

**[052] BCCM/ULC: A public culture collection for *ex situ* conservation of cyanobacterial diversity and support of taxonomic and genomic studies**

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Cyanobacteria are a phylum of morphologically diverse photosynthetic bacteria. During their long and complex evolutionary history, they successfully colonized a wide range of habitats from polar to temperate and tropical regions. They also show interesting adaptations to extreme habitats (e.g. high salinity, high or low temperature, light intensity, exposure to UV, freezing, desiccation) but their diversity is still insufficiently studied.

BCCM/ULC is a young public collection, currently hosting more than 500 cyanobacterial strains, of which approximately 140 derive from (sub)polar and alpine environments, followed by tropical, subtropical and Mediterranean biotopes as well as strains of Belgian origin. An ISO 9001 certificate covers the public deposition and distribution of strains, as part of a multi-site certification for the BCCM consortium.

All strains are studied by applying a polyphasic approach workflow (i.e., morphological, molecular, and ecological data). Furthermore, the collection includes more than 20 strains that are the reference (or ‘type’) for newly described taxa including *Plectolyngbya*, *Shackletoniella*, *Timaviella*, *Parakomarekiella*, *Petrachloros*, *Leptochromothrix*, *Vermifilum*, *Tigrinifilum*, *Affixifilum*, *Sirenicapillaria*, *Ophiophycus* and *Floridanema*. Recently, a set of taxonomically interesting strains of rock-inhabiting cyanobacteria from Finland as well as strains from freshwater, marine and terrestrial habitats from Florida, USA (Berthold–Laughinghouse Culture Collection) have been deposited into the collection.

Additionally, an integrated approach that combines whole-genome sequencing, metagenomics, phylogenomics and phylogenetic placement 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. Recently, the collection has developed a suite of highly reproducible genomic workflows (GEN-ERA; <https://github.com/Lcornet/GENERA>), coded in Nextflow and based on Singularity containers, that meet the requirements of open science and FAIR practices.