

# DEMERSAL FISH ASSEMBLAGES FROM THE CONTINENTAL SHELF AND UPPER SLOPE TRAWLING GROUNDS OFF SE SPAIN (WESTERN MEDITERRANEAN)

A. M. Fernández <sup>1</sup> \* and M. García-Rodríguez <sup>2</sup>

<sup>1</sup> IEO. Centro Oceanográfico de Murcia, Pedro del Pinatar, Spain - \* angel.fernandez@mu.ieo.es

<sup>2</sup> IEO. Servicios Centrales. Madrid, Spain

## Abstract

The continental shelf and upper slope fish communities off SE Spain were studied based on data collected during the LEDER cruise in June 2002. Cluster and MDS analysis allowed the identification of four groups of hauls related to depth, which result in well defined communities. Similarity percentage analysis was used to identify the most discriminating species between communities. Ecological parameters are provided for comparison with other areas.

*Key-Words:* Fish assemblages, Demersal communities, Western Mediterranean

## Introduction

Fish communities and the bathymetric distribution of their species are well known in some areas of the Spanish Mediterranean specially the Catalan Sea, the Balearic Islands and the Alborán Sea (1,2,3). The hydrological conditions of the continental shelf and upper slope off SE of Spain could be considered transitional between the north-western Mediterranean areas and the Alboran Sea. These characteristics could affect species distribution and community composition. The present study is the first analysis of the demersal fish communities in this area.

## Materials and methods

Data were collected in June 2002. A total of 54 samples (hauls) were taken with the MEDITS sampling gear between depths of 36 and 578 m. Abundance and biomass data were transformed by double square root to reduce the effects of extreme values. A total of 107 species were recorded but pelagic species from the continental shelf and mesopelagic or bathypelagic species from the upper slope were omitted from the analysis as well as species recorded only in a single sample, since they could introduce some noise in the analysis. Cluster analysis and multidimensional scaling (MDS) were used for grouping similar samples. The PRIMER package (4) was used to carry out the analysis, based on the Bray-Curtis similarity index, Complete Linkage Clustering and UPGMA (Unweighted Pair-Group Mean Analysis). To establish which species contribute to the (dis)similarity between groups of samples, the SIMPER (similarity percentage analysis) routine was used. To test the differences between groups of samples an one-way layout ANOSIM test was employed. The ecological parameters abundance, biomass, species richness (S), mean species richness, Shannon-Wiener diversity index (H') and evenness (J') were determined for each group identified by cluster and MDS analysis.

## Results and discussion

Analysis made on biomass and abundance data showed similar results. Cluster analysis and MDS (Fig. 1) showed four main groups of samples clearly related to depth which correspond to shallow areas (A), continental shelf (B), continental break (C) and upper slope (D) respectively. Similar bathymetric pattern has been described in other areas (1, 3). In shallow areas (less than 40 m deep) few samples were taken due to the existence of rocky bottoms and *Posidonia oceanica* sea-grass. The results of SIMPER for similarity within groups showed that in group B the most characteristic species were *Boops boops*,

*Mullus barbatus*, *Serranus hepatus*, *Spicara maena*, *Pagellus acarne*, *Cepola macrophthalmia*, *Mullus surmuletus* and *Lepidotrigla cavillone*. For group C, the most characteristic species were *Micromesistius poutassou*, *Helicolenus dactylopterus*, *Gadiculus argenteus* and *Lepidopus caudatus*. In the case of group D, the characteristic species were *Phycis blennoides*, *Lampanyctus crocodilus*, *Galeus melastomus*, *Etmopterus spinax*, *Nezumia aequalis* and *Hoplostetius mediterraneus*. ANOSIM test (R=0.868; significance level < 0.1%) confirmed the high dissimilarity between these assemblages. Species richness (S), diversity (H') and evenness (J') reached the highest values in group B whereas maximum values of abundance and biomass were obtained for group C. Group D showed the smallest values of abundance, biomass and S, but intermediate values of H' and J' (Table 1).

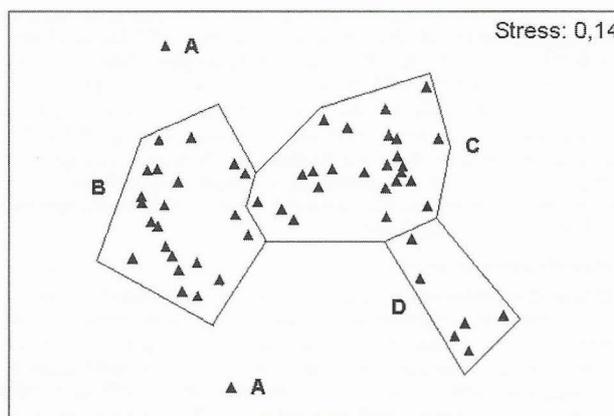


Fig.1. MDS plot of samples. Groups encircled by lines correspond to those obtained by cluster analysis.

## References

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Table 1. Ecological parameters of the groups of samples resulting from cluster and MDS analyses (group A was not included because of the small number of samples).

Parameter	Group		
	B	C	D
Abundance (N/10 <sup>3</sup> m <sup>2</sup> )	10.3	48.3	3.4
Biomass (g/10 <sup>3</sup> m <sup>2</sup> )	359.3	1022.3	188.6
Species richness	59	54	22
Mean species richness	18.0	12.9	11.3
Diversity (H')	1.98	0.96	1.19
Evenness (J')	0.70	0.37	0.49
Mean depth (m)	80.3	217.3	521.3
Number of hauls	22	24	6