

Analysis of bacterial communities of King George and Deception Islands, Antarctica using high-throughput sequencing

ABSTRACT

King George Island (KGI) and Deception Island (DCI) are members of the South Shetland Islands in Antarctica, each with their own landscape and local environmental factors. Both sites are suitable for longterm monitoring of bacterial diversity shift due to warming, as temperature rises relatively faster than East Antarctica. This study was conducted to determine and compare the baseline diversity of soil bacteria in KGI and DCI. 16S rDNA amplicons of bacteria from both sites were sequenced using Illumina next generation sequencer. Results showed that major phyla in KGI and DCI were Actinobacteria, Proteobacteria, Chloroflexi, Verrucomicrobia, Bacteroidetes and Acidobacteria. The distribution and evenness of the soil bacterial communities varied at genus level. The genera *Sphingomonas* sp. was predominant at both sites while the subsequent six major genera differed. Two bacterial genera, *Legionella* and *Clostridium* were also found in low abundance in both sites, both of which may contain pathogenic members. Further verification will be required to determine whether the pathogenic members of these genera are present in both sites.

Keyword: Antarctica; South Shetland Islands; Soil bacterial diversity; 16S rDNA; Pyrosequencing