

Analyses of soil bacterial diversity of the Schirmacher Oasis, Antarctica

Abstract

Schirmacher Oasis, Antarctica, is a region with relatively large exposed area and consisted of many freshwater lakes. Nevertheless, only a few studies were done on the bacterial diversity of this region. Hence, this project was undertaken to determine the bacterial community in soil samples collected from the Schirmacher Oasis using the denaturing gradient gel electrophoresis (DGGE) of amplified 16S rDNA fragments. A total of 79 partial 16S rDNA sequences were obtained from the excised DGGE bands, which corresponded to 63 different operational taxonomic units (OTUs) representing bacteria from seven different phyla. The most dominant phyla in descending order were Acidobacteria, Proteobacteria, Bacteroidetes, and Actinobacteria, Planctomycetes, Cyanobacteria and BRC1. There were 5.4 % of unclassified bacteria which cannot be grouped into any of the existing phyla. Eighty-seven percent of the OTUs had highest similarity with the uncultured bacteria from the NCBI GenBank database. Thirty-two percent of the OTUs were similar to bacteria reported in other parts of the Antarctica, while the others were related to bacteria found elsewhere outside the Antarctic.