

Diversity and Community Structure of Archaea in Deep Subsurface Sediments from the Tropical Western Pacific

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Archaeal 16S rRNA gene clone libraries using PCR amplicons from six different layers of the MD06-3059 core were obtained from the tropical Western Pacific sediments. A total of 543 clones were randomly selected, and 195 valid clones and 137 operational taxonomic units were identified after chimera check and C97% similarity analysis. Phylogenetic results showed that the archaeal diversity in the collected samples was very diverse, and the obtained OTUs were grouped into Crenarchaeota and Euryarchaeota, with the former dominated by Miscellaneous Crenarchaeotic Group (MCG, 54% of total archaeal clones) and the latter dominated

by Marine Benthic Group D (MBG-D), South African Gold Mine Euryarchaeotic Group (SAGMEG) and Marine Benthic Group B (MBG-B). Phylotypes in this study shared high similarity with those in subsurface sediments from Peru Margin sites, which indicated that different geographical zones might host similar members of archaeal populations based on similar sedimentary environments. In our study, MCG seemed to dominate certain layers of the nonhydrate sediments, suggesting a wide ecophysiological adaptation than previously appreciated. This might vary with the different geochemical gradients of the environment.