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Differences in demersal community structure and biomass size spectra within and outside the Maltese Fishery Management Zone (FMZ)

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SUMMARY: We examined the protection effect of a long-established fisheries protection zone by studying the demersal communities and the biomass size spectra of specific taxonomic groups. The results and the relevant management implications of the community analysis are discussed within the context of the MEDITS trawl survey program, from which the data was derived. The demersal fishery resources on the muddy bottoms of Maltese trawling grounds were found to be stratified in four main depth ranges: 83 to 166 m (outer continental shelf), 140 to 230 m (shelf break), 270 to 440 m (shallow slope), and 466 to 701 m (deep slope). Significant differences were detected between the inside and outside zones of the outer continental shelf. Stations from this stratum inside the protected zone had twice as much biomass as those outside as well as larger individuals of some species (e.g. elasmobranchs). The depth strata identified do not coincide with those sampled in existing trawl survey programmes in the Sicilian Channel, which were set up without reference to demersal assemblage structure and its relation to depth. It is therefore clear that characterisation of the biotic assemblages is important in order to obtain a better sampling representation of each depth-stratum/assemblage type, and this should be considered in the survey design.

Keywords: Sicilian Channel, biomass size spectrum, Maltese fishery, trawl surveys, Mediterranean Sea, demersal assemblages, Marine Protected Areas.

RESUMEN: Diferencias en la estructura de la comunidad demersal y espectros de biomasa dentro y fuera de la zona de gestión pesquera de Malta. – Examinamos el efecto de protección de una zona de protección pesquera establecida desde hace mucho tiempo mediante el estudio de las comunidades demersales y espectros de biomasa de grupos taxonómicos específicos. Los resultados del análisis de comunidades se discuten en el contexto de las campañas de arrastre MEDITS, que sirvieron para generar los datos, y se señalan las implicaciones para la gestión de recursos pesqueros de nuestros resultados. Los recursos pesqueros demersales de fondos de arrastre fangosos se encuentran estratificados en 4 rangos de profundidad: 83-166 m (plataforma continental externa), 140-230 m (límite entre la plataforma y el talud), 270-440 m (talud superior) y 466-701 (talud medio). El único grupo dentro de la zona de protección que resultó diferente significativamente del estrato equivalente fuera de la zona de protección fue el grupo de la plataforma continental externa. Las estaciones de este estrato dentro de la zona de protección resultaron tener el doble de biomasa que las estaciones equivalentes fuera de la zona de protección, así como individuos de tallas superiores para ciertas especies (e.g. elasmobranquios). Los estratos de profundidad identificados no coinciden con los estratos de muestreo de los programas de campañas de arrastre en el canal de Sicilia, que fueron establecidos sin tener en cuenta la estructura de comunidades y su relación con la profundidad. La caracterización de grupos bióticos es importante para mejorar la representación del muestreo en cada estrato de profundidad y tipo de comunidad y debe tenerse en cuenta para el diseño de los planes de campaña de arrastre demersal.

Palabras clave: Canal de Sicilia, espectro de biomasa, pesquerías de Malta, campañas de arrastre, mar Mediterráneo, comunidades demersales, Áreas Marinas Protegidas.

INTRODUCTION

Currently there is increasing interest in the ecosystem approach to fisheries management (Link, 2002; Pitkitch *et al*., 2004), and consequently a good knowledge of the components of the system is essential. In addition to the removal of target species, fishing with demersal towed gears can result in large-scale secondary ecological effects (Hall, 1999; Kaiser and de Groot, 2000; Kaiser *et al.,* 2006). In the Mediterranean Sea, demersal stocks are generally recognised as depleted, fully-exploited or over-exploited (Farrugio *et al*., 1993; Lleonart and Maynou, 2003; Rochet *et al*., 2005). This is mainly a consequence of fleet over-capacity and the use of very small mesh sizes in trawl cod-ends, which has increased fishing mortality and habitat degradation (Caddy, 1990; Fiorentini *et al*., 1997; Ragonese *et al*., 2002; Lleonart, 2005). This situation has raised concerns about the validity of the management actions implemented in the past (Corten, 1996). It has increased the pressure on scientists and stakeholders to adopt a precautionary and ecosystem-based approach in order to reduce the chances of overexploitation and/or collapse of fish stocks and prevent ecosystem degradation. Areas in which fishing is restricted, or Marine Protected Areas (MPAs), are one tool designed to protect populations of commercially important stocks from overexploitation as well as protecting other components of the ecosystem. In general, studies of MPAs have demonstrated that the abundance and size of harvested fish species increase when compared to unprotected adjacent areas (Rowley, 1994; Russ, 2002; Halpern, 2003). However, most studies are of areas that are either completely closed to fishing or have very limited fishing activities. In the present study, we focus on the 25 Nautical Mile Maltese Fisheries Management Zone (FMZ) that has strict controls on trawling pressure. The management regime in this MPA specifically addresses fisheries (EC 813/2004).

Bottom trawling is an important component of most Mediterranean fisheries and, in many cases, it yields the highest earnings among all the fishing sub-sectors. In the Mediterranean, the seabed is trawled by commercial fishers at depths ranging from 50 m to 800 m (Farrugio *et al*., 1993). The fishery has a multi-species composition and many of the commercially valuable species only appear seasonally in the catches (Caddy, 1993; Stergiou *et al*., 1997). Trawl catches are composed of a highly diverse mix of fish (teleosts and elasmobranchs), cephalopods and crustaceans (decapods and stomatopods), together with several epifaunal macrobenthic invertebrates (Relini *et al*., 1999; Sánchez *et al*., 2007).

The demersal fish, crustacean and cephalopod assemblages of Mediterranean trawl fishery grounds have been studied in the western (Abella *et al*., 1999; Abelló *et al*., 2002; Colloca *et al*., 2003; Massutí and Reñones 2005) and eastern (Tserpes *et al*., 1999; Ungaro *et al*., 1999; Labropoulou and Papaconstantinou, 2000; Kallianiotis *et al*., 2004) basins, but there have been very few studies on such assemblages in the Sicilian Channel (Patti *et al*., 1994; Dimech *et al*., 2005; Gristina *et al*., 2006), which is the biogeographical border between the western and eastern sectors of the Mediterranean (Bianchi, 2007). Some studies have examined the relationship between environmental factors (i.e. depth, water temperature, oxygen concentration and sediment type) and the distribution of the demersal assemblages (Biagi *et al*., 1989; Sardà *et al*. 2004); others have attempted to relate the demersal assemblages to the structuring role of macroepibenthic communities (Gaertner *et al*., 1999; Colloca *et al*., 2003; Massutí and Reñones, 2005). Most of these studies suggest that depth is a key driver of demersal assemblage composition and structure.

These studies provide important baseline information to underpin an ecosystem-based approach to the management of Mediterranean trawl fisheries. Understanding the relationship between restricted fishing zones, environmental factors and the communities of epibenthic invertebrates and those of demersal fish is important for management, especially if these relationships reveal links with different life-history stages or size-classes of target species (Blyth-Skyrme *et al.*, 2006). This knowledge becomes more critical since the collateral effects of the fishery can impact upon features (e.g. habitat or bioturbating fauna) that support key ecosystem functions (Kaiser and de Groot, 2000; Kaiser *et al*., 2006).

At present, information is lacking on the distribution of biotic assemblages in relation to zones in which fisheries are restricted and a wider range of environmental parameters for many areas of the Mediterranean, even if such information is essential for the management of its living resources.

The present work aimed to study the conservation effect of the Maltese 25-Nautical Mile restricted

fishing zone. The main hypothesis is that the exclusion of large-scale commercial fishing activities will have restricted overall fishing effort on demersal species. Specifically, the present study addressed the structure of the demersal assemblage, sediment characteristics, and the distribution of demersal resources on muddy bottoms in the depth range 80 m to 800 m inside the 25 Nautical Mile FMZ, and immediately outside it.

MATERIAL AND METHODS

Study area

Since 1971 Malta has managed a 25-Nautical Mile Exclusive Fishing Zone (Fig. 1) that covers an area of 11980 km^2, and which, after Malta became a member of the European Union in 2004, was retained as a Fisheries Management Zone (FMZ) (Council of the European Union, 2004). The objectives of the original Exclusive Fishing Zone (EFZ) were to protect the local artisanal fisheries from foreign large-scale fishing, especially trawling. Until recently, the fishing regulations in force in the EFZ were those published in 1934 (Fish Industry Act), with minor changes over the years (Camilleri, 2005), that included a restriction on trawling within Maltese territorial waters (3 nautical miles from the coastline; the restriction was maintained at 3 nautical miles even after the extension of Maltese territorial waters to 12 nautical miles). Prior to Malta's accession to the EU a new management regime was proposed, agreed upon and later implemented after accession through Council Regulation EC 813/2004, which, *inter alia*, limited trawling operations to specified areas based on the trawlable grounds identified during a survey in 1978 made in collaboration with the Food and Agriculture Organization of the United Nations (FAO) (Giudicelli, 1978).

Sampling methodology

The present study was conducted within the 25 NM FMZ around the Maltese islands and the sea area immediately outside this zone that comprises the General Fisheries Commission for the Mediterranean (GFCM) geographical sub-area 15, as part of the ongoing MEDITS trawl survey programme (Bertrand *et al*., 2002). Experimental otter trawl samples were collected by the RV *Sant`Anna* in

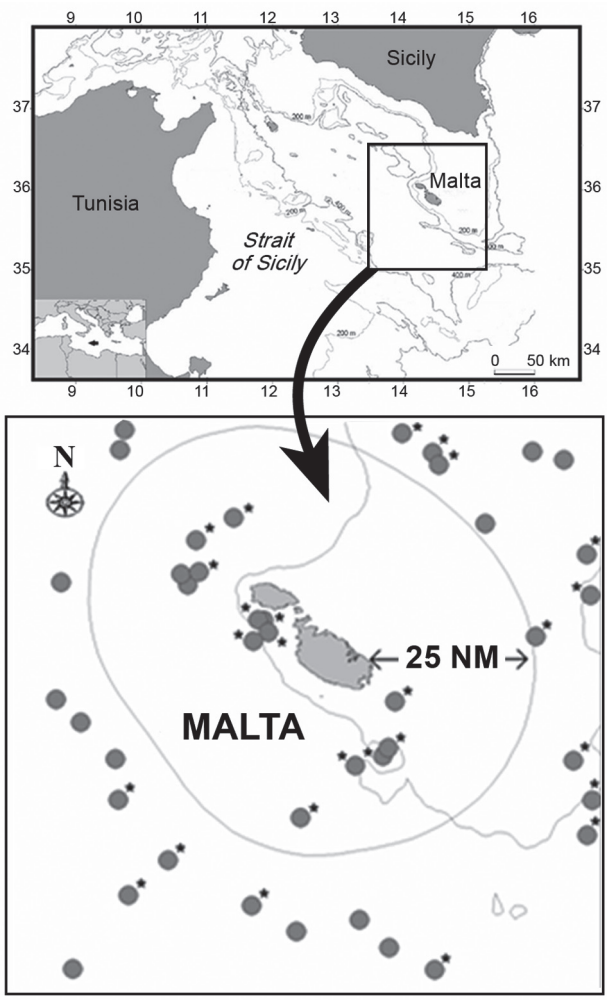

Fig 1. – Map of the study area showing the location the General Fisheries Commission for the Mediterranean geographical sub-area 15 (the quadrilateral south of Sicily). The oval around Malta represents the boundary of the Maltese 25 NM Fisheries Management Zone (FMZ). The filled circles mark the position of the trawl sampling stations; stations from where box-cores were collected are indicated by an asterisk. The 200 m depth contour is also shown.

June/July of 2003, 2004 and 2005 from 45 stations located at different depths between 80 m and 800 m (Fig. 1). Each haul lasted for 30 min at depths less than 200 m and 60 min at depths between 200 and 800 m, and trawl speed was ca. 3 knots. Samples were collected using a 20-22 m wide and 40 m long experimental otter trawl net with a 2-2.5 m vertical opening and a cod end stretched mesh size of 20 mm (IFREMER GOC 73) (Fiorentini *et al*., 1999). Seawater bottom temperature was measured using a temperature probe (Minilog Vemco©) attached to the net. The entire biotic component from each haul was sorted, after which the fauna were identified, weighed and counted.

In 2004 and 2005, 3 replicate samples for sediment analyses were collected from 26 stations (marked

with an asterisk in Fig. 1) using a WILDCO® 0.0625 m² box-corer. Of the 26 stations sampled, 12 were from the 100 to 200 m MEDITS depth stratum, seven were from the 200 to 500 m MEDITS depth stratum, and the other seven were from the 500 to 800 m MEDITS depth stratum. Sediment granulometry and the percentage of organic carbon were determined according to the procedures described by Buchanan (1984). The percentage dry weight of the different sediment fractions was calculated. Folk and Ward statistical sediment descriptors, including mean sediment grain size, sediment sorting, skewness and kurtosis, were calculated using the GRADISTAT version 4.0 software (Blott and Pye, 2001). Data for macrofauna (infauna and epifauna) from these box-core samples were not used in the present study since the total abundance was very low for all stations, ranging from ca. 2 to 10 individuals per core and averaging 64 ind./m^2 with high variability (Dimech *et al*., 2005).

Statistical analyses

Univariate indicators, including abundance indices, biodiversity indices and slopes and intercepts of biomass size spectra, were computed for the stations sampled inside and outside the FMZ including: the total number of individuals per km^2, total biomass per km^2, total number of species, Shannon-Weiner diversity (*H*') and Pielou's evenness (*J*'). Abundance data were used for calculating the diversity indices. These indicators were calculated for each assemblage group identified *a posteriori* from multivariate analysis of the data in order to eliminate the confounding effect of change in the demersal communities that occurs with depth in the large depth range examined (80 to 800 m).

The univariate indices (density, DI, and biomass, BI) for each station were standardised per km^2, and analysed using multivariate classification and ordination techniques. Species whose percentage abundance and biomass were less than 0.01% of the total sample were removed from the analyses. In order to reduce the influence of abundant species and increase the importance of less common species a similarity matrix was constructed from the fourth-root transformed data using the Bray-Curtis similarity index (Clarke and Warwick, 1994a). Non-metric multidimensional scaling (nMDS) ordination was applied. Since the biomass data yielded results that could be interpreted more clearly, only these are presented and used for further analysis. The SIMPER (similarity percentages) procedure was used to determine which species contributed most to the similarity within each grouping of stations and to the dissimilarity between the groupings that were defined *a posteriori* (Clarke and Warwick, 1994b). The Analysis of Similarities (ANOSIM) routine was used (Clarke and Warwick, 1994b) to check for temporal differences between the identified clusters that may affect the analysis between the stations inside and outside the FMZ.

Relationships between the measured abiotic parameters (depth, temperature and sediment characteristics) and the composition of the demersal assemblages were determined using the BIOENV procedure (Clarke and Ainsworth, 1993), and by superimposing scaled individual variables onto the sample locations on the two-dimensional nMDS ordination plots (Field *et al*., 1982; Clarke and Warwick, 1994a). All the analyses were undertaken using the PRIMER 6 statistical software package (Clarke and Warwick, 1994a).

Biomass size-spectra were plotted to determine if the assemblage groups identified *a posteriori* exhibit any differences in body-size distribution inside and outside the Maltese FMZ. Size spectra were calculated for each assemblage inside and outside the FMZ based on data from each of the three separate years, by using the weights of individuals from all taxonomic groups, including teleosts, elasmobranchs, crustaceans and cephalopods. Since different hauls did not sweep equal areas of the bottom, especially due to the large difference in the depth range, weights were standardised per km^2, after which each individual was assigned to a weight-class ($\log_{10}$ weight in g). The data were normalised and the logarithm of the biomass was calculated. Lower and upper size classes were excluded to avoid data artifacts due to poor retention in the gear (Duplisea *et al.,* 1997; Jennings *et al.,* 2001).

For the univariate abundance and biodiversity indices and slopes and intercepts of the biomass size-spectra a two-way GLM analysis of variance (2-Way GLM ANOVA) was used to test for significant differences between different assemblages (identified *a posteriori* from the multivariate analyses) and to detect significant differences between the stations for the groups identified inside and outside the FMZ.

TABLE 1. – Contribution of each taxon to the composition of the demersal assemblages in terms of density and biomass for the years under study.

Taxon	Relative Density (%)				Biomass (%)			
	2003	2004	2005	Mean ± s.d.	2003	2004	2005	Mean ± s.d
Teleosts	68.11	75.59	94.91	79.54 ±13.83	64.11	66.92	83.12	71.38 ±10.26
Elasmobranchs	1.32	1.40	0.60	1.11 ± 0.44	18.76	20.98	11.18	16.97 ±5.14
Decapods	17.36	19.16	3.15	13.22 ± 8.77	6.11	7.06	3.53	5.57 ±1.82
Molluscs	13.21	3.86	1.34	4.69 ± 6.26	11.02	5.04	2.17	6.08 ±4.52

RESULTS

A total of 189 species (26 elasmobranchs, 111 teleosts, 26 decapods and 26 molluscs) were identified; teleosts were the dominant taxon sampled by the fishing gear in terms of both density and biomass index (Table 1). When classified on the basis of biomass, five main groups resulted at a similarity of 46% (Fig 2). These groups represented two different geographical locations of the outer continental shelf (A and B, Fig. 2), the shelf break (140 to 273 m), shallow slope (240 to 440 m) and the deep slope (466 to 701 m). The species responsible for the four assemblages revealed by nMDS, as determined by SIMPER, show that a large number of species contributed to the overall similarity and there were clearly dominant species: Continental Shelf - *Scyliorhinus canicula*, *Mullus barbatus* and *Merluccius merluccius*; Shelf Break - *Capros aper*, *Argentina sphyraena*, *Scyliorhinus canicula* and *Merluccius merluccius*; Shallow Slope - *Chlorophthalmus agassizi*, *Merluccius merluccius* and *Caelorhynchus caelorhynchus*; Deep Slope - *Galeus melastomus*, *Aristaeomorpha foliacea*, *Hoplostethus mediterraneus* and *Merluccius merluccius* (Appendix 1).

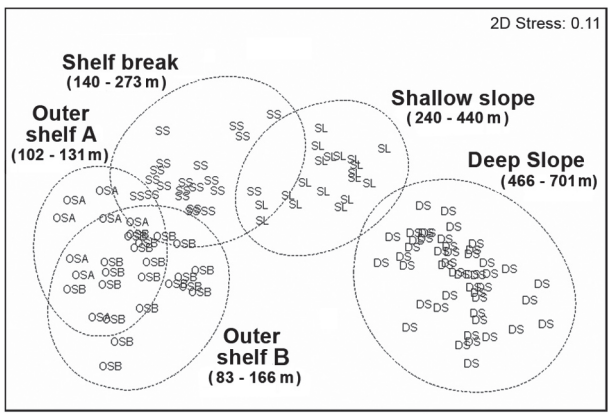

FIG 2. – Non-metric multidimensional scaling (nMDS) plot for the sampling stations for all the three years based on the biomass data. The ovals show the groups generated by cluster analysis. OSA, Outer Shelf A; OSB, Outer Shelf B; SS, Shelf Break; SL, Shallow Slope; DS, Deep Slope.

TABLE 2. – Average percentage dissimilarity between species for the groups obtained by the ordination techniques as determined by the ANOSIM procedure. See legend to Figure 2.

Group	OSA	OSB	SS	SL
OSB	55.56			
SS	59.03	54.29		
SL	77.31	71.81	60.46	
DS	91.58	87.72	83.19	65.22

Interestingly, some species are present in most of the assemblage types identified but they differ in their percentage contribution to assemblage structure; for example, *Merluccius merluccius* had different mean densities in the different groups identified (Appendix 1).

Analysis of similarities (ANOSIM) showed that the groups generated by nMDS were not significantly different ($R = 0.137$, $P < 0.05$) between the years under study. The lowest dissimilarity was between the shallower groups while the greatest dissimilarity was between the deep and shallow groups (Table 2). For the univariate parameters estimated (Fig. 3), differences between the station groups identified by the classification and ordination analyses were all significant (GLM ANOVA $P < 0.05$; Table 3) . Total density and the biomass index were highest for the Outer Shelf A (inside FMZ) and Shelf Break stations. Both biomass and abundance were very low in the Outer Shelf B (outside FMZ) group when compared to the other group of the same depth range, that is, Outer Shelf A. Significant differences (GLM ANOVA $P < 0.05$; Table 3) were only detected between the stations inside and outside the FMZ for the biomass index. Evenness and diversity values were fairly similar among groups, but were lowest for the Shelf Slope. Although the Deep Slope group had the lowest abundance and biomass values, diversity and evenness were relatively high when compared with the other groups.

The correlation analyses undertaken using the BIOENV procedure gave relatively high values of Spearman's coefficient for depth, temperature and

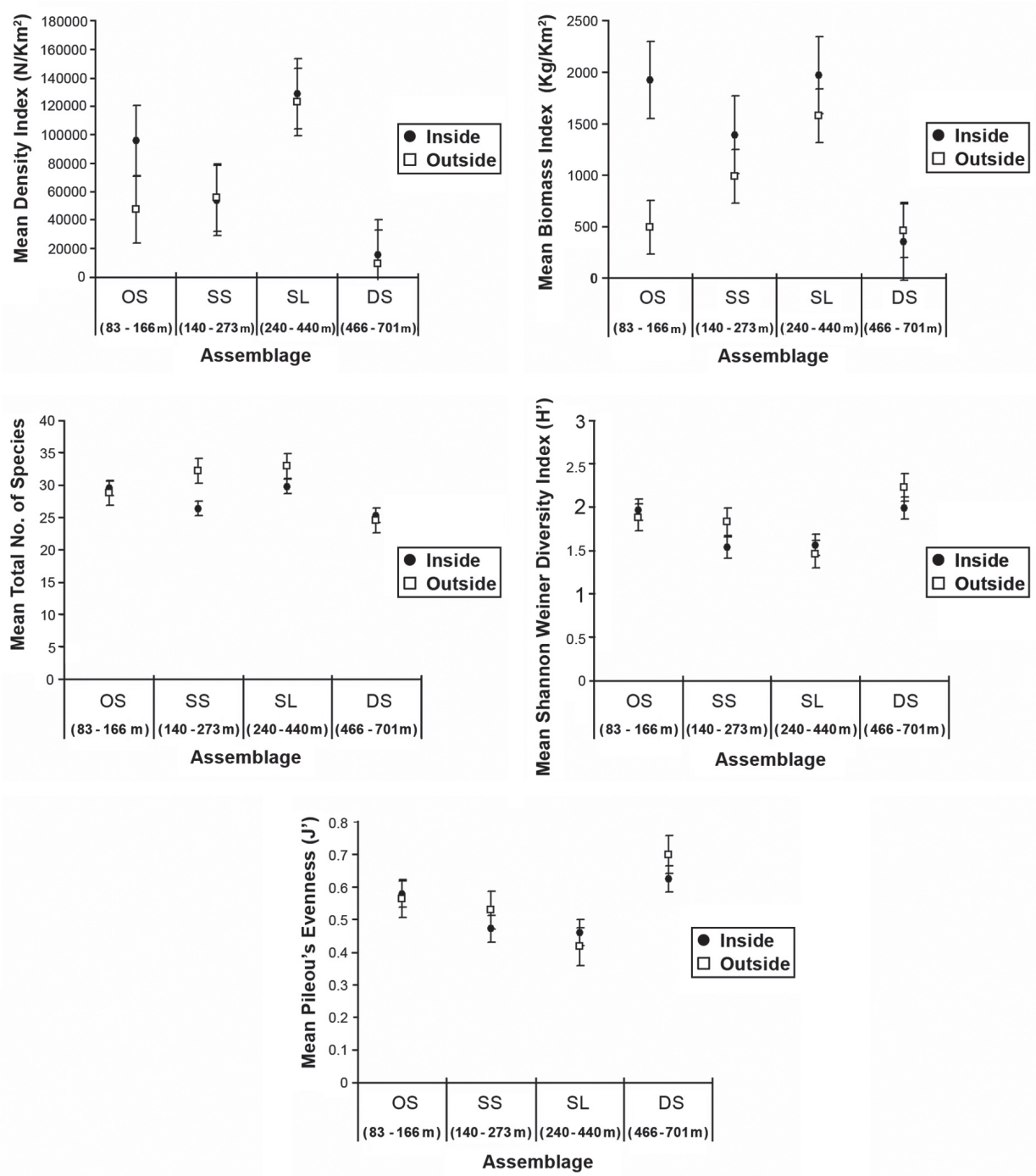

FIG 3. – Mean (± standard error) values of mean density index in N/km^2, mean Biomass index in kg/km^2, mean number of species, mean Shannon-Weiner diversity (*H'*) and mean Pielou`s evenness (*J'*) for each of the four main groups of stations. OS, Outer Shelf; SS, Shelf Break; SL, Shallow Slope; DS, Deep Slope.

any combination associated with these parameters (Fig. 4). For all the assemblage types, a combination of four sediment characteristics: % very coarse sand, % medium sand, % coarse sand and sorting coefficient, gave the highest Spearman correlation value (0.344) when sediment characteristics alone were considered. Most sediment granulometric parameters such as mean grain size and % very coarse sand, gave very low correlation values and do not seem to be important in predicting the structure in the demersal assemblages (Fig. 4).

For the biomass size-spectra slopes (Fig. 5) significant differences (GLM ANOVA $P< 0.05$; Table 3) were detected between the groups identified

TABLE 3. – Summary of the outcome of the 2-Way GLM ANOVA for the effects of assemblages and inside/outside the 25 nautical mile FMZ and the interaction between these factors (see Figs. 3 and 5) for Density Index (DI) in N/km^2, mean Biomass Index (BI) in kg/km^2, mean number of species (S), mean Shannon-Weiner diversity (*H'*) and mean Pielou`s evenness (*J'*) and slopes (s) and intercepts (i) of the biomass size spectra. The characters in bold show a significant differences at $P < 0.05$.

		DI		BI		S		*J'*		*H'*	
	df	F	P	F	P	F	P	F	P	F	P
Corr. Model	7	8.63	<0.01	6.73	<0.01	5.76	<0.01	12.81	<0.01	7.86	<0.01
Intercept	1	80.72	<0.01	91.65	<0.01	2391.83	<0.01	1803.75	<0.01	1636.76	<0.01
Assemblage	3	10.87	**<0.01**	6.65	**<0.01**	7.03	**<0.01**	16.08	**<0.01**	9.27	**<0.01**
Inside/Outside	1	0.98	0.32	4.94	**0.03**	2.42	0.12	0.54	0.47	0.95	0.33
As. *Ins/Out.	3	0.78	0.51	2.84	**0.04**	2.07	0.11	1.35	0.26	1.51	0.22
Error	109										
Total	117										
Corr. Total	116										

		All Taxa (s)		Teleosts (s)		Elasmobranchs (s)		Crustaceans (s)	
Corr. Model	7	4.13	0.01	11.99	<0.01	4.07	0.01	0.88	0.54
Intercept	1	449.15	<0.01	478.64	<0.01	28.02	<0.01	62.84	<0.01
Assemblage	3	6.10	**0.01**	21.27	**<0.01**	2.49	0.10	1.46	0.27
Inside/Outside	1	8.17	**0.01**	14.77	**<0.01**	2.69	0.12	0.65	0.43
As. *Ins/Out.	3	0.81	0.51	1.81	0.19	6.10	**<0.01**	0.16	0.92
Error	16								
Total	24								
Corr. Total	23								

		All Taxa (i)		Teleosts (i)		Elasmobranchs (i)		Crustaceans (i)	
Corr. Model	7	3.84	0.01	10.19	<0.01	8.57	<0.01	1.65	0.20
Intercept	1	2176.74	<0.01	2631.14	<0.01	828.88	<0.01	584.69	<0.01
Assemblage	3	5.61	**<0.01**	15.30	**<0.01**	6.24	**<0.01**	1.03	0.41
Inside/Outside	1	8.40	**<0.01**	17.10	**<0.01**	0.60	0.448	0.03	0.88
As. *Ins/Out.	3	0.55	0.65	2.77	0.08	13.56	**<0.01**	2.19	0.14
Error	16								
Total	24								
Corr. Total	23								

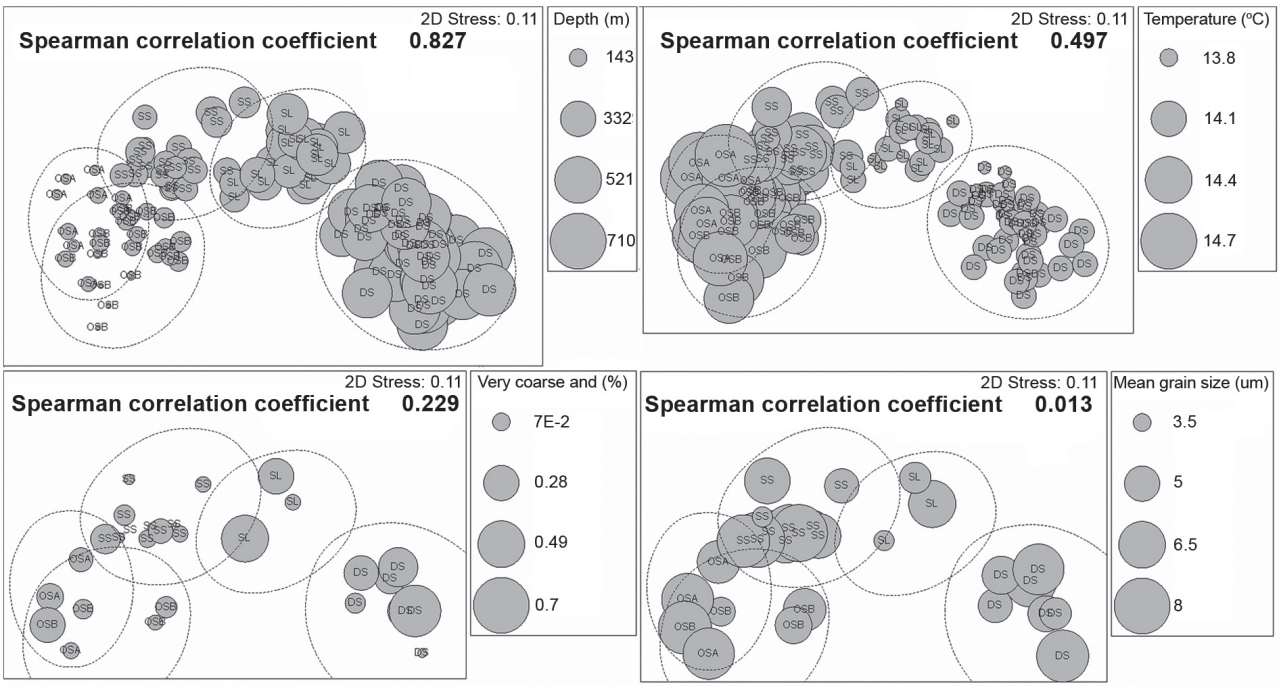

FIG 4. – The nMDS plot from Figure 2 with scaled values of (A) depth, (B) temperature, (C) % very coarse sand, and (D) % mean sediment grain size (μm). The Spearman correlation coefficient for each parameter is also shown.

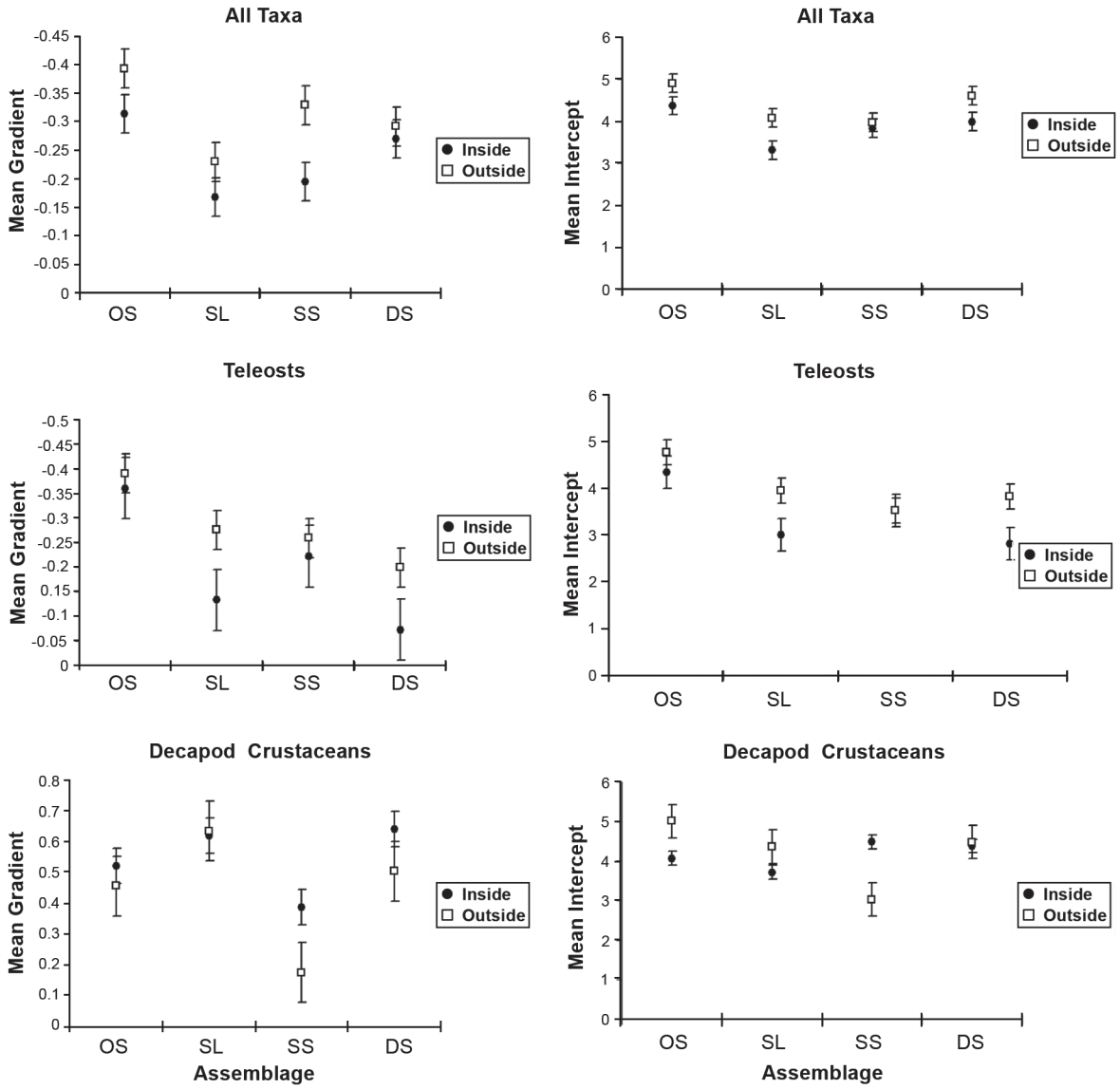

FIG 5. – Variation in the slopes and intercept (± 1 S.E.) of the biomass size-spectra for the different taxonomic groups, by assemblage type, and inside and outside the Maltese 25 Nautical Mile Fisheries Management Zone. OS, Outer Shelf; SS, Shelf Break; SL, Shallow Slope; DS, Deep Slope.

(assemblage) for all taxa grouped together and for teleosts only. For the intercepts (Fig. 5) significant differences (GLM ANOVA $P< 0.05$; Table 3) were detected between the groups identified for all taxa grouped together, for teleosts and for elasmobranchs, but not for crustaceans.

The relatively shallow stations exhibit steeper gradients (negative), most likely due to the higher number of large individuals present on the continental shelf, while the relatively deeper assemblages have less steep gradients possibly due to a shift in the composition of the demersal community from one dominated by fish species to one dominated by crustacean species. Nonetheless, the intercept values are quite similar.

When the biomass size spectra for the analysis between the inside and outside stations were considered, significant differences (GLM ANOVA $P< 0.05$; Table 3) were detected for all taxa grouped together and teleosts both for the slopes and gradients. For the elasmobranchs the frequency distribution of the $\log_{10}$ of the biomass size classes was plotted for each assemblage and for the inside and outside stations (Fig. 6). There is a clear, low number of size classes in the outside stations of the outer shelf and shelf break assemblages.

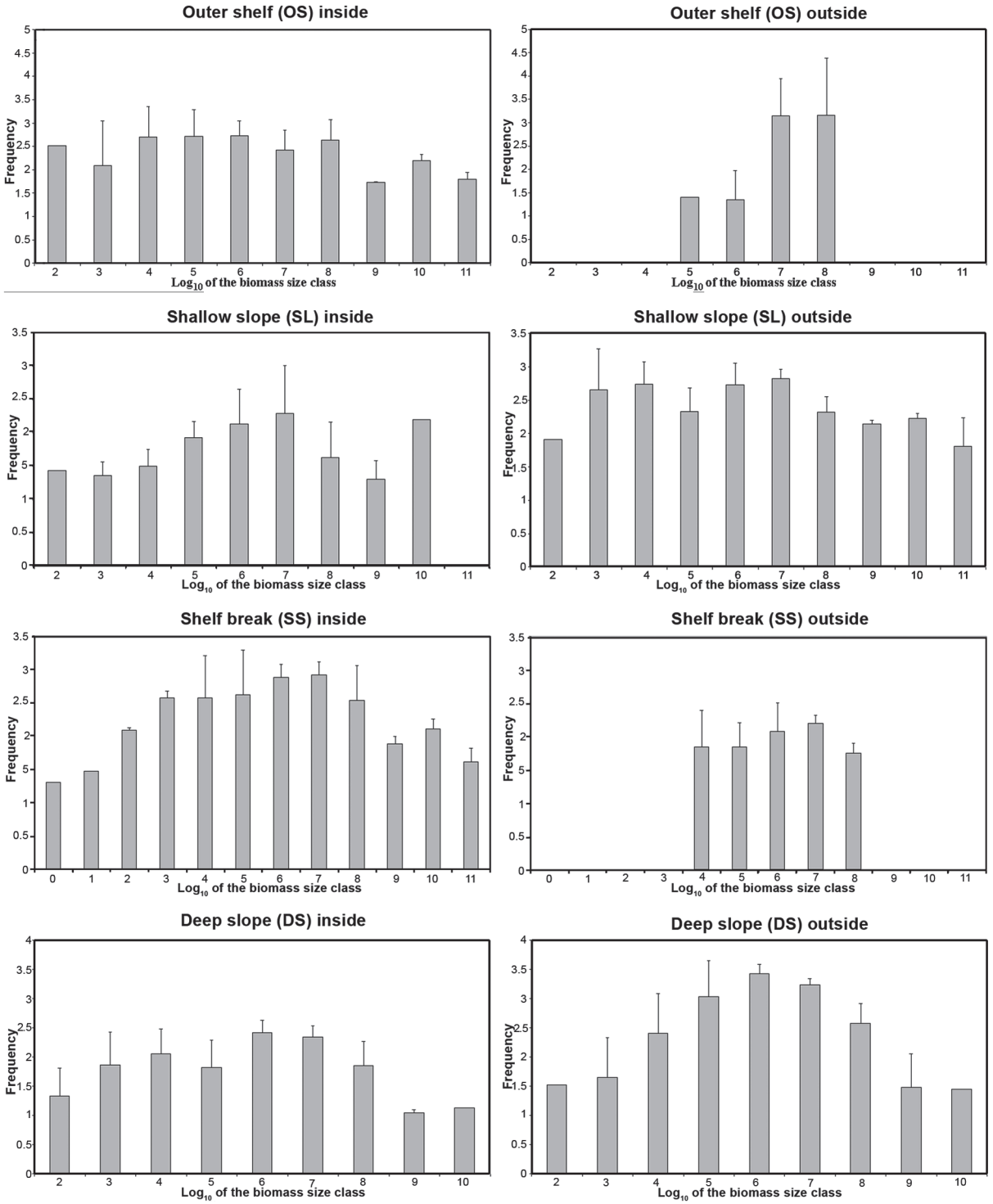

FIG 6. – Biomass size frequency distribution of elasmobranches (± 1 S.E.) by assemblage type, and inside and outside the Maltese 25 Nautical Mile Fisheries Management Zone. OS, Outer Shelf; SS, Shelf Break; SL, Shallow Slope; DS, Deep Slope.

DISCUSSION

Based on our results, the fishery resources of Maltese trawling grounds are stratified into four main depth ranges, which agrees with other studies in the Mediterranean that have shown similar depth ranges for deep water demersal assemblages (Table 4). The multivariate analyses also differentiated two different assemblages on the offshore continental shelf (Outer Shelf A and B). The only difference

TABLE 4. – A summary of studies on deep water assemblages in the Mediterranean. The studies marked with an asterix have used an *a posteriori* approach to determine the assemblage structure.

Authors	Location	Assemblage type	Depth ranges used in the analysis (m)	Years
Moranta *et al*., (1998)	Western Mediterranean	Fish assemblages	200-400; 400-800; 800-1400; 1400-1800	
Tserpes *et al*., (1999)	Eastern Mediterranean (Southern Aegean)	Demersal assemblages	0-100; 100-200; 200-500; 500-800	1996-97
Ungaro *et al*., (1999)*	Central Mediterranean (South Adriatic)	Fish assemblages	31-329; 281-551	1996-97
Labropoulou and Papaconstantinou (2000)	Eastern Mediterranean 1990-1993	Fish assemblages	100-200; 200-500	
Colloca *et al*., (2003)*	Central Mediterranean (Tyrrhenian sea)	Demersal assemblages	12-47; 32-133; 128-317; 195-496; 388-616	1997-98
		Cephalopod assemblages	16-407; 281-538; 315-547	1996-97
		Crustacean assemblages	29-131; 77-329; 346-551	1996-97
Kallianiotis *et al*., (2004)	Eastern Mediterranean (North Aegean Sea) Thracian sea	Fish assemblages	10-50; 50-100	1996-2000
	Thermaikos Gulf Central Aegean sea		10-100; 50-100; 100-200; 50-500 100-500; 200-600	
D'Onghia *et al*., (2004)*	Mediterranean	Fish assemblages	600-650; 800-1300; 1300-4000	2001
Massutí and Reñones (2005)*	Balearic Islands, NW Mediterranean	Demersal assemblages	41-76; 69-147; 139-235; 326-444; 472-686; 649-745	2001

between these two assemblages was that one is found inside the 25 NM FMZ while the other is found in the sea immediately outside the zone. None of the environmental parameters measured seemed to explain the difference between these two assemblages. Depth, temperature and sediment characteristics, which are the main factors that structure benthic and demersal assemblages, are similar in the two areas (Biagi *et al*., 1989).

The difference between these two assemblages may be related to fishing pressure since trawling effort is very limited on the continental shelf inside the FMZ. Only 15 trawlers that are restricted in power and length by regulation (Council of the European Union, 2004) are allowed to fish in the zone, while there are no legal restrictions on trawling outside the zone. Furthermore, most of the trawlers that fish inside the zone target red shrimp *Aristaeomorpha foliacea* at a depth of ca. 600 m due to the availability of good trawling grounds at the north western part of the islands which are very close to the shore. Italian trawling fleets regularly trawl the areas outside the 25 NM FMZ since it is very close to the main Sicilian fishing ports. The differences between the two continental shelf assemblages were mainly quantitative (Appendix 1) with species groups sensitive to trawling, such as elasmobranchs (for example, *Scyliorhinus canicula* and *Raja clavata*), being very common inside the zone, and practically absent outside the 25 NM FMZ. These species were also those most responsible for the difference between the two assemblages.The analysis of the size-spectra of the Outer Shelf also indicated that elasmobranchs were larger in size inside the FMZ. Furthermore, the $\log_{10}$ biomass size classes in the Outer Shelf and Shelf Break assemblages are less than half that of the inside stations, which indicates a clear impact on the community of elasmobranchs in the outside stations. The Outer Shelf region outside the FMZ has half the biomass (Camilleri, 2002) and abundance of the region inside the 25 NM zone (see Fig. 3), and reduced biomass and abundance is a common feature of heavily trawled areas (Kaiser and de Groot, 2000).

When the size-spectra over the entire depth range studied are considered, the Outer Shelf area is different from the deeper areas. The size spectra analysis also showed differences between the inside and outside stations for the Shelf Break, Shallow Slope and Deep Slope assemblages. These differences were not detected by univariate or multivariate community descriptors. The mean size spectra for the teleosts

show a clear pattern of decreasing mean body size with increasing depth. The Outer Shelf assemblages are dominated by high abundances of small body-sized fishes (Fig. 5) and as the depth increases, the preponderance of larger body-sized fishes increases although overall abundance decreases. There is a transition from one assemblage to another as the depth increases with a shift in the community from one dominated by fish to one dominated by decapods (mostly shrimps). The elasmobranchs for example in the shallower assemblages are dominated by larger body-sized individuals (e.g. *Raja clavata* and *Squalus blainvillei* and *Mustelus* spp.) but the large sized elasmobranchs decline in predominance in the deeper waters with the occurrence of smaller sized individuals (e.g. *Galeus melastomus* and *Etmopterus spinax*).

In this study, the assemblages were determined *a posteriori* followed by further analysis to determine changes in community descriptors between the inside and outside areas of the FMZ. A number of studies in the Mediterranean have analysed assemblages according to predefined depth strata, which usually depend on survey protocols formulated with little or no consideration to biologically relevant bathymetric zonation. For example, in the present study, the data used were obtained from the Mediterranean International Trawl Survey (MEDITS) programme, which samples the following predefined depth strata on muddy bottoms: 51 to 100 m, 101 to 200 m, 201 to 500 m, and 501 to 800 m. However, biologically relevant strata resulting from the *a posteriori* community analysis made here do not coincide with the MEDITS strata. It is therefore clear that characterisation of the biotic assemblages is important in order to obtain a better sampling representation of each biologically meaningful depth-zone/assemblage type, and this should be incorporated into the survey designs.

Furthermore, assemblages determined *a posteriori* are also important in order to enable abundance estimation (e.g. density and biomass indices) and indicators (diversity indices and size spectra), as well as assessment at a multispecies level (integrated also by environmental data) as requested by the precautionary and ecosystem based approach. Classic designs can be maintained to estimate abundance for single species but analysis of assemblages based on data gathered in the same surveys needs to be made to generate ecologically meaningful depth strata for the analysis of biotic communities. One also needs to take into consideration that a statistical design based on demersal assemblages in different countries in a large basin such as the Mediterranean Sea will result in a very heterogeneous sampling allocation and problems will emerge when comparing data across large distances, such as in the case of the Mediterranean Sea. Hence, a standard protocol for the collection of data aimed at allowing a comparison across large areas is more desirable; a post-stratification of sampling stations according to the assemblages identified can be used to improve local assessments and management advice. This may also apply to other trawl survey programmes implemented elsewhere outside the Mediterranean Sea.

In general, the transition from one assemblage to the next is gradual at the shallower depths and becomes sharper as the depth increases. For instance, the dissimilarity between the Deep Slope assemblage and the shallower assemblages is the highest (e.g. dissimilarity between DS and OSA = 91.58); dissimilarity was lowest between the deeper assemblages (e.g. dissimilarity between DS and SL = 65.22). The differences between the shelf break, shallow slope and deep slope were mostly qualitative (Appendix 1) since most of the species recorded in either one of the assemblages were not present in the other and this explains the high dissimilarity values obtained.

The main environmental variable that predicted the observed change in community structure over the depth range studied was depth. This has also been shown to be the case in other areas of the Mediterranean (Biagi *et al*., 1989). Temperature is the second most important factor responsible for the zonation of the assemblages (this is most likely because there is a strict correlation between depth and temperature). Although the observed variation in temperature is very small (ca. 1^{o}C) in the depth range studied, a slight variation in seawater temperature can have significant effects on the distribution of fish (e.g. Quéro *et al*., 1998). After these parameters, sediment fractions are the next most important, which includes the percentage contribution of very coarse sand, coarse sand, and medium sand. Factors such as median grain size and organic carbon, which were expected to affect the structure of the assemblages, were not found to be important in this respect.

The ordination techniques and the analysis of similarities did not detect any temporal change in assemblage structure between the years under study, which is not unexpected since sampling was always

conducted in the same month. A lack of temporal variation has also been found in other parts of the Mediterranean such as off the coasts of Tuscany in the Tyrrhenian Sea where assemblages persisted through time (Biagi *et al*., 2002). This suggests that changes in assemblage composition are consistent over short time scales. Nonetheless, it should be noted that a much longer series of data is necessary to track the temporal persistence of the deep water populations, since changes in the deep sea may be very gradual and occur on a decadal scale. However, shorter term, sudden temporal changes may occur in areas exposed to chronic disturbances such as heavy trawling (Jennings *et al.*, 2001).

Univariate community descriptors showed different trends with changes in depth. The total number of species, biomass, and abundance all decreased significantly with depth. In spite of this, both evenness and diversity (*H'*) did not decrease, which suggests that although secondary production in deeper waters is lower than in shallower waters, the habitat is still rich in species.

The analysis of assemblage structure has the potential to provide valuable inputs into fisheries management, particularly in multispecies fisheries such as the trawl fishery in the Mediterranean Sea. Such analyses can assist in: (i) determining geographical or spatial boundaries of fish and other demersal assemblages, especially in relation to depth zonation; (ii) subdividing the fishery into components affected by different conditions, e.g. different intensities of fishing pressure, and to differences in environmental conditions; and (iii) designing management interventions applicable to different components of the fishery or to different areas, based on the spatial distribution patterns of the assemblages. This work has clearly shown consistent trends in community descriptors of the demersal assemblages, with spatial partitioning of the assemblages present in all areas studied.

Based on the regional trends seen here, fisheries managers should request scientific advise on how assemblage structure and its relation to the depth ranges and fishing pressure could be used as a basis for revising existing fisheries zones and management units, as most of these are based on predetermined depth strata which may have no direct biological basis, may overlap different assemblages, and do not take into account the assemblage structure. Identifying assemblages can be a very useful tool for adaptive management especially in multi-species fisheries and would facilitate the implementation of management measures specific to the different assemblage types. In effect, geographical areas with distinct assemblages can be considered as different management units for the trawl fishery and this would be the first step towards an ecosystem approach in fisheries management.

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Appendix 1. – Species which contributed to 90% of the similarity as determined by the SIMPER procedure.

Species	Av. Density $\sqrt[4]{(kg/km^2)}$	sd	Cum.%	Species	Av. Density $\sqrt[4]{(kg/km^2)}$	sd	Cum.%
Outer Shelf A (OSA) Average similarity: 51.60				**Outer Shelf B (OSB)** Average similarity: 57.29			
Scyliorhinus canicula	2.36	0.7	7.22	*Merluccius merluccius*	2.42	0.5	9.49
Mullus barbatus	2.58	0.7	14.45	*Trachurus trachurus*	2.6	1.4	17.76
Raja clavata	2.57	1.6	21.28	*Parapenaeus longirostris*	2.41	1.06	25.89
Merluccius merluccius	2.31	1.4	27.6	*Illex coindetii*	2.07	1.2	32.52
Aspitrigla cuculus	2.03	0.4	33.49	*Argentina sphyraena*	1.77	0.79	38.21
Sepia orbignyana	2.14	0.5	39.38	*Alloteuthis media*	1.55	0.4	43.79
Serranus hepatus	1.96	0.4	45.26	*Mullus barbatus*	1.66	0.93	49.2
Lepidotrigla cavillone	2.06	1.3	50.65	*Trisopterus minutus capelanus*	1.45	0.8	54.12
Citharus linguatula	1.73	0.3	55.41	*Aspitrigla cuculus*	1.57	1.08	58.82
Spicara flexuosa	2.16	2.2	59.57	*Macrorhamphosus scolopax*	1.51	1.17	63.1
Trachurus trachurus	2.58	2.7	63.67	*Citharus linguatula*	1.17	0.51	67.24
Argentina sphyraena	1.68	1.1	67.55	*Scaeurgus unicirrhus*	1.22	0.9	71.05
Macrorhamphosus scolopax	2.41	2.6	71.2	*Serranus hepatus*	1.29	0.91	74.79
Serranus cabrilla	1.73	1.7	74.48	*Capros aper*	1.09	0.84	77.96
Dentex macrophthalmus	1.51	1.5	77.72	*Spicara flexuosa*	1.45	1.71	81.06
Scaeurgus unicirrhus	1.27	0.3	80.85	*Zeus faber*	1.33	1.32	84.12
Boops boops	1.38	1.5	83.25	*Lepidotrigla cavillone*	1.04	1.49	86.18
Mullus surmuletus	1.28	1.8	85.31	*Todaropsis eblanae*	0.81	1.09	87.87
Raja miraletus	1.41	2.9	86.93	*Sepia orbignyana*	0.8	1.21	89.35
Trisopterus minutus capelanus	1.06	1.5	88.49	*Sepiola* spp.	0.63	0.77	90.81
Alloteuthis media	0.93	1.3	89.91				
Illex coindetii	1.2	2.4	91.26				
Shallow Slope (SL) Average similarity: 59.58				**Shelf Break (SS)** Average similarity: 58.19			
Chlorophthalmus agassizi	3.48	1.5	8.46	*Capros aper*	3.82	1.32	8.68
Merluccius merluccius	2.61	0.4	16.07	*Argentina sphyraena*	2.84	1.1	15.48
Coelorhynchus coelorhynchus	2.84	1.4	23.15	*Scyliorhinus canicula*	2.64	1.35	22.06
Gadiculus argenteus	2.49	0.7	29.65	*Merluccius merluccius*	2.36	0.5	28.42
Parapenaeus longirostris	2.17	0.5	35.74	*Illex coindetii*	2.12	1.25	33.19
Scyliorhinus canicula	2.16	0.9	41.36	*Macrorhamphosus scolopax*	2.25	1.42	37.86
Raja clavata	2.51	1.8	46.88	*Scaeurgus unicirrhus*	1.58	0.27	42.1
Todaropsis eblanae	2	1.4	51.87	*Parapenaeus longirostris*	1.93	1.2	46.32
H. dactylopterus dactylopterus	1.94	0.9	56.58	*Todaropsis eblanae*	1.83	0.54	50.52
Phycis blennoides	1.76	0.8	61.05	*Raja clavata*	2.18	2	54.72
Nephrops norvegicus	1.79	1	65.39	*Peristedion cataphractum*	1.98	1.21	58.91
Peristedion cataphractum	1.72	0.8	69.52	*Trachurus trachurus*	1.69	1.24	62.17
Argentina sphyraena	1.72	1.1	73.59	*H. dactylopterus dactylopterus*	1.42	0.65	65.39
Lepidopus caudatus	2.01	2.1	77.04	*Sepia orbignyana*	1.38	0.94	68.26
Raja oxyrinchus	1.49	1.5	79.89	*Mullus barbatus*	1.5	1.55	71.02
Squalus blainvillei	1.56	2.1	82.31	*Alloteuthis media*	1.16	0.83	73.47
Capros aper	1.41	1.7	84.35	*Zeus faber*	1.46	1.39	75.91
Lophius budegassa	1.02	1.3	86.12	*Mullus surmuletus*	1.26	1.15	78.23
Hymenocephalus italicus	1	1.7	87.52	*Lepidotrigla dieuzeidei*	1.61	2.44	80.53
Scaeurgus unicirrhus	0.71	1	88.74	*Lophius budegassa*	1.27	1.35	82.68
Sepiola spp.	0.69	1	89.88	*Citharus linguatula*	1.03	0.93	84.74
Galeus melastomus	0.76	1	90.97	*Raja miraletus*	1.2	1.3	86.8
				Trigla lyra	1.3	1.69	88.83
				Aspitrigla cuculus	1.05	1.59	90.31
Deep Slope (DS) Average similarity: 59.45							
Galeus melastomus	2.45	0.9	9.44				
Aristaeomorpha foliacea	2.21	0.6	18.59				
Hoplostethus mediterraneus	1.98	0.6	25.82				
Merluccius merluccius	2.13	1.3	32.78				
Plesionika martia	1.64	0.4	39.57				
Nezumia sclerorhynchus	1.65	0.8	45.91				
Phycis blennoides	1.74	1	52.08				
Coelorhynchus coelorhynchus	1.67	0.9	57.79				
H. dactylopterus dactylopterus	1.93	1.4	63.47				
Etmopterus spinax	1.64	1	69.01				
Hymenocephalus italicus	1.2	0.4	73.71				
Nephrops norvegicus	1.32	0.9	77.51				
Todarodes sagittatus	1.22	1.7	80.62				
Parapenaeus longirostris	1.11	0.9	83.7				
Raja oxyrinchus	1.36	2.1	86.56				
Chlorophthalmus agassizi	1.45	1.8	89.39				
Chimaera monstrosa	1.19	1.7	91.7				