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Checking the concurrence among macrobenthic organism distribution patterns at different taxonomic scales in relation to environmental factors

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Abstract

The interaction of both natural conditions and anthropogenic environmental impacts can lead to different soft-bottom macrobenthic distribution patterns. Soft-bottom macrobenthic community was analysed at different taxonomic scales in order to evaluate whether diverse subset of organisms respond to the variability of the environmental pressures (natural and human induced) showing or not similar distribution patterns. Therefore, this long-term survey had been focused on a heterogeneous area, where both anthropogenic and natural stress may affect the community. Three perpendicular transects to the coast were established and stations at 4, 10 and 15 m depths were sampled at each transect twice a year (summer- winter) from 2004 to 2009. Non-parametric multivariate techniques were used to analyse soft-bottom macrobenthic community distribution and its relation to the environmental factors. Similar distribution patterns between investigated taxonomic levels were detected and they were mainly related to depth.

Keywords: Soft bottom, Macrobenthos, Polychaeta, Syllidae, Taxonomic scales, Mediterranean Sea.

1. Introduction

The knowledge about the composition and distribution of the benthic assemblages is of great interest because they have been considered a key element of marine ecosystems in terms of the role played by organisms in the maintenance and regulation of ecological processes (Gray and Mirza, 1979; Naeem et al., 1999). The benthic communities show different distribution patterns (Warwick, 1988) as a consequence of changes in their structure caused by the interaction of both natural conditions and anthropogenic environmental impacts. There is a cause-effect relationship between environmental conditions and the community structure. However, it is difficult to detect rules underpinning the dynamics of populations (Butler, 1994) because the relative importance of different factors influencing ecological systems will alter from place to place and time to time (Constable, 1999). The challenge is to identify the conditions under which different processes or factors may be important (Butler and Chesson, 1990). Changes in the environment features will be reflected on the benthic community structure but also on the polychaete assemblage and the Syllidae species composition (Simboura et al., 2000; Moreira et al., 2006; Cacabelos et al., 2010). Their distribution pattern and ecological functioning have traditionally been addressed by describing the taxonomic composition of assemblages (Bremmer, 2005).

Soft-bottom benthic communities are probably the most widely used indicators for environmental changes as they are composed of relatively immobile organisms and their quantitative sampling is quite easy (Warwick, 1993). Among soft-bottom benthic organisms, polychaetes are considered one of the most important groups in these

communities (Fauchald and Jumars, 1979). They are abundant and ecologically important (Glasby et al., 2000) and their assemblage structure are influenced by the heterogeneity of the habitat (Del-Pilar-Ruso et al., 2011). Among polychaetes, Syllidae is considered a complex and diverse family (Fauchald and Rouse, 1997; San Martín, 2003; Aguado and San Martín, 2008) and also constitutes one of the most widely distributed polychaete families worldwide, both in soft and hard bottoms, especially in shallow waters (Granados-Barba et al., 2003). In the Western Mediterranean, the Spanish sector is the one with the highest numbers of species and endemic forms described (Musco and Giangrande 2005)

We have focused on these different subsets of the whole soft-bottom benthic community because we were interested in checking the concordance of the organism distribution patterns in relation to the environmental features in a heterogenic area (characterized by the influence of both natural and human pressures). Therefore, soft-bottom macrobenthic community was analysed at different taxonomic scales and using different levels of taxonomic resolution with the aim of i) assessing the influence of the environment features on distribution pattern in this heterogeneous area and; ii) determinate whether the same environmental factors drive spatial distributions of community composition based on different taxonomic subsets of soft-bottoms macrobenthic organisms.

2. Material and methods

2.1. Sampling design and laboratory work

The study was carried out in Alicante coast (Western Mediterranean) (Fig. 1). In this area, a north–south pollution gradient, caused by sewage outfall and port activities, has taken place for decades. As a consequence of the increasing stress, the original habitat, mainly dominated by seagrass beds, has been altered and it has become a muddier area with a high coverage of dead *Posidonia oceanica* rhizomes (Ramos-Esplá, 1984; Fernández-Torquemada, 2012) and it has also been colonised by algae, mainly *Caulerpa prolifera* (personal observations). Besides, a new activity has also been set up in recent years (reverse osmosis desalination activity). The main impact on marine communities of reverse osmosis desalination plants is caused by the discharge of an effluent of high salinity. Brine discharge remains on the bottom because of its high density and affects marine benthic communities by leading to possible death of organisms which live in an osmotic balance with their environment (Einav et al., 2002; Fernández-Torquemada et al., 2005; Del-Pilar-Ruso et al., 2007, 2008). This activity started in September 2003, but there was an increase of brine dilution in 2006 reducing the salinity of the effluent. Due to the long-term impacts of different human pressures the study area is considered as disturbed.

In order to analyse the macrobenthic soft-bottom community three perpendicular transects to the coast were established (called A, B and C), each at a distance of around 400 m from each other. They are around 2 km to the south of the sewage and port activities (including a dock that was built from 2005 to 2007) and the brine discharge takes place in front of the transect B. Three depths were sampled at each transect (one station at 4 m, other one at 10 m and the third one at 15 m). A total of 9 station were compared from 2004 to 2009 and in each year, sampling was carried out in two seasons (winter and summer) (Fig. 1). Samples were taken out by scuba diving. To study macrobenthic organisms, three replicates were

collected at each station using a square box (22.5 x 22.5 cm). As a whole, 324 samples for biotic analyses were collected, sieved through a 0.5 mm mesh screen and preserved in buffered formalin. Once in the laboratory, the macrobenthos was sorted and analysed. The identification of organisms was done by means of microscope and stereomicroscope. An additional corer sample was collected at each station for sediment analysis. Immediately after its collection, pH was measured in undisturbed sediment cores using a pH-meter Crison with a sensor 52-00. Once in the laboratory, the sediment was dried in an oven to estimate both grain size and organic matter following Buchanan's methodology (1984). Organic matter content of dry sediment was estimated by loss of mass on ignition after being ashed at 400 °C for 4 h (Buchanan, 1984). Salinity surveys were made in summer and winter each year by means of a CTD sensor.

2.2. Statistical analyses

Non-parametric multivariate techniques were used to analyse benthic community distribution patterns at different taxonomic scales in relation to the environmental factors. Firstly, macrobenthic community was analysed at Phylum-Order level (either Phylum, Class or Order, depending on the taxonomic group). Among different taxonomic groups, polychaetes were selected and analysed at family level. Finally, the family Syllidae was chosen from all polychaete families and identified to genus and species level (Fig. 2). Triangular similarity matrices were calculated using the Bray-Curtis similarity coefficient on untransformed abundance data for all taxa identified throughout the study period (only the three replicates at each sampling station were averaged) and Euclidean distance on normalized data for environmental variables (Clarke and Warwick, 2001). Triangular

matrices were calculated from the untransformed abundance data because there are several studies that demonstrated that when the severity of transformation becomes higher the loss of information using higher taxonomic levels increases (Olsgard et al., 1997; Karakassis and Hatziyanni, 2000; Anderson et al. 2005; Puente and Juanes 2008; Bevilacqua et al. 2009). In order to determine the environmental features that characterized each station of the study area, a PCA procedure was applied. A graphical representation of multivariate patterns of the assemblages at different taxonomic scales was obtained by non-metric multidimensional scaling (nMDS). The similarity profile test (SIMPROF) permutation test was run to test the null hypothesis that a specific set of samples, which are not *a priori* divided into groups, do not differ from each other in multivariate structure. With respect to the distribution pattern detected previously, a similarity percentages (SIMPER) procedure was performed to determine the percentage contribution of each group at each taxonomic scale. The possible relationship between the benthic community at each taxonomic scale and abiotic factors was determined using the BEST routine (BIO-ENV option). Prior to conducting this procedure inter-correlations among environmental factors have been analysed. Spearman correlations between biotic data (the whole benthic community, polychaetes at family level and syllids at genus and species level) and abiotic factors (sediment grain size, organic matter, pH, salinity and depth) were determined using the RELATE procedure. A second-stage nMDS ordination was also plotted to visualize the relationships among similarity matrices at each taxonomic scale (Somerfield and Clarke, 1995). By means of second-stage analysis, Spearman's correlation coefficients are calculated between all pairs of matrices. The analysis was performed twice; taking into account temporal variability as well as calculating the mean values among years. All

multivariate analyses were performed using the PRIMER-E statistical package (Clarke and Gorley, 2006).

3. Results

3.1. Community composition

Analysing the benthic community a total of 23 taxonomic groups was collected and the most abundant taxa were polychaetes (49.44% of the total abundance), followed by Nematoda (21.20%), Bivalvia (13.80%) and Amphipoda (7.50%). Taking into account the polychaete assemblage, a total of 48 families were collected and the families Capitellidae (19.62%), Spionidae (13.72%), Paraonidae (10%), Syllidae (7.34%) and Nephtyidae (6.83%) were the most abundant ones. The rest of the families represented less than 5% of the total abundance (Table 1). With respect to the family Syllidae, a total of 1134 syllids belonging to 30 species and 12 genera from the total samples were identified (Table 2). The most abundant genera were *Syllis*, *Sphaerosyllis*, *Parapionosyllis*, *Exogone* and *Paraehlersia*. The most species-rich genera were *Syllis* with 8 species, with *Syllis garciai* (Campoy, 1982) being the most abundant one, and *Sphaerosyllis*, with 6 species, with *Sphaerosyllis taylori* Perkins, 1981 and *Sphaerosyllis pirifera* Claparède, 1968 the most abundant ones. Three species belonging to genus *Parapionosyllis* were identified and *Parapionosyllis labronica* Cognetti, 1965 was the most abundant one. *Exogone naidina* Örsted, 1845 was the most represented species of the genus *Exogone*. Only one species belonging to the genus *Paraehlersia* was collected; *Paraehlersia ferrugina* (Langerhans, 1881). The rest of the species were represented by a low number of specimens and some of them, such as *Prosphaerosyllis* sp., *Prosphaerosyllis campoyi* (San Martín, Acero,

Contonente and Gómez, 1982), *Salvatoria clavata* (Claparède, 1963), *Syllis corallicola* Verrill, 1900, *Syllis torquata* Marion and Bobretzky, 1875 and *Syllis vittata* Grube, 1840 were represented only by one specimen (Table 2).

3.2. Environmental factors

Analysing environmental features by means of PCA (Fig. 3), it was detected that 61.1% of the total variance was explained by the first two axes. Axis I (PC1) accounted for 34.3% of the total variance, and the main contributors were depth, organic matter, fine sand and mud. On the other hand, axis II (PC2) explained 26.7% of the residual variance; the variables contributing most were coarse sand, gravel and medium sand. Sediment grain size decreased with increasing depth. In the shallower areas (4 meters depth) sediments was either fine sand (A1 and C1) or medium sand (B1). In the intermediate areas (10 meters depth) sediment was mixed fine sand and mud, while in the deeper areas (15 meters depth) the percentage of mud was considerably increased ($15.28\% \pm 2.25$ (SE) at 4 m; $36.50\% \pm 3.08$ (SE) at 10 m and $51.5\% \pm 2.26$ (SE)). For organic matter, the highest values were obtained in the deeper stations ($2.72\% \pm 0.33$ (SE) at 4 m; $4.92\% \pm 0.51$ (SE) at 10 m; and $8.22\% \pm 0.75$ (SE) at 15 m). The pH and salinity values do not seem to have any influence on the variance of environmental features. The salinity was around 37.92 ± 0.05 in all the stations with the exception of stations closer to the discharge of the desalination plant, B1 at 4 meters, where salinity exceed 40 during the first two sampling periods (2004 and 2005). Once the brine dilution was applied in 2006 these salinity values decreased.

3.3. Distribution patterns at different taxonomic scales

The four nMDS analyses based on the benthic community at high taxonomic level (Phylum to Order), polychaete families and syllid genera and species abundances showed a main differentiation of the shallow stations from the deeper ones throughout the study period (Fig. 4). This pattern was corroborated by means of the SIMPROF procedure. This analysis indicated significant differences between a main group (where most of the deeper stations are included) and most of the shallower ones (that segregated from the main group) at different taxonomic scales (benthic community: $p=0.009$; polychaete families: $p=0.001$; syllids at genus level: $p=0.006$ and syllids at species level: $p=0.001$). The SIMPER procedure showed that most taxonomic groups showed an increasing abundance with depth, except nematodes that were more abundant at 4 meters. Likewise, most of the polychaete family abundances increased with the depth. In the family Syllidae, the genera *Parapionosyllis*, *Paraehlersia*, *Syllis* and *Exogone* were, mainly, responsible for the dissimilarities among depths. *Parapionosyllis*, mainly *Parapionosyllis labronica*, was more abundant in shallower stations. The genus *Paraehlersia*, represented by *Paraehlersia ferrugina*, and the genus *Exogone*, represented by *Exogone naidina*, were more abundant at 10 metres. The genus *Syllis*, with *Syllis garciai* being the most abundant species, dominated at 10 and 15 m. The genus *Sphaerosyllis* occurred in all the depth range; however, the spatial distribution between the two main species seems to be different. *Sphaerosyllis taylori* was more abundant between 4 and 10 m. *Sphaerosyllis pirifera* showed the opposite pattern, i.e. it was less abundant in the shallowest ones (Table 3; SIMPER procedure). These distribution patterns could be also related with differences in granulometric composition since sediment grain size decreased with increasing depth.

3.4. Distribution patterns vs. environmental factors

The BIO-ENV analysis showed that both the patterns derived from the benthic community as well as from the polychaete family distributions showed certain correlations with all the abiotic factors (there were not inter-correlations) throughout the six sampling years. Salinity, depth, medium sand and fine sand constituted the best combination for both the benthic community ($\rho=0.46$) and polychaete families ($\rho=0.57$). Among these abiotic factors, depth and fine sand seemed to be the main factors relating to the distribution pattern of polychaete families, while depth was the main factor relating to the distribution pattern of the whole community at low resolution level (Table 4). The distribution of Syllidae also showed correlations with environmental conditions, both at genus and species level ($\rho=0.48$ and $\rho=0.56$, respectively). The best combination included depth and fine sand (BEST procedure, BIO-ENV option). The RELATE procedure showed that both abiotic factors were correlated significantly at genus (Depth: $\rho=0.35$, $p=0.001$; fine sand: $\rho=0.44$, $p=0.001$) and at species level (Depth: $\rho=0.42$, $p=0.001$; fine sand: $\rho=0.42$, $p=0.001$) (Table 4).

The second-stage MDS derived from inter-matrix correlations showed that the distance between taxonomic scales reflects the degree to which the similarity matrices are correlated. Syllids at genus level (SG) showed lower similarity values (Fig. 5). The matrix derived from the benthic community abundances at high taxonomic level (BC) compared with the matrix derived from polychaete abundances at family level (PF) showed a correlation of 0.68. Selecting the family Syllidae of all polychaete families, the matrix derived from syllid assemblage at species level showed a correlation of 0.55 with respect to

polychaete families and 0.40 with respect to the benthic community; however these correlations decrease when syllids at genus level are considered ($\rho=0.50$ and $\rho=0.35$, respectively). As expected, higher correlations were obtained between syllid assemblage at both genera and species level ($\rho=0.86$) (Fig. 5A). This procedure was performed again regarding the average abundance data among years. In both cases similar pattern was detected, but it was more robust in the second approach (Fig. 5).

4. Discussion

The original habitat type (*Posidonia oceanica* meadows) of the study area has been changed since several anthropogenic impacts have been merging for decades. It has become a constantly disturbed area due to the high sedimentation rates derived from the port expansion and the eutrophication caused by the presence of a sewage discharge. Sampled stations analysed showed a heterogeneous bottom with differences in sediment type and organic matter content among them. Grain size decreases with increasing depth, with a higher percentage of mud and organic matter in deeper stations. Shallower stations are subjected to higher natural stress due to the hydrodynamics whereas deeper stations are homogeneously stable. These changes in sediment characteristics lead to differences in the distribution pattern of benthic communities.

The benthic community inhabiting these heterogeneous soft bottoms showed similar response to stress to that observed by Pearson and Rosenberg (1978) and Rhoads and Germano (1986) in their studies, where changes in benthic communities with respect to an

organic matter gradient were analysed. These models showed that environmental disturbances, lead to a lower species diversity, which drives an increase in the dominance and abundance of some species, mainly opportunistic polychaetes (Gray and Elliot, 2009). Class Polychaeta characterized the community of these heterogeneous soft bottoms and it was mainly dominated by organisms considered opportunistic such as Capitellidae, Paraonidae and Spionidae as it was detected in a previous study (Del-Pilar-Ruso et al., 2008). This polychaete assemblage composition seems to be consistent throughout the time. Family Syllidae was also present in the study area, though in lower abundances since this family is generally considered as a pollution-sensitive. However, though they are highly sensitive to pollution or to other kind of stress (Giangrande et al., 2004, 2005; Musco et al., 2004), some Syllid species with an opportunistic behaviour have been identified (Giangrande, 1988; Cognetti and Maltagliati, 2000; Giangrande et al., 2005). In this sense, it was observed that one of the five most abundant species, *Exogone naidina*, which is considered as a tolerant species (Simboursa and Zenetos, 2002) and other tolerant species such as *Exogone verrugera* (Claparède, 1868), *Syllis hyalina* Grube, 1863 and *Sphaerosyllis hyxtrix* (Claparède, 1863) (Simboursa and Zenetos, 2002) were present in the study area, though the last ones show low abundance values. However, the most abundant species in the study area, *Syllis garciai* (Campoy, 1982), is considered as a sensitive species (Bentix; Simboursa and Zenetos, 2002), but this species present a wide range of habitat preferences such as coarse sands, muddy habitats as well as *P. oceanica* rhizomes (San Martín, 2003), habitats that compose the heterogeneous soft bottom of the studied area.

In this long-term survey, it has been detected that macrobenthic soft-bottom community distribution is influenced by environmental features (caused by both natural and

anthropogenic perturbations) as it was detected previously (Del-Pilar-Ruso et al., 2007, 2008, 2009) and these correlations were detected at different taxonomic scales. However, in spite of the existence of different stresses that have altered the original habitat, the depth seems to be a key factor structuring the spatial distribution pattern at each of the different taxonomic scales. In conclusion, the heterogeneity of environmental features, which characterised the study area, determines a similar spatial pattern analysing the benthic community at high taxonomic level and the polychaete assemblage at family level. This pattern was also consistent at both syllid genus and species level and it was probably due to the dominance of few species in each genus level since environmental disturbances lead to a decrease of diversity, except in the case of *Sphaerosyllis*. This last genus was dominated by two species with a different spatial distribution pattern between 4 and 15 m. Musco et al. (2009) also detected that some syllid species of the same genus followed a different pattern of distribution. These differences in assemblage composition when considering syllid species, which correlate with depth, might also reflect strong relationship with granulometric composition (coarse vs fine sediments) as it was detected by other authors (Moreira et al., 2006) since sediment grain size decreased with increasing depth. Besides *S. taylori* is usually more abundant in coarser sandy sediments (shallower depths in the study area) than in muddy ones (deeper areas) (Moreira et al., 2006; San Martín, 2003).

Once the knowledge of the composition and distribution of each taxon of the study area has been analysed, the distribution patterns at different levels of hierarchy were compared in order to reveal some regularity among the above distribution patterns. The second stage analyses showed high correlations between matrices derived from the different taxonomic scales when mean abundance data over years were considered (abundance data averaged).

It is well recognised that community structure may vary temporally depending on the successional status (e.g. disturbance history) and seasonal effects (Magierowski and Johnson, 2006). In this sense, the second-stage correlations decreased when temporal variability was taken into account (when years were treated separately) (Fig. 5). These results highlight the importance of inter-annual changes in ecological processes.

5. Conclusions

Measuring changes in the distribution patterns of benthic community in a long-term study revealed a similar distribution pattern at different taxonomic scales. Benthic community distribution patterns, mainly related to the depth and granulometric composition, were found again when considering the syllid genus or species level, as well as when polychaete families or the benthic community at high taxonomic level were analysed. In conclusion, the soft bottom community spatial distribution pattern determined by the environmental heterogeneity keeps at different taxonomic scales.

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Fig. 1 Map of the study area showing the sampling stations (A, B, C: transect located north to south; 1, stations located at 4 m; 2, stations located at 10 m; 3, stations located at 15 m) (UTM coordinate system. Grid zone 30S)

Fig. 2 Schematic diagram of selecting each taxonomic scale

Fig. 3 Principal component analyses (PCA); contribution of main environmental features (depth, O.M: organic matter, pH, Sal: salinity, G: gravel, Cs: coarse sand, Ms: medium sand; Fs: fine sand; and M: mud) to Axis I and II

Fig. 4 MDS analyses based on the Bray-Curtis Similarity of non-transformed abundance data at each taxonomic scale considered throughout the sampling period: (A) benthic community at high taxonomic level; (B) polychaetes at family level; (C) syllids at genus level and (D) syllids at species level

Fig. 5 Second stage MDS and correlations among similarity matrices derived from each taxonomic scale: (A) taking into account temporal variability; (B) mean abundance data among years (averaged data). BC: benthic community, PF: polychaete families, SG: syllids at genus level, SS: syllids at species level

Table 1 Mean values of relative abundance (ind/m²) of the main taxonomic groups at different scales: benthic community; polychaete families and syllids at genus and species level

Transect	Stations								
	A	A	A	B	B	B	C	C	C
Depth	4	10	15	4	10	15	4	10	15
Station	A1	A2	A3	B1	B2	B3	C1	C2	C3
Benthic community									
Amphipoda	47.73	267.22	209.61	65.84	113.03	224.96	63.65	121.27	280.94
Bivalvia	186.56	309.47	302.88	62.00	356.11	288.07	137.73	432.38	502.60
Decapoda	10.43	104.80	46.09	21.95	32.37	50.48	6.59	37.86	64.75
Nematoda	834.02	70.23	92.73	1351.99	964.61	72.98	64.75	466.94	41.16
Polychaeta	639.23	1279.01	1542.92	311.66	776.41	1717.97	335.80	1079.29	1550.62
Polychaeta families									
Capitellidae	44.44	158.02	379.70	40.05	109.19	501.51	62.55	173.94	342.39
Nepthyidae	9.33	40.60	130.04	4.94	76.27	76.82	18.66	133.88	140.47
Paraonidae	27.43	183.26	212.35	13.17	49.93	170.10	15.91	112.48	134.43
Spionidae	226.61	81.76	159.12	55.42	154.73	186.56	79.56	189.30	133.88
Syllidae	47.74	147.60	43.33	90.53	92.73	79.56	24.69	46.09	105.90
Syllids genera and species									
<i>Exogone</i>	1.65	9.88	6.58	1.65	20.30	3.84	1.10	3.84	6.58
- <i>Exogone naidina</i>	0.00	9.33	1.10	1.65	19.75	2.74	0.55	1.10	2.19
<i>Paraehlersia</i>	2.74	8.23	0.55	1.65	6.04	3.84	0.00	4.94	4.94
- <i>Paraehlersia ferrugina</i>	2.74	8.23	0.55	1.65	6.04	3.84	0.00	4.94	4.94
<i>Parapionosyllis</i>	1.65	4.94	0.00	25.79	2.19	1.10	20.30	1.10	1.10
- <i>Parapionosyllis labronica</i>	1.65	0.00	0.00	25.79	1.10	0.00	19.20	1.10	0.00
<i>Sphaerosyllis</i>	7.13	55.42	8.23	49.93	31.28	15.36	0.55	8.78	29.08
- <i>Sphaerosyllis pirifera</i>	4.39	24.69	4.39	0.00	3.29	11.52	0.55	6.58	19.75
- <i>Sphaerosyllis taylori</i>	1.10	26.89	2.74	49.38	26.89	0.00	0.00	1.10	6.04
<i>Syllis</i>	30.73	56.52	23.59	2.74	20.85	48.29	0.55	21.40	48.83
- <i>Syllis garciai</i>	20.85	53.22	22.50	1.10	16.46	44.44	0.00	19.75	45.54

Table 2 List of species and summary of each species total abundance data at each station during the sampling period

Transect	Station									
	A	A	A	B	B	B	C	C	C	Total
	4	10	15	4	10	15	4	10	15	
Station	A1	A2	A3	B1	B2	B3	C1	C2	C3	
<i>Brania arminii</i> (Langerhans, 1881)	1		1	3					1	6
<i>Erinaceusyllis serratosetosa</i> (Hartmann-Schröder, 1982)				2				1		3
<i>Exogone dispar</i> (Webster, 1879)			1			2			1	4
<i>Exogone naidina</i> Örsted, 1845		17	2	3	36	5	1	2	4	70
<i>Exogone verugera</i> (Claparède, 1868)	3	1	9		1		1	5	7	27
<i>Haplosyllis granulosa</i> (Lattig, San Martín and Martín, 2007)		1			3			1	1	6
<i>Paraehlersia ferrugina</i> (Langerhans, 1881)	5	15	1	3	11	7		9	9	60
<i>Parexogone meridionalis</i> (Cognetti, 1955)					2					2
<i>Parapionosyllis brevicirra</i> Day, 1954		9			1	2			2	14
<i>Parapionosyllis labronica</i> Cognetti, 1965	3			47	2		35	2		89
<i>Parapionosyllis</i> cf. <i>macaronesiensis</i> Brito, Núñez and San Martín, 2000					1		2			3
<i>Perkinsyllis anophthalma</i> (Capaccioni and San Martín, 1989)							2			2
<i>Prosphaerosyllis campoyi</i> (San Martín, Acero, Contonente and Gómez, 1982)			1							1
<i>Prosphaerosyllis</i> sp.				1						1
<i>Salvatoria clavata</i> (Claparède, 1863)				1						1
<i>Salvatoria yraidæ</i> (San Martín, 1984)				8						8
<i>Sphaerosyllis glandulata</i> Perkins, 1981	1	3	1			1			1	7
<i>Sphaerosyllis austriaca</i> Banse, 1959	2	1						2	2	7
<i>Sphaerosyllis hystrix</i> Claparède, 1863		1		1	2					4
<i>Sphaerosyllis pirifera</i> Claparède, 1868	8	45	8		6	21	1	12	36	137
<i>Sphaerosyllis climenti</i> Del-Pilar-Ruso and San Martín, 2012		2	1			6			3	12
<i>Sphaerosyllis taylori</i> Perkins, 1981	2	49	5	90	49			2	11	208
<i>Syllis corallicola</i> Verrill, 1900						1				1
<i>Syllis garciai</i> (Campoy, 1982)	38	97	41	2	30	81		36	83	408
<i>Syllis gerlachi</i> (Hartmann-Schröder, 1960)		4	1		1			1	3	10
<i>Syllis hyalina</i> Grube, 1863	1						1			2
<i>Syllis</i> cf. <i>mauretanica</i> (Licher 1999)	17	2	1	3	7	4		1		35
<i>Syllis pontxioi</i> San Martin and López, 2000								1	3	4
<i>Syllis torquata</i> Marion and Bobretzky, 1875						1				1
<i>Syllis vittata</i> Grube, 1840						1				1
Total	81	247	73	164	152	132	43	75	167	1134

Table 3 Summary of the results of SIMPER dissimilarities among depths (4, 10 and 15 m) at different taxonomic levels (benthic community; polychaete families and syllids at genera and species level) (Av. Abund: average abundance, Contrib. %: percentage of contribution; Cum. %: cumulative percentage, A.D = average dissimilarity)

Benthic community				
	Av.Abund	Av.Abund	Contrib%	Cum.%
Depth (A.D= 64.56%)	4 m	10 m		
Polychaeta	428.9	1044.9	39.68	39.68
Nematoda	750.25	500.59	27.14	66.82
Bivalvia	128.76	365.98	13.54	80.36
Amphipoda	59.08	167.17	7.66	88.02
Depth (A.D= 67.56%)	4 m	15 m		
Polychaeta	428.9	1603.83	51.39	51.39
Nematoda	750.25	68.95	18.27	69.66
Bivalvia	128.76	364.52	11.9	81.57
Amphipoda	59.08	238.5	8.22	89.78
Depth (A.D= 43.72%)	10 m	15 m		
Polychaeta	1044.9	1603.83	43.18	43.18
Bivalvia	365.98	364.52	14.4	57.58
Nematoda	500.59	68.95	14.35	71.93
Amphipoda	167.17	238.5	12.93	84.86
Polychaete families				
Depth (A.D= 78.66 %)	4 m	10 m		
Spionidae	120.53	141.93	16.21	16.21
Capitellidae	49.02	147.05	10.69	26.91
Paraonidae	18.84	115.23	9.02	35.93
Syllidae	54.32	95.47	8.4	44.34
Nephtyidae	10.97	83.58	8.09	52.42
Depth (A.D= 82.91 %)	4 m	15 m		
Capitellidae	49.02	407.86	19.63	19.63
Spionidae	120.53	159.85	11.08	30.71
Paraonidae	18.84	172.29	10.64	41.35
Nephtyidae	10.97	115.78	7.2	48.55
Cirratulidae	5.85	107.73	5.56	54.12
Syllidae	54.32	76.26	5.26	59.37
Depth (A.D= 61.18 %)	10m	15 m		
Capitellidae	147.05	407.86	16.54	16.54
Spionidae	141.93	159.85	11.52	28.05
Paraonidae	115.23	172.29	9.11	37.17
Nephtyidae	83.58	115.78	7.58	44.74
Syllidae	95.47	76.26	6.3	51.05
Cirratulidae	33.47	107.73	5.34	56.39
Syllids genera level				
Depth (A.D= 87.84 %)	4 m	10 m		
<i>Syllis</i>	17.01	37.04	32.26	32.26

<i>Sphaerosyllis</i>	28.81	35.8	23.46	55.72
<i>Parapionosyllis</i>	23.87	3.09	21.02	76.74
<i>Exogone</i>	2.19	12.76	11.63	88.37
<i>Paraehlersia</i>	2.19	7.2	6.73	95.09
Depth (A.D= 87.35 %)	4 m	15 m		
<i>Syllis</i>	17.01	46.73	44.01	44.01
<i>Parapionosyllis</i>	23.87	0.85	20.94	64.95
<i>Sphaerosyllis</i>	28.81	20.39	18.86	83.81
<i>Exogone</i>	2.19	6.58	8.72	92.53
Depth (A.D=66.33 %)	10 m	15 m		
<i>Syllis</i>	37.04	46.73	42.94	42.94
<i>Sphaerosyllis</i>	35.8	20.39	27.8	70.73
<i>Exogone</i>	12.76	6.58	14.87	85.6
<i>Paraehlersia</i>	7.2	3.61	8.34	93.94
Syllids species level				
Depth (A.D= 93.56 %)	4 m	10 m		
<i>Syllis garciai</i>	10.97	33.54	26.16	26.16
<i>Parapionosyllis labronica</i>	23.32	0.82	19.22	45.38
<i>Sphaerosyllis taylori</i>	25.24	20.58	13.11	58.49
<i>Sphaerosyllis pirifera</i>	2.47	12.96	8.79	67.28
<i>Exogone naidina</i>	1.10	11.32	7.14	74.43
<i>Paraehlersia ferrugina</i>	2.19	7.20	6.32	80.74
Depth (A.D = 94.40 %)	4 m	15 m		
<i>Syllis garciai</i>	10.97	43.54	38.1	38.1
<i>Parapionosyllis labronica</i>	23.32	0.00	18.95	57.05
<i>Sphaerosyllis pirifera</i>	2.47	13.81	9.15	66.2
<i>Sphaerosyllis taylori</i>	25.24	3.40	7.77	73.97
<i>Exogone verugera</i>	1.10	3.40	5.56	79.52
Depth (A.D = 73.17 %)	10 m	15 m		
<i>Syllis garciai</i>	33.54	43.54	36.83	36.83
<i>Sphaerosyllis pirifera</i>	12.96	13.81	14.69	51.53
<i>Sphaerosyllis taylori</i>	20.58	3.40	10.5	62.02
<i>Exogone naidina</i>	11.32	2.34	8.61	70.63
<i>Paraehlersia ferrugina</i>	7.20	3.61	7.56	78.2
<i>Exogone verugera</i>	1.44	3.40	5.62	83.82

Table 4 Spearman correlations between each environmental feature and biotic data taking into account each taxonomic scale (ρ = correlation; sig. level= significance level, %)

	Benthic community		Polychaete families		Syllid genera		Syllid species	
	ρ	sig.level	ρ	sig.level	ρ	sig.level	ρ	sig.level
Total abiotic	0.38	0.1	0.50	0.1	0.42	0.1	0.44	0.1
Salinity	0.18	0.1	0.18	0.1	0.10	1.4	0.12	0.3
Depth (m)	0.39	0.1	0.44	0.1	0.35	0.1	0.42	0.1
pH	0.08	1.3	0.11	0.6	0.28	0.1	0.28	0.1
Organic matter (%)	0.01	39.8	0.04	21.4	0.13	0.4	0.10	2
Gravel (%)	0.08	3.6	0.14	0.3	0.08	3.8	0.19	0.1
Coarse sand (%)	0.05	17.9	0.12	2	0.06	9.9	0.11	2.4
Medium sand (%)	0.22	0.1	0.27	0.1	0.16	0.5	0.20	0.2
Fine sand (%)	0.21	0.1	0.34	0.1	0.44	0.1	0.42	0.1
Mud (%)	0.21	0.1	0.24	0.1	0.18	0.1	0.21	0.1

Fig 1

Fig 2

Fig 3

Fig 4

Fig 5

Highlights

- 1.-Similar distribution patterns were detected at different taxonomic scales
- 2.-These patterns are mainly determined by depth and granulometric composition.
- 3.-Similar response to stress to that observed by previous authors was detected.