

Diversity of Bacterioplankton in an Antarctic Ice-Margin Area Analyzed via Restriction Fragment Length Polymorphism (RFLP) and 16S rRNA Gene Sequence

ChungHun Oh and SangHoon Lee*

*Polar Research Center, Korea Ocean Research & Development Institute,
Ansan PO Box 29, Seoul 425-600, Korea*

ABSTRACT. Little is known about the community structures of natural bacteria, because of the methodological limitations in the cultivation and subsequent identifications of bacteria. Recent studies circumvented these limitations by utilizing the 16S rRNA genes (rDNA) obtained directly from natural mixed populations without cultivation. We studied the community structure and the biodiversity of bacterioplankton sampled from an Antarctic ice-margin area, using RFLP and 16S rDNA sequence. The 16S rDNA were PCR-amplified from the natural mixed-population DNA with primers designed for bacteria. The PCR products were cloned by ligation to pGEM-T easy vector, and 20 clones were obtained by transformation in *Escherichia coli*. Cluster analyses based on the RFLP of HpaII digestion grouped 17 clones into 5 clusters, and 3 clones belonged to none of the 5 clusters. These results suggest that many diverse species, rather than a few dominant ones, make up the natural community. However, the 16S rDNA sequences obtained from the PCR product belonged to one taxon group, the alpha-subdivision of purple bacteria. Although the sequences we found fall in a single subdivision, the potentially broad spectrum of bacterial species in nature makes our finding inconclusive and suggests further investigations.

*corresponding author (shlee@sari.kordi.re.kr)