

PHYLOGENETIC ANALYSIS OF BACTERIAL DIVERSITY IN TOPSOIL SAMPLES FROM FEILDS PENINSULA, ANTARCTICAH.R. Li¹, Y. Yu¹, B. Chen¹, D.M. Ren²¹*Polar Research Institute of China, SOA Key Laboratory for Polar Science, Shanghai, China,*²*State Key Lab of Genetic Engineering, Institute of Genetics, Fudan University, Shanghai, China*

Soils of Antarctic regions are subjected to harsh environmental conditions, in which the biological activity is mostly controlled by microorganisms due to less plant diversity in this ecosystem. Denaturing gradient gel electrophoresis (DGGE) profiles of PCR amplified V3 regions of 16S rDNA were used to assess bacterial diversity in the topsoil samples collected from Feilds Peninsula, the vicinity of the Great Wall Station, Antarctica. DGGE profile showed that bacterial phylogenetic composition varied in different soils. Sequences corresponding to 12 dominating excised bands were analyzed and fell into eight lineages of the domain Bacteria: beta-, gamma-, delta- proteobacteria; *Cytophaga-Flexibacter-Bacteroides* (CFB) group; Actinobacteria; *Acidobacteria*; *Cyanobacteria* and green nonsulfur bacteria. It was found that autotrophic bacteria (*Cyanobacteria*) and those can grow on a wide range of carbon sources (*Pseudomonas*) or various C1-substrates (*Methylophilus*) were dominant members in studied topsoil. The majority of the sequences were most closely related to the sequences from uncultured microorganisms in environmental (especially soils and sediments). The results suggest that most of the topsoil bacterial community has never been isolated and their function of its dominant members appears to be unknown.