

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

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**Abstract** Archaeal 16S rRNA gene clone libraries using PCR amplicons from eight different layers of the MD06-3051 core were obtained from the tropical Western Pacific sediments. A total of 768 clones were randomly selected, and 264 representative clones were sequenced by restriction fragment length polymorphism. Finally, 719 valid clones and 104 operational taxonomic units were identified after chimera-check and  $\geq 97\%$  similarity analysis. The phylogenetic analysis of 16S rDNA sequences obtained from sediment samples were very diverse and showed stratification with depth. Majority of the members were most closely related to uncultivated groups and physiologically uncharacterized assemblages. All phylotypes were affiliated with *Crenarchaeota* (76%) and *Euryarchaeota* (24%), respectively. Deep-sea archaeal group (DSAG, 41% of total clones) and miscellaneous crenarchaeotic group (MCG, 29% of total clones) belonging to *Crenarchaeota* were the most predominant archaeal 16S rDNA phylotypes in clone libraries. 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, members of DSAG and MCG seemed to dominate certain layers of the nonhydrate sediments, suggesting a wide eco-physiological adaptation than previously appreciated. The spatial distribution and community structure of these groups

might vary with the different geochemical gradients of the environment.

## Introduction

Subsurface sediments are the largest compartment of the global biosphere and are estimated to contain 1/10 to 1/3 of total living biomass on Earth [1, 2]. Recent studies have reported that microorganisms are ubiquitous in different geographically separated sites [3–8] and present a great phylogenetic diversity in marine subsurface sediments. On one hand, activities of subsurface microorganisms in the form of fermentation, methanogenesis, and sulfate reduction play important roles in global biogeochemical cycles, especially in global carbon cycle [2, 9–11]. Microorganisms take part in decomposition of organic matter, nutrient cycling, element transformation, and mobilization in sediments [9]. On the other hand, the geological and geochemical conditions greatly affect microbial diversity and community composition in subsurface environments [4]. However, microorganisms seem to be ecophysiolegically flexible [12], and the diversity range of metabolisms has evolved to adapt the variety of the biogeochemical settings such as the energy limitation in difficult and inhospitable environments [13].

Many factors account for the microbial diversity in various niches, such as temperature, geologic location, and chemical composition. In general, microorganisms show similar phylotypes based on the same environments. However, unexplained variation might occur even in areas that seem to be homogeneous and similar. For example, at the subsurface hydrate sites, methanogenic archaea in the Cascadian Margin shared little similarity with communities in the Nankai Trough [6, 14]. Consequently, with the development of newer methodology and technology of

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