

Metagenomic analyses of pelagic sediments in the Ross Sea (Antarctica)

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Microbial communities are critical to the functioning of marine ecosystems and the dominant players in carbon cycling and other biogeochemical cycles of organic matters and nutrients. Especially benthic prokaryotic community inhabiting the pelagic sediments may make up approximately 70% of the global prokaryotic biomass. The continental margin and deep-sea floor in the Ross Sea are considered to be differently affected by geological, biological and ocean physical factors. At inner continental shelf (ICS), higher export rates of primary production (PP) are expected than offshore due to summer algal bloom in coastal polynyas. Low temperature Shelf Water is a major water mass at ICS. Continental slope (CS) is influenced by intermediate PP export and warm water of Circumpolar Deep Water. Deep-sea floor (DSF) beyond the continental margin is characterized by low PP export and dense water mass of Antarctic Bottom Water. Therefore, the characteristics of the pelagic sediments may be different depending on the influence of those environmental factors, possibly affecting the structures and functions of benthic prokaryotic communities. To investigate community structures and potential functions of benthic prokaryotic community, both 16S amplicon sequencing and deep metagenome shotgun sequencing were performed for surface sediment samples at three sites (ICS, CS and DSF) in the Ross Sea. In the presentation, some results will be shown and discussed.

Key words: Metagenome, Prokaryote, Ross Sea, Sediment