



Monterey Bay cold seep infauna: quantitative comparison of bacterial mat meiofauna with non-seep control sites

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Cold seeps in Monterey Bay are sites of low fluid discharge from sea floor sediments mediated by one of several geologic processes (Barry et al. 1996, 1997). Sediment in the upper 10 cm of seeps is usually enriched in either hydrogen sulphide or methane or both. The presence of these compounds relatively close to the sediment-water interface supports the development of dense mats of sulphur-oxidizing bacteria (*Beggiatoa* sp. and *Thioploca* sp.) and vesicomyid clams (*Calyptogena* sp.) or other megafauna that utilize sulphide indirectly via nutritional reliance on endosymbiotic chemolithoautotrophic bacteria. Chemosynthetic production at these deep (600-900 m) cold seeps may stimulate other assemblages that either graze directly on seep organisms or indirectly via trophic links with seep and non-seep biota. In shallow water (<10 m) sites dominated by sulphide-oxidizing chemoautotrophic species, up to 50% of the infaunal respiration demands were met through this pathway (Fenchel & Bernard, 1995). Other sulphide-rich marine habitats are also linked to trophic enrichment from chemosynthetic production (Montagna & Spies, 1985 and references therein).

This study focuses on the protistan and other meiofaunal organisms inhabiting sediments of cold seeps in Monterey Bay. We present quantitative estimates of their abundance in samples collected from sedimentary habitats at seeps and nearby non-seep control sites.

Infaunal biota were sampled from push cores (7 cm diameter x ~15 cm deep) collected from the Clam Field cold seep site at 906 m depth in Monterey Bay, California, U.S.A. between September 1996 and September 1997 using the ROV *Ventana*. Cores were taken from mats of chemolithoautotrophic bacteria (*Beggiatoa* sp. and *Thioploca* sp.; seep, n=13) or from an area outside the seep boundary (3-50 m) as defined by the distribution of clams and bacterial mats (control, n=12). Cores were subsampled

using a 60 cc syringe (2.6 cm diameter) with its Luer end removed. The top centimeter of sediment was preserved with 2% glutaraldehyde in filtered seawater (FSW). Aliquots of the preserved, mixed sediment slurry were placed on a density gradient of 50% FSW-50% Percoll and centrifuged to separate organisms from sediment particles (Starink et al., 1994). After staining with the fluorochrome DAPI, the supernatant was filtered onto a 3 µm pore size polycarbonate filter, and organisms were observed and counted under epifluorescence microscopy. Biovolumes were determined using standard geometric formulas. Differences among sites in the mean biovolume of each taxon were assessed by ANOVA, and multiple comparisons were performed using a Student-Newman-Keul test.

Five major groups of eukaryotic organisms were present in both seep and control samples: euglenoids, ciliates, atestate Foraminifera (allogromiids), testate Foraminifera and nematodes. The total biovolume of organisms from seep samples was only slightly higher than at control site cores (Fig. 1). Nematodes dominated the biovolume of the seep samples and Foraminifera were the largest component of the controls. A two-way analysis of variance on site (seep/control) and taxa (euglenoids, ciliates, allogromiids, Foraminifera and nematodes) resulted in a significant ($P=0.00077$) seep-taxon interaction term, suggesting that the difference in mean biovolume between seep and control samples was associated with some, but not all, taxa. Subsequent analyses showed that mean nematode and ciliate biovolumes were significantly higher at seep than control sites ($P=0.008$ and 0.003 respectively), while no significant differences were observed for other taxa. In addition, biovolumes of nematodes and Foraminifera were significantly ($P<0.05$) higher than other meiofaunal taxa at the seep and control sites. Many species of seep euglenoids and ciliates possessed either endo- or epibiotic bacteria.

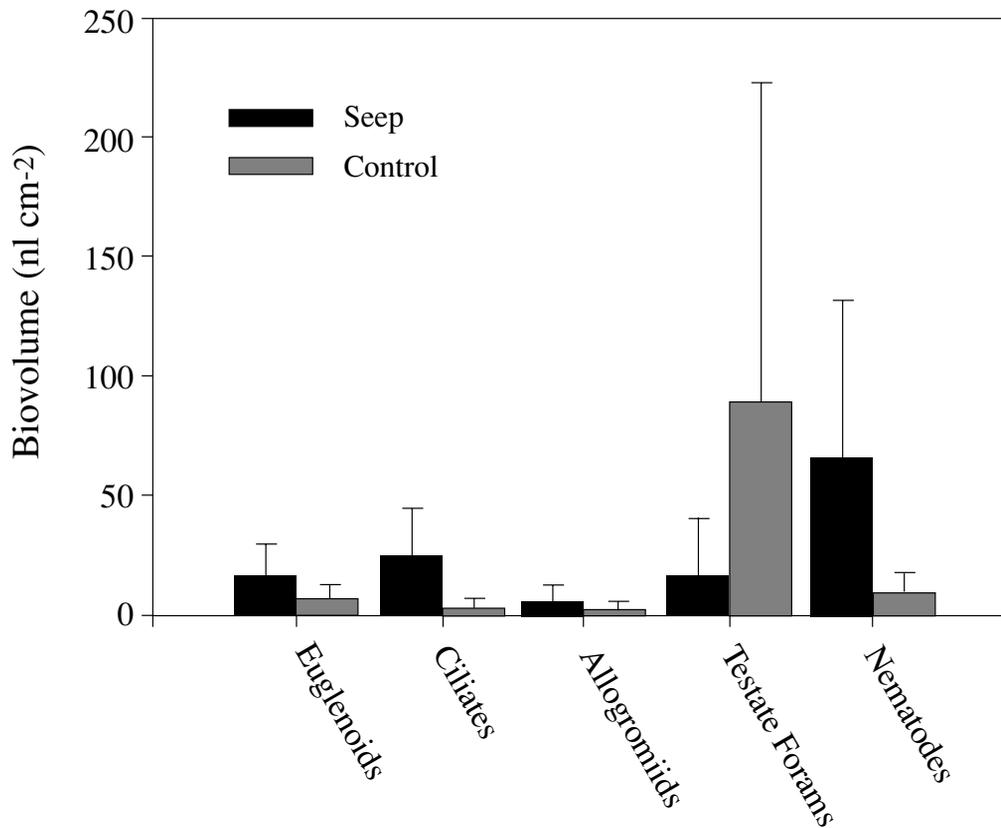


Figure 1. Mean (\pm S.D.) biovolume of 5 meiofaunal taxa from seep ($n=13$) and control ($n=12$) sites at 906 m in Monterey Bay, California, USA.

The high incidence of symbiotic relationships between bacteria and seep protists is unusual compared to previously studied sedimentary habitats, and suggests that processes other than phagotrophic uptake of free-living chemoautotrophic bacterial productivity may be important at these seeps.

Bernard & Fenchel (1995), who present the only other comprehensive survey of protists from bacterial mats, report a range of protistan biovolumes from 12 to 170 nl cm⁻² for eight samples from a shallow (<10 m) *Beggiatoa*-dominated environment. We measured protistan biovolumes of 10-87 nl cm⁻² in seep samples and 3-36 nl cm⁻² from control cores at the 906 m site.

In contrast to surveys of protistan fauna, several studies have documented the larger organisms from various seeps. In concordance with our findings, nematodes are the predominant metazoan in a number of other studies (Bernard & Fenchel, 1995; Montagna & Spies, 1985; Shirayama & Ohta, 1990; Montagna et al., 1989; Kamenev et al., 1993). The range of nematode abundance reported from these studies is 0.1 to 338 nematodes cm⁻² for seeps, compared to our estimates of 9 to 307 cm⁻². Studies

including estimates of nematode abundance from seep and control sites (Shirayama & Ohta, 1990; Montagna & Spies, 1985) do not report enhanced nematode abundance in seep samples. We observed significantly ($P<0.05$) elevated nematode abundance at seep sites (179 ± 184 cm⁻²) compared to control samples (82 ± 52 cm⁻²).

Thiobiotic nematodes have been observed to have a more slender morphology than oxybiotic species (Jensen, 1987). We found no difference in the relationship of body length (log-transformed) and body diameter (log-transformed) between seep and control samples (Fig. 2). In fact, the nematodes with the largest body diameter were from seep samples.

It is evident from this preliminary work that considerable variability exists in the composition of meiofauna assemblages associated with the bacterial mats at cold seeps and corresponding control sites we have examined for this study. Nevertheless, several trends concerning faunal patterns are evident; 1) nematodes are the dominant biomass contributor to the meiofauna of bacterial mat assemblages, 2) Foraminifera are the dominant component at control sites, 3) nematodes in Monterey Bay do not share the

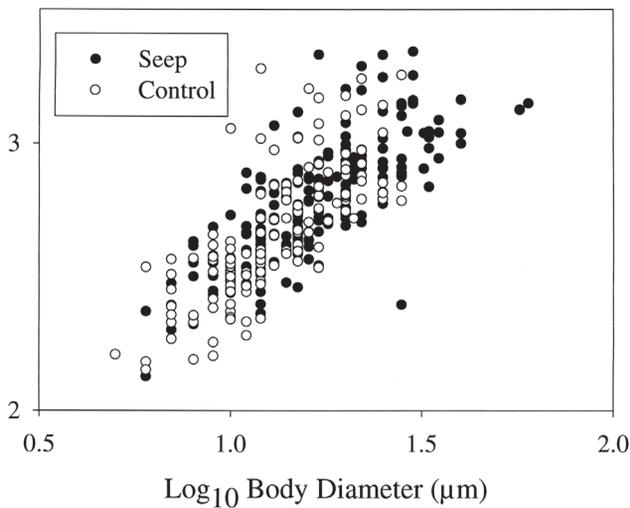


Figure 2. Body length vs body diameter for nematodes collected from seep and control sites at 906 m in Monterey Bay, California, USA.

morphology peculiar to thiobiotic and oxybiotic nematodes of shallow bacterial mats, and 4) symbiotic relationships between bacteria and protists may play an important role in the survival of eukaryotic organisms in this environment. These conclusions are somewhat speculative considering the limited scope and small sample size of this study, but may form the basis for testable hypotheses concerning factors regulating the faunal composition of low oxygen sites in Monterey Bay and elsewhere.

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