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הקשורים בפעילויות חיפוש וקידוח נפט וגז בים – דו"ח סופי**

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**מוגש למנהל אוצרות טבע  
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## תקציר בעברית

מטרת המחקר היא לאפיין כמותית את מאפייני חי תוך המצע של קרקעית הים העמוק במים הכלכליים של ישראל בטווח העומקים 100-1900 מטר. דגימות מחפר קופסא נאספו ב- 50 אתרים ביוני-יולי 2013. חי תוך המצע הגדול מ- 250 מיקרון נספר והוגדר לרמה הפרטנית ביותר שהתאפשרה (37% של המינים הוגדרו לרמת המין. זוהו שלש חברות חי החיות בשלשה בתי גידול, שולי מדף היבשת, מדרון היבשת ומישור הבתיאל. ההטרוגניות בתוך כל בית גידול הוערכה בעזרת ממוצע אינדקס הדמיון של חאו-סורנסן ובעזרת חישוב של  $(\exp(\gamma) = \text{beta-diversity} - \exp(\alpha \text{ diversity}))$  . התקבלו ערכים בטווחים של 0.64-0.7 ו- 1.73-2.77, בהתאמה, כאשר נעשה שימוש בדגימות מאוחדות ממישור הבתיאל. הערכים המקבילים מדגימות שלא אוחדו מראים הטרוגניות גדולה יותר, עם ערכים של 0.26 ו- 6.27, בהתאמה. הסיבה היא כנראה דיגום בלתי מספק. צפיפות חי תוך המצע בבתי הגידול השונים (ממוצע גאומטרי של 59-2220 פרטים למטר רבוע, מראה ירידת צפיפות לוגריתמית עם עליית העומק. המספר המוערך של מספר המינים בכל אחד מבתי הגידול חושב בשיטת ההתקלשות (rarefaction) הן בהקשר לשטח הנדגם והן בהקשר למספר הפרטים שנדגמו. התוצאות היו 203 מינים (בהקשר לשטח נדגם) ו- 206 מינים (בהקשר למספר הפרטים שנדגמו) בשולי מדף היבשת, 170 ו- 163 במדרון היבשת ו- 130-144 במישור הבתיאל. ערכי  $\alpha$  diversity מוקלשים ביחס לשטח נדגם קטנים לכוון בתי הגידול העמוקים. יחד עם זאת ערכי  $\alpha$  diversity מוקלשים ביחס למספר פרטים נדגם עולים בצורה דומה בכל בתי הגידול עם עליית מספר הפרטים. עומק המים, השכיח של התפלגות גודלי הגרגר, אחוז החרסיות ותכולת הסיידן הפחמתי הראו במשותף קורלציה גבוהה להרכב חברת החי. עומק המים כגורם בודד הראה את הקורלציה הגבוהה ביותר.

## Deep-sea soft bottom infaunal communities of the Levantine Basin (SE Mediterranean) and their shaping factors

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**Abstract** - The present study sought to quantify the infauna and environmental characteristics of the deep SE Levantine Basin, Mediterranean Sea (33.4-31.7 N, 31.3-34.9 E; 100-1900 m water depth). Box corer samples were collected at 50 sites in June-July 2013. The infauna (> 250  $\mu\text{m}$ ) were enumerated and identified to the lowest possible taxonomic level (~ 37% to the species level). Three faunal assemblages were identified, inhabiting three biotopes, the shelf margin (SM), the continental slope (CS) and the bathyal plain (BP). The within-biotope heterogeneity was evaluated by the average Chao-Sørensen similarity index and the beta diversity ( $\exp(\text{gamma diversity}) - \exp(\text{alpha diversity})$ ), revealing values of 0.64-0.7 and 1.73-2.77, respectively, upon applying the pooled bathyal plain samples. The corresponding non-pooled samples revealed higher heterogeneity, with values of 0.26 and 6.27, respectively, likely due to insufficient sampling. The infaunal density in the various biotopes (geometric mean 59-2220 ind  $\text{m}^{-2}$ ) exhibited a logarithmic decline with water depth. The estimated number of taxa per biotope was calculated by rarefaction analysis in relation to the sampled area and the number of sampled individuals, resulting in 203 (sampled area) -206 (number of individuals) (SM), 170-163 (CS) and 144-130 (BP) taxa. The rarified alpha diversity in relation to the sampled area revealed decreasing values toward the deeper biotopes. However, similar rarified alpha diversities were found in all the biotopes in relation to the number of sampled individuals. Water depth, sediment grain size mode,  $\text{CaCO}_3\%$ , and clay% were jointly correlated with faunal composition; water depth provided the single strongest correlate.

## **Introduction**

The Mediterranean deep sea is characterized by unique environmental conditions in comparison to the adjacent eastern Atlantic. Its water temperatures below ~300 m are homogenous and high (~13-14°C), its salinity is high, and its primary production is relatively low. These parameters vary from the west to the east through the Mediterranean, reaching their extremes in the Levantine Basin (LB), where the highest temperature and salinity and the lowest primary production occur (Sarda et al. 2004; Danovaro et al. 2010). Oligotrophy was identified by Pusceddu et al. (2010) and Baldrighi et al. (2014) as the major determinant of the decreasing abundance and biomass of benthic fauna along the Mediterranean west-east axis, with the LB as an extremely low-nutrient, low-chlorophyll, and ultra-oligotrophic environment (Kress and Herut 2001; Siokou-Frangou et al. 2010). Understanding the Mediterranean ecology and its shaping factors requires, among other studies, the elucidation of the poorly investigated ecology of the southeastern LB, the easternmost point of these biotic and oceanographic gradients.

The deep-sea infauna of the southeast corner of the LB off the Israeli coast has been qualitatively reported previously, including its zoogeographic relationships with the western Mediterranean and the eastern Atlantic (Galil 2004 and literature therein). However, the quantitative characterization of this province in terms of its infaunal density, diversity, and composition in relation to environmental variation has only been partially performed (Kröncke et al. 2003; Baldrighi et al. 2014). Kröncke et al. (2003) sampled the entire LB from Crete to Israel and from Egypt to Cyprus, and Baldrighi et al. (2014) studied the deep sea south of Crete as part of a wider Mediterranean survey. Tselepides et al. (2000) studied the comparable environment of the adjacent deep Aegean Sea. The latter authors included detailed determinations of faunal assemblages from the shelf, continental slope, and bathyal plain, with data on faunal density and diversity and a variety of environmental parameters. Here, we aim to provide a comparable quantitative assessment of the infaunal benthos of the LB based on a particularly extensive broad-scale survey of the region.

## **Materials and methods**

### Surveyed area and sampling design

The area covered by the present study encompasses approximately 23,000 km<sup>2</sup> of the southeastern LB. It was recently mapped (Hall et al. 2015), enabling the distinction of a variety of bottom terrain features (supplementary Fig. S1), and providing insight into the studied area geological evolution (Gvirtzman et al. 2015). The continental shelf margin (SM) and its continuation on the continental

slope (CS) are located between 100-1000 m water depths and contain diverse terrain, including a steep canyon area in the north and the prominent Dor and Palmahim gravitational sediment slumps in the center of the coast, with a moderately inclined CS between them, marked with numerous smaller sediment slides (Katz et al. 2015). The bathyal plain (BP), located between 1000-1900 m water depths, is generally flatter than the CS but is crossed by southeast-northwest channels, frequent ridges and trenches.

Seabed sediments were sampled at 50 sites (Fig. 1 and supplementary Fig. S1) from the RV Shikmona (Israel Oceanographic and Limnological Research). Offshore transects on the SM and the CS crossed the canyon area in the north and the Palmahim gravitational slump in the south. Other transects were located in the relatively featureless CS. BP samples were collected along approximate continuations of these transects. Details of the sampling operations are given in supplementary Table S1. A total of 150 box core sediment samples, three at each site, were collected with a 0.0625-m<sup>2</sup> box corer (Ocean Instruments BX 700 AL) during June-July 2013. A 5.4-cm diameter sub-sample core was taken from each box corer sample for the measurement of the sediment chemical and sedimentological characteristics. The fauna from the remaining box corer content were sorted (0.0602 m<sup>2</sup>).

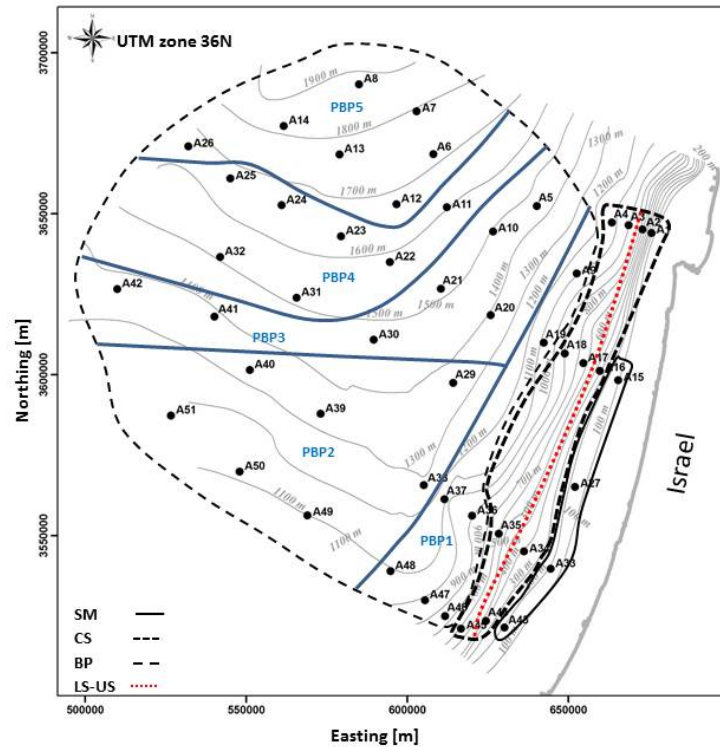
#### Environmental parameters

The 0-1 cm sediment horizons of the three sub-samples at each site were mixed, dried and used for all required sediment-related measurements. A Mastersizer (Malvern, UK) was used to characterize the grain size distribution following the protocol of Crouvi et al. (2008). The samples were characterized by their grain size mode and their clay (<8 µm), silt (8-63 µm), and sand (>63 µm) volume proportions. The upper clay limit (<8 µm) was set following Konert and Vandenberghe (1997). The sediment total organic carbon (TOC) weight percentage was measured from the 0-1 cm sediment horizon by dichromate digestion and potentiometric titration according to Gaudette et al. (1974) with a detection threshold of 0.02%. The sediment CaCO<sub>3</sub> weight percentage was evaluated by reaction with concentrated HCl (Jones and Kaiteris 1983). The water temperatures at three depth ranges, 100-200, 200-1000 and 1000-1900 m were estimated from a large dataset collected from 1980-present off the Mediterranean coast of Israel (<http://isramar.ocean.org.il/isramar2009/>).

#### Faunal sampling and processing

Previous experience at water depths of 40-1900 m off the Israeli coast suggested the effective absence of live infauna below a sediment depth of 7 cm (Hadas Lubinevsky, perscomm); hence, only the 0-

10 cm sediment horizon was sampled in the present study. The samples were processed on a 250- $\mu\text{m}$  mesh size sieve, and the resultant residue was preserved in 99% ethanol on board. In the laboratory, the samples were stained in an ethanol/rose bengal solution of  $\sim 1$  mg/ml and left for



**Fig. 1** - Sampling locations and biotopes identified. The red dotted line designates the division added by the clustering of the NT data. The blue lines delimit the areas of the pooled samples and PBP1-5 are the designations of the pooled samples. SM - shelf margin, US - upper continental slope, LS - lower continental slope, CS - continental slope, BP - bathyal plain.

at least 24 hours prior to further processing. The stained specimens were sorted under a stereoscope and identified to the lowest possible taxonomic rank with the assistance of a group of taxonomists (see acknowledgements). All identified infaunal taxa were included in the subsequent analyses regardless of their status as macrofauna or meiofauna or the Linnaean rank of their identification.

### Statistical methods

Very low specimen counts per sample initially led us to pool the three replicates from each site, corresponding to a sampled site area of  $0.18 \text{ m}^2$ . However, in the case of the BP site data, the specimen counts remained rather low. Consequently, the samples from the 35 deep sites were pooled into groups of seven sites in depth order to yield five “pooled samples”, each having a sampled area

of 1.26 m<sup>2</sup> (Fig. 1 and supplementary Table S1). Following these manipulations, the average specimen counts per site were 403 and 138 individuals, respectively, for the SM and the CS and 99 individuals per pooled sample from the BP.

Differences among univariate sets of faunal and abiotic parameters were tested by ANOVA followed by post hoc pairwise t-tests (Excel, Microsoft) or by the non-parametric Kruskal-Wallis rank sum test with Bonferroni's P value adjustment, followed by the post hoc pairwise Wilcoxon rank sum test with Bonferroni's P value adjustment, using the R software environment. Spearman's rank correlation was used to test the correlation between two univariate variables (R Core Team 2016).

Faunal assemblages were determined by cluster analysis of the quantitative sample data (specimen counts normalized to the area sampled). Both non-transformed (NT) and square root (SR)-transformed sample profiles were subjected to the PRIMER-v7 (Clarke et al. 2014; Clarke and Gorley 2015) and PERMANOVA+ (Anderson et al. 2008) software packages. The Bray-Curtis similarity measure was applied to both the NT- and SR-transformed data matrices. Sample clusters were visualized using a dendrogram that was created by applying the group average clustering method and relative differences among samples were visualized by the nMDS ordination. The resultant clusters were tested by pairwise PERMANOVA (applying a maximum of 10,000 permutations and using the Monte Carlo correction) to test for significant differences among the identified assemblages. The bottom area encompassing a significantly different faunal assemblage was termed a biotope.

The Chao-Sørensen similarity index between samples at a scale of 0 (no similarity) to 1 (complete identity) (Chao et al. 2005) was calculated by the EstimateS 9.1.0 software package (Colwell 2013), evaluating the homogeneity of the faunal assemblages of each biotope by averaging the Chao-Sørensen similarity values obtained for each pair of compared samples. The entropy Shannon "number equivalents" ( $\exp(\text{gamma diversity}) - \exp(\text{alpha diversity})$ ) were calculated to evaluate the beta diversity values in different biotopes following the approach of Jost (2007; equations 17a-c), also a measure of heterogeneity within each biotope.

The EstimateS 9.1.0 software was used also to evaluate the relationships between alpha diversity and the sampled area or the number of sampled individuals using rarefaction analysis. The estimated series of alpha diversity values enables diversity comparisons between biotopes based on a common number of sampled individuals or number of samples. The sample size or the number of samples which is related to an asymptotic value of alpha diversity signifies a sufficient sampling effort to represent the examined biotope. Rarefaction was also used to determine the maximal estimated number of taxa in each biotope (Colwell et al. 2012).

A matrix of the abiotic parameters sampled at each site was constructed: water depth, TOC%, CaCO<sub>3</sub>%, grain size mode, clay%, and clay+silt%. These variables were rescaled prior to assessing

their potential correlations with faunal composition (SR-transformed data) using the BIOENV program (Clarke and Ainsworth 1993; PRIMER v7). The analyses were based on the Bray-Curtis similarity of faunal composition and on Euclidean distance measures for the abiotic variables.

## Results

### Faunal variation

A total of 232 taxa were identified; 92 were identified to the species level, 86 to the genus level, 37 to the family level, and 17 to higher taxonomic levels. Three assemblages were identified by the analysis of the SR-transformed faunal composition (Fig. 2A): the shelf margin (SM), the continental slope (CS), and the bathyal plain (BP). Analysis of the NT data divided the CS into two units, the upper (US) and the lower slope (LS) (Fig. 2B). The nMDS presentation of the similarity among samples is presented in Fig. 3. Supplementary Table S2 provides primary data on the infauna of each assemblage, and average biotope-specific biotic characteristics are presented in Table 1.

The relationship between faunal density and water depth at each sampled site is presented in Fig. 4, described by a log-linear function. Significant variation in the infaunal density was detected among all of the biotopes (ANOVA, post hoc multiple t-tests, log-transformed data, Table 1).

The maximal numbers of taxa per biotope and their 95% confidence limits were estimated using two rarefaction analyses in relation to the number of samples and the number of sampled individuals. The results are presented in Fig. 5A, B. As not all the sampled individuals were identified to the species level, the obtained maximal numbers of taxa represent a minimum number of species. The alpha diversity values calculated by both rarefaction methods within the range of the actual samples or number of sampled individuals are presented in Fig. 6.

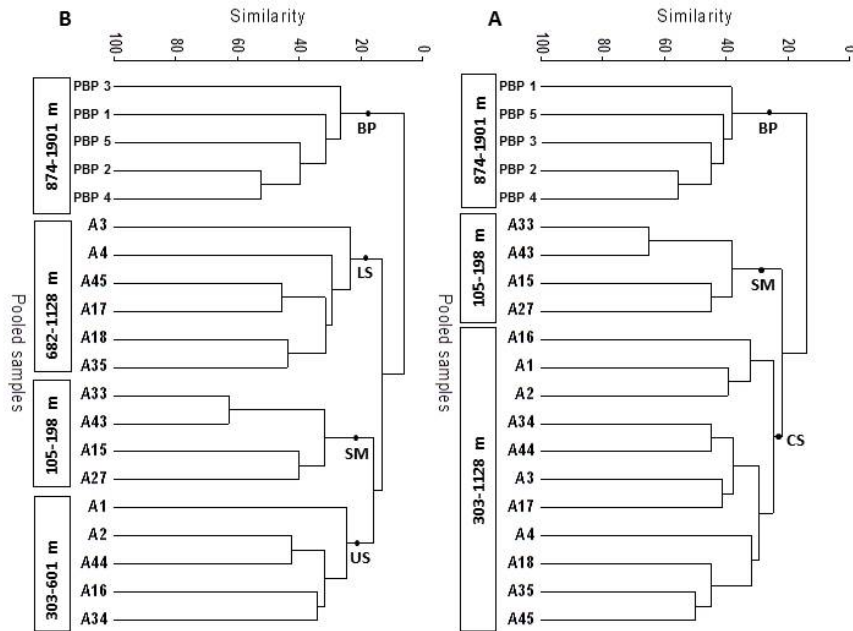
Two approaches were followed to evaluate the heterogeneity within each biotope, the average Chao-Sørensen similarity index and the beta diversity, presented in Table 1.

### Environmental variation

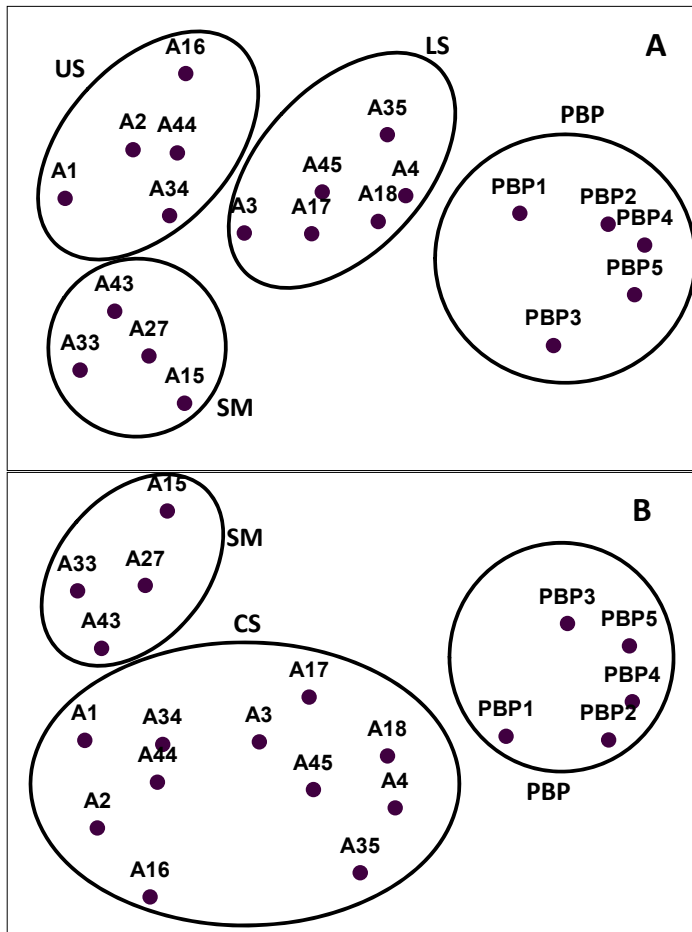
Table 2 presents the average values for the available environmental parameters in each of the identified biotopes and general biotope characteristics, size, depth and multi annual temperature regime which were at the LB minimum for the CS and the BP. The BP values of the CaCO<sub>3</sub>% and the sediment mode were significantly different from their values in the other two biotopes. Other parameters revealed minor differences or no differences at all.



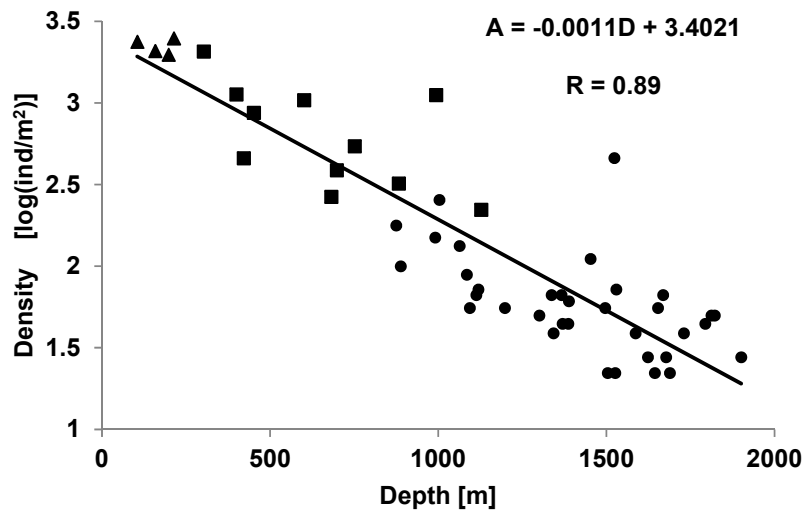
Two parameters, water depth and grain size mode, were significantly correlated with faunal composition (Table 3). No such correlation was observed for the other four parameters, tested individually, but certain tests of these latter parameters in concert with other ones, revealed significant correlations. Water depth revealed the strongest rank correlation of a single parameter with sample faunal composition (Rho of 0.78). Water depth, CaCO<sub>3</sub>%, and clay% revealed the strongest rank correlation of multiple parameters (Rho of 0.81).



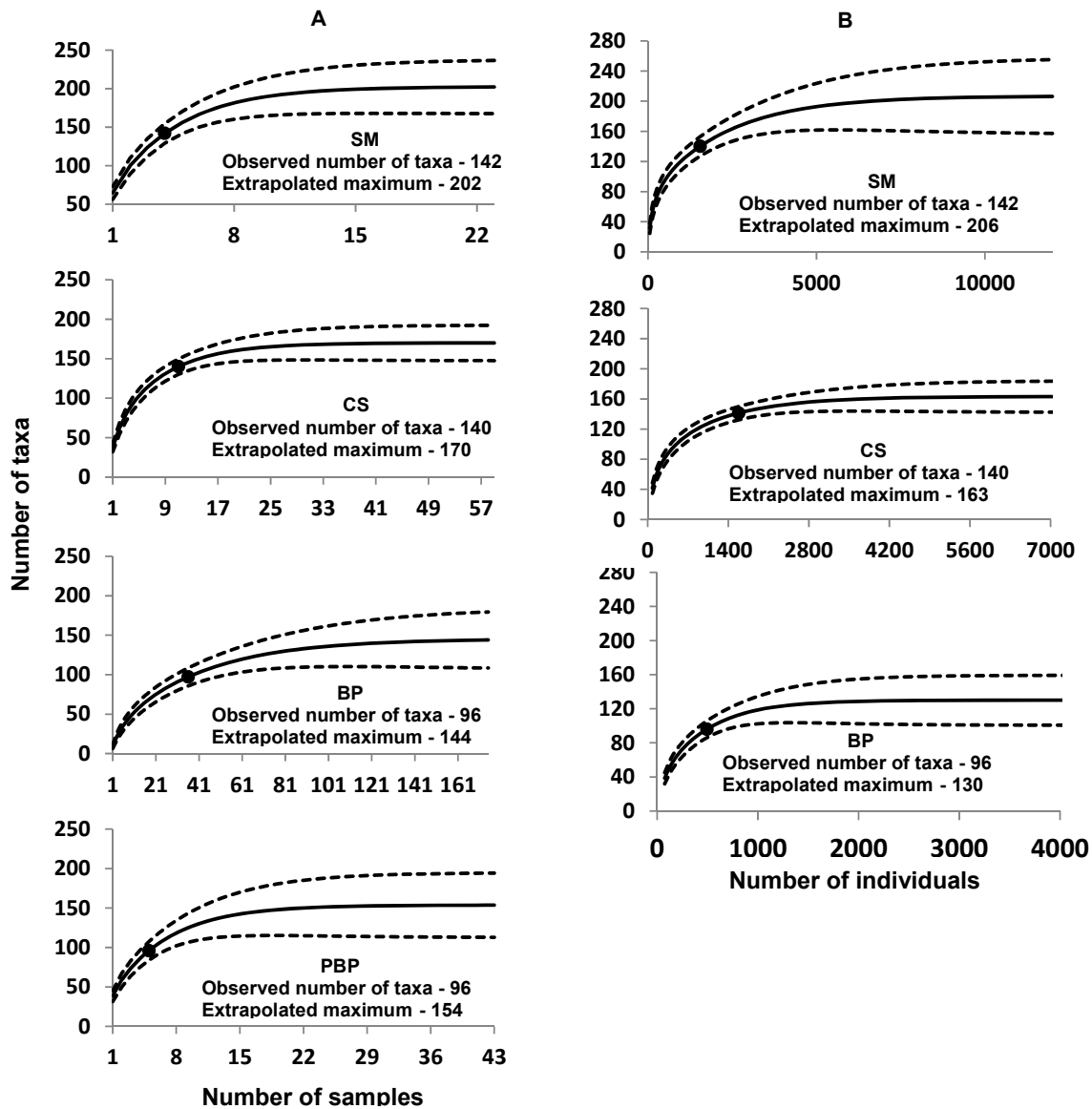
**Fig. 2** - Cluster analysis of (A) - SR-transformed, and (B) - non-transformed sample profiles based on Bray-Curtis similarity index and group average clustering. The black dots label roots of statistically significant clusters (in A, pairwise PERMANOVA,  $t$  statistic(7-9)=1.86-2.53,  $P(\text{MC})=0.0019-0.0011$ ; B, pairwise PERMANOVA,  $t$  statistic(7-13)=1.83-2.74,  $P(\text{MC})=0.0005-0.003$ ). SM - shelf margin, US - upper continental slope, LS - lower continental slope, CS - continental slope, BP - bathyal plain. Depth ranges of the assembled samples are depicted in the vertical framed rectangles.



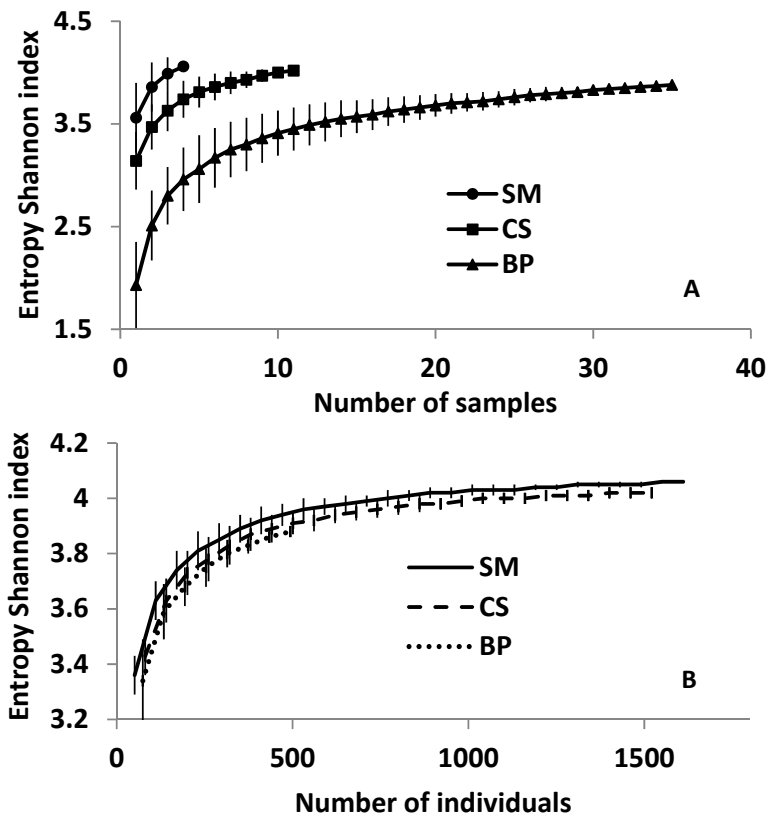
**Fig. 3** - nMDS analysis of (A) - non-transformed, and (B) - SR-transformed sample profiles. The ellipses label roots of statistically significant clusters (see Fig. 2). SM - shelf margin, US - upper continental slope, LS - lower continental slope, CS - continental slope, PBP - bathyal plain, pooled samples.



**Fig. 4** - Regression of log infaunal density on water depth. A -  $\log(\text{density})$ , D - water depth (m), R - correlation coefficient. SM - Triangles, CS - rectangles, BP - circles.



**Fig. 5** – Rarefied, intrapolated and extrapolated number of taxa in the three identified biotopes related to the number of samples (A) and to the numbers of sampled individuals (B). The black dot in each graph designates the last actually sampled site or the actual number of individuals sampled. Black line - the estimated number of taxa, dashed lines - 95% confidence limits. SM - shelf margin, CS - continental slope, BP - bathyal plain, PBP - BP pooled samples.



**Fig. 6** - The relationships between the estimated Shannon alpha diversity index related to the number of samples (A) and to the number of sampled individuals (B). SM - shelf margin, CS - continental slope, BP - bathyal plain. The vertical thin lines are estimated standard deviations.

Table 1 - Characteristics of the faunal assemblages in the three biotopes

<sup>a</sup> Biotope	Depth range [m]	number of pooled or non-pooled samples	Number of sampled individuals	<sup>b</sup> Density [geometric mean of the number of individuals /m <sup>2</sup> ]	Number of biotope-specific taxa	<sup>c</sup> Chao-Sørensen - similarity index	<sup>d</sup> The “number equivalents” of the Beta diversity [entropy Shannon index]
SM	105-198	4	1611	*2220	57	0.7±0.15	1.73
CS	303-1128	11	1521	*610	37	0.64±0.17	2.77
BP	874-1901	35	494	*59	29	*0.26±0.23	6.27
PBP	874-1901	5	494	*59	29	0.7±0.15	1.96

<sup>a</sup> SM - shelf margin, CS -continental slope, BP - Bathyal plain, PBP - pooled bathyal plain samples.

<sup>b</sup> Values designated by asterisk are significantly different from all others (one way ANOVA of log-transformed values,  $F = 87.8$ ,  $df = 2$ ,  $P = 1.34 \cdot 10^{-16}$  followed by a post-hoc Pairwise t-tests with  $P < 0.0011$ ).

<sup>c</sup> Values designated by asterisk are significantly different from all others (Kruskal-Wallis rank sum test with the Bonferroni P value adjustment, chi-squared = 125.66,  $df = 3$ ,  $p\text{-value} < 2.2e-16 \cdot 10^{-16}$  followed by a post-hoc pairwise Wilcoxon rank sum tests with  $P < 0.0015$ ).

<sup>d</sup> Calculated according to Jost (2007; equations 17a-c).

Table 2 - Abiotic characteristics of the three biotopes

<sup>a</sup> Biotope	Depth range [m]	Number of samples	Biotope area [km <sup>2</sup> ]	<sup>b</sup> Temperature [°C]	<sup>c</sup> TOC [%]	<sup>c</sup> CaCO <sub>3</sub> [%]	<sup>c</sup> Sediment mode [μm]	<sup>c</sup> Sediment clay fraction [%]	<sup>c</sup> Sediment clay+silt fraction [%]
SM	105-198	4	650	16.5 ± 0.7	0.99 ± 0.22	7.79 ± 0.63	7.53±0.46	<sup>a</sup> 47.3±1.2	95.6±2.1
CS	303-1128	11	2500	13.9 ± 0.4	<sup>1</sup> 0.81 ± 0.18	7.93 ± 1.15	6.44±0.63	60.4±6.3	98.6±2
BP	875-1901	35	19400	13.6 ± 0.1	<sup>1</sup> 0.75 ± 0.11	*23.54 ± 10.29	*4.89±0.55	<sup>a</sup> 66.1±4.5	96.8±2.8

<sup>a</sup> SM - shelf margin, CS -continental slope, BP - Bathyal plain.

<sup>b</sup> The multiannual average temperature in each habitat was calculated from 67,717, 270,022 and 90,644 temperature measurements taken off the Israeli coast of the Mediterranean roughly within the MS, CS and BP depth ranges, respectively, between the years 1980-present.

<sup>c</sup> Values designated by asterisk are significantly different from all others. Values which are designated by superscript numbers are significantly different from each other. (Kruskal-Wallis rank sum tests with Bonferroni P adjustment, P<0.01 followed by post-hoc pairwise Wilcoxon rank sum tests with P < 0.01).

Table 3 – Spearman’s rank correlations between combinations of abiotic parameters and faunal assemblages (BIOENV analysis, PRIMER-v7)

Significant Rho value		Rho>0.526
Abiotic parameter	Significant Rho tested alone	Maximal Rho value in concert with other parameters
Depth ([m]	0.784	0.811 - with CaCO <sub>3</sub> and Clay
Grain Size mode [µm]	0.631	0.761 - with CaCO <sub>3</sub> and Clay
CaCO <sub>3</sub> [%]	Rho<0.526	0.759 - with Clay
Clay [%]	Rho<0.526	0.759 - with CaCO <sub>3</sub>
Clay+silt [%]	Rho<0.526	Always reduces Rho when added
Total Organic carbon [%]	Rho<0.526	0.537 - with Clay

## Discussion

### General

This study is the first to comprehensively sample the benthic infauna of the LB in the southeastern Mediterranean and to examine the correlations between three defined biotopes and environmental parameters. The Levantine Basin is the warmest, saltiest, and least productive area in the Mediterranean. It should be noted that the studied area did not encompass the deepest part of the LB (>2000 m) and is characterized by a relatively shallow CS in comparison to many other Mediterranean CSs. The density in the studied area is low and logarithmically decreases with depth. The Shannon diversity index rarified according to the largest mutually sampled area unit (4 samples) also decreased with increasing depth, assumedly due to the decreasing density. However, almost no change in the Shannon index was observed among the biotopes rarified to the unit of sampled individuals (494 ind). The biotopes identified are clearly water depth-related, but their distributions are likely governed by a suite of depth-related factors rather than exclusively water depth per se. These parameters include the characteristics of the fine sediment grain fraction and the sediment CaCO<sub>3</sub> percentage but are hypothesized also to include local bottom terrain variables and the quantity and quality of food sources.

### Faunal assemblages

Three significantly different faunal assemblages were identified here using the SR-transformed abundance profile of the various samples. Repeating the analysis with the NT data enabled the

division of the CS assemblage into two depth-related ones, likely due to the different densities of several taxa between the two parts of the CS and slight differences in the faunal composition. The CS assemblage was demonstrated to be more heterogeneous than the SM and the BP by its relatively high beta diversity (Table 1) and by the larger differences among its samples as demonstrated by the nMDS presentation distances, both indicating the potential existence of more than one assemblage (Fig. 2; NT data). The differences among the faunal compositions in the various biotopes are also demonstrated by the high number of biotope-specific taxa, 53% of the total number. A study by Tselepides et al. (2000) along the north coast of Crete was conducted considering a bottom terrain and depth range that were similar to those of the present studied area. Their study revealed similar biotopes to those of the present one, located at similar depths, 100-200 m (comparable to the present shelf margin), 540-940 m (continental slope) and 1570 m (bathyal plain).

The present assessment of faunal assemblages was based on data of variable taxonomic resolution and that crossed the traditional boundaries of meio- and macrobenthos. The representation of faunistic groups containing individuals that cross the sieving threshold distorts the abundance profile of certain taxa but on the other hand is assumed to enhance the power of distinction among biotopes, providing more comprehensive data. The identification of fauna to the species level was not always achieved, and it was assumed that identification to higher taxonomic levels reduces the distinctions among faunal assemblages but would not introduce any false distinctions. Bett and Narayanaswamy (2014) previously assessed the influence of taxonomic level on the ecological assessment of deep-sea macrobenthos, noting that genus-level alpha and beta diversity measures were highly correlated to and are good predictors of their species-level equivalents. They further argued that given the complexity of the West Shetland slope environment, it may be reasonable to expect these conclusions to hold for other deep-sea environments. We suggest that the ecological coherence of our results generally support this approach. Nevertheless, the need to improve taxonomic accuracy in ecological studies using both conventional and genetic approaches is evident.

### Faunal density

The infaunal density logarithmically declined with water depth (Fig. 4). Table 4 presents density data from the present study along with those from three previous studies in the eastern Mediterranean (Tselepides et al. 2000; Kröncke et al. 2003; Baldrighi et al. 2014). Comparisons among these studies are hampered by the different years of sampling, low sample numbers, and different sieve mesh sizes, permitting only general conclusions: (a) a well-established exponential decline in faunal density with water depth (Fig. 4 and Tselepides et al. (2000)); (b) relatively low densities (100s -1000s ind m<sup>-2</sup> on the continental slope and 10s - 100s ind m<sup>-2</sup> on the bathyal plain); (c) consistently higher values



observed by Kröncke et al. (2003) in comparison to those found in the present study and those of Baldrighi et al. (2014) may reflect temporal changes; (d) no obvious west-east faunal density reduction in the LB was observed, applicable at the scale of the entire Mediterranean (Sardà et al. 2004; Baldrighi et al. 2014).

Table 4 - Selected comparable parameters related to faunal assemblages in the Eastern Mediterranean

Citation	Sampling year	Sampling site designation in the article	Depth [m]	Lower threshold mesh size [ $\mu\text{m}$ ]	Density [Ind/m <sup>2</sup> ]	Number of taxa
West to Israel						
<sup>a</sup> Present study	2013	A4	1128	250	221	26
Kröncke et al. (2003)	1993	35	1024	500	1240	29
Present study	2013	A5	1453	250	111	11
Kröncke et al. (2003)	1993	36	1522	500	324	3
Present study	2013	A26	1678	250	28	5
Kröncke et al. (2003)	1993	37	1875	500	162	6
South to Crete						
Baldrighi et al. (2014)	2008	EM1	1237	300	199	18
Kröncke et al. (2003)	1993	18	1431	500	582	15
Baldrighi et al. (2014)	2008	EM2	1907	300	37	4
North of Crete						
Tselepides et al. (2000a)	1995	A-E2	200	500	<sup>b</sup> ~800	~33
Tselepides et al. (2000a)	1995	A-E5	700	500	~500	~22
Tselepides et al. (2000a)	1995	A-E7	1570	500	191	~10

<sup>a</sup> Pairs of samples highlighted by the same background are comparable, sampled at adjacent sites.

<sup>b</sup> ~ - Values estimated from a graph.

It has been indicated on a global scale that specific biotic groups display different density proportions along an increasing depth gradient accompanied by a smaller size and lower biomass of individuals, namely, the larger megafauna and macrofauna are replaced by smaller meiofaunal species. This leads to a faunal change into denser communities containing taxa that are smaller-sized but more adaptable to shortages in available food and its differential availability to different biotic groups (Rex et al. 2006; Wei et al. 2010). The global-scale findings are also supported by the foraminiferal density demonstrated in the framework of the present sampling effort, showing only minor density changes in the various biotopes (Orit Hyams-Kaphzan and Ahuva Almogi-Labin, unpubl data).

Primary production in the eastern Mediterranean is rather low, e.g., 59 g C m<sup>-2</sup> y<sup>-1</sup> recorded in the Cretan Sea (Siokou-Frangou et al. 2010), with export flux through the water column likely declining exponentially with water depth (Marsay et al. 2015). Hence, Danovaro et al. (1999) reported for the Cretan Sea flux values of 1-2 g C m<sup>-2</sup> yr<sup>-1</sup> at 1540 m water depth. This latter study evaluated a 10% contribution of vertically transported labile carbon to the deep water in the western Mediterranean compared to 2-3% in the Cretan trough. The low rate of vertical sedimentation described in the LB supports the low vertical supply of particulate organic matter from the euphotic zone. Van Santvoort et al. (1996) demonstrated for the deep eastern Mediterranean, >2000 m depth, 3 cm kyr<sup>-1</sup>, converted to 0.0021 g cm<sup>-2</sup> y<sup>-1</sup> using a specific gravity of 0.7 g cm<sup>-3</sup> (Basso et al. 2004). The preliminary results of Schirone et al. (2014) in the present studied area showed a vertical sedimentation rate of 0.08±0.01 g cm<sup>-2</sup> y<sup>-1</sup> in the Israeli CS and even a much lower, non-significant level for its BP. Hence, the above indications of low vertical flux to the LB deep waters may explain at least partially the sharp density decline with depth of the >250 µm infauna. The comparable characteristics of the smaller meiofauna in the studied area are still missing.

Lateral transport from terrestrial or shelf sources across the CS may partially explain the density gradient towards the BP. A phenomenon termed “downwelling” of downhill wintertime currents was reported by Rosentraub and Brenner (2007) and Rosentraub et al. (2010) flowing from the Israeli shelf to the slope down to the 500-m depth contour. In addition, a turbidity current across the CS was indicated to be created by dense water development along continental margins of the LB (Oszoy et al. 1989; Chronis et al. 2000). Transport from the Nile delta by the general counter-clockwise Mediterranean current (Schattner et al. 2015) is another assumed mechanism of lateral transport. Chemo-synthetic bacterial mats were recently found on the CS, estimated to cover 3% of the CS bottom (Rubin-Blum et al. 2014), and may also be considered a potential food source.

The distributions of TOC concentrations on the sediment surface here are quite uniform, and although their small changes are correlated with depth (Table 5), they are unlikely to explain the huge differences in biotope densities. This difference is likely caused by labile carbon and its availability to different biotic groups, which should be evaluated in the future. The TOC percentages found in this study are in agreement with previously presented levels, which are twice those found on the western side of the LB (Romankevich 1984).

Table 5 - Spearman's rank correlations of abiotic parameters with depth [m]

Abiotic parameter	Spearman's Rho in	P value
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	relation with depth	
Grain Size mode [ $\mu\text{m}$ ]	-0.806	2.2E-16
CaCO <sub>3</sub> [%]	0.796	2.2E-16
Total Organic carbon [%]	-0.606	5.14E-06
Clay [%]	0.396	4.72E-3
Clay+silt [%]	-0.374	7.47E-3

## Faunal diversity

Assumed faunal assemblage uniformity within each of the biotopes underlies the comparison of a variety of ecological aspects among them. The area required to fully represent a biotope's fauna depends on the faunal density. However, within-biotope variation at different spatial scales may also exist, increasing the required representative area. The pooling of the BP samples demonstrates the effect of density. The increased representative area reduced the heterogeneity of the pooled samples, as demonstrated by the increased Chao-Sørensen and decreased beta diversity indices (Table 1). Higher within-biotope heterogeneity in the CS in comparison to other biotopes is indicated by its higher beta diversity and by the larger area for CS in the nMDS representation (Fig. 3), leading also to the separation of the CS into two biotopes when using the NT data. Within-biotope heterogeneity is a well-documented phenomenon even in communities with much higher population densities than the present one (Grassle and Maciolek 1992). The existence of natural patchiness resulting from the presence of a variety of micro-habitats in an apparently uniform muddy bottom is well established in the deep-sea literature (Grassle and Morse-Porteous 1987; Grassle and Maciolek 1992; Snelgrove et al. 1992; Gage 2004 and literature therein).

The relationships between alpha diversity and the number of sampled individuals indicates high alpha diversity similarity across biotopes, as the three biotope-specific curves overlap and reach a mutual asymptote at least for the SM and the CS and partially for the BP (Fig. 6B). However, a different sampling area is required in each biotope to approach this asymptotic level (Fig. 6A), likely due to the lower densities in deeper waters. However, this analysis needs to be interpreted with caution, as the ranges of both the sampling area and the number of sampled individuals are incomplete in the rarified alpha diversity curves. Hence, it is not known if all curves of the sample-dependent alpha diversity would reach a common asymptote similar to the one of the number of individuals-dependent alpha diversity of the CS and SM curves. It is also doubtful that the rarified alpha diversity level in the number of individuals-dependent BP curve would maintain its overlap with the curves of the SM and the CS at higher numbers of sampled individuals. This doubt is

supported by the different estimated maximal numbers of taxa in the various biotopes (Fig. 5), which may lead to different asymptotic alpha diversity values.

Tselepides et al. (2000) presented taxa accumulation curves for their various sampled depth ranges. Their 23 samples did not reach an asymptote, and the expected number of taxa reached ~160 taxa in the SM, ~100-130 in the CS and ~60 in the BP, revealing a similar trend to that observed in the present study, showing a decreasing number of species with increasing depth. The alpha diversity in the study by Tselepides et al. (2000) declined with depth, similar to the present observed results; these results are compatible with the general trend in Mediterranean alpha diversity with depth (Danovaro et al. 2010). However, the study by Tselepides et al. (2000) lacks the evaluation of estimated alpha diversity, with its above-indicated similarity when rarified to the number of sampled individuals. The limited sampling effort of both Kröncke et al. (2003) and Baldrighi et al. (2014) at the relevant sites (Table 4), in addition to the other above-mentioned differences in identification accuracy, size threshold and sampling date, permits only a general statement claiming a roughly similar number of sampled taxa.

#### Ecology of the region

Two approaches were applied to examine the potential correlations between abiotic parameters and changes in the composition of the fauna: sample-wise (Table 3) and biotope-wise (Table 2). The sample-wise approach revealed water depth as the major correlated parameter, which is also evident from observing the depth-related distribution of the biotopes (Figs. 1, 2). However, it is likely not water depth per se (hydrostatic pressure) that is responsible for this correlation but a number of underlying parameters that co-vary with depth. Sediment is widely recognized to be a strong driver of infaunal ecology, both generally (Gray 1974) and in the deep sea (Etter and Grassle 1992), although it may be a complex relationship (Snelgrove and Butman 1994). In the present study, in addition to water depth, the grain size mode showed significant correlation with the sample biotic profiles. Percentage clay and CaCO<sub>3</sub>% in concert increased the rank correlation of both water depth and grain size mode with the faunal composition (Table 3). Table 5 provides the Spearman's rank correlation between all the abiotic parameters and depth. Although all five examined abiotic parameters demonstrated a significant rank correlation with depth, only the grain size mode, the CaCO<sub>3</sub>% and the TOC% revealed strong correlations with depth. The importance of the effect of the TOC percentage on biotope densities is discussed above. The higher percentage of CaCO<sub>3</sub> in the BP results from the higher biogenic content of planktonic foraminifera and pteropod shells (Elyashiv et al. 2014). The siliciclastic and less biogenic, closer-to-shore sediment originated from the sediment province formed by the Nile sediment transportation (Maldonado and Stanley 1976).

The three biotopes are related to three different bottom terrains; this strong affiliation is supported by several preliminary sedimentological indications that led us to put forward a working hypothesis for future studies suggesting that bottom sediment stability is a determining factor of faunal composition, with a much less stable CS in comparison to the SM and the BP. Sediment stability is generally a result of its fluidity, mixing processes, bottom inclination and overlying currents. Preliminary results reported higher sediment water content in the slope region of the studied area in comparison to both the shelf margin and the bathyal plain (Barak Herut, unpubl data).

Barsanti et al. (2011) studied and reviewed the sediment mixing processes in the Mediterranean deep sea (>2000 m) and in the LB, they found mixing processes mainly in the upper 2 cm caused by bioturbation. Bottom mixing was preliminarily examined in the SM, CS and BP of the present studied area by Schirone et al. (2014) using the  $^{210}\text{Pb}$  and  $^{137}\text{Cs}$  radionuclide and metal contaminant depth profiles. The present studied bottom area is much shallower than the bottom examined in Barsanti et al. (2011) and the results demonstrated a 2- and 4-cm mixed layer in the SM and the BP, respectively, and a much thicker mixed horizon in the CS. The intensively mixed, and hence less stable, CS bottom is assumed to result from the stronger inclination of the CS in comparison to its neighboring provinces coupled with the downhill currents and gravitational slides described and discussed above. Interestingly, one of the LB sites examined by Barsanti et al. (2011) in the much deeper mid-slope near Rhodes revealed a 6-cm mixed layer indicated to result from physical factors rather than bioturbation, similar to our interpretation of the results of Schirone et al. (2014) from the Israeli CS.

#### Future research directions

The present study comprehensively characterized the biotic parameters of the >250  $\mu\text{m}$  benthic fauna of the southeastern corner of the LB and their assumedly shaping abiotic factors. This is the first detailed study of the benthic ecology of this region, the eastern edge of the Mediterranean west-east axis. Future studies in this area should technically include more accurate faunistics and more intensive sampling in view of the low infaunal density. Scientifically, the characterization of other benthic faunal communities, mainly those of smaller meiofauna and bacteria are needed, as well as a better characterization of the sediment features that potentially affect the faunal composition and density.

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### **Compliance with ethical standards**

#### **Conflict of interest:**

The authors declare that they have no conflict of interest.

#### **Ethical standards:**

All applicable international, national and institutional guidelines for the care and use of animals were followed.

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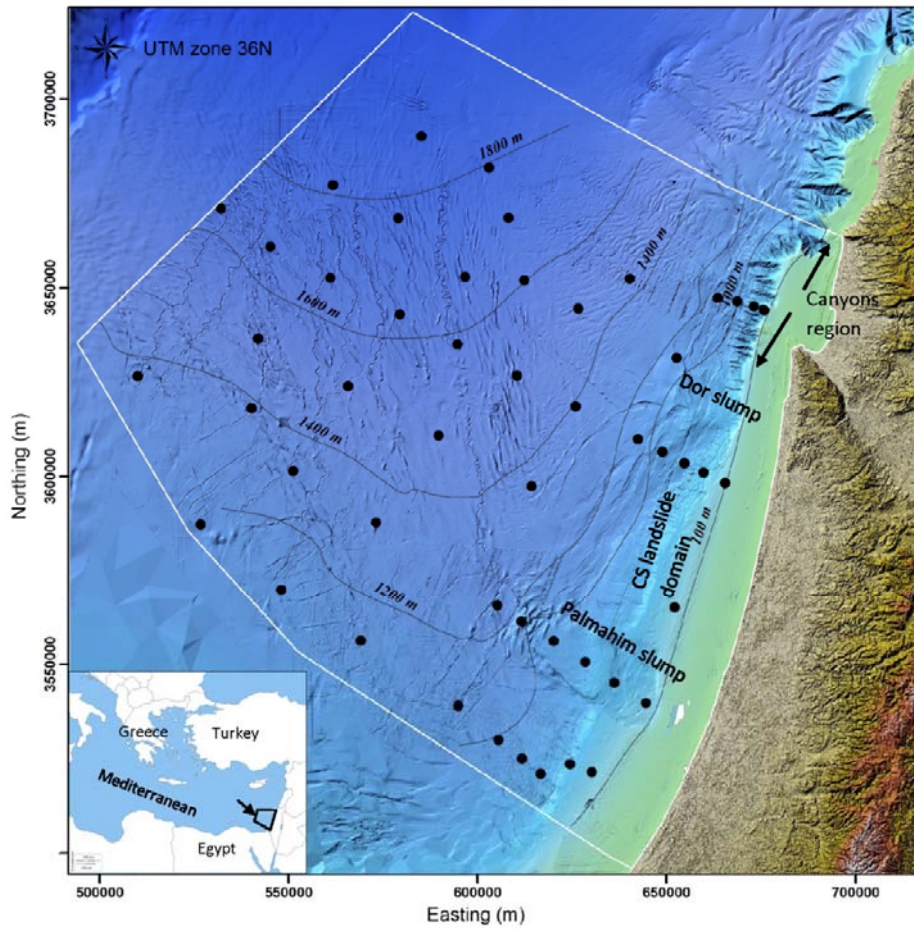
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## נספחים



**Fig. S1** – Bathymetric hillshade map of the Mediterranean deep sea off Israel. The map was copied upon permission from Hall et al. (2015). The white line delimits the studied area. The sites which were sampled during this study were overlaid on the map to show their proximity to features of the bottom terrain. No labels were added to the sampling sites for sake of clarity and they are depicted in Fig. 2. CS - continental slope. The location of the study site within the eastern Mediterranean is marked by an arrow in the inset.

Table S1 - Sampling site IDs and their sampling dates, location (longitude, latitude, degrees and decimal points), depth [m] and biotopes' names. SM - shelf margin, US - upper continental slope, LS - lower continental slope, CS - continental slope, PBP1-5 - bathyal plain pooled samples (Fig. 1).

Site ID	Sampling date	Latitude North [degrees.decimal]	Longitude East [degrees.decimal]	Bottom Depth [m]	Biotope's name	Division of the CS to US and LS as revealed by the cluster analysis of the NT data
A15	6/18/13	32.50915	34.76186	105	SM	
A27	6/26/13	32.21213	34.61426	158	SM	
A33	6/26/13	31.98365	34.5299	214	SM	
A43	7/10/13	31.82122	34.37614	198	SM	
A16	6/18/13	32.53582	34.70177	422	CS	US
A1	6/16/13	32.92022	34.88022	303	CS	US
A2	6/16/13	32.9301	34.85027	601	CS	US
A34	6/26/13	32.0335	34.44307	400	CS	US
A44	7/10/13	31.84061	34.31507	452	CS	US
A4	6/17/13	32.95127	34.74994	1128	CS	LS
A18	6/18/13	32.58682	34.58645	883	CS	LS
A35	6/26/13	32.08417	34.36107	682	CS	LS
A45	7/10/13	31.81884	34.23343	698	CS	LS
A3	6/16/13	32.94198	34.80518	994	CS	LS
A17	6/18/13	32.55835	34.64795	752	CS	LS
A46	7/10/13	31.85524	34.18125	875	PBP1	
A36	6/26/13	32.13511	34.27435	889	PBP1	
A37	6/26/13	32.18269	34.18409	991	PBP1	
A47	7/10/13	31.89999	34.11605	1003	PBP1	
A19	6/18/13	32.61742	34.51763	1063	PBP1	
A9	6/17/13	32.8101	34.63036	1085	PBP1	
A48	7/10/13	31.98254	34.00383	1094	PBP1	
A49	7/10/13	32.14102	33.73207	1113	PBP2	
A50	7/9/13	32.26447	33.5099	1120	PBP2	
A51	7/9/13	32.422	33.28377	1198	PBP2	
A38	6/26/13	32.22232	34.11639	1301	PBP2	
A40	7/8/13	32.54945	33.54486	1337	PBP2	
A39	7/8/13	32.42481	33.77777	1343	PBP2	
A29	6/25/13	32.50828	34.21691	1367	PBP2	
A42	7/9/13	32.77681	33.10673	1370	PBP3	
A20	6/18/13	32.6971	34.34348	1387	PBP3	
A41	7/8/13	32.69912	33.42872	1388	PBP3	
A5	6/17/13	33.00051	34.50117	1453	PBP3	
A10	6/17/13	32.93073	34.35471	1496	PBP3	
A30	6/25/13	32.63119	33.95552	1504	PBP3	
A21	6/19/13	32.77205	34.17918	1524	PBP3	
A31	6/25/13	32.75078	33.70127	1526	PBP4	
A32	7/8/13	32.86613	33.44788	1529	PBP4	
A22	6/19/13	32.84864	34.01176	1587	PBP4	
A11	6/23/13	33.00035	34.20252	1624	PBP4	

A23	6/20/13	32.92207	33.84939	1644	PBP4	
A24	6/20/13	33.01028	33.65298	1653	PBP4	
A25	7/8/13	33.08593	33.48353	1669	PBP4	
A26	7/9/13	33.17673	33.3437	1678	PBP5	
A12	6/19/13	33.01051	34.03511	1689	PBP5	
A6	6/24/13	33.14991	34.15951	1730	PBP5	
A13	6/20/13	33.15169	33.84684	1794	PBP5	
A14	6/24/13	33.23211	33.66236	1812	PBP5	
A7	6/24/13	33.27046	34.10534	1822	PBP5	
A8	6/20/13	33.34743	33.91411	1901	PBP5	

Table S2 - The names of the elucidated taxa, their four-level taxonomic classification: Phylum, Class, Order, Family, their size-related type, their density in each of the biotopes [Number of individuals /m<sup>2</sup>] and the number of samples in which they were present per biotope. SM - continental shelf margin; CS - continental slope; BP - bathyal Plain. Taxonomic assignment was done using the World Register of Marine Species (WoRMS) database (<http://www.marinespecies.org/>).

Taxon	Faunal size-related type	Phylum	Class	Order	Family	Number of individuals /m <sup>2</sup> in each biotope			Number of samples of presence per biotope		
						SM	CS	BP	SM	CS	BP
						4 samples	11 samples	35 samples	4 samples	11 samples	35 samples
Monticellina sp.	Macrofauna	Platyhelminthes	Rhabditophora	Rhabdocoela	Umagillidae	44.30	0	0	4	0	0
Nematoda	Meiofauna	Nematoda				6.92	3.02	1.27	3	4	6
Sipuncula	Macrofauna	Sipuncula				2.77	1.51	1.11	2	3	5
Phascolion strombus strombus	Macrofauna	Sipuncula	Sipunculidea	Golfingiida	Phascolionidae	0	0.50	0	0	1	0
Apionsoma murinae bilobatae	Macrofauna	Sipuncula	Phascolosomatidea	Phascolosomatida	Phascolosomatidae	0	0	0.95	0	0	3
Clitellata	Macrofauna	Annelida	Clitellata			2.77	2.01	1.27	1	1	3
Amphinomidae	Macrofauna	Annelida	Polychaeta	Amphinomida	Amphinomidae	0	0.50	0	0	1	0
Dorvilleidae	Macrofauna	Annelida	Polychaeta	Eunicida	Dorvilleidae	1.38	1.01	0	1	1	0
Protodorvillea sp.	Macrofauna	Annelida	Polychaeta	Eunicida	Dorvilleidae	0	0	0.16	0	0	1
Abyssoninoe sp.	Macrofauna	Annelida	Polychaeta	Eunicida	Lumbrineridae	1.38	0	0.16	1	0	1
Gallardoneris sp.	Macrofauna	Annelida	Polychaeta	Eunicida	Lumbrineridae	12.46	20.64	0	2	10	0
Lumbrineridae	Macrofauna	Annelida	Polychaeta	Eunicida	Lumbrineridae	1.38	0	0	1	0	0
Ninoe sp.	Macrofauna	Annelida	Polychaeta	Eunicida	Lumbrineridae	0	0.50	0	0	1	0
Scoletoma sp.	Macrofauna	Annelida	Polychaeta	Eunicida	Lumbrineridae	0	1.01	0	0	2	0
Drilonereis sp.	Macrofauna	Annelida	Polychaeta	Eunicida	Oeononidae	1.38	0	0	1	0	0
Oeononidae	Macrofauna	Annelida	Polychaeta	Eunicida	Oeononidae	1.38	0	0	1	0	0
Aphroditiformia	Macrofauna	Annelida	Polychaeta	Phyllodocida		0	0	0.32	0	0	2
Glycera lapidum	Macrofauna	Annelida	Polychaeta	Phyllodocida	Glyceridae	15.23	5.03	1.74	4	4	11
Hesionidae	Macrofauna	Annelida	Polychaeta	Phyllodocida	Hesionidae	13.84	1.51	0	3	2	0
Oxydromus sp.	Macrofauna	Annelida	Polychaeta	Phyllodocida	Hesionidae	2.77	0	0	2	0	0
Podarkeopsis sp.	Macrofauna	Annelida	Polychaeta	Phyllodocida	Hesionidae	0	1.01	0	0	2	0

Nephtyidae	Macrofauna	Annelida	Polychaeta	Phyllodocida	Nephtyidae	12.46	2.01	0	2	2	0
Nephtys sp.	Macrofauna	Annelida	Polychaeta	Phyllodocida	Nephtyidae	15.23	0.50	0.32	4	1	2
Ceratocephale loveni	Macrofauna	Annelida	Polychaeta	Phyllodocida	Nereididae	0	12.58	0.16	0	8	1
Pholoe sp.	Macrofauna	Annelida	Polychaeta	Phyllodocida	Pholoidae	2.77	0	0	2	0	0
Ancistrosyllis groenlandica	Macrofauna	Annelida	Polychaeta	Phyllodocida	Pilargidae	1.38	1.51	0.16	1	2	1
Pilargis sp.	Macrofauna	Annelida	Polychaeta	Phyllodocida	Pilargidae	0	0	0.16	0	0	1
Sigambra sp.	Macrofauna	Annelida	Polychaeta	Phyllodocida	Pilargidae	16.61	0	0	3	0	0
Pholoides dorsipapillatus	Macrofauna	Annelida	Polychaeta	Phyllodocida	Sigalionidae	0	0	0.32	0	0	2
Sphaerodoridae	Macrofauna	Annelida	Polychaeta	Phyllodocida	Sphaerodoridae	1.38	0	0	1	0	0
Sphaerodoropsis sp.	Macrofauna	Annelida	Polychaeta	Phyllodocida	Sphaerodoridae	1.38	3.52	1.27	1	3	2
Brania sp.	Macrofauna	Annelida	Polychaeta	Phyllodocida	Syllidae	9.69	12.08	1.90	2	8	8
Eusyllinae	Macrofauna	Annelida	Polychaeta	Phyllodocida	Syllidae	2.77	1.01	0	1	1	0
Exogone sp.	Macrofauna	Annelida	Polychaeta	Phyllodocida	Syllidae	4.15	0	0.16	1	0	1
Sphaerosyllis sp.	Macrofauna	Annelida	Polychaeta	Phyllodocida	Syllidae	5.54	7.05	0.32	1	5	2
Syllis (Eusyllis) cf. hyperioni	Macrofauna	Annelida	Polychaeta	Phyllodocida	Syllidae	1.38	0	0	1	0	0
Syllis sp.	Macrofauna	Annelida	Polychaeta	Phyllodocida	Syllidae	1.38	5.03	0	1	5	0
Galathowenia oculata	Macrofauna	Annelida	Polychaeta	Sabellida	Oweniidae	5.54	0	0.95	1	0	6
Megalomma sp.	Macrofauna	Annelida	Polychaeta	Sabellida	Sabellidae	2.77	0	0	1	0	0
Capitellidae	Macrofauna	Annelida	Polychaeta	Sedentaria (subclass)	Capitellidae	1.38	1.01	1.27	1	2	8
Mediomastus sp.	Macrofauna	Annelida	Polychaeta	Sedentaria (subclass)	Capitellidae	1.38	2.01	0	1	2	0
Neomediomastus sp.	Macrofauna	Annelida	Polychaeta	Sedentaria (subclass)	Capitellidae	0	7.05	0.16	0	4	1
Notomastus sp.	Macrofauna	Annelida	Polychaeta	Sedentaria (subclass)	Capitellidae	4.15	4.53	2.85	2	4	12
Pseudocapitella incerta	Macrofauna	Annelida	Polychaeta	Sedentaria (subclass)	Capitellidae	0	0.50	0.16	0	1	1
Spiochaetopterus sp.	Macrofauna	Annelida	Polychaeta	Sedentaria (subclass)	Chaetopteridae	0	0	0.32	0	0	2
Cossura sp.	Macrofauna	Annelida	Polychaeta	Sedentaria (subclass)	Cossuridae	51.22	1.01	0	2	2	0
Clymenella sp.	Macrofauna	Annelida	Polychaeta	Sedentaria (subclass)	Maldanidae	5.54	0	0	3	0	0
Euclymene sp.	Macrofauna	Annelida	Polychaeta	Sedentaria (subclass)	Maldanidae	0	2.52	0	0	1	0

Maldanidae	Macrofauna	Annelida	Polychaeta	Sedentaria (subclass)	Maldanidae	5.54	1.01	0.16	1	2	1
Metasychis sp.	Macrofauna	Annelida	Polychaeta	Sedentaria (subclass)	Maldanidae	2.77	0	0	1	0	0
Praxillella gracilis	Macrofauna	Annelida	Polychaeta	Sedentaria (subclass)	Maldanidae	2.77	0.50	0	2	1	0
Rhodine sp.	Macrofauna	Annelida	Polychaeta	Sedentaria (subclass)	Maldanidae	8.31	0	0	2	0	0
Opheliidae	Macrofauna	Annelida	Polychaeta	Sedentaria (subclass)	Opheliidae	15.23	6.54	0.47	3	8	3
Ophelina sp.	Macrofauna	Annelida	Polychaeta	Sedentaria (subclass)	Opheliidae	0	0	0.16	0	0	1
Leitoscoloplos sp.	Macrofauna	Annelida	Polychaeta	Sedentaria (subclass)	Orbiniidae	0	0.50	0	0	1	0
Orbiniidae	Macrofauna	Annelida	Polychaeta	Sedentaria (subclass)	Orbiniidae	0	0.50	0	0	1	0
Aricidea (Aedicira) sp.	Macrofauna	Annelida	Polychaeta	Sedentaria (subclass)	Paraonidae	106.59	0	0	4	0	0
Aricidea (Allia) antennata	Macrofauna	Annelida	Polychaeta	Sedentaria (subclass)	Paraonidae	15.23	0	0	1	0	0
Aricidea (Allia) monicae	Macrofauna	Annelida	Polychaeta	Sedentaria (subclass)	Paraonidae	13.84	9.06	0	3	3	0
Aricidea (Aricidea) wassi	Macrofauna	Annelida	Polychaeta	Sedentaria (subclass)	Paraonidae	22.15	2.01	0	2	3	0
Aricidea sp.	Macrofauna	Annelida	Polychaeta	Sedentaria (subclass)	Paraonidae	13.84	24.67	0.47	3	8	3
Cirrophorus branchiatus	Macrofauna	Annelida	Polychaeta	Sedentaria (subclass)	Paraonidae	0	0.50	0	0	1	0
Cirrophorus sp.	Macrofauna	Annelida	Polychaeta	Sedentaria (subclass)	Paraonidae	0	1.51	0	0	3	0
Levinsenia sp.	Macrofauna	Annelida	Polychaeta	Sedentaria (subclass)	Paraonidae	30.45	33.22	0	3	10	0
Paraonidae	Macrofauna	Annelida	Polychaeta	Sedentaria (subclass)	Paraonidae	102.44	12.08	3.01	4	8	10
Paraonides sp.	Macrofauna	Annelida	Polychaeta	Sedentaria (subclass)	Paraonidae	0	0	0.16	0	0	1



Apistobanchus sp.	Macrofauna	Annelida	Polychaeta	Spionida	Apistobanchidae	1.38	0	0	1	0	0
Heterospio mediterranea	Macrofauna	Annelida	Polychaeta	Spionida	Longosomatidae	0	0.50	0	0	1	0
Heterospio sp.	Macrofauna	Annelida	Polychaeta	Spionida	Longosomatidae	0	0	0.16	0	0	1
Magelona sp.	Macrofauna	Annelida	Polychaeta	Spionida	Magelonidae	11.07	0	0	1	0	0
Poecilochaetus sp.	Macrofauna	Annelida	Polychaeta	Spionida	Poecilochaetidae	1.38	0	0	1	0	0
Prionospio sp.	Macrofauna	Annelida	Polychaeta	Spionida	Spionidae	81.67	15.60	0.32	4	6	1
Scolelepis sp.	Macrofauna	Annelida	Polychaeta	Spionida	Spionidae	5.54	0	0	2	0	0
Spionidae	Macrofauna	Annelida	Polychaeta	Spionida	Spionidae	31.84	15.60	3.96	4	8	16
Spiophanes sp.	Macrofauna	Annelida	Polychaeta	Spionida	Spionidae	5.54	27.69	0.95	3	8	5
Acrocirridae	Macrofauna	Annelida	Polychaeta	Terebellida	Acrocirridae	0	0	0.47	0	0	3
Ampharetinae	Macrofauna	Annelida	Polychaeta	Terebellida	Ampharetidae	2.77	0.50	0	1	1	0
Amphicteis sp.	Macrofauna	Annelida	Polychaeta	Terebellida	Ampharetidae	8.31	0	0	1	0	0
Anobothrus gracilis	Macrofauna	Annelida	Polychaeta	Terebellida	Ampharetidae	0	2.01	0	0	3	0
Melinna sp.	Macrofauna	Annelida	Polychaeta	Terebellida	Ampharetidae	0	0.50	0	0	1	0
Aphelochaeta sp.	Macrofauna	Annelida	Polychaeta	Terebellida	Cirratulidae	1.38	0	0	1	0	0
Cirratulidae	Macrofauna	Annelida	Polychaeta	Terebellida	Cirratulidae	155.04	7.05	1.42	4	3	8
Tharyx sp.	Macrofauna	Annelida	Polychaeta	Terebellida	Cirratulidae	0	0.50	0	0	1	0
Brada sp.	Macrofauna	Annelida	Polychaeta	Terebellida	Flabelligeridae	0	0.50	0	0	1	0
Pectinaria sp.	Macrofauna	Annelida	Polychaeta	Terebellida	Pectinariidae	0	1.01	0	0	2	0
Sternaspis sp.	Macrofauna	Annelida	Polychaeta	Terebellida	Sternaspidae	52.60	0.50	0	3	1	0
Amaeana sp.	Macrofauna	Annelida	Polychaeta	Terebellida	Terebellidae	0	0	0.16	0	0	1
Terebellidae	Macrofauna	Annelida	Polychaeta	Terebellida	Terebellidae	0	1.51	1.42	0	1	9
Terebellides stroemii	Macrofauna	Annelida	Polychaeta	Terebellida	Trichobanchidae	8.31	1.51	0.63	2	3	3
Trichobanchidae	Macrofauna	Annelida	Polychaeta	Terebellida	Trichobanchidae	0	0	0.16	0	0	1
Ostracoda	Macrofauna	Arthropoda	Ostracoda			29.07	17.62	0.95	4	7	5
Phoxichilidiidae	Macrofauna	Arthropoda	Pycnogonida	Pantopoda	Phoxichilidiidae	4.15	0.50	0	1	1	0
Copepoda	Macrofauna	Arthropoda	Copepoda (subclass)			0	0	0.16	0	0	1
Harpacticoida	Meiofauna	Arthropoda	Copepoda (subclass)	Harpacticoida		12.46	9.06	2.21	3	6	8
Aegisthidae	Meiofauna	Arthropoda	Copepoda (subclass)	Harpacticoida	Aegisthidae	15.23	10.07	0	2	4	0
Cervinia bradyi	Meiofauna	Arthropoda	Copepoda (subclass)	Harpacticoida	Aegisthidae	44.30	67.45	8.54	3	2	1
Cerviniella talpa	Meiofauna	Arthropoda	Copepoda (subclass)	Harpacticoida	Aegisthidae	55.37	4.03	0.63	3	4	2

Cerviniopsis sp.	Meiofauna	Arthropoda	Copepoda (subclass)	Harpacticoida	Aegisthidae	26.30	24.67	0.32	3	6	1
Argestidae	Meiofauna	Arthropoda	Copepoda (subclass)	Harpacticoida	Argestidae	0	2.01	0.63	0	2	4
Argestidae sp2	Meiofauna	Arthropoda	Copepoda (subclass)	Harpacticoida	Argestidae	0	1.51	1.27	0	3	4
Eurycletodes oblongus	Meiofauna	Arthropoda	Copepoda (subclass)	Harpacticoida	Argestidae	0	1.01	0	0	2	0
Mesocletodes sp.	Meiofauna	Arthropoda	Copepoda (subclass)	Harpacticoida	Argestidae	0	3.52	0.32	0	6	2
Elanella haifensis	Meiofauna	Arthropoda	Copepoda (subclass)	Harpacticoida	Canuellidae	6.92	0	0	2	0	0
Scottolana sp.	Meiofauna	Arthropoda	Copepoda (subclass)	Harpacticoida	Canuellidae	8.31	0	0	2	0	0
Dactylopodopsis sp.	Meiofauna	Arthropoda	Copepoda (subclass)	Harpacticoida	Dactylopusiidae	0	7.05	3.16	0	6	13
Ectinosomatidae	Meiofauna	Arthropoda	Copepoda (subclass)	Harpacticoida	Ectinosomatidae	27.69	9.56	1.11	3	3	1
Halectinosoma sp.	Meiofauna	Arthropoda	Copepoda (subclass)	Harpacticoida	Ectinosomatidae	2.77	0.50	0	2	1	0
Microsetella norvegica	Meiofauna	Arthropoda	Copepoda (subclass)	Harpacticoida	Ectinosomatidae	1.38	0	0	1	0	0
Longipedia sp.	Meiofauna	Arthropoda	Copepoda (subclass)	Harpacticoida	Longipediidae	4.15	1.51	0	1	2	0
Miraciidae	Meiofauna	Arthropoda	Copepoda (subclass)	Harpacticoida	Miraciidae	0	1.01	0	0	2	0
Typhlamphiascus typhlops	Meiofauna	Arthropoda	Copepoda (subclass)	Harpacticoida	Miraciidae	1.38	1.01	0	1	2	0
Danielsseniinae	Meiofauna	Arthropoda	Copepoda (subclass)	Harpacticoida	Pseudotachidiidae	0	2.01	0	0	1	0
Paranannopus sp.	Meiofauna	Arthropoda	Copepoda (subclass)	Harpacticoida	Pseudotachidiidae	0	3.02	0	0	2	0
Pseudotachidius coronatus	Meiofauna	Arthropoda	Copepoda (subclass)	Harpacticoida	Pseudotachidiidae	0	12.08	0.16	0	4	1
Thalestridae	Meiofauna	Arthropoda	Copepoda (subclass)	Harpacticoida	Thalestridae	22.15	5.03	2.06	1	4	4

Amphipoda	Macrofauna	Arthropoda	Malacostraca	Amphipoda		6.92	1.51	0.32	3	3	2
Ampelisca jaffaensis	Macrofauna	Arthropoda	Malacostraca	Amphipoda	Ampeliscidae	15.23	0	0	3	0	0
Ampelisca sp.	Macrofauna	Arthropoda	Malacostraca	Amphipoda	Ampeliscidae	5.54	0	0	2	0	0
Carangoliopsis spinulosa	Macrofauna	Arthropoda	Malacostraca	Amphipoda	Carangoliopsidae	60.91	14.09	0	3	5	0
Corophium sp.	Macrofauna	Arthropoda	Malacostraca	Amphipoda	Corophiidae	0	0	0.16	0	0	1
Rhachotropis sp.	Macrofauna	Arthropoda	Malacostraca	Amphipoda	Eusiridae	0	0.50	0	0	1	0
Jassa oia	Macrofauna	Arthropoda	Malacostraca	Amphipoda	Ischyroceridae	1.38	0	0	1	0	0
Leucothoe lilljeborgi	Macrofauna	Arthropoda	Malacostraca	Amphipoda	Leucothoidae	1.38	1.01	0	1	2	0
Leucothoe sp.	Macrofauna	Arthropoda	Malacostraca	Amphipoda	Leucothoidae	1.38	0	0	1	0	0
Lysianassidae	Macrofauna	Arthropoda	Malacostraca	Amphipoda	Lysianassidae	2.77	0	0.63	1	0	1
Oediceroides pilosa	Macrofauna	Arthropoda	Malacostraca	Amphipoda	Oedicerotidae	0	0	0.16	0	0	1
Westwoodilla caecula	Macrofauna	Arthropoda	Malacostraca	Amphipoda	Oedicerotidae	1.38	0.50	0	1	1	0
Harpinia antennaria	Macrofauna	Arthropoda	Malacostraca	Amphipoda	Phoxocephalidae	33.22	4.53	0	2	5	0
Harpinia crenulata	Macrofauna	Arthropoda	Malacostraca	Amphipoda	Phoxocephalidae	44.30	0	0	3	0	0
Harpinia pectinata	Macrofauna	Arthropoda	Malacostraca	Amphipoda	Phoxocephalidae	12.46	0.50	0	1	1	0
Harpinia sp.	Macrofauna	Arthropoda	Malacostraca	Amphipoda	Phoxocephalidae	24.92	2.01	0	3	2	0
Paraphoxus oculatus	Macrofauna	Arthropoda	Malacostraca	Amphipoda	Phoxocephalidae	1.38	0	0	1	0	0
Phoxocephalidae	Macrofauna	Arthropoda	Malacostraca	Amphipoda	Phoxocephalidae	5.54	1.01	0	1	2	0
Stenothoe sp.	Macrofauna	Arthropoda	Malacostraca	Amphipoda	Stenothoidae	1.38	0	0	1	0	0
Pseudotiron bouvieri	Macrofauna	Arthropoda	Malacostraca	Amphipoda	Synopiidae	0	0	0.32	0	0	2
Cumacea	Macrofauna	Arthropoda	Malacostraca	Cumacea		0	0.50	0	0	1	0
Cyclaspis longicaudata	Macrofauna	Arthropoda	Malacostraca	Cumacea	Bodotriidae	0	1.01	0	0	1	0
Diastylodes serratus	Macrofauna	Arthropoda	Malacostraca	Cumacea	Diastylidae	8.31	2.01	0.32	2	3	2
Makrokyllindrus longipes	Macrofauna	Arthropoda	Malacostraca	Cumacea	Diastylidae	0	0	0.16	0	0	1
Eudorella truncatula	Macrofauna	Arthropoda	Malacostraca	Cumacea	Leuconidae	1.38	0	0	1	0	0
Leucon (Crymoleucon) macrorhinus	Macrofauna	Arthropoda	Malacostraca	Cumacea	Leuconidae	0	3.52	0	0	2	0
Leucon (Epileucon) ensis	Macrofauna	Arthropoda	Malacostraca	Cumacea	Leuconidae	1.38	1.01	0.16	1	2	1
Leucon (Macrauloleucon) siphonatus	Macrofauna	Arthropoda	Malacostraca	Cumacea	Leuconidae	4.15	1.01	0.32	2	2	2
Leucon sp.	Macrofauna	Arthropoda	Malacostraca	Cumacea	Leuconidae	0	0.50	0.16	0	1	1
Procampylaspis armata	Macrofauna	Arthropoda	Malacostraca	Cumacea	Nannastacidae	0	0.50	0	0	1	0
Procampylaspis sp.	Macrofauna	Arthropoda	Malacostraca	Cumacea	Nannastacidae	0	0.50	0.16	0	1	1
Anthuroidea	Macrofauna	Arthropoda	Malacostraca	Isopoda		0	0	0.16	0	0	1
Asellota	Macrofauna	Arthropoda	Malacostraca	Isopoda		9.69	14.09	0.47	1	3	2
Cymothoida	Macrofauna	Arthropoda	Malacostraca	Isopoda		0	1.01	0.32	0	1	2

Gnathiidae	Macrofauna	Arthropoda	Malacostraca	Isopoda	Gnathiidae	1.38	0	0	1	0	0
apseudomorpha	Macrofauna	Arthropoda	Malacostraca	Tanaidacea		0	0	0.16	0	0	1
Tanaidomorpha	Macrofauna	Arthropoda	Malacostraca	Tanaidacea		2.77	0	0	2	0	0
Paranarthrura intermedia	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Agathotanaidae	0	4.53	0	0	3	0
Paranarthrura sp.	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Agathotanaidae	0	2.01	0.32	0	2	2
Paranarthrura sp1	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Agathotanaidae	62.29	1.51	0.16	2	3	1
Paranarthrura sp2	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Agathotanaidae	2.77	0	0	1	0	0
Parakanthophoreus nanopsenos	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Akanthophoreidae	65.06	0	0	4	0	0
Tumidochelia sp.	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Akanthophoreidae	15.23	1.51	0	3	2	0
Anarthrura sp.	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Anarthruridae	0	2.01	0	0	3	0
Anarthruridae	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Anarthruridae	1.38	0	0	1	0	0
Apseudes holthuisi?	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Apseudidae	1.38	0	0	1	0	0
Apseudes sp.?	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Apseudidae	0	3.02	0.95	0	1	1
Apseudopsis acutifrons?	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Apseudidae	0	5.54	0	0	1	0
Leviapseudes sp.	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Apseudidae	0	3.52	0.47	0	5	3
Collettea cf. cylindrata	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Colletteidae	0	0	0.32	0	0	2
colletteidae	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Colletteidae	1.38	3.52	0.16	1	2	1
colletteidae sp1	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Colletteidae	0	1.51	1.27	0	2	7
colletteidae sp4	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Colletteidae	0	0	0.16	0	0	1
colletteidae sp6	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Colletteidae	0	0	1.74	0	0	9
colletteidae sp7	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Colletteidae	5.54	0.50	0	2	1	0
colletteidae sp8	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Colletteidae	13.84	0	0	2	0	0
Haplocope sp.	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Colletteidae	0	10.07	0	0	4	0
Leptognathiella sp1	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Colletteidae	0	5.54	0.16	0	5	1
Leptognathiella sp2	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Colletteidae	2.77	1.01	0	1	2	0
Leptognathiella sp3	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Colletteidae	0	2.52	0.32	0	4	2
Leptognathiopsis sp.	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Colletteidae	6.92	0.50	0	2	1	0
Leptognathia sp.	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Leptognathiidae	35.99	6.54	0	3	3	0
Cristatotanaeis sp.	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Paratanaoidea incertae sedis	0	3.02	0	0	3	0
Parafilitanaeis sp.	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Paratanaoidea incertae sedis	0	0.50	0	0	1	0
Mystricentrus sp.	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Pseudotanaidae	0	0	0.47	0	0	3
Pseudotanaeis sp1	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Pseudotanaidae	0	2.01	0.32	0	2	1
Pseudotanaeis sp2	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Pseudotanaidae	0	1.01	0	0	2	0
Pseudotanaeis sp3	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Pseudotanaidae	0	13.59	0	0	6	0

Pseudotanais stiletto	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Pseudotanaidae	59.52	2.52	0	4	1	0
Araphura sp. ?	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Tanaellidae	1.38	0	0.32	1	0	1
Araphura sp1	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Tanaellidae	0	0.50	0	0	1	0
Tanaella sp.	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Tanaellidae	1.38	0	0.95	1	0	5
tanaellidae sp.	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Tanaellidae	0	0.50	0	0	1	0
Protanaissus sp.	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Tanaissuidae	0	1.01	0	0	1	0
Tanaopsis laticaudata	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Tanaopsidae	1.38	0	0	1	0	0
Typhlotanaiidae	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Typhlotanaiidae	0	1.01	0	0	1	0
Typhlotanais angstromensis	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Typhlotanaiidae	2.77	0	0	1	0	0
Typhlotanais sp.	Macrofauna	Arthropoda	Malacostraca	Tanaidacea	Typhlotanaiidae	16.61	0	0	1	0	0
Alpheus sp.	Macrofauna	Arthropoda	Malacostraca	Decapoda	Alpheidae	1.38	0	0	1	0	0
Ebalia sp.	Macrofauna	Arthropoda	Malacostraca	Decapoda	Leucosiidae	1.38	0	0	1	0	0
Aplacophora	Macrofauna	Mollusca	Aplacophora			18.00	0	0	1	0	0
Cardiomya costellata	Macrofauna	Mollusca	Bivalvia	Anomalo- desmata	Cuspidariidae	0	0	0.79	0	0	4
Bathyarca pectunculoides	Macrofauna	Mollusca	Bivalvia	Arcoida	Arcidae	0	0	0.16	0	0	1
Thyasira sp.	Macrofauna	Mollusca	Bivalvia	Lucinoida	Thyasiridae	0	0	0.16	0	0	1
Thyasira alleni	Macrofauna	Mollusca	Bivalvia	Lucinoida	Thyasiridae	168.88	11.07	0	3	5	0
Thyasira exintermedia	Macrofauna	Mollusca	Bivalvia	Lucinoida	Thyasiridae	4.15	17.11	0	2	7	0
Thyasira oblonga	Macrofauna	Mollusca	Bivalvia	Lucinoida	Thyasiridae	8.31	97.15	0	2	10	0
Saccella commutata	Macrofauna	Mollusca	Bivalvia	Nuculanoida	Nuculanidae	13.84	2.01	0.16	2	3	1
Yoldiella wareni	Macrofauna	Mollusca	Bivalvia	Nuculanoida	Yoldiidae	0	5.03	7.44	0	2	18
Ennucula aegeensis	Macrofauna	Mollusca	Bivalvia	Nuculida	Nuculidae	2.77	8.05	0	2	6	0
Ennucula tenuis	Macrofauna	Mollusca	Bivalvia	Nuculida	Nuculidae	1.38	0	0	1	0	0
Nucula sulcata	Macrofauna	Mollusca	Bivalvia	Nuculida	Nuculidae	1.38	0	0	1	0	0
Kelliella miliaris	Macrofauna	Mollusca	Bivalvia	Veneroida	Kelliellidae	11.07	4.03	1.90	2	4	9
Abra cfr. alba	Macrofauna	Mollusca	Bivalvia	Veneroida	Semelidae	1.38	0	0	1	0	0
Abra longicallus	Macrofauna	Mollusca	Bivalvia	Veneroida	Semelidae	2.77	2.01	0	1	3	0
Timoclea ovata	Macrofauna	Mollusca	Bivalvia	Veneroida	Veneridae	1.38	0	0	1	0	0
Caudofoveata sp.	Macrofauna	Mollusca	Caudofoveata			69.21	14.60	0	3	4	0
cfr. Falcidens gutturosus	Macrofauna	Mollusca	Caudofoveata	Chaeto- dermatidae	Chaeto- dermatidae	45.68	3.52	0	2	2	0
Gastropteridae	Macrofauna	Mollusca	Gastropoda	Cephalaspidea	Gastropteridae	1.38	0	0	1	0	0
Megastomia conoidea	Macrofauna	Mollusca	Gastropoda	Heterobranchia (subclass)	Pyramidellidae	1.38	0	0	1	0	0

Ringicula conformis	Macrofauna	Mollusca	Gastropoda	Heterobranchia (subclass)	Ringiculidae	4.15	0	0	1	0	0
Crenilabium exile	Macrofauna	Mollusca	Gastropoda	Heteronemertea (subclass)	Acteonidae	0	0.50	0.16	0	1	1
Eulima glabra	Macrofauna	Mollusca	Gastropoda	Littorinimorpha	Eulimidae	1.38	0	0	1	0	0
Fusculima minuta	Macrofauna	Mollusca	Gastropoda	Littorinimorpha	Eulimidae	1.38	0	0	1	0	0
Benthomangelia macra	Macrofauna	Mollusca	Gastropoda	Neogastropoda	Mangeliidae	0	0	0.32	0	0	2
Nassarius turulosus	Macrofauna	Mollusca	Gastropoda	Neogastropoda	Nassariidae	4.15	2.52	0	2	3	0
Antalis cfr. Agilis	Macrofauna	Mollusca	Scaphopoda	Dentaliida	Dentaliidae	0	0	0.16	0	0	1
Antalis cfr.vulgaris	Macrofauna	Mollusca	Scaphopoda	Dentaliida	Dentaliidae	0	1.01	0.16	0	1	1
Cadulus subfusiformis	Macrofauna	Mollusca	Scaphopoda	Gadilida	Gadilidae	0	0.50	0.47	0	1	2
Dischides politus	Macrofauna	Mollusca	Scaphopoda	Gadilida	Gadilidae	1.38	0	0	1	0	0
Entalina tetragona	Macrofauna	Mollusca	Scaphopoda	Gadilida	Entalinidae	0	2.52	0.95	0	5	4
Pulsellum lofotense	Macrofauna	Mollusca	Scaphopoda	Gadilida	Pulsellidae	1.38	4.53	0.16	1	5	1
Heteronemertea	Macrofauna	Nemertea	Anopla			1.38	0	0	1	0	0
Lineidae	Macrofauna	Nemertea	Anopla	Heteronemertea (subclass)	Lineidae	0	0	0.16	0	0	1
Echinoidea	Macrofauna	Echinodermata	Echinoidea			1.38	0.50	0	1	1	0
Ophiuroidea	Macrofauna	Echinodermata	Ophiuroidea			85.83	3.02	0	4	5	0
Spengelidae	Macrofauna	Hemichordata	Enteropneusta	[unassigned] Enteropneusta	Spengelidae	1.38	0	0	1	0	0