

ORIGIN AND PHYLOGENY OF BACTERIA LIVING IN PERMANENT ANTARCTIC LAKE ICE AND SOILS

C.M.V.L. Wong¹, S. Radu², H.K Tam¹, H.Y Yong¹, F.Y Wong²

¹*Biotechnology Research Institute, University Malaysia Sabah, Kota Kinabalu, Sabah, Malaysia,* ²*Department of Food Science, Faculty of Food Science and Technology, Universiti Putra Malaysia, Serdang, Selangor, Malaysia*

Antarctica harbours a diverse population of unique microorganisms. The diversities of bacteria of various parts of Antarctica were well-documented. However, there were only few reports on the bacterial diversity of the Schirmacher oasis. Schirmacher oasis is an area of relatively ice-free, low lying-hills, in the Eastern Dronning Maud land, East (70°46'04"-70°44'21"S; 11°49'54"-11°26'03"E) Antarctica, about 70km away from Prince Astrid coast. The objective of this project was to analyse the bacterial diversity in the permanent Antarctic lake ice of the Schirmacher Oasis. This was a collaborative research between the Academy of Sciences, Malaysia and the National Centre for Antarctica and Ocean Research, India. Samples were collected from the permanent Antarctic lake ice and soils within the Schirmacher oasis during the Austral summer in 2004. Bacteria were isolated by incubating these samples in nutrient and Luria-Bertani media. Purified bacteria were analysed by Gram-staining and light microscope. Universal primers 25f, 518r, 530f, 907r, 926f, 1114f, 1392r and 1525r were used in various combinations to amplify the 16S rDNA of bacteria. Amplified 16S rDNA were sequenced and analysed using the basic local alignment search tool (BLAST) to identify the bacteria. *Arthrobacter spp.*, *A. oxydans*, *Bacillus spp.*, *B. cereus*, *B. polyfermenticus*, *B. pumilus*, *Pseudomonas fluoresceus*, *P. putida*, *P. syringae*, *Nocardioides*, *Frigoribacterium*, *Rubrobacter*, *Rhodococcus*, and *Flavobacterium* were among the strains isolated. These strains were not unique to the Schirmacher oasis but were also found in other parts of Antarctica and temperate countries. Nevertheless, there were fourteen strains of bacteria which have unique 16S rDNA sequences. These unique sequences indicated that this group of bacteria could be novel and unique to the Schirmacher oasis. Additionally, we were able to culture two of the unique strains which were previously reported to be "unculturable". These unique bacteria are interesting, and their novelty is currently being ascertained by various biochemical tests.