

# NEW PERSPECTIVES AND CHALLENGES IN THE STUDY OF DEEP-SEA PROKARYOTES - THEIR ROLE IN BIOGEOCHEMICAL CYCLES, AND THEIR POTENTIAL INDUSTRIAL APPLICATIONS

Gerhard Herndl<sup>1</sup>\*, Christian Tamburini<sup>2</sup> and Laura Giuliano<sup>3</sup>

<sup>1</sup> Department of Biological Oceanography, Royal Netherlands Institute for Sea Research, P.O. Box 59, 1790 AB Den Burg, Texel, The Netherlands - herndl@nioz.nl

<sup>2</sup> CNRS/INSU - UMR 6117. Campus de Luminy - Case 901. TPR2, 7ème étage. 163 avenue de Luminy. 13288, Marseille CEDEX 09, France

<sup>3</sup> CIESM, 16, Bd. De Suisse, MC 98000 Monaco; Institute for the Coastal Marine Environment (IAMC) 98122 Messina, CNR, Italy

## Abstract

Deep-sea prokaryotes (DSP) adapted, diversified and evolved over billions of years and represent a virtually untapped resource for industrial purposes. Recently, a number of novel metabolic pathways have been discovered shedding new light on the dark ocean's prokaryotes. Non-thermophilic Archaea have been recently discovered to represent the major source of autochthonously produced organic carbon in the deep sea and play a major role in deep-water nitrification outnumbering bacterial nitrifiers in the oxygen minimum zones of the mesopelagic ocean. Anaerobic ammonium and methane oxidizers have been found in the dark ocean's sediments and even more recently, in the deep oceanic water column. The Mediterranean Sea offers unique opportunities to study these DSP as it represents one of the very few seas with warm deep-waters. Field results from the CIESM-SUB campaigns have begun to address some key issues in the microbial oceanography of the Mediterranean Sea.

**Keywords :** *Bacteria, Deep Sea Processes, Organic Matter.*

Microbes are the main drivers of the energy and matter flux in the sea. Essentially all our knowledge on the functioning of the microbial food web in the ocean originates from the surface ocean. However, more than 70% of the ocean's volume is considered the deep ocean and this dark oceanic realm, particularly the bathypelagic water column has been poorly studied. Consequently, our knowledge on the vertical distribution and functional variability of deep-sea prokaryotes in the ocean's interior are still poorly known despite recent advances in elucidating their phylogenetic and metabolic characteristics.

While the abundance of prokaryotes decreases from the sunlit surface waters to the deep ocean by one to two orders of magnitude and their overall activity by at least two orders, the diversity of DSP is only about 25% lower than in surface waters. Despite their overall low activity, DSP are play a major role in the biogeochemical cycling of material due to the sheer volume of the dark ocean. Heterotrophic DSP are responsible for the processing of refractory organic matter sinking from the sunlit surface layers into the dark ocean's realm. This substrate processing is done under high hydrostatic pressure conditions leading to specific adaptations. Piezophilic (barophilic) bacteria have been isolated from the deep ocean. Based on molecular analyses, the notion emerges that deep-sea bacteria originate from psychrophilic bacteria. This finding, however, is based on studies performed in the deep Atlantic and Pacific. The warm deep waters of the Mediterranean Sea offer here a great opportunity for comparative studies on DSP. It has been shown, using clone libraries and sequencing, that the bacterial community composition of the deep Mediterranean is substantially different from that in the deep Atlantic [1]. Anaerobic ammonia oxidizers have been isolated in the marine environment first in sediments, however, these anammox bacteria have been found recently also in the suboxic waters of the Black Sea and in the mesopelagic waters of the Benguela and Peruvian upwelling area. Anaerobic methane oxidizers, discovered less than 10 years ago, are now found consistently in slope and deep sediments frequently in close association with sulfate reducers. Non-thermophilic Archaea contribute similarly to the total abundance of DSP as Bacteria [2]. While one of the major groups of the Archaea, the Euryarchaea, do not exhibit major variations in their abundance throughout the water column, the other major group, the Crenarchaea, increase in their relative abundance with depth. A major fraction of the mesopelagic crenarchaeal community is oxidizing ammonia [3] and using inorganic carbon as carbon source [4]. Thus, they represent dark ocean chemoautotrophs. Quantitative PCR using the *amoA* gene of Bacteria and Crenarchaea revealed that crenarchaeal *amoA* genes dominate over bacterial *amoA* genes in the oxygen minimum layer of the Atlantic. Whether crenarchaeal nitrification prevails over bacterial nitrification in the oxygen minimum layers of the ocean remains to be shown, however. Generally, the richness of archaeal phylotypes is only about half of the bacterial richness in the deep ocean. Noteworthy, however, is the fact the bathypelagic Crenarchaea are apparently not chemoautotrophs but heterotrophs, utilizing efficiently D-amino acids commonly considered refractory for microbial utilization [5].

Using a genomic approach, [6] detected a number of functional genes from prokaryotic communities of the deep North Pacific responsible for the expression of specific enzymes and the synthesis of polysaccharides and antibiotics. Unexpected pathways for utilizing specific components of organic matter such as D-amino acids, chitin, pullulan and cellulose are mediated by DSP [7].

From all what we know thus far on deep-water microbial food webs, the role of the highly diverse prokaryotic community and its interaction with the unexplained high viral abundance remains enigmatic and awaits investigation. Since the deep waters of the Mediterranean Sea are besides the Sulu Sea the only warm deep waters in the global ocean, the Mediterranean Sea offers unique opportunities for microbial oceanography.

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