

Metagenomics of the deep Mediterranean

September 19 2007

Metagenomics is a revolutionary approach to study microbes. Rather than isolating pure cultures, the power of high-throughput sequencing is applied directly to environmental samples to obtain information about the genomes of the prokaryotic cells present in a specific habitat studied. The ocean is an ideal subject of this approach because of its enormous microbiota, whose biomass equals that of all other living organisms on earth is mostly microbial, and also because most of these microbes are extremely fastidious to cultivate.

Craig Venter pioneered these studies and has sampled the surface of the World oceans, but has only scraped the surface. Only one study carried out in Hawaii Ocean Time Series (or HOT) station has analyzed the metagenome of different depths down to 4000m showing the enormous diversity hidden there.

This article describes the second study of the bathypelagic region, in this case at a station located over the Ionian abyssal plain, a flat deep basin occupying most of the space between Sicily and Greece in the Eastern Mediterranean. The deep waters of the Mediterranean are special in being free from the intrusion of polar waters that feed most the bottom of the global ocean. The Ionian sample comes from 3000 m deep and is submitted to a continuous pressure of 300 Kg/cm² but contrastingly to most deep ocean habitats this has a relatively warm temperature of nearly 14°C.

In general, a remarkable number of similarities were found with the deep meso-pelagic Pacific and a convergence at the level of taxa found

and types of metabolism with the soil microbiota is starting to be perceived. The authors use the term “invisible soil” paraphrasing the “invisible forest” coined by Paul Falkowski to refer to the hidden but gigantic primary productivity found in the photic zone.

The diversity of metabolic enzymes involved in resilient organic compounds degradation was very high. However, many microbes could complement their heterotrophic metabolism with chemolithotrophic energy supplies and, specifically in the Mediterranean, the oxidation of carbon monoxide, probably released by tectonic activity, could be important.

There is also evidence that the microbes rarely live isolated. The free living planktonic lifestyle is probably not very popular in this extremely depleted environment. Quorum sensing genes indicate that instead, microbes tend to aggregate in particles and they could become luminescent maybe to attract and be eaten by animals. This strategy could provide the cells with a sporadic visit to the nutritious oasis of an animal gut. Overall, this paper shows that the deep ocean possesses a rich and mostly unknown microbiota that deserves much more studies.

A recent analysis of a metagenomic library from the deep Mediterranean shows a surprising high number of quorum sensing or lux genes that are only expressed when bacteria live in colonies. The deep ocean might be too depleted in resources for microbes to live independently. Instead the association to detritus particles might give them a rich microenvironment. Now, some of the genes detected have been positively identified as luxA, directly involved in bioluminescence.

Why would deep sea bacteria be luminescent? One possible explanation is that they become attractive to animals that at these depths are very photosensitive. Being swallowed by one of these creatures would give the bacteria a temporary oasis of nutrient-rich conditions before another

long dip in the abyssal black.

Citation: Martín-Cuadrado A-B, López-García P, Alba J-C, Moreira D, Monticelli L, et al (2007) Metagenomics of the Deep Mediterranean, a Warm Bathypelagic Habitat. PLoS ONE 2(9): e914. doi:10.1371/journal.pone.0000914

Source: Public Library of Science

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