

Cyanobacterial molecular diversity and distribution in microbial mats from antarctic lakes

P. De Carvalho Maalouf, A. Lambion, F. Zakhia
and *A. Wilmotte

Center for Protein Engineering, B6, University of Liège, 4000, Liège, Belgium

1. Introduction

Antarctica is a vast continent submitted to extreme conditions. The few coastal deglaciated areas contain **lakes** that offer milder conditions where microbial mats can develop. The latter are dominated by **cyanobacteria**. In the frame of the **AMBIO** project (www.ambio.ulg.ac.be), we aim to assess the influence of ecological and historical factors on the distribution of cyanobacteria in antarctic aquatic habitats.

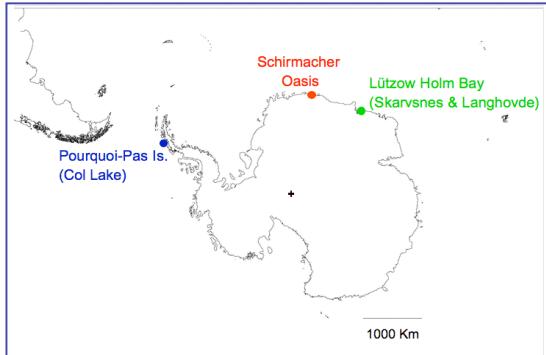


Fig. 1 - Map of Antarctica showing the sampled regions.

3. Results

The sequences grouped into 14 OTUs. **Seven are potentially endemic to the Antarctic** (OTUs 3, 6, 9, 10, 11, 12 and 13). The others have a cosmopolitan distribution. Each lake from SK and LA have a different OTU composition (Fig. 2).

4. Conclusion and perspectives

These preliminary results show the existence of **potential endemic cyanobacterial taxa in Antarctica**, corroborating previous studies (7). They also indicate that lakes separated by small distances can have different microbial communities highlighting the **importance of the ecological factors in shaping the microbial community**.

The integration of the results of the 80 samples that are now being analyzed will allow us to assess the **influence of the (more or less) extreme conditions on the geographic distribution of cyanobacteria along the 3 biogeographic regions of Antarctica**.

2. Methods

13 samples from 10 lakes from Skavnes (SK), Langhovde (LA), Schirmacher Oasis (SC) and Pourquoi-Pas Island (Col Lake, CL) were analyzed (Fig. 1). SK, LA and SC were sampled during the MERLIN campaign in 2007 and CL was sampled in 2003 during the Sledge Bravo campaign. DNA was isolated following a modified protocol of Smalla *et al* (1). A semi-nested PCR was performed (2) and the obtained amplicons were screened by DGGE (3). Our sequences and their closest relatives (RDP II, <http://rdp.cme.msu.edu>) were aligned using GENEIOUS (4) and a distance tree was constructed using TREECON (5 ; Fig. 2). Finally, sequences sharing more than 97.5% of similarity were grouped into Operational Taxonomic Units (OTUs) using PHYLIP and DOTUR (6).

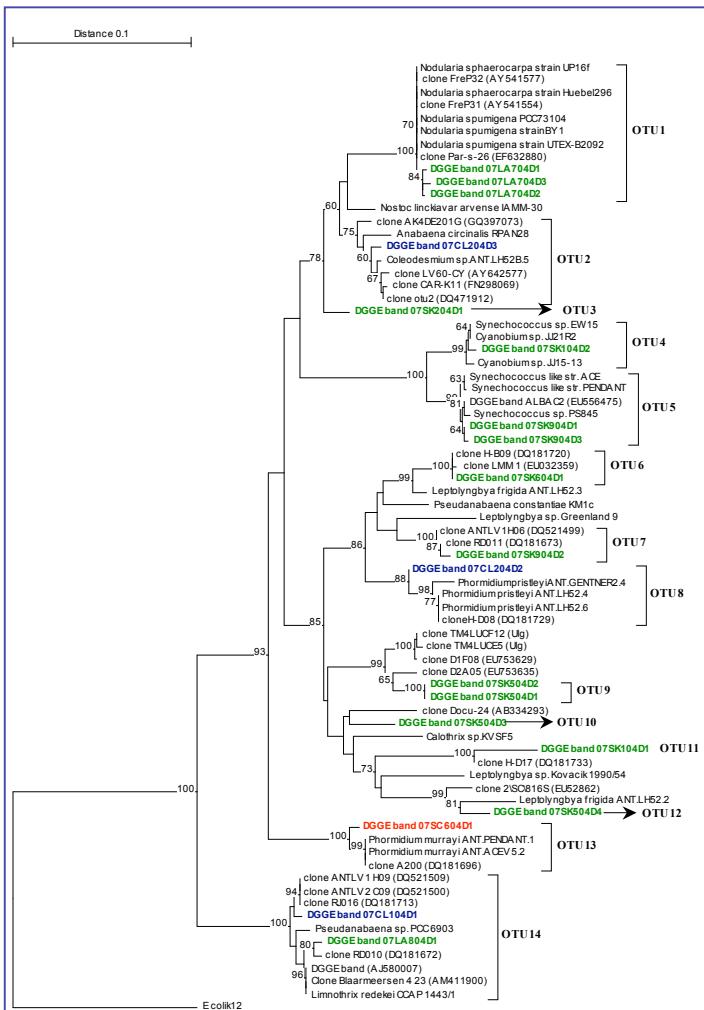


Fig. 2 - Distance tree (Neighbor Joining, bootstrap with 100 iterations) of the obtained DGGE sequences and their closest relatives. Sequences from SK and LA are in green, SC in red and CL in blue.