

# MICROBIAL COMMUNITY CHANGE OF THE BIOFILM FORMED IN THE MARINE ENVIRONMENT OF ANTARCTICA

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The microbial community change of biofilms formed on the artificial surfaces in the marine environment of Antarctica for seven days was investigated. 16S rRNA gene amplicons were directly sequenced using GS-FLX sequencing machine. Approximately 4,000 to 5,000 sequence reads were obtained from each sample. They were clustered into 262 to 938 phylotypes by 97% similarity cutoff. Most of phylotypes were affiliated to *Bacteroidetes* and *Gammaproteobacteria*. The minor phyla were included *Alphaproteobacteria*, *Firmicutes*, *Cyanobacteria*, *Actinobacteria*, GN02, and OD1. The relative abundance of phylotypes assigned to *Proteobacteria* changed as follows for 7 days; 38.0% - 59.4% - 66.5% - 80.6% - 57.6% - 28.0% - 43.1%. Phylotypes assigned to *Bacteroidetes* were the major at the initial stage, decreased down to 12.7% at the fourth day and increased in the later stage. The most predominant phylotype comprising 65.3% on the fourth day was closely related to *Pseudoalteromonas prydzensis* (98.4% similarity).