

Archaeal and bacterial communities in the potential gas hydrate bearing sediments at Formosa Ridge, offshore Taiwan

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Gas hydrate is a high potentially alternative energy resource. Due to the interest in marine gas hydrate, the research team from Taiwan has been demonstrated the intensive BSR distribution, high methane and shallow depth of SMI at SW offshore Taiwan that indicated this area are potential gas hydrate region. In this study, the composition of the Archaeal and Bacterial communities were determined by 16S rRNA phylogenetic analyses of clone libraries and metagenomic analyses from piston core KP-10N from MD 178 cruise and two gravity cores obtained from the potential gas hydrate bearing area (station G1) and control normal area (station G2) from OR3-1672 cruise at Formosa Ridge. High methane and low SMI were detected at station KP10N at Formosa Ridge. Among them, ANME and *Gammaproteobacteria* sulfur reducer *Desulfobacterium* and *Desulfomonas* were detected at SMI area. The occurrence of archaeal phylotypes DSAG with MCG or MGI, and the dominant bacterial phylotypes (*Chloroflexi*, *Planctomycetes*, JS1) were dominant in station KP10N. These microbial community structures are closely related to the microbial community compositions in methane hydrate bearing sediment. Total 1322 archaeal and 9809 bacterial 16S rDNA sequence reads were extracted from six metagenomic datasets from gravity cores G1& G2 and classified based on SILVA taxonomy. Bacterial dominant phylotypes in all datasets are *Chloroflexi*, *Planctomycetes*, *Deltaproteobacteria* and *Gammaproteobacteria*. The bacterial phylotypes with significantly different occurrences is JS1 and OD1 only detected in GH region (G1) core, not in the control G2 core. Dominant archaeal phylotypes are DSHVG-6, MBGD/DHVEG-1, and *Thaumarchaeota*, MBG-B and MGI. In addition, the gas hydrate related phylotypes of ANME-2, ANME-3 and JS1 were detected in the bottom of G1 core. Both phenomena indicated that the bottom of G1 core may be the region of sulfate-methane interface. The characterization of microbial community at gas hydrate area is essential to gain a better understanding of microbial diversity, contribution and the effects of microbial activities in hydrate ecosystems.