

ARCHAEAL DIVERSITY AT SHALLOW HYDROTHERMAL SYSTEM OFF PANAREA (EOLIAN ARCHIPELAGO, ITALY) AS REVEALED BY 16S rDNA PCR-DGGE ANALYSIS

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Abstract

A molecular phylogenetic survey of occurring archaeal diversity at four different shallow hydrothermal vents was carried out by using the 16S rDNA PCR-DGGE fingerprinting method. Most of retrieved archaeal sequences did not match with those of yet-described *Archaea*, suggesting the presence of new archaeal genotypes.

Keywords: *Aeolian Arc, Biodiversity, Thermal Vents*

The shallow marine hydrothermal vents of the Eolian Islands in the Tyrrhenian Sea are located in tectonically active areas and despite their accessibility, several aspects concerning microbial ecology of these ecosystems have been much less investigated than those of deep-sea vents. Among Eolian Islands, thermal springs and shallow hydrothermal vents of Vulcano are considered the "type locality" of hyperthermophilic *Archaea*. Very few studies have been concerned the microorganisms living at near hydrothermal system of Panarea Island [1,2,3]. On the basis of culture-dependent techniques, microbial communities of extreme environments were thought to be dominated by *Archaea* [4,5]. The recent application of molecular methods revealed a different picture, in which *Bacteria* dominated the microbial communities in most of these environments [2,3]. Here we report the archaeal diversity studied by molecular tools in environmental samples collected from four shallow thermal sites characterised by different temperatures and depths located off Panarea Island. Archaeal diversity was investigated by means of 16S rDNA PCR-DGGE fragment analysis, as previously described [2]. DGGE profiles showed that total number of bands, equivalent to the archaeal richness, was higher in water (24) than in sediment samples (18). Comparison among the DGGE profiles, performed on the basis of Bray-Curtis similarity coefficient, showed low similarity levels among vents, suggesting that archaeal community was differently distributed at four sites, according to physico-chemical parameters. The similarity matrices were also used for constructing a non-metric multidimensional scaling (NMDS) diagram (Fig. 1).

low similarity levels of sequences with yet-described clones of *Archaea* suggest the presence of new indigenous archaeal phylotypes.

References

- 1 - Gugliandolo C., Italiano F. and Maugeri T.L., 2006. The submarine hydrothermal system of Panarea (Southern Italy): biogeochemical processes at the thermal fluids - sea bottom interface. *Ann. Geophysics*, 49: pp 783-792.
- 2 - Maugeri T.L., Lentini V., Gugliandolo C., Italiano F., Cousin S. and Stackebrandt E., 2009. Bacterial and archaeal populations at two shallow hydrothermal vents off Panarea Island (Eolian Islands, Italy). *Extremophiles*, 13: 199-212.
- 3 - Manini E., Luna G.M., Corinaldesi C., Zeppilli D., Bortoluzzi G., Caramanna G., Raffa F., and Danovaro R., 2008. Prokaryote diversity and virus abundance in shallow hydrothermal vents of the Mediterranean Sea (Panarea Island) and the Pacific Ocean (North Sulawesi-Indonesia). *Microb. Ecol.*, 55: 626-639.
- 4 - Stetter K.O., Fiala G., Huber R. and Seegerer A., 1990. Hyperthermophilic microorganisms. *FEMS Microbiol. Rev.*, 75: 117-124.
- 5 - Baross J.A. and Deming J.W., 1995. Growth at high temperatures: isolation and taxonomy, physiology, and ecology. In: Karl DM (ed.), *The microbiology of deep-sea hydrothermal vents*. CRC Press. Boca Raton, pp 169-217.
- 6 - Amend J.P., Meyer-Dombard D.R., Sheth S.N., Zolotova N. and Amend A.C., 2003. *Palaecoccus helgesonii* sp. nov., a facultatively anaerobic, hyperthermophilic archaeon from a geothermal well on Vulcano Island, Italy. *Arch. Microbiol.*, 179: 394-401.

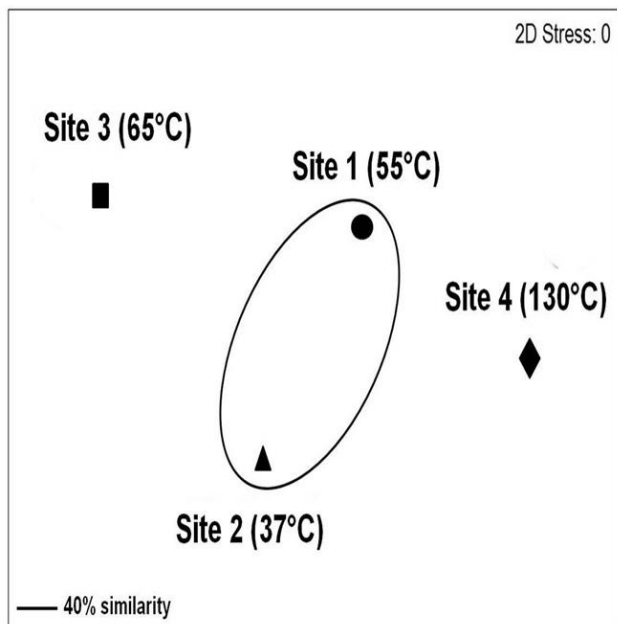


Fig. 1. NMDS diagram showing the clustering of the archaeal community

Phylogenetic analysis revealed that most of the archaeal DGGE 16S rRNA gene sequences matched with uncultivated *Archaea* and these results did not allow us to speculate about their physiology. Only two sequences, obtained from sites 1 and 4, were distantly affiliated (<96% similarity) with *Palaecoccus helgesonii*, an obligate chemo-heterotrophic, hyperthermophilic, microaerophilic euryarchaeon, recently isolated from a geothermal well at Vulcano Island [6]. The