

# BENTHIC COMMUNITY STRUCTURE AND FUNCTION OF THE DEEP EASTERN MEDITERRANEAN SEA

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## Abstract

During the last 20 years, new technological developments and the application of advanced environmental monitoring methods in concert with a proliferation of multidisciplinary research programmes have gradually changed our perception of the structure and function of the deep Mediterranean deep Sea. It is now considered a dynamic environment linked to upper water column processes and also influenced by major geo-morphological features (abyssal basins, seamounts, submarine canyons, etc.) that shape its benthic community structure.

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Reviews on the biology and ecology of the Mediterranean deep sea have been published in recent years [1-3]. Studies of the Eastern Mediterranean bathyal and abyssal fauna have revealed significant correlations between faunal abundances and biomass, and factors indicating food availability, all being at very low levels compared to temperate regions [4]. The abyssal basins of the Eastern Mediterranean are extremely unusual deep-sea systems. With water temperatures at 4000 m in excess of 14°C (rather than <4°C for the deep oceanic basins) the entire benthic environment is as hot as the water around a hydrothermal vent system, but lacks the vents rich chemical energy supply.

The Mediterranean also differs from other deep-sea ecosystems in terms of its species composition [5]. *Acanthephyra eximia* appears to have functionally replaced *Eurythenes gryllus*, the dominant deep-sea scavenging crustacean throughout most of the world's oceans, while *Chalinura mediterranea* (a much smaller grenadier) has retained the role of *Coryphaenoides armatus*. Typical deep-water groups, such as echinoderms, glass sponges and macroscopic foraminifera (Xenophyophora) are absent in the deep Mediterranean, while other faunistic groups (fishes, decapod crustaceans, mysids and gastropods) are poorly represented compared to the NE Atlantic.

Barriers to colonisation of the Mediterranean include the differences in temperature, salinity, and food supply between the Atlantic and Mediterranean, as well as the existence of shallow sills. Despite these difficulties and the relative youth of the system a deep-sea fauna has developed, although it is impoverished compared to that of the oceans. Even if the deep Mediterranean is generally considered a "biological desert", times do come when certain areas display such high benthic activity as to be characterised as "benthic hotspots" [4]. These areas are in most cases located at the mouth of submarine canyons that transport, through flush flooding, sediment failure and dense shelf water cascading, large amounts of sediment and organic matter to the deep sea [6]. Large-scale hydrographic changes (Eastern Mediterranean Transient, EMT) have also been implicated in enhancing the productivity of the euphotic zone and indirectly the structure of the underlying deep benthic communities [7].

Recently it was concluded that deep-sea fauna is highly vulnerable to environmental alteration, and that deep-sea biodiversity can also be affected by very small temperature changes [7]. Thus the potential large-scale consequences of climate change are already evident in the structure of deep-sea communities. The impoverished "energy-thirsty" deep-sea benthic microbial community in the Eastern Mediterranean has been found to respond rapidly to inputs of fresh organic matter [8]. Microbial communities have been investigated at several sites around the deep Eastern Mediterranean Sea [9] and found to be characterised by the existence of a well developed (consisting of several levels) benthic microbial loop.

The use of molecular-based techniques and the construction of large clone libraries of the 16S rRNA genes have revealed that the total sequence richness of bacterial communities inhabiting the energy poor sediments of the Eastern Mediterranean is extremely high (Figure 1) and comparable to estimates obtained from microbiota inhabiting terrestrial ecosystems [9]. This could be an adaptation that has evolved so that a system under starvation stress is able to utilise any quantity or quality of organic matter available.

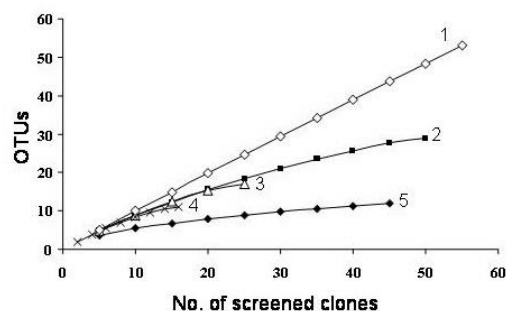


Fig. 1. Rarefaction analysis of 16S rDNA sequence heterogeneity in clone libraries from deep-sea sediments worldwide. Total numbers of screened clones are plotted against unique operational taxonomic units (OTUs). Library 1 derived from the deep Eastern Mediterranean Sea from a depth of 2970 m [9]. Libraries 2 and 5 originated from the Japan Trench at a depth of 6400 m (Li et al., 1999. *Mar. Biotechnol.* 1: 391-400). Library 3 derived from the Suruga Bay at a depth of 1159 m and library 4 from the Japan Trench at a depth of 6379 m (Li et al., 1999. *Biodivers. Conserv.* 8: 659-677).

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