

The BCCM/ULC collection to conserve the biodiversity and study the secondary metabolites of Antarctic cyanobacteria

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On the Antarctic continent, Cyanobacteria are key primary producers and main drivers of the food webs in a wide range of aquatic to terrestrial habitats. For example, they build benthic microbial mats in lakes and soil crusts. Their success in these harsh cold conditions can probably be explained by particular adaptations to survive freeze/thaw cycles, seasonally contrasted light intensities, high UV radiations, desiccation and other environmental stresses.

The BCCM/ULC public collection is funded by the Belgian Science Policy Office since 2011. A Quality Management System ensures that the services of deposits (both public and safe) and distribution are well documented and efficient for the clients' satisfaction. It has obtained the ISO 9001 certification for deposition and distribution of strains, as part of the multi-site certification for the BCCM consortium. This collection aims to gather a representative portion of the Antarctic cyanobacterial diversity with different ecological origins (limnetic mats, soil crusts, cryoconites, endoliths...) and make it available for researchers to study the taxonomy, evolution, adaptations to harsh environmental conditions, pigments, and genomic make-up. It presently includes 216 cyanobacterial strains, of which 119 are of Antarctic origin (catalogue: <http://bccm.belspo.be/catalogues/ulc-catalogue-search>).

As shown by morphological identification, the strains belong to five orders (Synechococcales, Oscillatoriales, Pleurocapsales, Chroococciopsidales and Nostocales). The 16S rRNA and ITS sequences of the strains are being characterized. The first 85 Antarctic strains already studied are distributed into 25 Operational Taxonomic Units (OTUs = groups of sequences with > 97,5% 16S rRNA similarity), and thus represent a quite large diversity. Moreover, strains identified as members of the genera *Leptolyngbya* or *Phormidium* appear in several lineages. This supports the idea that there is a need to revise the taxonomy of these polyphyletic genera with a simple filamentous morphology.

In addition, cyanobacteria are known to produce a wide range of secondary metabolites (e.g. alkaloids, cyclic and linear peptides, polyketides) with bioactive potential. Genome sequencing of 11 strains has been started to enable genome mining for biosynthetic clusters. Pair-read data from illumina MiSeq runs were obtained and submitted to a bioinformatic pipeline dedicated to the assembly of genomes and search of sequences involved in the biosynthesis of secondary metabolites. Gene cluster prediction analysis allowed to characterize 20 clusters of NRPS, PKS and hybrid NRPS-PKS from 2 to 66kb. Surprisingly, none of the characterized operons had previously been described in the literature.