

BCCM/ULC public collection of cyanobacteria: A tool for microbial research and innovation

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Cyanobacteria represent an ancient group of morphologically diverse oxyphototrophic bacteria. Their long and complex evolutionary history is considered to have contributed to the successful colonization of a wide range of habitats including those, which are, from an anthropocentric point of view, hostile to life and are known as 'extreme' environments. Cyanobacteria thriving in mesophilic environments have been extensively studied in respect to their taxonomy. However, little is known about the diversity and taxonomy of extremophilic cyanobacteria. Nonetheless, the discovery of several new taxa through the investigation of just a limited number of extreme habitats suggests a high degree of novel biological diversity that remains unexplored.

The BCCM/ULC public culture collection, funded by the Belgian Science Policy Office since 2011, currently hosts more than 500 cyanobacterial strains, of which approximately 140 derive from polar, subpolar, and alpine environments, followed by tropical, subtropical and mediterranean biotopes. In addition, strains of Belgian origin (lakes, soils) are also represented in the collection. All strains are studied by applying a polyphasic approach workflow, which includes a combination of morphological (microscopy), molecular (16S rRNA gene and ITS region) and ecological data.

Cyanobacteria are also known producers of a variety of natural products. Indeed, there have been more than 2000 functionally diverse and structurally complex bioactive metabolites identified from cyanobacteria, including alkaloids, cyclic and linear peptides, polyketides and nonribosomal peptides. These metabolites range from toxins to biologically active molecules showing promise as potential drug leads. As part of an ongoing effort to discover new molecules with potential pharmaceutical applications, the strains are being evaluated for their antibacterial and/or antifungal activities.

Furthermore, whole-genome sequencing is applied to study taxonomically interesting morphotypes and bioactive metabolite-producing strains. Genome sequencing has already been performed for 25 strains, 10 of them being currently analysed within the collection. The bioinformatic analysis of genomes of the strains ULC007, ULC065 and ULC129 revealed the presence of biosynthetic gene clusters encoding for a wide range of natural products with potential biomedical applications. Polar strains of the recently described genus *Laspinema* are also studied from a phylogenomic and comparative genomic perspective to understand the basis of adaptations to cold environments. Lastly, the collection has developed a series of containerized bioinformatics workflows that correspond to the open science practices.