The role of suprabenthic and epibenthic communities in the diet of a deep-sea fish assemblage (Le Danois Bank, Cantabrian Sea, N Spain)

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INTRODUCTION

In 2003 and 2004 two multidisciplinary surveys (ECOMARG Project) were carried out between 400 and 1000 m depths to study the benthic-demersal ecosystem of the Le Danois Bank (Figure 1), as well as the fish and crustacean trophic ecology (Serrano *et al*., 2005). Two depth intervals were identified: 400-700 m and 701-1000 m. The nine fish species under study were selected on the basis of their relative abundance and the composition of the deep-water demersal fish assemblages in the study area. The aim of this work was to analyse the feeding habits of these species and to determine possible shifts on diet composition between the two depth intervals studied. A detailed taxonomic study of the most characteristic prey groups has been conducted in order to estimate the degree of predation on the different benthic compartments: suprabenthic and epibenthic assemblages.

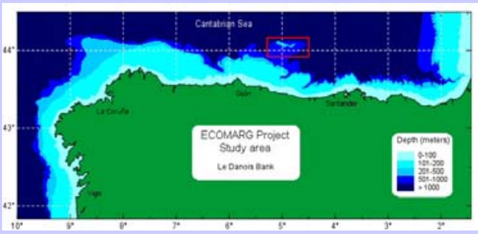

Figure 1.- Study area showing the Le Danois Bank.

RESULTS AND DISCUSSION

Stomach contents of 602 specimens belonging to 9 deep-sea fish species (Table 1) were examined. *Alepocephalus rostratus* preyed mainly on the suprabenthic mysid *Gnathophausia zoea*, together with plankton prey such as scyphozoans and salps (Figure 2), whereas *Chlorophthalmus agassizii* fed on smaller prey, like copepods, fish larvae, amphipods, euphausiids, mysids and chaetognaths among others. The macrourid *Coryphaenoides rupestris* was the most specialised predator with the lowest taxonomic diversity feeding mainly on copepods and the mysid *G. zoea*. The shark *Deania calcea* consumed a high proportion of ostheichthyes (68 %), while other sharks such as *Etmopterus spinax* and *Galeus melastomus* fed both on suprabenthic prey and fish. Interestingly, euphausiids were the dominant prey ingested by *G. melastomus*. The species *Hoplostethus mediterraneus* consumed a high variety of amphipods, euphausiids and mysids, with a high prey diversity (H' = 3.8). However, the macrourid *Nezumia sclerorhynchus* was the predator with the highest taxonomic diversity (H' = 4.9) with a diet composition based on a great variety of amphipods, and endobenthic preys such as polychaetes. Finally, in *Trachyscorpia cristulata*, the crab *Geryon trispinosus* made up almost the 50 % of the diet.

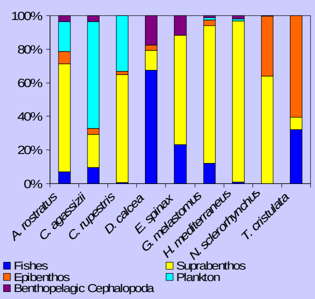

Figure 2.- Diet composition of the nine fish species analysed. Percentage in number (% N) of main prey.

Table 1.- Diet composition (% Number) of the nine selected fish species. Only preys with more than 2% are shown. Intervals of depth analysed: A = 400-700 m, B = 701- 1000 m. Abbreviations: Ale ros = *Alepocephalus rostratus*; Chl aga = *Chlorophthalmus agassizii*; Cor rup = *Coryphaenoides rupestris*; Dea cal = *Deania calcea*; Etm spi = *Etmopterus spinax*; Gal mel = *Galeus melastomus*; Hop med = *Hoplostethus mediterraneus*; Nez scl = *Nezumia sclerorhynchus*; Tra cri = *Trachyscorpia cristulata*.

Prey taxon	Ale ros	Chl aga	Cor rup	Dea cal	Etm spi	Gal mel	Hop med	Nez scl	Tra cri
Crustacea	46.4	58.6	97.2	11.8	63.9	85.1	97.3	67.1	58.5
Geryon trispinosus									47.2
Natantia	7.1	2.2	2.8	11.8		5.3	7.3		1.9
Acanthephyra pelagica	3.6								
Natantia unid.				2.9					1.9
Pasiphaea multidentata							2.3		
Pasiphaea spp.				5.9			1.4		
Sergia robusta				2.9		1.8			
Systellaspis debilis	3.6	1.1							
Euphausiacea		5.0			59.0	71.9	30.1		
Euphausia sp.		1.1			3.3				
Meganyctifanes norvegica		1.7			24.6	11.5	2.3		
Euphausiacea unid.					27.9	59.7	27.4		
Amphipoda		6.6	3.5			1.5	17.8	45.5	
Ampelisca sp							1.8	17.5	
Amblyops sp							1.4	2.4	
Amphipoda unid.							3.2	1.2	
Laetmatophilus tuberculatus								2.0	
Pardaliscidae unid.								2.9	
Pseudotiron bouvieri			1.6				3.2	1.6	
Hyperiidae		2.8				1.2			
Mysidacea	35.7	5.0	51.2		1.6	3.0	38.8	5.5	3.8
Boreomysis arctica			2.4				3.2		1.9
Boreomysis spp.			1.2				2.3		
Eucopia hanseni		3.3	2.0						
Gnathophausia zoea	35.7	1.1	45.7		1.6	2.4	5.9		1.9
Mysidacea unid.							25.1		
Isopoda			5.9				1.4	9.6	1.9
Anthuridae								2.9	
Eurycope grimaldii			5.5				1.4		
Copepoda Calanoidea		38.7	32.7				1.4	3.1	
Ostracoda Cypridinidae	3.6								
Mollusca Cephalopoda	3.6	3.3		17.7	11.5	1.5	1.8		
Cephalopoda	3.6	3.3		17.7	11.5	1.3	1.8		
Sepiolidae unid.		2.8							
Todarodes sagittatus				2.9					
Histioteuthis reversa				2.9	6.6				
Cephalopoda unid.				11.8	4.9				
Cnidaria Scyphozoa	17.9								
Ctenophora	3.6								
Annelida Polychaeta	3.6	1.7	1.6	2.9				26.6	5.7
Laetmonice philicornis	3.6			2.9				1.4	5.7
Aphroditidae unid.		1.7						2.4	
Nephtys sp.									3.8
Hyalinoecia spp.								19.7	
Echinodermata								3.9	
Tunicata Salpidae	14.3	1.7							
Chaetognatha		5.0							
Pisces	7.1	25.4		67.7	23.0	12.1			32.1
Argyropelecus spp.	3.6								
Alepocephalidae unid.				8.8					
Micromesistius poutassou				17.7	9.8	4.3			1.9
Myctophoidei		6.1		11.8					
Diaphus spp.		2.2		5.9					
Gonostoma spp.				2.9					
Myctophoidei unid.		3.9		2.9					
Scomber scombrus				2.9					
Synaphobranchus kaupii									9.4
Sternoptychidae	3.6	1.7							
Stomias boa				2.9					
Fish larvae		16.0							
Ostheichthyes unid.	3.6	1.1		23.5	9.8	5.6			15.1
Stomachs with food	19	17	25	29	33	119	34	35	35
Empty stomachs	44	0	2	52	32	26	27	8	53
Depth	B	A	B	A, B	A	A, B	A, B	A, B	A, B
Number of taxa	11	35	25	15	13	54	39	86	15
Trophic diversity (H')	2.8	3.5	2.4	3.4	3.0	2.6	3.8	4.9	2.7

MATERIALS AND METHODS

A total of 602 stomach contents of 9 demersal deep fish species were analysed. Quantitative diet estimation was obtained for the main fish species present in the bank, sampled using a Porcupine baca trawl. A suprabenthic sledge and a beam trawl were used to study suprabenthic and epibenthic communities, respectively. In the present study the stomach content analysis was based on prey number, as percentage abundance (%N). Suprabenthos abundance is given in individuals/100m^2 and epibenthos in individuals/haul. Only stomachs with food have been taken into account. Prey were separated and identified to species level whenever possible. When, due to the digestion stage, it was not possible to identify the prey it was assigned to the lowest taxa level. Clustering methods were applied to analyse prey affinities between the fish-depth groups. SIMPER analysis was used to identify prey species that contribute most to the dissimilarity between the groups resulting from the hierarchical analysis.

The relevance of the suprabenthic and epibenthic communities in the diet of demersal fish species was examined by comparing stomach content data with their abundance in the environment. To evaluate the degree to which the suprabenthic and epibenthic communities were selected in favour of other prey we used the Ivlev index.

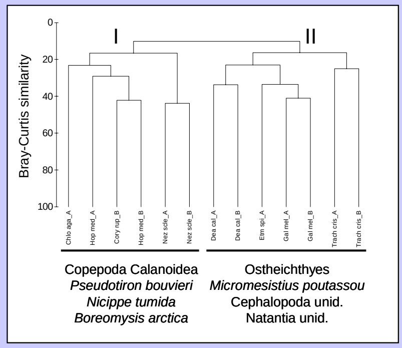

Figure 3.- Dendrogram of fish-depth groups based on Bray-Curtis similarity of prey number. Taxa below contain species that contribute most to the similarity of two groups according to the SIMPER analysis. Abbreviations and depth intervals are given in Table 1.

The cluster analysis of prey affinities between fish-depth groups (Figure 3) depicted two major blocks: one consisting of fish species mainly feeding on suprabenthic prey (group I: *C. agassizii*, *C. rupestris*, *H. mediterraneus*, *N. sclerorhynchus*); the other consisting of fish preying on ostheichthyes, cephalopoda and a variety of decapod crustaceans (group II: *D. calcea*, *E. spinax*, *G. melastomus*, *T. cristulata*). SIMPER analysis revealed that Calanoid copepods, *Pseudotiron bouvieri*, *Nicippe tumida* and *Boreomysis arctica* contributed most to the similarity of group I. By contrast, unidentified ostheichthyes, *Micromesistius poutassou*, cephalopods and unidentified Natantia were prey (on average larger in size to those characterizing group I) most contributing to the similarity of group II.

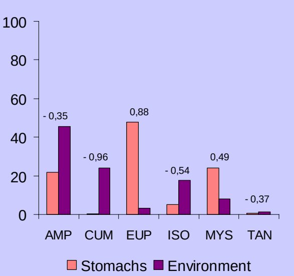

Figure 4.- Comparison between abundance (% Number) of the main suprabenthic groups in the stomachs and in the environment. Numbers show the Ivlev index. AMP = Amphipoda, CUM = Cumacea, EUP = Euphausiacea, ISO = Isopoda, MYS = Mysidacea, TAN = Tanaidacea

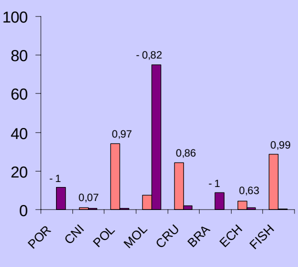

Figure 5.- Comparison between abundance of the main epibenthic groups in the stomachs and in the environment. Numbers show the Ivlev index. POR = Porifera, CNI = Cnidaria, POL = Polychaeta, MOL = Mollusca, CRU = Crustacea, BRA = Brachiopoda, ECH = Echinodermata, FISH = Pisces

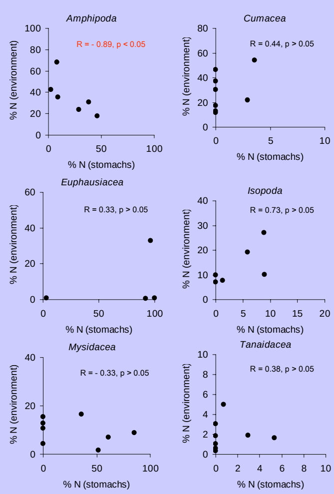

Figure 6.- Relationships between % N of the main suprabenthic groups in the stomachs and in the environment (R = Spearman rank correlation). Points represent each haul.

Euphausiacea and Mysidacea appeared to be the only positively selected prey, whereas the rest of the taxa were negatively selected (Figure 4). Regarding epibenthic communities, the Ivlev index was positive for Polychaeta, Crustacea, Echinodermata and Pisces and negative for Porifera, Mollusca and Brachiopoda (Figure 5). The main reason is due to the high densities in the environment of the sponge *Pheronema grayi*, the bivalve *Limopsis aurita* and the brachiopod *Gryphus* vitreus. The predators selected did not use all these prey as a food resource.

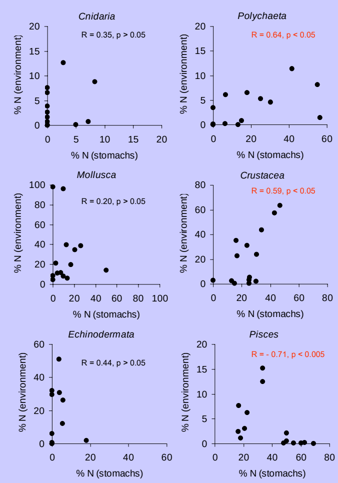

Figure 7.- Relationships between % N of the main epibenthic groups in the stomachs and in the environment (R = Spearman rank correlation). Points represent each haul.

When analyse the relationships between the abundance in the stomachs and in the environment, we found a negative correlation ($p < 0.05$) for the Amphipoda (Figure 6). No significant correlations were found for the rest of suprabenthic taxa. However, concerning epibenthic communities, significant correlations were found for polychaetes, crustaceans and fishes, the first two being positively correlated and the latter negatively correlated (Figure 7). The main discrepancies found were due to the methodology used, because the beam trawl appeared to be a good sampler for some taxa (polychaetes and crustaceans), but not for fish.

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