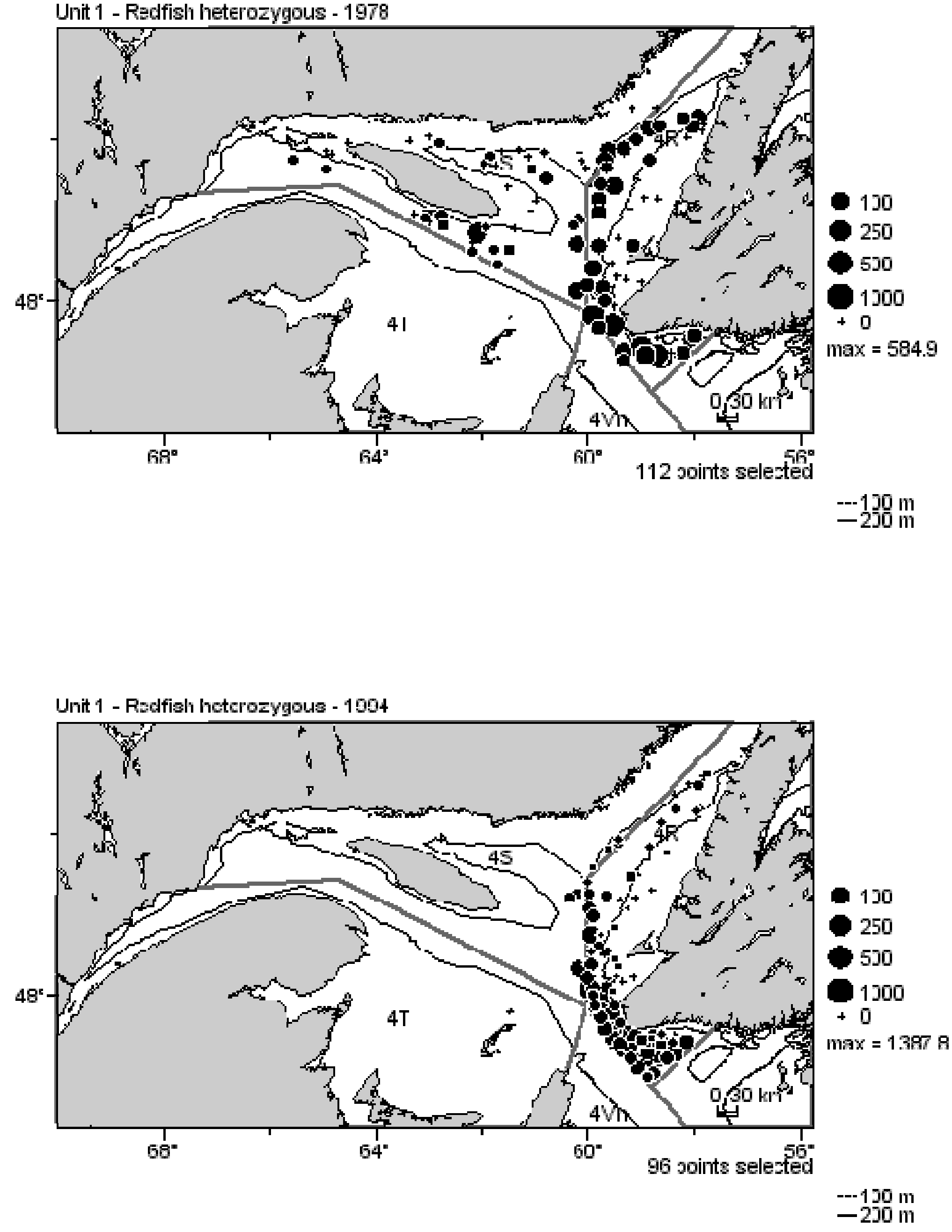

Figure 24. Distribution of redfish heterozygous individuals in the 1978 and 1994 surveys of *Gadus Atlantica*.

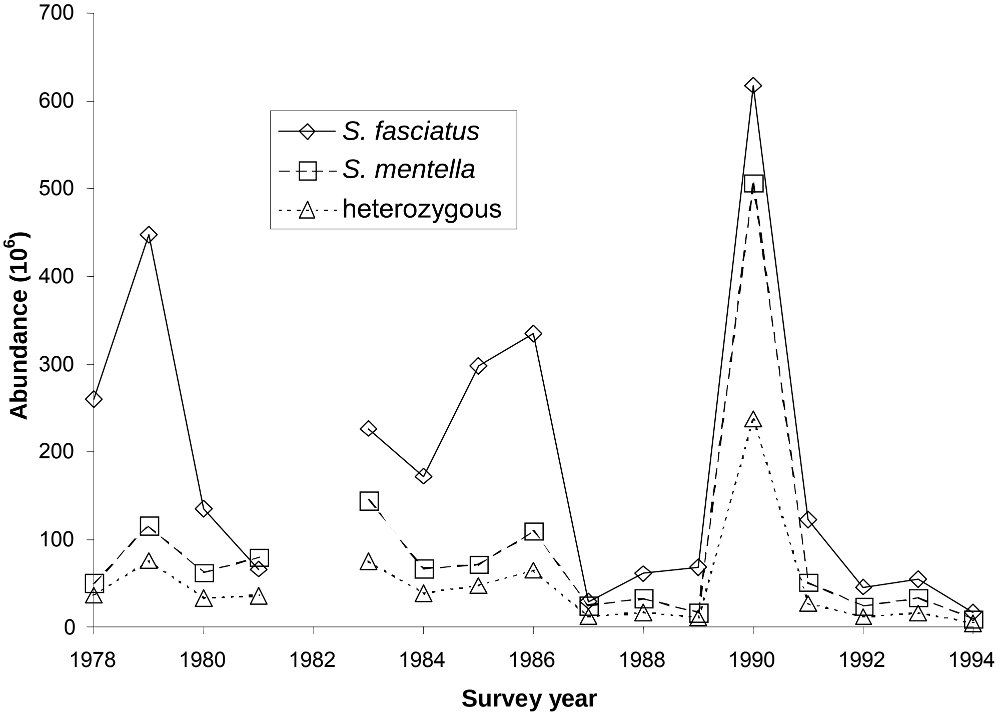

Figure 25. Indices of abundance from *Gadus Atlantica* winter survey. Species were separated after genotype proportions by depth in 1983 for the 1978-1989 period and in 1994 for the 1990 to 1994.

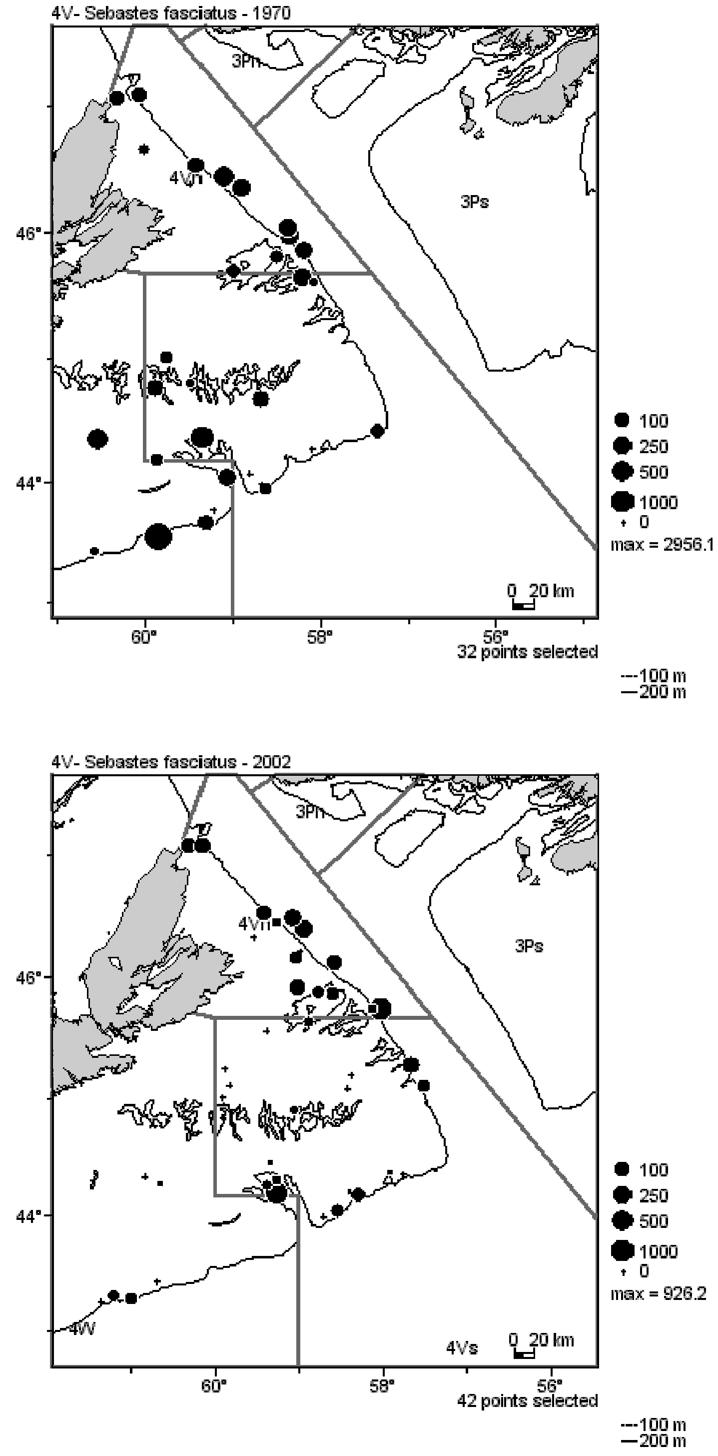

Figure 26. Distribution of *S. fasciatus* in the 1970 and 2002 surveys of 4V.

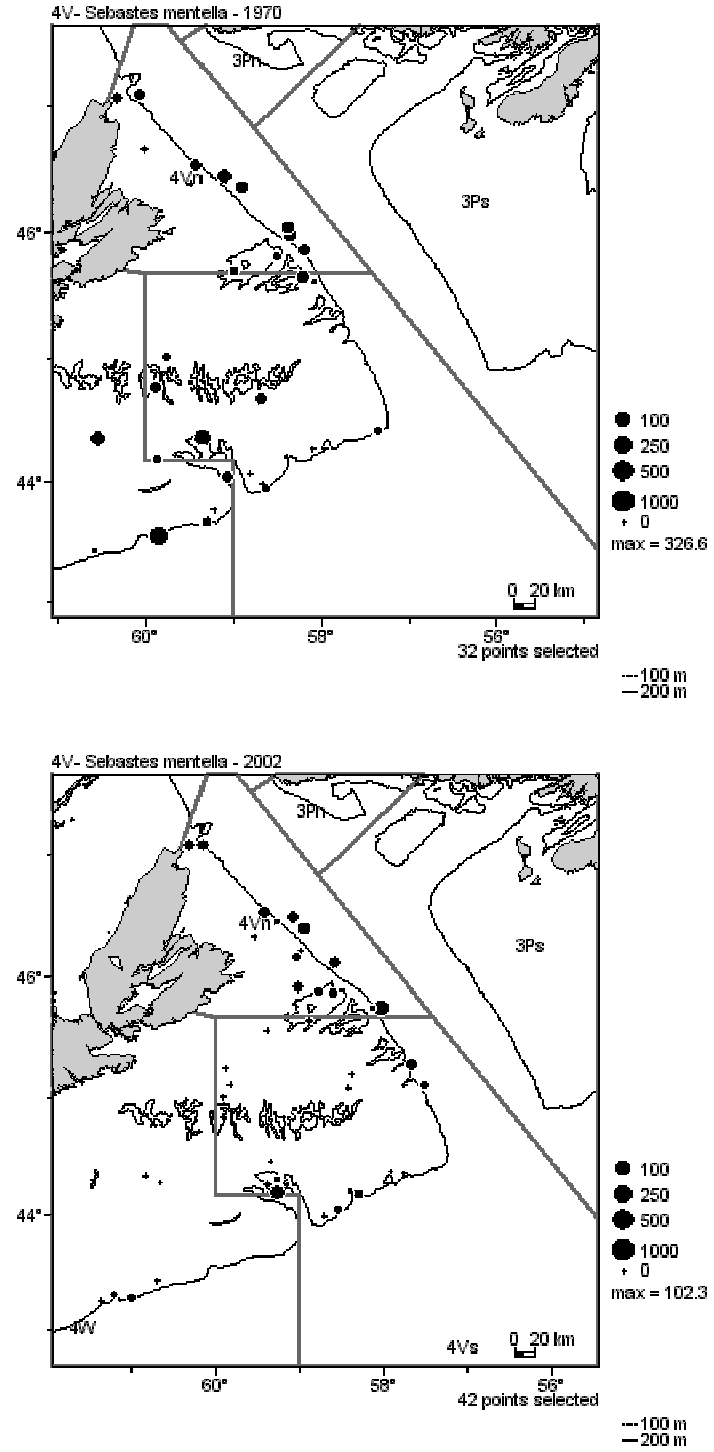

Figure 27. Distribution of *S. mentella* in the 1970 and 2002 surveys of 4V.

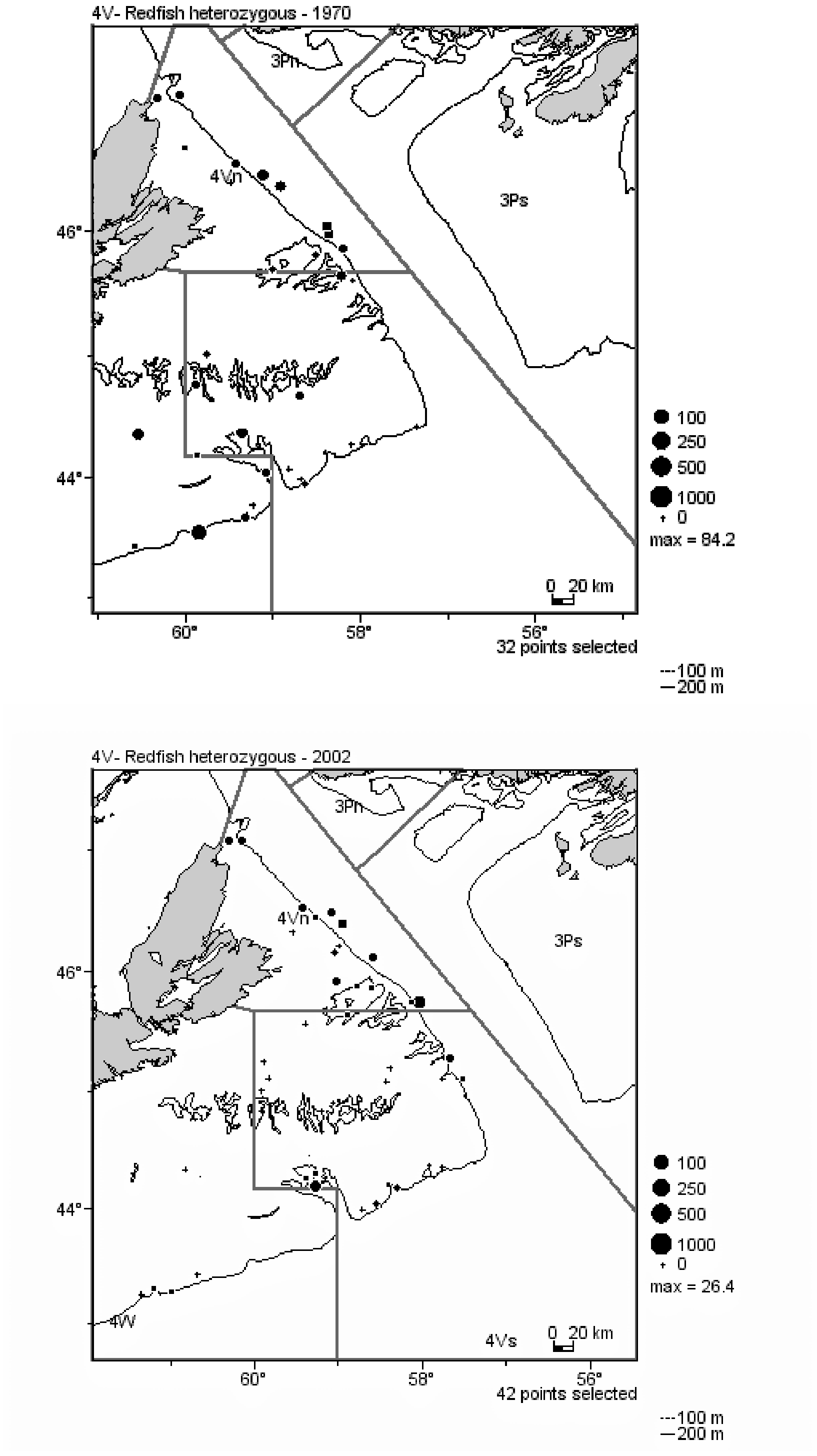

Figure 28. Distribution of redfish heterozygous individuals in the 1970 and 2002 surveys of 4V.

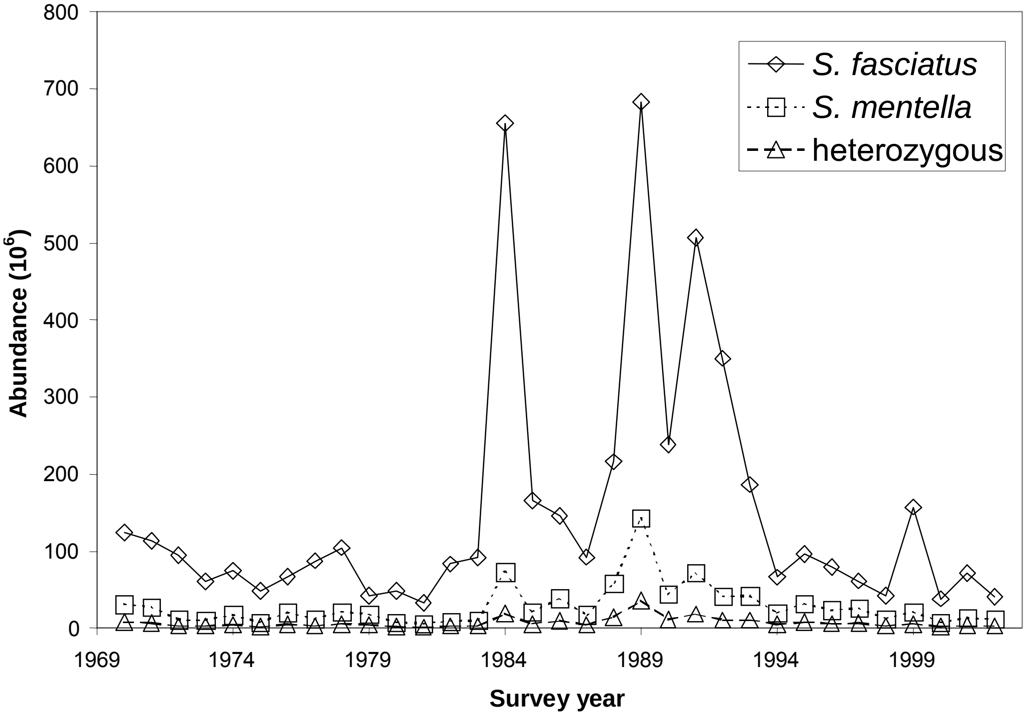

Figure 29. Indices of abundance from the 4V surveys. Species are separated using genotype proportions by depth from the Redfish Multidisciplinary Research Program data (1995-1999).