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## First insights into the structure and environmental setting of cold-seep communities in the Marmara Sea

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### Abstract:

A brackish-water cold seep on the North Anatolian Fault (NAF) in the Marmara Sea was investigated with the Nautilie submersible during the MarNaut cruise in 2007. This active zone has already been surveyed and revealed evidence of active seeping on the seafloor, such as bubble emissions, patches of reduced sediments, microbial mats and authigenic carbonate crusts. MarNaut was the first opportunity to sample benthic communities in the three most common microhabitats (bioturbated and reduced sediments, carbonate crust) and to examine their relationships with environmental conditions. To do so, faunal communities were sampled and chemical measurements were taken close to the organisms. According to diversity indices, the bioturbated microhabitat exhibited the highest taxonomic diversity and evenness despite a lower number of samples. Conversely, the reduced sediment microhabitat exhibited the lowest taxonomic diversity and evenness. The carbonate crust microhabitat was intermediate although it had the highest biomass. Multivariate analyses showed that (1) fauna were relatively similar within a single microhabitat; (2) faunal community structure varied greatly between the different microhabitats; (3) there was a link between faunal distribution and the type of substratum; and (4) chemical gradients (i.e. methane, oxygen and probably sulphides) may influence faunal distribution. The estimated fluid flow velocity (0.4–0.8 m/yr) confirmed the presence of fluid emission and provided evidence of seawater convection in the two soft-sediment microhabitats. Our results suggest that the reduced sediments may represent a harsher environment with high upward fluid flow, which restrains seawater from penetrating the sediments and inhibits sulphide production, whereas bioturbated sediments can be viewed as a bio-irrigated system with sulphide production occurring at greater depths. Therefore, the environmental conditions in reduced sediments appear to prevent the colonization of symbiont-bearing fauna, such as vesicomid bivalves, which are more often found in bioturbated sediments. Fluid flow appears to control sulphide availability, which in turn influences the horizontal and vertical distribution patterns of fauna at small spatial scales as observed at other seep sites

**Keywords:** Marmara Sea; Cold seep; Benthic fauna; Biological diversity; Environmental conditions; Chemosynthetic.

69

70 Cold-seep ecosystems are home to chemosynthetic communities composed of a  
71 number of endemic vesicomyid, solemyid and mytilid bivalves, as well as several  
72 siboglinid polychaetes that are often the dominant macro- and megafauna (Bergquist  
73 et al. 2003, 2005; Levin and Mendoza 2007; Levin et al. 2003; Luth et al. 1999; Olu  
74 et al. 1996, 1997; Olu-Le Roy et al. 2004, 2007; Paull et al. 1984; Sahling et al. 2002;  
75 Sibuet and Olu, 1998). One of the key adaptations of species to seep habitats is their  
76 association with bacterial endosymbionts, which ensure chemosynthetic primary  
77 production through the oxidation of the reduced compounds contained in the seeping  
78 fluids (Cavanaugh, 1983; Childress et al., 1986; Dubilier et al., 2008; Fisher, 1990).  
79 Thus, these taxa rely on seeping fluids for their nutrition and survival, and their  
80 spatial distribution is a reliable indicator of the presence of chemical fluxes at the  
81 sediment-water interface (Levin, 2005; Sibuet and Olu, 1998). Other heterotrophic  
82 species live in association with seep chemosynthetic species, benefiting from these  
83 enriched environments (Tunnicliffe et al., 2003) and also relying on organic inputs  
84 derived from neritic (coastal) and terrestrial organic material (Gage, 2003).

85

86 Recent studies on seep ecosystems have highlighted the vast heterogeneity of  
87 habitats and associated faunal assemblages at small spatial scales that range from  
88 the sampling unit (dm scale) to the geological structure (km scale) on which the  
89 assemblages are found (Vanreusel et al., 2009). Although there are some similarities  
90 between structures and regions, each newly discovered seep area may have its own  
91 signature in terms of faunal structure, diversity and chemical conditions. Previous  
92 studies have suggested that the composition and intensity of fluid seepage are the  
93 major factors structuring the distribution of seep fauna (Levin, 2005; Sibuet and Olu,  
94 1998). Other driving forces, such as depth (Sibuet and Olu, 1998), substratum type  
95 (Olu et al., 1996; Sahling et al., 2003), oxygen concentration (Bergquist et al., 2005;  
96 Levin and Gage, 1998), biological interactions (Bergquist et al., 2003) and  
97 hydrographic regime (Luth and Luth, 1998; Luth et al., 1999) have also been  
98 suggested to play a role on species distribution patterns.

99

100 Recently, the deep-sea sites of the Marmara Sea (40-41°N; 26-30°W) have received  
101 more attention from the scientific community, mainly because of the seismic hazard  
102 in the Istanbul area. This intra-continental sea, located on the North-Anatolian Fault

103 zone (NAF), is tectonically active (Armijo et al., 2004; Le Pichon et al., 2001; Sengor  
104 et al., 2005). Submarine earthquakes constitute a potential threat for human  
105 populations (Ambraseys, 2000; Ambraseys and Finkel, 1991; Ansal et al., 2009;  
106 Hubert-Ferrari et al., 2000; Oglesby et al., 2008). These earthquakes influence gas  
107 emissions (Hovland et al., 2002) as confirmed by the presence of gas flares in the  
108 Izmit Gulf following the 1999 Kocaeli earthquake (Alpar, 1999). Subsequent  
109 investigations have revealed cold seeps in the deep basins of the Marmara Sea  
110 along the main fault, on secondary fault branches and on the anticline ridges (Armijo  
111 et al., 2005; Geli et al., 2008; Halbach et al., 2004; Zitter et al., 2008). The most  
112 common evidence for fluid expulsion in the Marmara Sea is the presence of black  
113 patches of reduced sediments associated with microbial mats and authigenic  
114 carbonate crusts (Zitter et al., 2008). While these generally correspond to zones of  
115 diffuse flow, focused flow of brackish water has been observed at two sites (Zitter et  
116 al., 2008). Moreover, cold seeps can release hydrocarbons as a separate gas phase,  
117 and even as oil (Bourry et al., 2009; Geli et al., 2008). Seeps can be thus  
118 characterised by gas flares, brackish-water springs or diffuse emission, depending on  
119 the dominant mode of fluid emission.

120

121 In 2007, the MarNaut cruise represented the first opportunity to sample the fauna  
122 associated with the cold-seep ecosystems of the Marmara Sea and to characterise  
123 the abiotic conditions of this basin of the eastern Mediterranean Sea. The present  
124 study aims to describe the structure of the benthic communities in the three most  
125 common microhabitats of a brackish-water cold seep and relate community structure  
126 to local environmental factors. Even though these objectives were hindered by  
127 sampling limitations, this study represents a fundamental step in advancing our  
128 understanding of the ecology and biogeography of chemosynthetic seep species  
129 within the larger Mediterranean context.

130

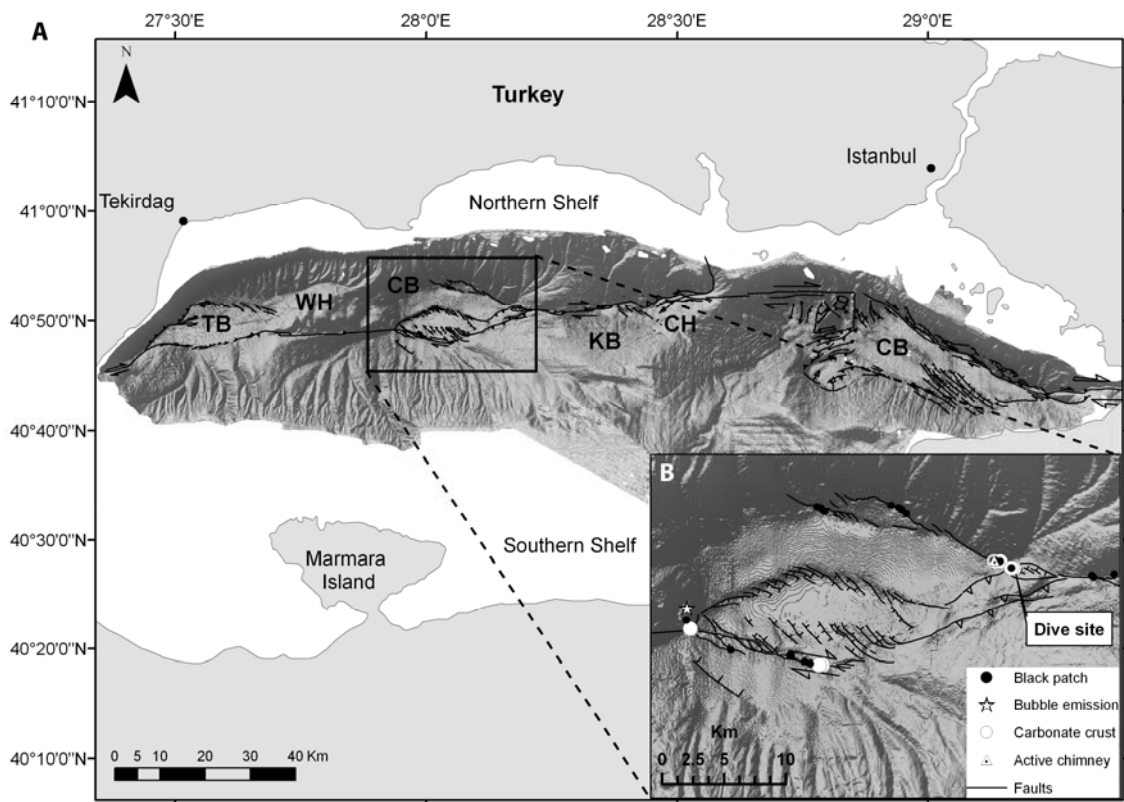
## 131 **2. Materials and methods**

### 132 **2.1. Study area**

133 Located between 40-41°N and 26-30°W, the Marmara Sea is the easternmost semi-  
134 enclosed basin of the Mediterranean Sea, and connects the Black Sea to the Aegean  
135 Sea via the Bosphorus and Dardanelles Straits. It is subdivided into four major basins

136 from east to west: the Çınarcik, Kumburgaz, Central and Tekirdağ basins, with a  
137 maximum depth of about 1260 m in the Central basin (Figure 1).

138



**Fig. 1.** (A) General bathymetric map of the Marmara Sea showing the fault traces (from Le Pichon et al., 2001), the different geological basins and (B) details of the study area in the Central Basin. The presence of black patches on the seafloor (black dots), carbonate crusts (white dots), active chimney (white triangle) and bubble emission (white star) were mapped according to the observations reported during the MARMARASCARPS cruise (Zitter et al., 2008) and exploratory MarNaut dives. The dive site corresponds to the site dedicated to environmental and faunal sampling during the MarNaut cruise in 2007. Abbreviations: TB, Tekirdağ Basin; CB, Central Basin; CB, Çınarcik Basin; KB, Kumburgaz Basin; WH, Western High; CH, Central High.

139

140 Preliminary visual observations of the Marmara Sea seafloor and the associated  
141 epibenthic communities were carried out using the ROV *Victor 6000* during the  
142 MARMARASCARPS cruise in 2002 (Armijo et al., 2005; Zitter et al., 2008). Our  
143 observations and sampling were carried out five years later during the MarNaut  
144 cruise (2007) on the R/V *L'Atalante* with the manned submersible *Nautilus*. During this  
145 cruise, exploratory dives were carried out to map seepage occurrences and faunal  
146 distributions at selected sites in the four major basins. Five sampling dives took place  
147 at the brackish-water spring described in this study. One of these dives was  
148 dedicated to sampling the mega- and macrofauna and characterising the

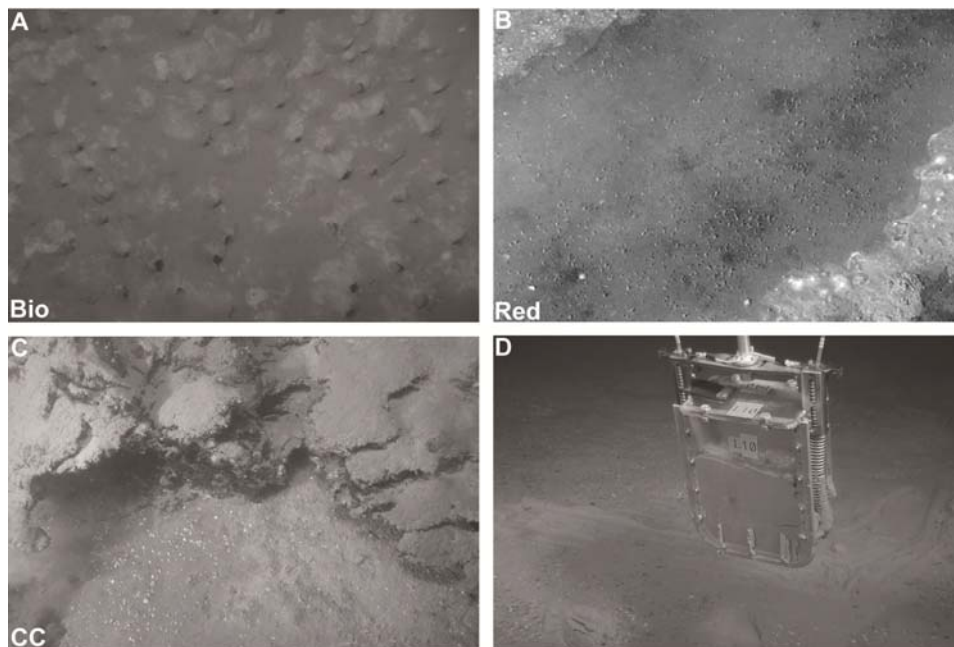
149 environmental features in the north-east Central basin (40°51.27'N - 28°10.19'W) at a  
150 depth of 1 120 m (Figure 1).

151

## 152 2.2. Sampling site

153 The chosen seep site harboured a mosaic of microhabitats. Three of these were  
154 selected and sampled: (1) the bioturbated sediment microhabitat (Bio) was  
155 characterised by brown sediments with small bioturbation holes (Figure 2a); (2) large  
156 patches of reduced sediment microhabitat (Red) were covered by short polychaete  
157 tubes and were surrounded by Bio patches (Figure 2b); and, (3) sparse carbonate  
158 crusts were located a couple of meters from Red patches and collectively constitute  
159 the Carbonate Crust microhabitat (CC, Figure 2c).

160



**Fig. 2.** Photographs of each of the three most common microhabitats of the Marmara cold seeps: (A, Bio) bioturbated sediments, (B, Red) reduced sediments and (C, CC) carbonate crusts (MarNaut cruise, 2007). (D) blade corer used for sampling chemosynthetic communities with the submersible.

161

162 Environmental characterisation of each microhabitat was conducted before sampling  
163 fauna to avoid any disturbance that could be caused by this sampling. Temperature  
164 and salinity measurements were performed using the MicroCat autonomous sensor  
165 (F. Harmegnies, Ifremer). Mean values were computed after deploying the sensor for  
166 1 min above the organisms and as close as possible to the seafloor using *Nautilé's*  
167 manipulator arm. Water and sediment samples were then taken for chemical  
168 analyses using 200 ml titanium bottles and tube corers (30 cm long; 5.4 cm inner

169 diameter), respectively. Complete sampling details are given in Table 1.  
170 Unfortunately, due to time constraints imposed by the use of a manned submersible,  
171 the physico-chemical sampling could not be completed above Bio and was not  
172 performed above CC. Sediments were also sampled with blade corers (Bayon et al.,  
173 2009; Menot et al., 2009, area:0.02m<sup>2</sup>, Figure 2d) deployed by *Nautilie's* arm to  
174 collect the epi- and endofauna. The number of samples for each microhabitat varied,  
175 depending on time and number of tools available (Table 1).

176

### 177 2.3. Physico-chemical analyses

178 The 200 ml water samples were used to determine pH as well as methane  
179 concentrations. pH measurements were performed on board with a pH-meter  
180 connected to a glass electrode (Metrohm) and were corrected for ambient  
181 temperature (25°C) and atmospheric pressure. Reproducibility of the method was  
182 ±0.01 pH units. Methane concentrations were measured in the laboratory using the  
183 headspace technique coupled with a gas chromatograph equipped with a flame-  
184 ionisation detector (error of 4%, see details in Sarradin and Caprais, 1996).

185

186 Sediments from tube corers were split horizontally on board and pore water was  
187 extracted by centrifugation of the different sediment layers (every cm for the first 2  
188 cm and every 2 cm until the end of the core) to measure chlorinity and sulphate  
189 concentrations with an ionic chromatograph on an isocratic system DX 120  
190 (DIONEX). Intact cores, along with supernatant water, were used for oxygen  
191 measurements. Oxygen profiles within supernatant water and sediments were  
192 obtained by using a microsensor OX 100 coupled to a pico-ammeter 5PA 2000  
193 (Unisense) and a micro-manipulator using the Profix data acquisition software  
194 (Unisense). The resolution of the sensor was <200 µm. Kendall rank correlations ( $\tau$ )  
195 (Kendall, 1938) were computed between chlorinity and sulphate profiles for the Red  
196 and Bio microhabitats.

197

### 198 2.4. Carbonate mineralogy

199 The mineralogy of the diagenetic carbonates was determined by X ray diffraction.  
200 The oxygen and carbon isotopic compositions of carbonates have been measured to  
201 characterize the water and carbon sources of the fluids from which the carbonates  
202 have precipitated. They are expressed in the conventional  $\delta$  notation defined as:

203  $\delta = [(Rs/Rr) - 1] * 1000$ , where  $R = {}^{18}\text{O}/{}^{16}\text{O}$  or  ${}^{13}\text{C}/{}^{12}\text{C}$  respectively in the sample (Rs)  
204 and in the reference (Rr). The reference for  $\delta^{18}\text{O}$  and  $\delta^{13}\text{C}$  is the V-PDB (Craig, 1957;  
205 Gonfiantini et al., 1995). The  $\text{CO}_2$  gas extracted from the carbonate by attack with  
206 100% phosphoric acid at  $90^\circ\text{C}$  was analysed with a triple collector mass  
207 spectrometer (ISOPRIME). The analytical precision  $2\sigma$  is 0.01‰ for both  $\delta^{18}\text{O}$  and  
208  $\delta^{13}\text{C}$ ; the reproducibility is 0.05‰ for  $\delta^{18}\text{O}$  and  $\delta^{13}\text{C}$ .

209

## 210 2.5. Estimation of fluid velocity in sediments

211 Since fluid flow velocity influences the distribution of seep faunal assemblages, we  
212 have used models of geochemical gradients to estimate fluid flow for the different  
213 microhabitats. It is known that the transport of dissolved species such as chloride  
214 occurs both through molecular diffusion and advection of interstitial water. The  
215 magnitude of diffusive flux and the velocity of advective flow provide constraints for  
216 models that can be estimated from the observed chlorinity profiles, a conservative  
217 aqueous species. If a steady-state condition is assumed for approximate calculation  
218 of the flow velocity, the concentration of dissolved chloride can be described by a  
219 partial differential equation (Berner, 1974):

220

$$221 D_s (d^2C/dx^2) + v(dC/dx) = 0$$

222

223 where  $C$  is the concentration of dissolved chloride (mmol/l),  $x$  is the absolute depth  
224 (cm) measured downward from the sediment-water interface,  $D_s$  is the diffusion  
225 coefficient of chloride in sediments ( $\text{m}^2/\text{yr}$ ), and  $v$  is the absolute upward vertical  
226 velocity of interstitial water relative to the sediment-water interface ( $\text{m}/\text{yr}$ ). The  
227 diffusion coefficient used here for this model was  $0.036 \text{ m}^2/\text{yr}$  at  $14^\circ\text{C}$  for a porosity of  
228 70% and a tortuosity factor of 1.4 (Henry et al., 1996; Li and Gregory, 1974). For all  
229 three tube cores, the chlorinity of seawater and of the emissions were assumed to be  
230 equal to 583 mmol/l and 496 mmol/l, respectively. Average velocity was fitted to each  
231 core. The diffusion coefficient of sulphate in marine sediments is half that of chloride  
232 (Iversen and Jørgensen, 1993) and sulphate profiles that would result from the sole  
233 effect of diffusion and advection, without any sulphate reduction, were computed  
234 assuming a seawater sulphate concentration of 30 mmol/l and an incoming fluid  
235 concentration of 0 mmol/l.

236

## 237 2.6. Faunal sorting and identification

238 Sediments from blade corers dedicated to faunal sampling and sampled at Bio and  
239 Red were photographed and split horizontally (0-1, 1-3, 3-5, 5-10, >10 cm)  
240 immediately after recovery. Core slices were passed through a sieve column (2 mm,  
241 1 mm, 500  $\mu\text{m}$ , 250  $\mu\text{m}$ ) and the retained residues were preserved in 10% buffered  
242 formalin. In the laboratory, all sediments were rinsed and invertebrates were sorted  
243 under a dissecting microscope and identified to the lowest taxonomic level possible.  
244 The CC samples were also washed over a 250  $\mu\text{m}$  mesh and the organisms retained  
245 were processed in the same way as those on the soft sediments. Due to space  
246 limitations on *Nautila*, two of the crust samples (CC1 and CC2) were put in the same  
247 sampling box. While the crusts themselves were treated separately, it was impossible  
248 to determine the origin of the material that had fallen to the bottom of the box. This  
249 was treated as a combined "sample" (CC<sub>box</sub>) that was only used when pooling all the  
250 carbonate crust data for  $\alpha$ -diversity analyses.

251

252 The surface of the sampled carbonate crusts was estimated using the IPLab  
253 Spectrum® image analysis software. Quantitative 2-D surface analyses were  
254 performed on video images, three times for each frame to reduce error resulting from  
255 on-screen tracing (Sarrazin and Juniper, 1999). Total surface area was used to  
256 calculate area-related indicators, such as density and biomass. However, because it  
257 does not take topography into account, this method probably underestimates surface  
258 area and in turn overestimates density and biomass.

259

260 In this study, we considered macrofauna *sensu stricto* (>250  $\mu\text{m}$ , Hessler and Jumars  
261 1974), so any meiofaunal taxa such as Nematoda, Copepoda and Ostracoda were  
262 considered separately. Nevertheless, the resulting meiofaunal list was very  
263 incomplete. Meiofauna *sensu stricto* were underestimated since only the fauna  
264 retained by a 250  $\mu\text{m}$  mesh was analysed instead of the 32  $\mu\text{m}$  to 62  $\mu\text{m}$  mesh size  
265 usually used for this faunal compartment (Hessler and Jumars, 1974; Thistle, 2003;  
266 Van Gaever et al., 2006). For most identified taxa, we achieved the family level  
267 except for Demospongia, Scyphozoa, Nematoda. While in the first two groups, only  
268 one morphology could be distinguished among the specimens, suggesting the  
269 presence of a single family, in the latest, several morphologies were identified.



270

271 The mean wet weight (ww) was measured for each microhabitat. To do so,  
272 individuals of all major macrofaunal taxa (bivalves, polychaetes, gastropods  
273 crustaceans) present in a sample were pooled, pat-dried on absorbent paper and  
274 weighed on a micro-scale balance with an error of 0.1 mg.

275

## 276 2.7. Faunal diversity analyses

### 277 2.7.1. Alpha-diversity

278 Alpha-diversity analyses were only performed for macrofauna and at the family level,  
279 with the exception of Demospongia and Scyphozoa. For meiofauna, only family  
280 richness for copepods, ostracods and mites is reported as a measure of alpha-  
281 diversity. Rarefaction curves (*sensu* Gotelli and Colwell, 2001) were computed on  
282 macrofaunal data for each microhabitat. Rarefaction curves plot expected taxonomic  
283 richness against sampling effort (Gauthier et al., 2010; Gotelli and Colwell, 2001;  
284 Hurlbert, 1971) and helps in evaluating sampling adequacy in different groups of  
285 samples. Because of the single sample from Bio, individual-based rarefaction was  
286 used in all microhabitats although this assumes homogeneous distribution of  
287 individuals and species among samples (Gotelli and Colwell, 2001)

288

289 Observed family diversity was also evaluated with commonly used diversity indices  
290 as well as more robust intrinsic diversity-based ordering methods. Taxonomic  
291 richness ( $S$ ), Shannon's entropy ( $H'$ , Shannon, 1948) and the Gini-Simpson diversity  
292 index ( $D$ , Gini, 1912; Simpson, 1949) as well as their numbers equivalents were  
293 computed. Numbers equivalents express the richness of a hypothetical perfectly  
294 even community that is as diverse as the one observed (Jost, 2007; Jost, 2006; Patil  
295 and Taillie, 1982). Community evenness was also determined using Pielou's index of  
296 evenness ( $J'$ , Pielou, 1969).

297

298 The right tail-sum method (RTS) is a diversity ordering method that allows graphical  
299 comparisons of communities (Liu et al., 2007; Patil and Taillie, 1982; Tothmérész,  
300 1998). It was shown to be more robust and stringent than other methods (Liu et al.,  
301 2007). Taxonomic groups are ranked by decreasing relative abundance, and the  
302 diversity profile is computed as:

303 
$$T_i = \sum_{j=i+1}^S p_{[j]} \text{ for } i = 1, 2, \dots, S - 1$$

304

305 where  $T_i$  is the RTS value at scale  $i$  and  $p_{[j]}$  is the relative abundance of the  $j^{\text{th}}$   
306 most abundant taxa. RTS is based on a clear definition of taxonomic diversity and is  
307 easily interpretable: communities that systematically have higher  $T_i$  values are more  
308 diverse. However, if the profile for two communities cross, no conclusion can be  
309 drawn (Liu et al., 2007).

310

### 311 2.7.2. Beta-diversity

312 Despite the modest number of samples, multivariate analyses were conducted to  
313 better illustrate the similarities and differences among faunal samples. Principal  
314 component analysis (PCA) and Ward's hierarchical clustering were used for this  
315 purpose. Macrofaunal and meiofaunal data sets were treated separately and  
316 ordination results compared with a Procrustean randomization test (Jackson 1995).  
317 The lowest available taxonomic level was used. Abundance data were first Hellinger-  
318 transformed in order to preserve Hellinger, rather than Euclidian, distances in PCA  
319 (Legendre and Gallagher, 2001). The Hellinger distance has been shown to  
320 adequately estimate community resemblance (Legendre and Gallagher, 2001). The  
321 equilibrium contribution circle was computed to identify taxa having an important  
322 impact on the position of samples in the ordination (Legendre and Legendre, 1998).  
323 These results were used to formulate hypothesis about the influence of habitat  
324 conditions on the variation in taxonomic composition within and between  
325 microhabitats.

326

327 Finally, the Jaccard's similarity ( $S_{jacc}$ ) coefficient was used to quantify similarity in  
328 terms of shared taxa among samples within microhabitats (Jaccard, 1901). This  
329 coefficient does not consider the absence of taxa in both samples and has value  
330 between 0 and 1. Mean Jaccard similarity in each microhabitat was computed to  
331 evaluate within-group variation.

332

333 All analyses were performed in the R environment (R, Development Core Team  
334 2009). Rarefaction curves, diversity indices and diversity profiles were computed

335 both with the Biodiversity R package (Kindt and Coe, 2005) and functions in Gauthier  
336 et al. (2010). Multivariate analyses were carried out using the Vegan package  
337 (Oksanen et al., 2008).

338

### 339 **3. Results**

#### 340 3.1. Physico-chemical characterisation of microhabitats

##### 341 3.1.1. Sediment appearance

342 The length of the tube cores varied from 12 to 20 cm depending on the nature of  
343 substratum (Table 1). Bio and Red exhibited visible differences in the upper 10 cm of  
344 sediment (Table 2). Based on the photographs taken on board, the oxygenated layer  
345 of brown sediments into the Bio sediment cores was thick (about 2 cm) and clearly  
346 distinct from the black sediment below. On the contrary, only black sediment was  
347 visible in the cores from the Red microhabitat (Table 2).

348

##### 349 3.1.2. Salinity, temperature and pH at the sediment-water interface

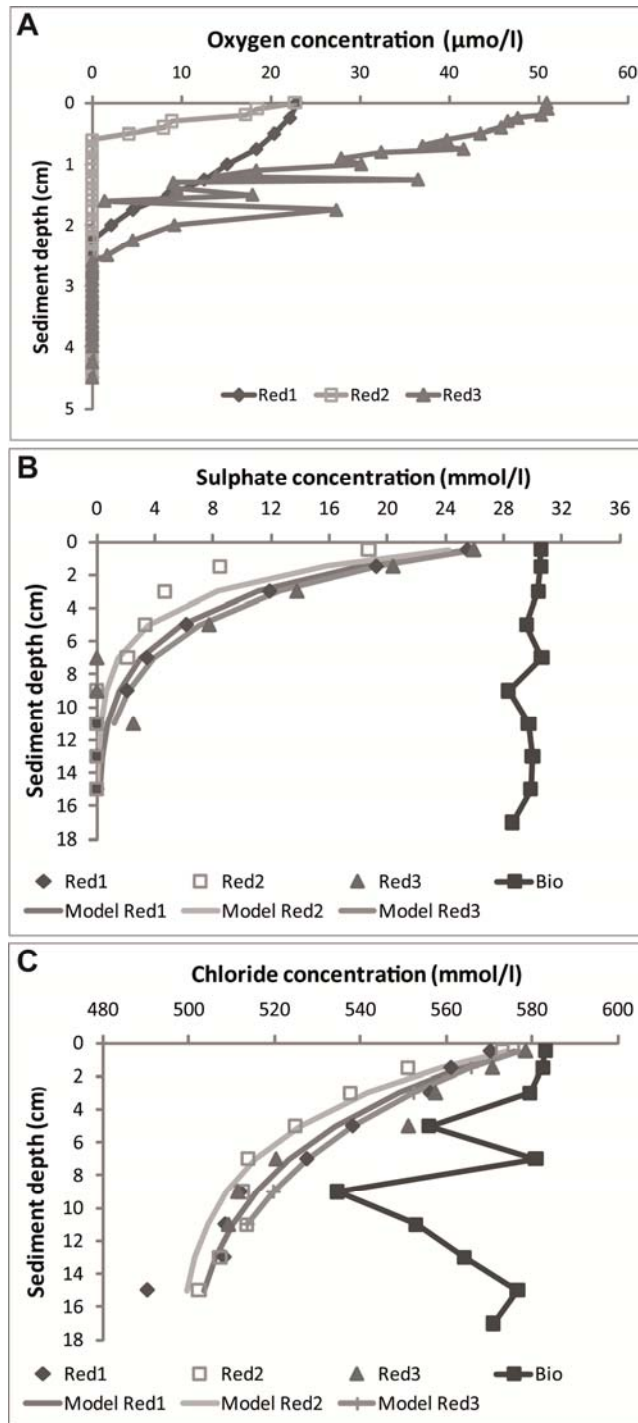
350 Continuous measurements at the sediment-water interface showed no variation in  
351 salinity or temperature, either between the replicates of the Red microhabitat, or  
352 between the Red and Bio microhabitats. Overall, mean salinity was 38.8‰ and mean  
353 temperature 14.5°C (Table 2). pH in water samples from Red ranged from 7.89 to  
354 7.94 (Table 2) and did not show important variation between replicates.

355

##### 356 3.1.3. Oxygen concentrations in pore water and methane concentrations at the 357 sediment-water interface

358 Oxygen data were only available for Red. Oxygen concentrations at the sediment-  
359 water interface varied from 22.8 to 50.9  $\mu\text{mol/l}$  among the three replicates (Table 2).  
360 Concentrations were much lower above Red2 where the oxygen depth penetration  
361 was the lowest (0.6 cm, Figure 3a). This sample also exhibited by far the highest  
362 methane concentration at the sediment-water interface (0.7  $\mu\text{mol/l}$ , Table 2). Oxygen  
363 concentration at the sediment-water interface appeared positively correlated to  
364 oxygen depth penetration and negatively correlated to methane concentration at the  
365 water-sediment interface, but could not be statistically tested due to the small number  
366 of samples ( $n=3$ , Table 2, Figure 3a).

367



**Fig. 3.** (A) Dissolved oxygen, (B) sulphate and (C) chloride profiles measured in pore water extracted from sediment cores sampled in the bioturbated sediment (solid line  $n=1$ ) and reduced sediment ( $n=3$ ) microhabitats in the Marmara Sea (MarNaut cruise, 2007). The model profiles are represented by dotted lines and explained in the text.

368

369 3.1.4. Isotopic signatures of the carbonate crust

370 The cm-thick carbonate crust sampled is composed of magnesian calcite. Three

371 isotopic measurements were realized on this crust; the upper mm-thick white layer is

372 underlain by a mm-thick light grey layer that covers a medium grey compact layer.  
373 The  $\delta^{18}\text{O}$  values (+2.40 to +2.09 ‰ V-PDB) are characteristic of calcite precipitated  
374 in equilibrium with the Marmara Sea bottom water ; the very low  $\delta^{13}\text{C}$  values (-35.17  
375 to -45.35 ‰ V-PDB) testify in favour of methane as the major source of carbon,  
376 oxidized as  $\text{CO}_2$  by methanotrophic bacteria (Aloisi et al., 2000; Gontharet et al.,  
377 2007; Pierre and Fouquet, 2007).

378

### 379 3.1.5. Sulphate and chloride concentrations in pore water and estimation of the 380 upward flux velocity

381 In terms of sulphate and chlorinity, Bio and Red microhabitats exhibited distinctive  
382 profiles (Figures 3b, c). The single sulphate profile from Bio was higher than all those  
383 from Red. Sulphate concentrations in Bio stayed almost unchanged throughout the  
384 different sediment layers, varying from 28.3 to 30.6 mmol/l (Figure 3b). On the other  
385 hand, sulphate concentrations in Red decreased sharply in the first 2-3 cm. All  
386 dropped to zero at depths of 7 to 11 cm, but Red3 showed a new, slight surge at 11  
387 cm (Figure 3b). The chlorinity profile in Bio presented sharp variations that were  
388 apparently independent of depth. Concentrations varied from 535 to 583 mmol/l and,  
389 as for sulphate, chloride concentration was higher at Bio than at Red (Figure 3c).  
390 Sulphate and chlorinity profiles were positively correlated within each microhabitat  
391 (Kendall's  $\tau = 0.9$ ,  $p < 0.01$  in Bio;  $\tau = 0.7$ ,  $p < 0.001$  in Red).

392

393 The theoretical advection-diffusion profiles of sulphate showed closer fits with actual  
394 data for Red1 and Red3. At Red2, the measured sulphate concentrations were lower  
395 in the first 4 cm, but match the theoretical advection-diffusion profile at greater depths  
396 (Figure 3b). It is not possible to determine whether sulphate reduction occurs in Red.

397

398 The shape of the chloride concentration profiles in Red1, Red2 and Red3 reflects  
399 upward migration of interstitial water through the sediment layer (Figure 3c). Based  
400 on the advection-diffusion model, mean square best fits were obtained for upward  
401 velocities ( $v$ ) of  $0.58 \pm 0.08$  m/yr,  $0.75 \pm 0.1$  m/yr and  $0.51 \pm 0.07$  m/yr for Red1, Red2  
402 and Red3, respectively (Figure 3c). Despite the uncertainty linked to certain factors  
403 and the problems inherent to the diffusion of salts, we assumed that the effective  
404 diffusivity at our site ranged from 0.03 to 0.04  $\text{m}^2/\text{yr}$ . Even though the pressure  
405 gradient was not measured, it is possible to give a lower bound to permeability in the

406 Red microhabitat from the assumption that the pore pressure gradient probably does  
407 not exceed the local lithostatic pressure gradient. Therefore, for a porosity of 70%  
408 and hence a density of 1500 kg/m<sup>3</sup>, this lower bound ranges from 2 to 4 × 10<sup>-15</sup> m<sup>2</sup>.

409

### 410 3.2. Macro- and meiofaunal community description

#### 411 3.2.1. Composition, abundance, density and $\alpha$ -diversity

412 Overall, a total of 524 and 4 975 individuals were sampled from Bio and Red  
413 sediments, respectively, of which 35.5% and 4.2% were macrofauna *sensu stricto*.  
414 On carbonate crusts, a total of 3 170 individuals were collected, among which 60.5%  
415 were macrofauna *sensu stricto*.

416

417 Relative macrofaunal abundances varied between both soft-sediment microhabitats  
418 (Bio and Red) and carbonate crusts and even between replicates of the same  
419 microhabitat (Table 3). In bioturbated sediments, bivalves and polychaetes were the  
420 dominant macrofaunal groups constituting 50% and 36% of the total abundance,  
421 respectively. Other groups were present, but in much lower abundances (<5.4%,  
422 Table 3). In the reduced sediments, all three replicates were very similar with a  
423 dominance of polychaetes that represented a mean of about 96% of the total  
424 macrofaunal abundance (Table 3). A few bivalves and gastropods were present.  
425 Finally, all three carbonate crust replicates were similar in terms of composition, but  
426 dominant taxa varied between samples. While CC1 and CC2 were dominated by  
427 rissoid gastropods (*Laevipithus verduini*, Van Aartsen et al., 1989, from 64.6 to  
428 72.2%), CC3 was dominated by an undescribed species of mytilid bivalve (68.8%,  
429 Table 3). These bivalves shared morphological similarities with *Idas modioliformis*  
430 (Sturany, 1896) from the eastern Mediterranean Sea and a preliminary molecular  
431 study suggests that they may belong to the Bathymodiolinae family and even  
432 represent a new genus (Ritt et al. unpublished data). We also have molecular  
433 evidence suggesting that this mytilid may harbour symbiotic bacteria (Ritt et al.  
434 unpublished data). Cnidarians, polychaetes and crustaceans were also present on  
435 CC but in lower abundances. The fauna found at the bottom of the combined-sample  
436 box (CC<sub>box</sub>) was largely dominated by rissoid gastropods (40.5%, Table 3).

437

438 Despite the large sieve mesh size used (250  $\mu$ m), numerous meiofaunal specimens  
439 were found in our samples (Table 4). When added to macrofauna, they contributed

440 from 17.7% to 98.3% of the total faunal abundance, with a lower impact in CC (Table  
441 4). Nematodes were consistently the dominant taxon, representing >79% of the  
442 meiofauna (Table 4). Copepods were the second most dominant meiofaunal taxon in  
443 Bio and CC, but were absent in Red. Only a few ostracods were observed in soft-  
444 sediment microhabitats (<0.5%, Table 4).

445

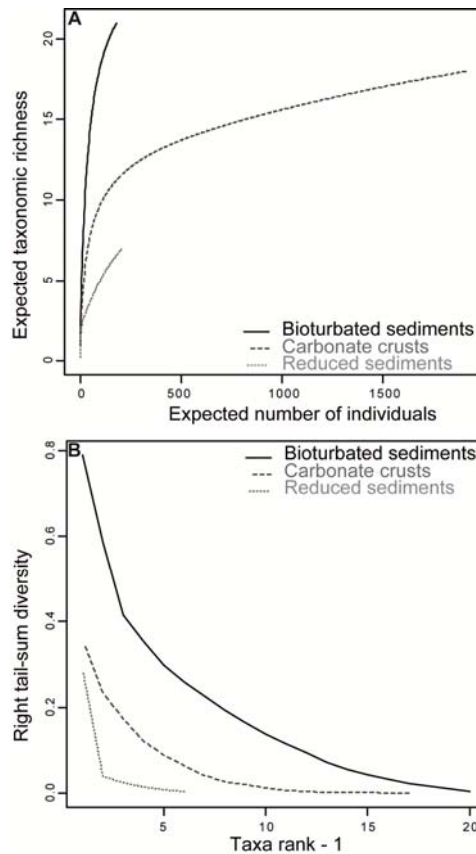
446 Average macrofaunal densities varied from 3 433 ind./m<sup>2</sup> in Red, to 15 325 ind./m<sup>2</sup> in  
447 CC with an intermediate value of 9 300 ind./m<sup>2</sup> in Bio (Table 5). Compared to  
448 macrofauna, the meiofaunal density ranking showed the opposite trend with  
449 minimum densities in CC (10.4 ind./10 cm<sup>2</sup>) and maximum densities in Red (79.4  
450 ind./10 cm<sup>2</sup>). They were intermediate in the Bio microhabitat (16.9 ind./10 cm<sup>2</sup>, Table  
451 5).

452

453 Rarefaction curves based on macrofaunal data (Figure 4a) show that the sampling  
454 effort was insufficient, especially in Bio (n=1) and Red (n=3). Nevertheless, the single  
455 sample from Bio had the highest taxonomic richness. For CC (n=3), the curve seems  
456 to level off, suggesting that most macrofaunal taxa was sampled (Figure 4a).  
457 However, the ranking of the three curves would probably remain the same with the  
458 addition of new macrofaunal samples and we can conclude with some confidence  
459 that the total taxonomic richness (S) was highest in Bio, lowest in Red and  
460 intermediate in CC (Figure 4a). Finally, the sharp increase of the Bio curves (Figure  
461 4a) indicates that, with each additional individual sampled, the probability of it  
462 representing a new taxon was high. This pattern also demonstrates that Bio showed  
463 a more even taxon distribution than the two other microhabitats, a result that was  
464 confirmed by Pielou's index ( $J$ , Table 5). Meiofaunal samples were largely  
465 dominated by nematods (from 79 to 100%) that were not identified below the phylum  
466 level and most likely include several families and species. Hence, only family  
467 richness for copepods, ostracods and mites is reported in Table 5 as a measure of  
468 alpha-diversity.

469

470



**Fig. 4.** Rarefaction curves (A) and right tail-sum (B) intrinsic diversity profiles according to the different microhabitats (MarNaut cruise, 2007). The  $CC_{Box}$  data were included.

471

472 The right tail-sum (RTS) intrinsic diversity profiles (Figure 4b) confirmed that Bio had  
 473 the highest evenness. The Bio curve is positioned above the two others and the most  
 474 abundant taxon represented only about 20% of the total macrofaunal abundance. In  
 475 Red, the dominant taxon represented nearly 70% of macrofaunal abundances  
 476 (Figure 4b). Classical diversity indices, and their numbers equivalents (Table 5), give  
 477 the same alpha-diversity ranking. Classic diversity indices gave a consistent ranking  
 478 (CC>Bio>Red; Table 5).

479

### 480 3.2.2. Symbiont-bearing fauna versus heterotrophic fauna

481 Symbiont-bearing fauna were present in various proportions in Bio and CC  
 482 microhabitats, and totally absent in Red. Overall, they represented about 3.8% of the  
 483 abundance in the Bio microhabitat, compared to 8.9 to 68.8% in CC. Symbiont-  
 484 bearing fauna were represented by various bivalve families, including the  
 485 Vesicomidae, Lucinidae and Mytilidae. Live mytilids (adult and post-larvae) were  
 486 only observed in CC (Table 3). However, dead specimens (post-larvae) were found



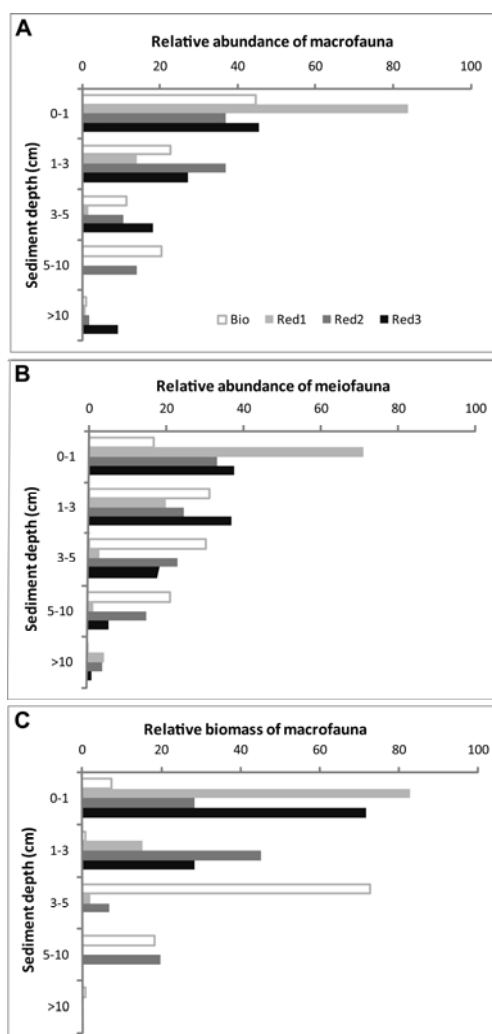
487 in large numbers in both soft-sediment microhabitats, reaching higher densities in  
488 Red. No data were available on the presence of symbiont-bearing fauna in the  
489 meiofaunal compartment.

490

### 491 3.2.3. Vertical distribution of the fauna within the sediments

492 The vertical distribution of the macrofauna varied among the two soft sediment  
493 microhabitats (Bio & Red, Figure 5a). Although the distribution pattern varied slightly  
494 between the three Red replicates, the macrofauna observed in Red was  
495 concentrated in the uppermost sediment layers with most (up to 80%) located within  
496 the top 3 cm (Figure 5a). In Bio, the fauna was more abundant in the very first layer  
497 (0-1 cm, 45%) and distributed more evenly among the others. Abundance reached  
498 minimum values below 10 cm in all samples (Figure 5a).

499



**Fig. 5.** Vertical distribution of (A) macrofaunal and (B) meiofaunal relative abundances and (C) relative biomass of macrofaunal taxa according to depth in the two soft-sediment microhabitats. Bio= bioturbated sediments, n=1; Red = reduced sediments, n=3.

500 Between 30 to 80% of meiofaunal abundance was observed in the first layers (0-1  
501 cm) of Red and then decreased gradually with depth (Figure 5b). In Bio, the  
502 distribution of meiofauna reached higher abundances in the 1-5 cm sediment layers.  
503 Nematodes were present at all depths (even >10 cm) whatever the microhabitat,  
504 whereas copepod crustaceans were restricted to the upper 10 cm. As for  
505 macrofauna, meiofauna were rare in the deep sediment layer [>10 cm], they  
506 represented less than 5% of the total faunal abundance (Figure 5b).

507

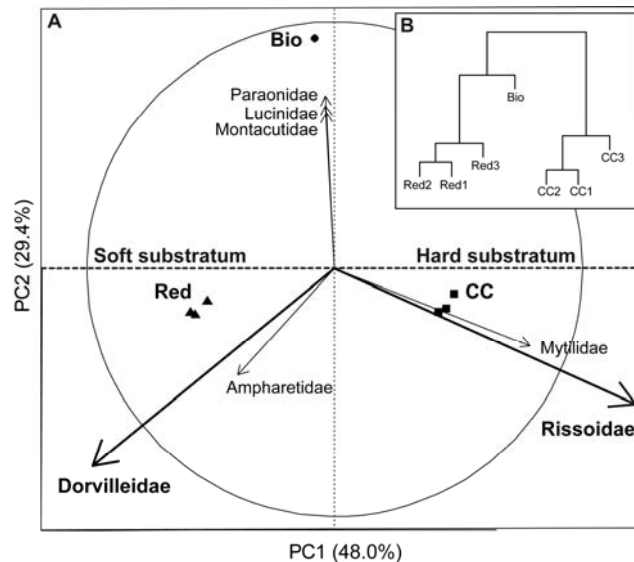
#### 508 3.2.4. Macrofaunal biomass

509 The highest macrofaunal biomass was found on CC reaching an average of 0.806 kg  
510 ww/m<sup>2</sup> (Table 5). Mytilids were the main contributors of this relatively high biomass.  
511 The biomass found at the bottom of the combined-sample box (CC<sub>box</sub>), was  
512 negligible, only reaching 0.0033 kg. In the two other microhabitats, the mean  
513 biomass was 0.0018 kg ww/m<sup>2</sup> on Bio and 0.0019 kg ww/m<sup>2</sup> on Red (Table 5). The  
514 low values of biomass found in these microhabitats, compared to the crusts, were  
515 related to the presence of small organisms. Most of the biomass was found in the  
516 upper 5 cm of the sediments (Figure 5c). While it was mostly concentrated in the top  
517 3 cm in Red, it was highest at 3-5 cm depth in the Bio microhabitat (Figure 5c).

518

#### 519 3.2.5. Within and among microhabitat variation

520 Hierarchical clustering and PCA on macrofaunal abundances sensu stricto illustrate  
521 variations between the carbonate crusts and the two soft substratum microhabitats  
522 (Figure 6). The ordination clearly separates the three microhabitats along the two first  
523 axes that represent 77.4% of the total variance (Figure 6a). The three microhabitats  
524 are separated along the first axis, which contains 48% of the variance in the faunal  
525 variation. Inter-microhabitat variability was larger than intra-microhabitat variability as  
526 all replicate samples from Red and CC microhabitats grouped together. On the  
527 second axis, the Red and CC microhabitats grouped together while Bio stood alone.  
528 This axis explained 29.4% of the variance in the faunal variation (Figure 6a). In terms  
529 of structuring taxa, the rissoid gastropods *Laeviphitus verduini* and the dorvilleid  
530 polychaetes contributed significantly to the two first axes, characterizing the CC  
531 microhabitat and the Red microhabitat, respectively (Figure 6a). Other taxa, such as  
532 the mytilid bivalves, were important, but to a lesser extent, in the positioning of the  
533 microhabitats on the two first axes (Figure 6a).



**Fig. 6.** (A) Ordination graph (PCA, scaling type 1) with the circle of equilibrium contribution (radius=0.77) and the two first axes representing 77.4% of the total variance. Vectors shorter than 0.42 were removed. (B) Ward's hierarchical clustering performed with Hellinger-transformed macrofaunal abundances of high taxonomic level data for each microhabitat type, Bio = bioturbated sediments, Red = reduced sediments, CC = carbonate crust.

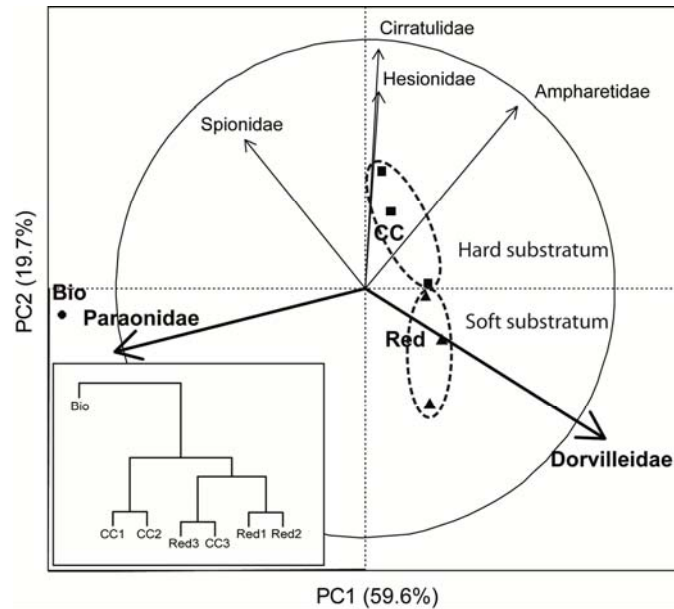
534

535 Interestingly, a PCA with Hellinger transformed meiofaunal data only (not shown)  
 536 exhibited the same general distance patterns as the one with macrofauna *sensu*  
 537 *stricto* (Procruste Test stat=0.83,  $p=0.006$ , 1000 permutations). However, meiofauna  
 538 sampling was very incomplete, especially on hard substratum, and these results  
 539 might reflect this paucity of observations.

540

541 The three microhabitats could also be distinguished when considering only the  
 542 polychaetes at the family level. Most families observed in the Bio microhabitat were  
 543 absent in Red and vice versa (Table 3). Moreover, while at least eight families were  
 544 present in the single Bio sample, and seven in CC, only four were observed in the  
 545 three Red samples (Table 3). Siboglinid polychaetes were absent from our samples  
 546 and were not observed in the seep areas that we explored in the Marmara Sea.  
 547 Multivariate analysis performed on just the polychaete family abundances also  
 548 separated the microhabitats along the two first axes, representing 79.3% of the total  
 549 variance (Figure 7a). Bio was clearly distinct from Red and CC along the first axis,  
 550 which explained 59.6% of the variance whereas the distinction along the second axis  
 551 was not as clear (Figure 7a). Paraonidae and Dorvilleidae were the most important  
 552 taxa in structuring the position of samples in the ordination. Cirratulidae, Hesionidae

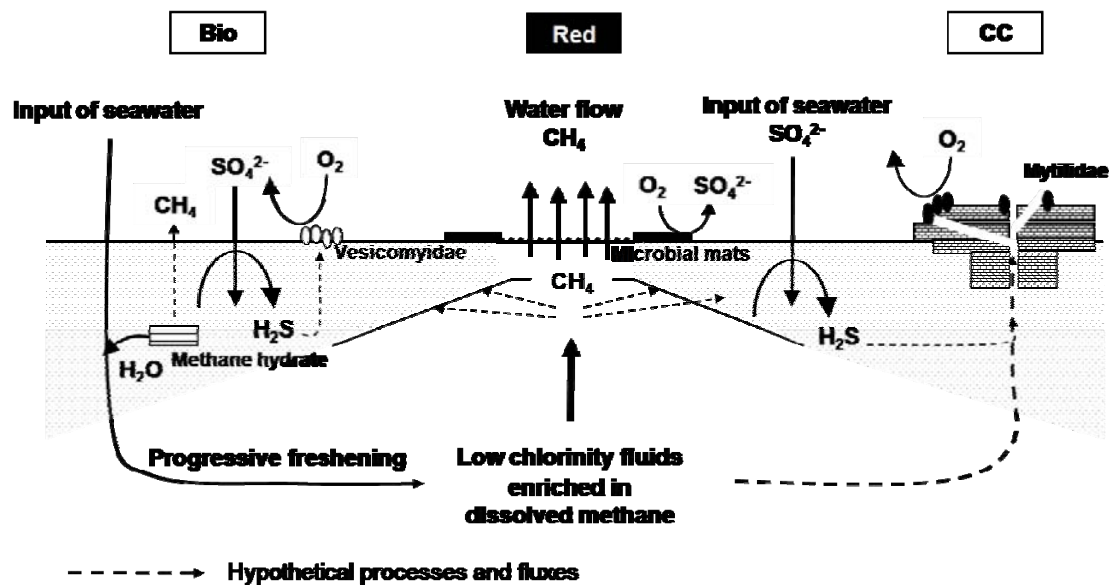
553 and Ampharetidae also had an important contribution on the second axis. Ward's  
 554 hierarchical clustering corroborated this separation (Figure 7b). However, no clear  
 555 distinction between the polychaete composition in CC and Red was established.  
 556



**Fig. 7.** (A) Ordination graph (PCA, scaling type 1) with the circle of equilibrium contribution (radius=0.72) and the two first axes representing 79.3% of the total variance. Vectors shorter than 0.56 were removed. (B) Ward's hierarchical clustering performed with Hellinger-transformed abundances of polychaete families data for each microhabitat type, Bio = bioturbated sediments, Red = reduced sediments, CC = carbonate crust. The possible link between the second axis and substratum type is noted.

557  
 558 The environmental and faunal results suggest a model of fluid circulation (Figure 8)  
 559 that relates faunal composition and their patchy distribution to the flux of low-  
 560 chlorinity fluid emissions. The upward flux was hypothesized to be higher under the  
 561 Red microhabitat and lower under the Bio and CC microhabitats, where symbiont-  
 562 bearing bivalves, vesicomysids and mytilids, respectively, were living. Thus, these  
 563 taxa appear to be reliable indicators of the presence of chemical fluxes, especially  
 564 sulphides, at the sediment-water interface.

565  
 566  
 567  
 568  
 569  
 570



**Fig. 8.** Schematic hypothetical representation (modified from Henry et al., 1996 and Olu et al., 1996) of physical and chemical processes in the first few centimetres of sediments at each microhabitat type, Bio = bioturbated sediments, Red = reduced sediments, CC = carbonate crust. Dotted line = hypothetical processes and fluxes. The distance between microhabitats is not drawn to scale.

571

572 4. Discussion

573 4.1. Environmental conditions in the Marmara Sea

574 The cold seeps of Marmara Sea illustrate an example of an active margin setting with  
 575 low-chlorinity upward fluids. Contrary to other seep sites, the regions of the Marmara  
 576 Sea explored in this study did not reveal spectacular evidence of fluid emissions on  
 577 the seafloor, such as mud volcanoes, pockmarks or brine pools (Milkov, 2000;  
 578 Hovland et al., 2002; Judd and Hovland, 2007). Instead, fluid fluxes appeared to be  
 579 unevenly distributed along active faults where fractures allow released gas to escape  
 580 or to filter through sediments (Geli et al., 2008; Zitter et al., 2008). Thermogenic  
 581 methane-rich bubble emissions occur (Bourry et al., 2009) and brackish water can be  
 582 expelled through chimneys on the seafloor (Zitter et al., 2008). Furthermore, black  
 583 patches (reduced sediments) throughout the different basins have been observed  
 584 within the larger Çınarcık basin where the dissolved oxygen concentration is the  
 585 lowest. In fact, a gradient of dissolved oxygen in the water column is observed from  
 586 the western to the eastern basins with concentrations reaching 50  $\mu\text{mol/kg}$  in the  
 587 Tekirdag basin, 25  $\mu\text{mol/kg}$  in the Central basin and 8  $\mu\text{mol/kg}$  in the Çınarcık basin  
 588 (Lionel Finchel, INSU). The Marmara Sea is not as anoxic as the Black Sea, but  
 589 pollution in the Marmara Sea due to anthropogenic activities (Cetecioglu et al., 2009)  
 590 and the proximity of land lead to high inputs of organic matter that can reach the  
 591 seafloor, enhancing microbial activity and organic matter degradation there. This is

592 supported by the observation of huge fluxes of marine snow during diving, even in  
593 the deeper part of the Central basin at depths of up to 1200 m.

594

595 Tectonic processes appear to play a major role in the occurrence of fluid emissions in  
596 this region and their highly dynamic nature may induce high spatial and temporal  
597 variation that may in turn influence faunal distribution (Zitter et al., 2008). This high  
598 spatial heterogeneity was apparent in the Red microhabitat, where replicates  
599 separated by only a couple of meters varied by as much as five fold in methane  
600 concentrations. The chemical data at the sediment-water interface (i.e. methane) as  
601 well as in pore water (i.e. sulphates, oxygen) confirmed the presence of fluid  
602 emission and provided evidence for seawater convection between the two soft-  
603 sediment microhabitats. Despite the incompleteness of our environmental factor  
604 dataset and the large within-microhabitat variations observed, our data suggest that  
605 both soft sediment microhabitats had a distinct chemical signature.

606

## 607 4.2. Microhabitat characteristics

### 608 4.2.1. Bioturbated sediment microhabitat

609 The Bio microhabitat was characterised by deeper oxygen and sulphate penetration.  
610 We can assume that the penetration of these elements in the sediments is favoured  
611 by the presence of burrows, probably built by crustaceans. It has been shown that  
612 complex burrows may influence the overall sedimentology and geochemistry of the  
613 seafloor and especially oxygen penetration (Aller, 1988; Ziebis et al., 1996). The  
614 jagged chlorinity profile can be interpreted as the consequence of transient diffusion-  
615 advection resulting from bio-irrigation. The sulphate concentrations remained  
616 relatively high and, with the exception of the lowest point at 16-18 cm depth, were  
617 compatible with mixing between seawater and a fluid of 100 mmol/l chlorinity and 0  
618 mmol/l sulphate, representative of fossil pore water originating from the ancient  
619 Marmara lake (Zitter *et al.*, 2008). The top of the sulphate reduction zone lays 16 cm  
620 below the seafloor and likely to the end of the bio-irrigated zone. This type of system  
621 has already been observed at Nankai (Henry et al., 1992; Toki et al., 2004) or on the  
622 Barbados Trench (Henry et al., 1996), as explained below for the Red microhabitat.

623

624 The observed taxonomic richness was highest in the Bio microhabitat, even though  
625 only a single sample was collected. This microhabitat had intermediate macrofaunal

626 densities and was dominated by bivalves — especially Montacutidae and  
627 Vesicomidae —, polychaetes and nematodes. It is interesting to note that the  
628 vesicomid *Isorropodon perplexum* (Sturany, 1896) and another symbiont-bearing  
629 species, the lucinid *Lucinoma kazani* (Salas and Woodside, 2002) have only been  
630 observed at Mediterranean Sea cold seeps where they are fuelled by the Anaerobic  
631 Oxydation of Methane (AOM) that induces H<sub>2</sub>S production (Boetius et al., 2000).  
632 Vesicomidae beds have already been observed at numerous cold seep sites with  
633 higher densities such as that around the centre of the Atalante mud volcano where  
634 they reach up to 10 ind./m<sup>2</sup> (Olu et al., 1996), or at the Nankai Trench where they  
635 reach 1 000 ind./m<sup>2</sup> (Henry et al., 1992). Vesicomid and lucinid densities in Bio were  
636 much lower with up to 200 and 150 ind./m<sup>2</sup> respectively, but their presence was not  
637 only an indication of fluid venting but also of shallow sulphide production in this  
638 microhabitat. Both families are known to live half-buried in the sediments where they  
639 are able to extend their foot to capture sulphide (Barry and Kochevar, 1998;  
640 Wallmann et al., 1997). As supposed by the diffusion-advection model, the sulphide  
641 production in Bio may occur deep within sediments.

642

#### 643 4.2.2. Reduced sediment microhabitat

644 The presence of methane at the interface of reduced sediment was the main  
645 evidence of seepage activity at the study site. This microhabitat was also  
646 characterised by low dissolved oxygen concentrations at the water-sediment  
647 interface and the sulphate profiles showed a sharp decrease in the first 10 cm.  
648 However, contrary to dissolved oxygen, we cannot assume that sulphates decreased  
649 only by simple consumption in sediments. The model based on chlorinity profiles  
650 supported the hypothesis that the Red microhabitat corresponded to a zone of fairly  
651 uniform Darcian flow (i.e. within fluid velocities ranging 0.5-0.75 m/yr) for a fluid of  
652 constant chlorinity (496 mmol/l) and containing no sulphates. The ascending fluid  
653 appears to be a mix of seawater and brackish pore fluid that dilutes the chloride. In  
654 fact, the salinity of the brackish pore fluids contained in the Marmara Sea sediments  
655 a few tens of meters below the seafloor is only about 100 mmol/l (Zitter et al., 2008).  
656 This mixing model implies that convection occurs around the brackish springs at a  
657 larger scale (1-100 m) than the one investigated here. Hydrate dissociation may also  
658 explain the progressive freshening of seawater within sediments in seeps.  
659 Nevertheless, no gas hydrates were found in our samples, although they do occur in

660 different basins of the Marmara Sea where the conditions of pressure and  
661 temperature corresponded to the hydrate stability zone (Bourry et al., 2009).

662  
663 According to the proposed fluid circulation model, the Red microhabitat was  
664 dominated by advective fluxes (0.4-0.8 m/yr) that were sufficient to inhibit inflow and  
665 to extend the sulphate reduction to the sediment surface. Hence, the depth at which  
666 sulphate penetrated into the sediments did not appear to be controlled by reaction  
667 rates but rather by competition with molecular diffusion in the vigorous ascending  
668 fluid flow. More sophisticated modelling would be required to determine actual  
669 reaction rates. Similar geochemical processes were also observed at the Nankai  
670 Trench (Henry et al., 1992; Toki et al., 2004) and at the Barbados accretionary  
671 prisms (Henry et al., 1996), two sites also characterised by low chlorinity upward  
672 fluxes.

673  
674 In terms of fauna, the Red microhabitat was characterised by low taxonomic  
675 diversity, the absence of symbiont-bearing fauna, the lowest macrofaunal densities  
676 and the large dominance of two ubiquitous polychaete families: the non-sedentary  
677 Dorvilleidae and the tube-building Ampharetidae. These two families are typical of  
678 areas enriched in organic matter (Fauchald and Jumars, 1979). The presence of low-  
679 diversity polychaete assemblages, dominated by one or two families, has been  
680 already observed in microbial mats from the Eel River basin, Hydrate Ridge and Gulf  
681 of Mexico (Levin et al., 2003; Sahling et al., 2002; Robinson et al., 2004). In our  
682 study, Ampharetidae were the second-ranked polychaete taxa. Members of this  
683 family have been observed in large numbers at other reduced sediments sites such  
684 as at the Hikurangi Margin (New Zealand) where they reach a density of up to 72 000  
685 ind./m<sup>2</sup> (Sommer et al., 2009b). This site lies on an active margin at a depth similar to  
686 our study site (~ 1050 m) with high concentrations of dissolved oxygen and methane  
687 at the water-sediment interface (197 µmol/l and 1 962 µmol/l, respectively; Table 6).  
688 In our study, dorvilleid and ampharetid polychaetes may represent the main  
689 consumers of dissolved oxygen at the surface of the Red microhabitat and account  
690 for the low oxygen concentration, which never exceeded 51 µmol/l.

691  
692 Meiofaunal densities, dominated by nematodes, were highest in the Red  
693 microhabitat, four times as great as those observed in the two other microhabitats.



694 They were higher (from 1 058 to 134 800 ind./m<sup>2</sup>) than those observed in the Black  
695 Sea at shallower depth (250 m, from 2 397 to 52 593 ind./m<sup>2</sup>, Sergeeva and Gulin.,  
696 2007). Nevertheless, our meiofaunal densities were much lower than those observed  
697 on the Atalante mud volcano at the Barbados accretionary prism where nematode  
698 density reaches up to 8 300 000 ind./m<sup>2</sup> (Olu et al., 1997). However, the large sieve  
699 size used (250 µm) lead to the underestimation of meiofaunal density in our study.  
700 The low similarity between replicates mostly reflected the differences in abundance  
701 due to the high spatial heterogeneity of meiofauna, but also to the sampling strategy  
702 used.

703

#### 704 4.2.3. Carbonate crust microhabitat

705 Carbonate crusts are known to be formed in reducing environments with methane  
706 inputs being oxidized by micro-organisms involved in the AOM (Aloisi et al., 2002;  
707 Aloisi et al., 2000). However, their immediate environment may change after they  
708 have formed. The carbonate crusts sampled here occur as a cm-thick layer that  
709 covers a meter-high mound covered by sediments; this structure may be considered  
710 as chemoherms (Teichert et al., 2005) that are built by fluid flow and/or escape of  
711 free methane gas into the water column. The crust is composed of magnesian calcite  
712 that was the product of anaerobic oxidation of methane as evidenced by the very low  
713  $\delta^{13}\text{C}$  value. However, additional chemical data will be necessary to gain a better  
714 understanding of this microhabitat and to position it within the gradient of  
715 environmental conditions observed in the two other microhabitats.

716

717 In terms of fauna, the CC microhabitat was characterized by intermediate diversity,  
718 the highest biomass and the highest macrofaunal densities, largely dominated by  
719 rissoid gastropods and by symbiont-bearing mytilids. The CC microhabitat exhibited  
720 the highest proportion of symbiont-bearing fauna and the occurrence of the latter was  
721 evidence of sufficient fluid flow and of exchanges between seawater and sediments  
722 to sustain symbiotic processes. Furthermore, this microhabitat harboured the highest  
723 percentage of symbiont-bearing fauna represented by mytilids that constitute the  
724 major part of the total biomass. Like *Idas* sp. from the Nile deep-sea fan, that lives in  
725 association with up to six different microbial symbionts (Duperron et al., 2008), the  
726 new mytilid species found in the Marmara Sea may harbour both thiotrophic and  
727 methanotrophic endosymbionts. To date our preliminary analyses only confirm the

728 presence of thiotrophic endosymbionts (Ritt et al. unpublished data). As on the giant  
729 pockmark off West Africa (Olu-Le Roy et al., 2007), carbonate crusts with mytilids  
730 appear to be under the influence of high fluid flow, higher than in sediments with  
731 vesicomysids, but lower than in reduced sediments in our study case (Table 6).

732

#### 733 4.3. Comparison between microhabitats (at the local scale)

734 Multivariate analyses showed a first distinction between communities found on hard  
735 and soft substratum microhabitats. The second axis could be related to a gradient of  
736 seepage influence (methane, oxygen and possibly sulphide). However, our chemical  
737 dataset was insufficient to establish statistical links between faunal distribution and  
738 environmental conditions and additional sampling would be necessary to further  
739 explore this hypothesis. The two distinct sediment microhabitats were characterized  
740 by contrasting methane supply and, probably, sulphide production. The Red  
741 microhabitat was dominated by upward advection of pore fluid that causes strong  
742 chemical gradients in the first few cm. At the Bio microhabitat, the production of  
743 hydrogen sulphide probably occurs below the bioturbated layer and is most likely  
744 controlled by bioirrigation fluxes (Wallmann et al., 1997). While the strong chemical  
745 gradients at Red can be exploited by free-living bacteria, more complex species  
746 interactions such as symbiosis could become advantageous at a site where sulphide  
747 production and oxygen supply are separated by at least 15 cm, as in Bio. Sulphide-  
748 tolerant polychaetes and nematodes lived on the surface of Red, whereas symbiont-  
749 bearing fauna, such as Vesicomysidae bivalves, were more evenly distributed and  
750 buried in Bio. The distribution patterns observed in our study support the hypothesis  
751 voiced by other authors suggesting that Ampharetidae and Dorvilleidae have a higher  
752 tolerance to sulphides (Levin et al., 2003; Sahling et al., 2002). Focusing only on  
753 polychaete families gives a different portrait. First of all, within-microhabitat variations  
754 appear to be proportionally more important than when considering the entire  
755 community. Also, Bio comes out as markedly different from all the others and the  
756 distinction between hard and soft substratum communities almost disappears.

757

758 These observations indicate that the faunal distribution at the Marmara Sea seeps is  
759 patchy and somewhat linked to the nature of the substratum and physico-chemical  
760 conditions that constrain the composition of the assemblages. Thus, within the same  
761 type of substratum (soft sediments), fluid flow velocities and chemical gradients such

762 as methane, oxygen and possibly sulphide concentrations appear to play a role in  
763 faunal composition.

764

#### 765 4.4. Comparison between microhabitats (at the global scale)

766 A total of 60 taxa, including meiofauna, were identified at our study site among which  
767 8 were also observed at eastern Mediterranean sites so far (Olu-Le Roy et al., 2004).  
768 This suggests that exchanges between the eastern Mediterranean Sea and the  
769 Marmara Sea seep sites continue to occur or occurred in the past. However,  
770 Siboglinidae polychaetes were not observed, neither during the MARMARASCARPS  
771 cruise (Zitter et al., 2008), nor during our cruise. This is surprising since siboglinids  
772 are present at most Mediterranean seep sites studied (Olu-Le Roy et al., 2004; Ritt et  
773 al., in prep.). This may simply be due to the lack of sampling in this area. In fact, a  
774 siboglinid tube was found at 1000 m depth during a recent Turkish cruise in 2008 (L.  
775 Artüz, pers. com.). Another hypothesis is that the geographic barrier induced by the  
776 Dardanelle sill (70 m) may have limited siboglinid larval dispersion within the  
777 Marmara Sea but only additional sampling will help resolve this conundrum.

778

779 The flow velocity observed at our study site (0.4-0.8 m/yr) was much lower than  
780 those previously reported in the Nankai Trough accretionary wedge (Henry et al.,  
781 1992), the Cascadia subduction zone or the Peru continental margin (Linke et al.,  
782 1994), all of which fall into a much larger range of 10-1 000 m/yr. These high rates  
783 are probably due to the combination of different factors, such as the geological  
784 setting, the presence of active thrusts, and the permeability of sediment layers  
785 (Henry et al., 2002). Furthermore, the distribution of the faunal communities in the  
786 Marmara Sea appears to differ from some large seep sites where a zonation of  
787 faunal communities has been observed at the 100 m to km scale (Le Pichon et al.,  
788 1990; Olu et al., 1996). This kind of ecological zonation has already been observed  
789 at larger scale on the Atalante mud volcano (Olu et al., 1996), the Håkon Mosby mud  
790 volcano (Niemann et al., 2006b), or the Hydrate Ridge (Sahling et al., 2002). The  
791 centre of the Atalante mud volcano is controlled by high fluid flux and colonised by  
792 high densities of nematodes, whereas clam beds are observed on the "Ridge zone",  
793 where the upward flux is lower. At the Håkon Mosby mud volcano, the active centre  
794 is only colonized by meiofaunal organisms, fauna form concentric belts around the  
795 active centre of the mud volcano (Jerosch et al., 2006) and this faunal distribution

796 appears to be directly related to chemical gradients (Jerosch et al., 2006; Niemann et  
797 al., 2006b). At Hydrate Ridge, the flux under microbial mats is controlled by the  
798 dissociation of gas hydrate and the abiotic conditions are much harsher (30 mmol/l  
799 sulphide) than within the surrounding sediments where the clams beds are found  
800 (Sahling et al., 2002). At sites such as the Hydrate and Blake ridges, changes in the  
801 faunal composition are linked to smaller spatial scales (Sahling et al., 2002; Van  
802 Dover et al., 2003). There, microbial mats colonise hydrate deposits with high  
803 sulphide concentrations; they are surrounded by vesicomid beds and, further away,  
804 by solemyid beds, following a gradient in sulphide concentrations. The faunal  
805 distribution in the Marmara Sea appears to be characterised by similar small-scale  
806 patterns. Patches of reduced sediments were dominated by ampharetid and  
807 dorvilleid polychaetes and nematodes surrounded by microbial mats and the entire  
808 area was also surrounded by more highly oxygenated sediments colonised by  
809 Vesicomidae and Lucinidae symbiont-bearing bivalves.

810

811 On soft sediments, the faunal distribution seems strongly reliant on sulphide  
812 production, which relies on the intensity of fluid flow. Indeed, a biological zonation  
813 was observed along a sulphide concentration gradient related to the occurrence of  
814 gas hydrates on the Cascadia margin (Sahling et al., 2002). Likewise, on the Håkon  
815 Mosby mud volcano, fluid flux gradient was related to faunal distribution patterns  
816 from the centre to the periphery (Niemann et al., 2006b). Methane concentrations  
817 measured above reduced sediments (Red, from 0.14 to 0.70  $\mu\text{mol/l}$ ) match the  
818 lowest ranges observed at other seep sites (Table 6). Indeed, measured methane  
819 concentrations above seep faunal assemblages within reduced sediment  
820 microhabitats range from 0.14  $\mu\text{mol/l}$  (this study) to 1 962  $\mu\text{mol/l}$  on the New Zealand  
821 margin (Sommer et al., 2009b, Table 6). Sediments filled with gas hydrates (and  
822 microbial mats) show the highest methane concentrations of all with concentrations  
823 of up to 6 500  $\mu\text{mol/l}$  (Table 6). Methane has been shown to influence the distribution  
824 of the fauna at other seep sites (Olu et al. 1997, Olu-Le Roy et al. 2007, Sergeeva  
825 and Gulin al., 2007).

826

827 Carbonate crusts may constitute an intermediate environment in terms of chemical  
828 gradients, and probably fluid intensity in the Marmara Sea, whereas they appear to

829 be associated with highest methane concentrations and probably highest fluid flow at  
830 the Regab pockmark (Olu-Le Roy et al., 2007).

831

#### 832 4.5. Conclusion and perspective

833 The Red microhabitat showed low taxonomic diversity and was dominated by surface  
834 deposit-feeders, whereas the Bio microhabitat harboured symbiont-bearing,  
835 burrowing species. In addition to chemical measurements and models based on  
836 them, we deduce that the Red microhabitat was influenced by fluids that prevent the  
837 establishment of non-tolerant species or even symbiotic species. On the other hand,  
838 Bio was also influenced by fluids but to a lesser extent, allowing an increase in  
839 diversity in association with an increase in trophic complexity and specialisation (i.e.  
840 symbioses). Interestingly, the CC microhabitat may sustain up to 69% of symbiont-  
841 bearing fauna and especially mytilids, suggesting that fluid-flux exchanges between  
842 seawater and sediments are high enough to sustain symbiotic processes. These  
843 hard substratum microhabitats would be characterised by intermediate environmental  
844 conditions, harbouring higher biomass and densities and intermediate diversity.  
845 Additional sampling will be necessary to further explore the links between faunal  
846 distribution and environmental conditions in the Marmara Sea and to validate the  
847 proposed model.

848

849 We will soon complete the molecular phylogeny and morphological description of the  
850 new mytilid found on the Marmara carbonate crusts. Thus, our preliminary results  
851 suggested, that even though this species shared morphological similarities with *Idas*  
852 *modioliformis* (Sturany, 1896) from the eastern Mediterranean Sea, it may represent  
853 a new genus in the Bathymodiolinae family (Ritt et al. unpublished data). In addition,  
854 further analyses will be done to confirm the status of the bacteria as symbionts,  
855 visualize their distribution in the gills and define their nutritional role in this bivalve  
856 species.

857

858 Finally, adequate and representative sampling of the meiofaunal and microbial  
859 compartments, their activities and their trophic interactions as well as a complete  
860 environmental characterization would be helpful in understanding the fine structure  
861 and functioning of the seep communities found in the Marmara deep basins.

862

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877

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Table 1

Sample locations, depth, sampling effort, and gear used to perform physico-chemical and faunal sampling in the three most common microhabitats of the north-eastern Central basin in the Marmara Sea explored during the MarNaut cruise in 2007. The length of the sediment cores and the estimated surface area of each carbonate crust sample are also reported.

Microhabitat types	Latitude (°N)	Longitude (°E)	Depth (m)	Physico-chemical sampling		Faunal sampling
				Interface water	Pore water in sediments	
Bioturbated sediments (Bio)	40°51.28'	28°10.20'	1122	1x1 minute MicroCat measurements: temperature, salinity	2 tube cores: SO <sub>4</sub> <sup>2-</sup> , Cl <sup>-</sup> profiles	1 blade core: Bio (13 cm)
Reduced sediments (Red)	40°51.27'	28°10.19'	1121	3x1 minute MicroCat measurements: temperature, salinity  3x2 water samples: CH <sub>4</sub> , pH	3x2 tube cores: O <sub>2</sub> , SO <sub>4</sub> <sup>2-</sup> , Cl <sup>-</sup> profiles	3 blade cores: Red1 (12 cm) Red2 (20 cm) Red3 (12 cm)
Carbonate crusts (CC)	40°51.27'	28°10.19'	1111	None	None	3 pieces of crust: CC1 (459 cm <sup>2</sup> ) CC2 (368 cm <sup>2</sup> ) CC3 (189 cm <sup>2</sup> ) + CC <sub>Box</sub>

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**Table 2**

Visual observations of sediment colour in the Bio and Red microhabitats. Temperature, salinity, dissolved oxygen and methane concentrations and pH measurements at the sediment-water interface in microhabitat samples from the Marmara Sea are also given (MarNaut cruise, 2007).

	Visual observations	Temperature	Salinity	[O <sub>2</sub> ]	[CH <sub>4</sub> ]	pH
<b>Bio</b>	Brown sediments at the top, reduced sediments the bottom	14.52	38.77	-	-	-
<b>Red1</b>	Reduced sediments throughout core	14.52	38.76	22.9 ± 13.1 µM	0.33 ± 0.04 µM	7.93 ± 0.01
<b>Red2</b>		14.52	38.76	22.8 µM	0.7 ± 0.28 µM	7.94 ± 0.02
<b>Red3</b>		14.52	38.77	50.9 ± 0.3 µM	0.14 ± 0.03 µM	7.89 ± 0.04

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**Table 3**

Relative macrofaunal (>250 µm) abundances (%) and total absolute abundances in the three microhabitats studied: bioturbated sediment (Bio, n=1), reduced sediment (Red, n=3) and carbonate crust (CC, n=3) microhabitats. Specimens recovered at the bottom of the sampling box (CC<sub>Box</sub>) are also reported. Total relative abundance from each taxonomic group is highlighted in bold. All samples are from the north-eastern Central basin in the Marmara Sea (MarNaut cruise, 2007). \* Taxonomic level used for alpha-diversity analyses.

Taxonomic groups	Reduced sediments					Carbonate crusts				
	Bio	Red1	Red2	Red3	Avg. ± SD	CC1	CC2	CC3	Avg.±SD	CC <sub>Box</sub>
<b>Porifera (Total)</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0.65</b>
Demospongia*	0	0	0	0	0	0	0	0	0	0.65
<b>Cnidaria (Total)</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>8.24</b>	<b>1.16</b>	<b>1.08</b>	<b>3.49±4.11</b>	<b>0</b>
Anthozoa - Zoantharia										
Parazoanthidae*	0	0	0	0	0	7.62	0.12	0	2.58±4.37	0
<i>Isozoanthus</i> sp.1	0	0	0	0	0	0.12	0.12	0	0.08±0.07	0
<i>Isozoanthus</i> sp.2	0	0	0	0	0	7.50	0	0	2.50±4.33	
Anthozoa - Actiniaria										
Sagartiidae*	0	0	0	0	0	0.62	1.04	1.08	0.84±0.23	0
<i>Sagartiogeton</i> sp.	0	0	0	0	0	0.62	0.81	1.08	0.84±0.23	0
Medusozoa – Scyphozoa*	0	0	0	0	0	0	0.23	0	0.08±0.13	0
<b>Polychaeta (Total)</b>	<b>36.02</b>	<b>99.23</b>	<b>98.25</b>	<b>90.90</b>	<b>96.13±4.54</b>	<b>16.60</b>	<b>17.58</b>	<b>3.23</b>	<b>12.47±8.02</b>	<b>32.03</b>
Ampharetidae*	0.54	29.46	3.52	54.54	29.17±25.52	4.31	7.45	2.15	4.64±2.67	11.77
Capitellidae*	0	0	0	0	0	0	0.12	0	0.04±0.07	0
Cirratulidae*	0	0	0	0	0	4.55	0.35	0	1.63±2.53	1.96
Cossuridae*	1.61	0	0	0	0	0	0	0	0	0
Dorvilleidae*	0	69.77	91.23	27.27	62.76±32.55	5.04	6.17	1.08	4.10±2.68	2.61
Flabelligeridae*	1.08	0	0	0	0	0	0	0	0	0
Hesionidae*	0	0	0	0	0	1.72	1.40	0	1.04±0.91	1.96
Lumbrineridae*	2.69	0	0	0	0	0	0	0	0	0
Paraonidae*	20.43	0	0	0	0	0	0	0	0	0
Pholoidae*	0	0	1.75	0	0.58±1.01	0	0	0	0	0
Phyllodocidae*	0.54	0	0	0	0	0	0	0	0	0.66
Spionidae*	5.90	0	0	0	0	0.98	2.09	0	1.03±1.05	13.07
Syllidae*	3.23	0	0	0	0	0	0	0	0	0
Unid. Families*	0	0	1.75	9.09	3.62±4.82	0	0	0	0	0
<b>Bivalvia (Total)</b>	<b>50.01</b>	<b>0.77</b>	<b>0</b>	<b>0</b>	<b>0.26±0.45</b>	<b>10.33</b>	<b>8.96</b>	<b>68.81</b>	<b>29.37±34.17</b>	<b>24.84</b>
Lucinidae*	19.89	0	0	0	0	0	0	0	0	1.31
<i>Lucinoma kazani</i>	1.61	0	0	0	0	0	0	0	0	0
<i>Myrtea amorpha</i>	0	0	0	0	0	0	0	0	0	1.31
Unid. Lucinidae	18.28	0	0	0	0	0	0	0	0	0
Mytilidae*	0	0	0	0	0	10.08	8.84	68.81	29.25±34.27	9.15
Mytilidae nov. sp.	0	0	0	0	0	10.08	8.84	68.81	29.25±34.27	9.15
Vesicomomyidae*	2.15	0	0	0	0	0	0	0	0	7.84
<i>Isorropodon perplexum</i>	1.61	0	0	0	0	0	0	0	0	7.84
Unid. Vesicomomyidae	0.54	0	0	0	0	0	0	0	0	0
Yoldiidae*	5.38	0.77	0	0	0.26±0.45	0	0	0	0	0
<i>Yoldiella striolata</i>	5.38	0.77	0	0	0.26±0.45	0	0	0	0	0
Sareptidae*	2.69	0	0	0	0	0	0	0	0	0
Montacutidae*	16.67	0	0	0	0	0	0	0	0	0
Unid. Families*	3.23	0	0	0	0	0.25	0.12	0	0.12±0.12	6.54

<b>Gastropoda (Total)</b>	<b>1.61</b>	<b>0</b>	<b>1.75</b>	<b>9.10</b>	<b>3.62 ± 4.82</b>	<b>64.58</b>	<b>72.18</b>	<b>26.88</b>	<b>54.54±24.26</b>	<b>40.52</b>
Pyramidellidae*	0.54	0	0	0	0	0	0	0	0	0
<i>Odostomia</i> sp.	0.54	0	0	0	0	0	0	0	0	0
Trochidae*	0	0	0	0	0	0	0	1.08	0.36±0.62	0
<i>Putseysia wiseri</i>	0	0	0	0	0	0	0	1.08	0.36±0.62	0
Elachisnidae*	0	0	0	0	0	64.58	72.18	25.80	54.18±24.87	40.52
<i>Laeviphitus verduini</i>	0	0	0	0	0	64.58	72.18	25.80	54.18±24.87	40.52
Xyladisculidae*	0	0	0	4.55	1.52±2.62	0	0	0	0	0
<i>Xylodiscula</i> sp.	0	0	0	4.55	1.52±2.62	0	0	0	0	0
Unid. Families*	1.07	0	1.75	4.55	2.10±2.29	0	0	0	0	0
<b>Aplacophora (Total)</b>	<b>2.14</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>
Chaetodermatidae*	2.14	0	0	0	0	0	0	0	0	0
<i>Falcidens guttuosus</i>	1.61	0	0	0	0	0	0	0	0	0
<i>Prochaetoderma</i> sp.	0.53	0	0	0	0	0	0	0	0	0
<b>Crustacea (Total)</b>	<b>5.38</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0.25</b>	<b>0.12</b>	<b>0</b>	<b>0.12±0.12</b>	<b>1.96</b>
Amphipoda-Gammarida										
Oedicerotidae*	3.76	0	0	0	0	0	0	0	0	0
<i>Perioculodes</i> aff. <i>longimanus</i>	3.76	0	0	0	0	0	0	0	0	0
Lysianassidae*	0	0	0	0	0	0.25	0.12	0	0.12±0.12	1.96
<i>Lysianassa longicornis</i>	0	0	0	0	0	0.25	0.12	0	0.12±0.12	1.96
Cumacea										
Diastylidae*	0.54	0	0	0	0	0	0	0	0	0
<i>Diastylodes serrata</i>	0.54	0	0	0	0	0	0	0	0	0
Unid. Families (juvenile)*	1.08	0	0	0	0	0	0	0	0	0
<b>Echinodermata (Total)</b>	<b>2.15</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>
Echinoida-Spatangoida										
Brissidae*	2.15	0	0	0	0	0	0	0	0	0
<i>Brissopsis</i> sp.	2.15	0	0	0	0	0	0	0	0	0
<b>Total abundances (number of individuals)</b>	<b>186</b>	<b>129</b>	<b>57</b>	<b>22</b>	<b>69±55</b>	<b>813</b>	<b>859</b>	<b>93</b>	<b>588±430</b>	<b>153</b>

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**Table 4**

Relative meiofaunal abundances (%) and total absolute abundances in the three microhabitats studied: bioturbated sediment (Bio, n=1), reduced sediment (Red, n=3) and carbonate crust (CC, n=3) microhabitats. All samples are from the north-eastern part of the Central basin of the Marmara Sea (MarNaut cruise, 2007). (\*\*) This proportion is largely underestimated since only the meiofauna >250 µm was sampled. No meiofauna was found in CC<sub>Box</sub>. \* Taxonomic level used for alpha-diversity analyses.

Taxa	Reduced sediments					Carbonate crusts			
	Bio	Red1	Red2	Red3	Avg.±SD	CC1	CC2	CC3	Avg.±SD
<b>Nematoda* (Total)</b>	<b>79.88</b>	<b>99.81</b>	<b>99.74</b>	<b>100</b>	<b>99.85±0.13</b>	<b>79.03</b>	<b>95.68</b>	<b>85.00</b>	<b>86.58±8.43</b>
<b>Crustacea (Total)</b>	<b>18.66</b>	<b>0.19</b>	<b>0.26</b>	<b>0</b>	<b>0.15±0.13</b>	<b>20.97</b>	<b>4.32</b>	<b>15.00</b>	<b>13.43±8.44</b>
Copepoda-Harpacticoida									
Miraciidae*									
<i>Typhamphiascus confusus</i>	13.12	0	0	0	0	16.83	0.32	15.00	10.72±9.05
<i>Typhamphaiscus</i> sp.	0.29	0	0	0	0	0	0	0	0
Ameiridae*									
<i>Amphiascus</i> sp.	0	0	0	0	0	1.65	1.28	0	0.98±0.87
<i>Ameira longipes</i>	0	0	0	0	0	0.33	0	0	0.11±0.19
Ameridae n. gen.	0	0	0	0	0	0.17	1.12	0	0.43±0.60
<i>Haifamera archibenthica</i>	1.46	0	0	0	0	0	0.16	0	0.05±0.09
Pseudotachidiidae*									
<i>Pseudotachidius coronatus</i>	0.29	0	0	0	0	0	0	0	0
Tisbidae*									
<i>Tisbella</i> sp.	0	0	0	0	0	0.83	0.64	0	0.49±0.43
Laophontidae*									
<i>Archesola typhlops</i>	0	0	0	0	0	0.17	0	0	0.06±0.10
Harpacticoida Juvenile	1.75	0	0	0	0	0.99	0.64	0	0.54±0.50
Copepoda-Cyclopoida									
Cyclopinidae*									
<i>Cyclopina</i> sp.1	0.88	0.15	0	0	0.05±0.09	0	0	0	0
<i>Cyclopina</i> sp.2	0.29	0	0	0	0	0	0	0	0
Copepoda-Calanoidea									
Unid. Calanoidea*	0	0	0	0	0	0	0.16	0	0.05±0.09
Ostracoda									
Cytherellidae*									
<i>Cytherella vulgata</i>	0.29	0	0	0	0	0	0	0	0
Potocypridae*									
<i>Proponcypris</i> cf. <i>levis</i>	0.29	0.04	0	0	0.01±0.02	0	0	0	0
<i>Proponcypris</i> sp.1	0	0	0.13	0	0.04±0.07	0	0	0	0
<i>Proponcypris</i> sp.2	0	0	0.13	0	0.04±0.07	0	0	0	0
<b>Chelicerata (Total)</b>	<b>1.46</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>
Unid. family Acarina*	1.46	0	0	0	0	0	0	0	0
% meiofauna / Total fauna**	64.8	95.4	93.3	98.3	95.7±2.5	42.7	42.2	17.7	34.2±14.3
<b>Total abundances (number of individuals)</b>	<b>343</b>	<b>2 696</b>	<b>797</b>	<b>1 274</b>	<b>1 589±988</b>	<b>606</b>	<b>626</b>	<b>20</b>	<b>417±344</b>

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**Table 5**

Biological descriptors of the three sampled microhabitats in the Marmara Sea. The numbers equivalents of Shannon and Simpson indices are given in italics. The highest values are highlighted in bold. Meiofaunal data is presented notwithstanding the incomplete sampling protocol.

Biological descriptors	Bioturbated sediments	Reduced sediments	Carbonate crusts
Macrofauna -dominant	Bivalves and polychaetes, reaching respectively 50 and 36% of total abundance	Large dominance of polychaetes, reaching a mean of 96.1% of total abundance (Dorvilleidae, Ampharetidae)	Gastropods and bivalves in various proportions, reaching a mean of 54.5 and 29.4% of total abundance, respectively
Macrofauna -others	Gastropods, crustaceans, aplacophora, chelicerates, echinoids	Bivalves, gastropods	Cnidarians, polychaetes, crustaceans
Macrofaunal densities	9 300 ind/m <sup>2</sup>	3 433 ± 2 740 ind/m <sup>2</sup>	<b>15 325 ± 9 440 ind/m<sup>2</sup></b>
Jaccard's similarity coefficient <sup>a</sup>	-	0.44	0.54
Symbiont-bearing fauna	3.8%	0%	<b>8.9 – 68.8%</b>
Mean total biomass (kg ww/m <sup>2</sup> )	0.0018	0.0019 ± 0.001	<b>0.806 ± 0. 25</b>
<b>Macrofaunal diversity indices</b>			
Richness (S) <sup>b</sup>	<b>21</b>	7	18
Shannon (H <sub>e</sub> ) <sup>b</sup> <i>Exp (H<sub>e</sub>)</i>	<b>2.42</b> <i>11.25</i>	0.77 <i>2.16</i>	1.37 <i>3.94</i>
Simpson (D <sub>GS</sub> ) <sup>b</sup> <i>(1 / 1 - D<sub>GS</sub>)</i>	<b>0.87</b> <b>7.73</b>	0.43 <i>1.76</i>	0.56 <i>2.29</i>
Evenness (J') <sup>b</sup>	<b>0.79</b>	0.39	0.47
Meiofauna -dominant	Nematodes with 81% of the total abundance	Nematodes with nearly 99.9% of the total abundance	Nematodes with 86.6% of the total abundance
Meiofauna -others	Copepods, nauplii, ostracods (19%)	Copepods, ostracods (0.1%)	Copepods (13.4%)
Meiofaunal densities	16 900 ind/m <sup>2</sup>	<b>79 450 ± 49 396 ind/m<sup>2</sup></b>	10 424 ± 8 331 ind/m <sup>2</sup>
Jaccard's similarity coefficient <sup>a</sup>	-	0.50	0.52
<b>Meiofaunal diversity indices</b>			
Total richness (S) <sup>b</sup>	<b>9</b>	3	6
Copepoda richness (S) <sup>b</sup>	<b>5</b>	1	5
Ostracoda richness (S) <sup>b</sup>	<b>2</b>	1	0
Acarina richness (S) <sup>b</sup>	<b>1</b>	0	0
Shannon (H <sub>e</sub> ) <sup>b</sup> <i>Exp (H<sub>e</sub>)</i>	<b>0.76</b> <i>2.14</i>	0.01 <i>1.01</i>	0.47 <i>1.60</i>
Simpson (D <sub>GS</sub> ) <sup>b</sup> <i>(1 / 1 - D<sub>GS</sub>)</i>	<b>0.35</b> <b>1.53</b>	0.002 <i>1.00</i>	0.22 <i>1.28</i>
Evenness (J') <sup>b</sup>	<b>0.34</b>	0.01	0.26

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<sup>a</sup> Mean Jaccard's similarity coefficient computed without  $CC_{Box}$ ,

<sup>b</sup> Diversity indices are given for macrofaunal and meiofaunal data with  $CC_{Box}$  included in both case.

**Table 6**

Review of the characteristics of different cold seep sites described by different authors, in terms of habitat, dominant fauna and related environmental conditions. This non-exhaustive list was compiled according to the availability of environmental data. SS: soft sediments, Co: concretions, Co/SS: concretions surrounded by soft sediments, GH/SS: gas hydrates within soft sediments.

Sites	Habitat type	Substratum	Dominant fauna	O <sub>2</sub> µmol/l	CH <sub>4</sub> µmol/l	SO <sub>4</sub> <sup>2-</sup> mmol/l	Authors
Gulf of Cadiz Cap. Arutyunov MV	Siboglinidae fields	SS	<i>Siboglinum poseidoni</i>	No data	0.3 – 1.1	30	Niemann et al., 2006a; Sommer et al., 2009a
Hydrate Ridge Southern Summit	Clam beds	SS	<i>Calyptogena pacific,</i> <i>C. kilmeri</i>	20	0.6	28	Sahling et al., 2002; Torres et al., 2002
	Microbial mats	GH/SS	<i>Beggiatoa sp.</i>	20	1	28	“
Olimpi field - MedRidge Napoli MV	Siboglinidae bushes	SS	<i>Lamelibranchia aff. anaximandri</i>	202 – 212	0.35	31	Ritt et al., in prep.
	Carbonate crusts	Co	<i>Lurifax vitreus,</i> Porifera	196 – 199	2.27 – 4.29	31	“
Anaximandre Mounds Amsterdam MV	Reduced sediments	SS	<i>Isorropodon aff. perplexum</i>	188 - 192	12.5	28 - 31	“
	Carbonate crusts	Co	Serpulid polychaetes	194 – 202	0.25 – 0.6	31	“
Nile deep-sea fan Cheops MV	Reduced sediments	SS	Spionid, hesionid polychaetes	No data	3.7 – 7.7	No data	“
Eel River Basin	Clam beds	SS	<i>Calyptogena pacific</i>	25-100	1 000	6.5	Levin et al., 2003; Orphan et al., 2004
	Microbial mats	GH/SS	<i>Beggiatoa sp.</i>	< 0.1	6500	6.3	“
Gulf of Mexico Green Canyon	Mussel beds	SS	<i>Bathymodiolus childressi</i>	129	21	30	Aharon et Fu, 2003; Bergquist et al., 2005
Alaska margin off Unimak island	Clam beds	SS	<i>Vesicomya extenta,</i> <i>V. diagonalis</i>	200	No data	28	Rathburn et al., 2009
	Siboglinidae fields	SS	<i>Siphonobranchia sp.</i>	140	No data	28	“
New Zealand margin	Ampharetidae fields	SS	Ampharetid polychaetes	197	1962	No data	Sommer et al., 2009b
Gulf of Guinea Giant pockmark Regab	<i>Calyptogena</i> beds	SS	<i>Calyptogena regab,</i> <i>Vesicomya aff. chuni</i>	211 – 238	0.4 – 3.4	No data	Olu-Le Roy et al., 2007
	Mytilidae Beds	SS/Co	<i>Bathymodiolus aff. boomerang</i>	230 – 240	0.7 – 23.2	No data	“

	Siboglinidae fields	Co	<i>Escarpia southwardae</i>	218 – 232	0.63 – 2.43	No data	“
Norwegian margin Håkon Mosby MV	Siboglinidae fields	SS	<i>Oligobrachia haakonmosbiensis</i> , <i>Siboglinum contortum</i>	270	0.7	28	Niemann et al., 2006b
	Microbial mats	SS	<i>Beggiatoa sp.</i>	270	0.3	28	“
	Centre	SS	Meiofauna (Copepoda)	270	5.7	28	Niemann et al., 2006b; Van Gaever et al., 2006
Nankai Trench Off Kumano	Clams beds	SS	<i>Calyptogena spp.</i>	No data	0.006	28.3	Toki et al., 2004
	Tubeworms	SS	Vestimentiferan?	No Data	0.006 – 300	28.2	“
	Microbial mats	SS		No Data	0.2 – 300	28.5	“
<b>This study</b>	Reduced sediments	SS	Ampharetid, dorvilleid polychaetes	18 – 51	0.14 – 0.7	19 – 26	Ritt et al.
	Bioturbated sediments	SS	Paraonid polychaetes, lucinid bivalves	No data	No data	31	“
	Carbonate crusts	Co	<i>Idas sp. nov.</i>	No data	No data	No data	“

Resume of the range of chemical concentrations for the different substratum and assemblage types (all studies combined). Higher values are highlighted in bold.

	Substratum	Dominant fauna	O <sub>2</sub> µmol/l	CH <sub>4</sub> µmol/l	SO <sub>4</sub> <sup>2-</sup> mmol/l
	GH/SS	Microbial mats	< 0.1 - 20	1 – <b>6 500</b>	6.3 - 28
	SS	Polychaetes	18 - <b>270</b>	0.14 - 1962 (0.006)	19 - <b>31</b>
		Bivalves	20 - 238	0.4 - 1000 (0.006)	6.5 - <b>31</b>
		Microbial mats	<b>270</b>	0.2 - 300	28 - 28.5
		Copepods	<b>270</b>	5.7	28
	SS/Co	Bivalves	230 - 240	0.7 - 23.2	
	Co	Gastropods		2.27 - 4.29	
		Polychaetes	194 - 232	0.25 - 2.43	31

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