

Environmental DNA as a tool for biomonitoring the Antarctic marine ecosystem

Aiko Tachibana¹, Ryosuke Makabe^{1,2}, Masato Moteki^{1,2}

¹ *Tokyo University of Marine Science and Technology*

² *National Institute of Polar Research*

Monitoring biological community structure and diversity is essential to understanding the impact of global climate change on the Antarctic marine ecosystem. Here, we introduce a new monitoring tool using environmental DNA (eDNA) metabarcoding and discuss the effectiveness of using eDNA to clarify biodiversity and community structure in polar regions. Seawater containing eDNA was sampled from 60°S to 65°S along the 110°E transect off Wilkes Land, East Antarctica, in January 2019. Analysis of nuclear 18S rDNA provided broad taxonomic coverage across the eukaryotic domain from a single filtered sample. Mitochondrial COI and nuclear 18S showed similar taxonomic coverage across metazoan phyla, although more taxa could be resolved to species level with the use of COI than with 18S. Mitochondrial COI analysis detected all major zooplankton species in the Southern Ocean, with distribution patterns similar to those observed in previous studies. However, the detection frequencies of larger zooplankton (Euphausiacea and Amphipoda) and micronekton (Myctophidae) are likely to underrepresent the occurrence of these taxa in reality. Our results suggest that eDNA metabarcoding is a useful technique, at the very least, for biomonitoring of lower trophic levels in Antarctic marine ecosystems.

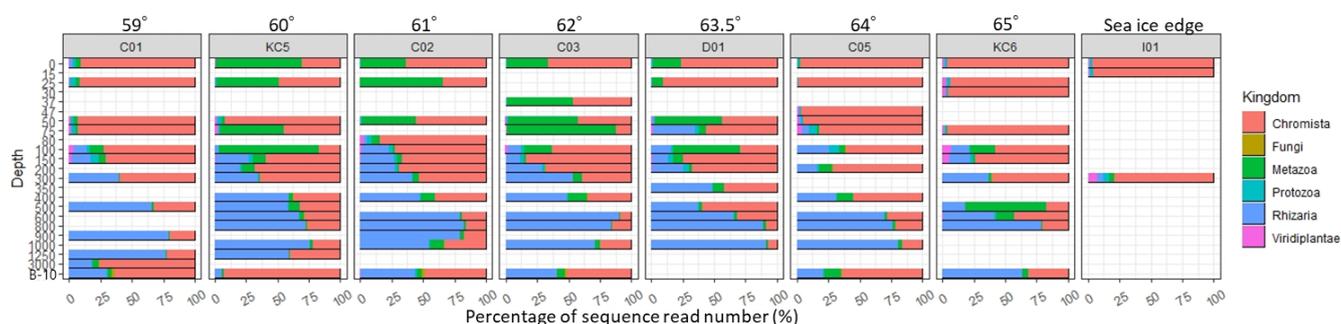


Figure 1. Relative abundance (sequence read number) and distribution of the eukaryote domain revealed by 18S from each sampling station along the 110°E transect in January 2019.