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BACTERIAL DIVERSITY IN ENVIRONMENTAL SAMPLES FROM ANTARCTICA

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Molecular methods were used to investigate bacterial diversity of Antarctic environmental samples collected from three different base stations- Signy (United Kingdom), Maitri (India) and Casey (Australia).

A description of the diversity of the bacterial population in the various sites was obtained from total community genomic DNA using PCR- DGGE (denaturing gradient gel electrophoresis) and 16S rDNA clone libraries. A nested PCR–DGGE approach was used with specific 16S rRNA primers for large bacterial groups as well as for actinomycetes. These specific 16S rDNA fragments were also cloned and screened using DGGE. Analyses showed spatial heterogeneity in different bacterial and actinomycete communities.