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**BCCM/ULC : genomic research on Polar cyanobacteria**

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The BCCM/ULC public collection of cyanobacteria aims to gather a representative portion of Polar cyanobacterial diversity from different ecological origins (microbial mats, soil crusts, cryoconites, endoliths, etc.) and ensure their ex-situ conservation in a context of global change. These strains are available for researchers to study the biodiversity, taxonomy, evolution, adaptations to harsh environmental conditions, and genomic make-up of Polar cyanobacteria. Currently, there are 120 unicyanobacterial strains of Polar origin in the collection (catalogue: http://bccm.belspo.be/catalogues/ulc-catalogue-search). The collection is ISO 9001 certified for depositing and distributing strains, as part of the multi-site certification of the Belgian Co-ordinated Collections of Micro-organisms (BCCM) consortium. Morphological and molecular identification (based on 16S rRNA sequences) indicate that the strains belong to the orders Chroococcales, Chroococcidiopsidales, Nostocales, Oscillatoriales, Pleurocapsales, and Synechococcales. This broad genotypic distribution makes the BCCM/ULC collection particularly interesting for phylogenomic studies. The first genome of an axenic Antarctic strain, Phormidesmis priestleyi ULC007, was sequenced. To investigate the occurrence of genes involved in the cold stress response, a selection of 42 PEGs (protein encoding genes) linked to cold adaptation was studied in 72 cyanobacterial genomes. By comparing the genes copy numbers as a proxy of adaptation, our results underline the importance of different functions in the adaptation mechanisms to the polar environment (e.g. DNA repair, Heat shock proteins, EPS biosynthesis). We also described a metagenomic pipeline that enables the easy recovery of genomes from non-axenic cultures, tested on 17 cyanobacterial strains from the BCCM/ULC collection. In parallel, we assembled 31 co-cultivated bacteria (12 nearly complete) from the same cultures and showed that they mostly belong to Bacteroidetes and Proteobacteria.