

Surface protistan microplankton community along 110°E in the Southern Ocean during austral summer 2012

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The vast amounts of phytoplanktonic production followed by heterotrophic protist production supports high productivity of metazoan species in the Southern Ocean. Distribution and community structures of microplanktonic protists were mostly investigated by pigments analysis and morphological observation. However, protists are thought to be more genetically heterogeneous than their morphological diversity. Therefore, gene-based survey of protistan microplankton community is also important. In the present study, we revealed the diversity and community structures of protistan microplankton in the Southern Ocean using High-Throughput Sequencing (HTS) technique.

Six surface seawater samples were taken along 110°E (41°S: Subantarctic Zone; SAZ - 62°S: Southern Antarctic Circular Current Frontal Zone; SACCFZ) in December 2012 during 54th Japanese Antarctic Research Expedition cruise. Each sample was size fractionated (10–100 µm), trapped by membrane filter and fixed in Lugol's solution. Meta-genomic DNA were extracted and purified from the samples. The V9 region of 18S rRNA gene was amplified using the eukaryotic universal primers; 1389F-1510R. The indexed amplicon libraries were sequenced on Illumina Miseq. The obtained sequences were processed on gene analysis software MacQIIME. Assignments of representative sequences were made against the database.

In total, 512,078 sequences were obtained and clustered into 1,849 OTUs at the 97% similarity. This analysis covered most of the protistan species in the amplicon libraries, since every sequence data showed more than 0.98 coverage. Biodiversity (Shannon index) were lower at the Antarctic Zone (AAZ) and the SACCFZ than the northern zones. Community structure at the phylum level showed significant presence of Chlorophyta sequences in the SAZ, and drastic decrease to the Polar Frontal Zone (PFZ). The clonal frequency of Dinoflagellata increased from SAZ to AAZ and reached at approximately 90% of total sequences at the AAZ. Such great dominance of Dinoflagellata can not be seen in the previous reports. However, further discussions will be needed to assess whether the clonal frequency actually reflects the cell numbers. We also revealed the protistan communities in the genus or species level. For example, genus *Prorocentrum*, an autotrophic dinoflagellata was frequently detected in the SAZ and PFZ but not in the AAZ and SACCFZ. Meanwhile, genus *Paulsenella*, "diatom killer" heterotroph shared approximately 60% in the total Dinoflagellata sequences in the AAZ and SACCFZ. On the other hand, Diatom *Chaetoceros rostratus* or closely related species was commonly detected in all the zones.

Although detailed analyses are still in progress, the results expand our knowledge on taxonomy and ecology of protistan microplankton living in the Southern Ocean.