

## **Diversity and abundance of *Bathyarchaeota* (MCG) in the South China Sea sediments and implication of its ecological roles**

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The archaea phylum Bathyarchaeota which is composed of a large number of diverse lineages, are widespread and abundant in marine sediments. The environmental factors controlling the distribution and evolution of this largely diversified archaeal phylum are currently unknown, also our understanding on its biogeochemical roles are still limited. In this study, a novel pair of specific primers targeting the major marine subgroups of bathyarchaeotal 16S rRNA genes was successfully designed and evaluated to investigate the distribution and abundance of Bathyarchaeota in marine sediments. The abundance of Bathyarchaeota in two sediment gravity cores from South China Sea (Dongsha and Shenhu area, each) was shown to strongly correlate with the TOC content. Sediment depth was identified as one of the key environmental factors shaping the community structure of the members of Bathyarchaeota. Subgroups Bathy-2, Bathy-8 and Bathy-10 were dominant bathyarchaeotal members in the SCS sediments, and Bathy-8 was found predominantly within the reducing and deeper sediment layers, while Bathy-10 occurred preferentially in the oxidizing and shallower sediment layers. Our study indicates that members of Bathyarchaeota may play important roles in organic carbon remineralization in marine subsurface sediments and support the hypothesis that different subgroups of the phylum may have distinct ecological niches and physiological properties.