

Molecular Diversity of Bacteria in Antarctic and Arctic soils

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The diversity of bacterial and actinobacterial community in soil samples from Signy Station, Antarctica and Dasan Station, Arctic was studied by PCR amplification and Denaturing Gradient Gel Electrophoresis (DGGE) of 16S rRNA gene fragments. Non-metric multidimensional scaling plots (MDS) analysis of DGGE profiles suggested that the Antarctica and Arctic soils used in this study have around 20% similarity of bacterial diversity. Major DGGE bands were excised from the gels, re-amplified and sequenced. The main bacterial groups in the Antarctica and Arctic soils fell into the *Bacterioidetes*, *Actinobacteria* and *Gemmatimonadetes*. There were several sequences which were not related to any known bacteria group. In addition, the presence of actinobacteria from the family *Micromonosporineae*, *Frankineae*, *Micrococcineae*, *Streptosporangineae* and *Pseudonocardineae* was detected in the Antarctica and Arctic soils. These results showed the presence of a diverse community of bacteria and actinobacteria in soils collected from the Signy Station, Antarctic and Dasan Station, Arctic. The correlation of environmental variables including soil water content, pH, electrical conductivity, carbon, hydrogen and nitrogen on the bacterial and actinobacterial community in this study is also presented.