

Studies on bacterial community on Antarctic ice sheet by 16S rRNA gene sequencing analysis

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Analyses of ice cores have often been used as a means to reconstruct past environments. However, analysis of the biological contents of ice cores has been relatively rare. Recently, snow algae that grew in the snow and ice on the glacier and stored in ice cores has been used as environmental markers in the analyses of ice cores from lower latitude regions such as Himalaya and Patagonia. In Antarctica, the possibility of microbial activity in the ice sheet is very small due to the cold and dry environment. But, the ice cores from Antarctica could preserve microorganisms in the ancient atmosphere trapped in the snow and ice of the ice sheet. The biomass and species composition of the microorganism in the ice cores could reflect the global environmental condition at that time. Thus, microorganisms in Antarctic ice cores could be useful to reconstruct past environments. However, analysis of microorganisms in the Antarctic ice is still very limited. In this study, we examined bacterial community in surface snow samples and ice cores samples in Antarctica by 16S rRNA gene sequencing analysis. Genes of 16S rRNA were subjected to PCR amplification and nucleotide sequencing. Homology search suggested that 16S rRNA sequences related to Actinobacteria and Proteobacteria. Although the sample availability has limited the study as a preliminary level, our results imply that bacterial diversity in snow and ice samples in Antarctica could be used as new environmental markers for past environmental conditions.