Cyanobacteria of Polar Regions: Focus of the BCCM/ULC Culture Collection

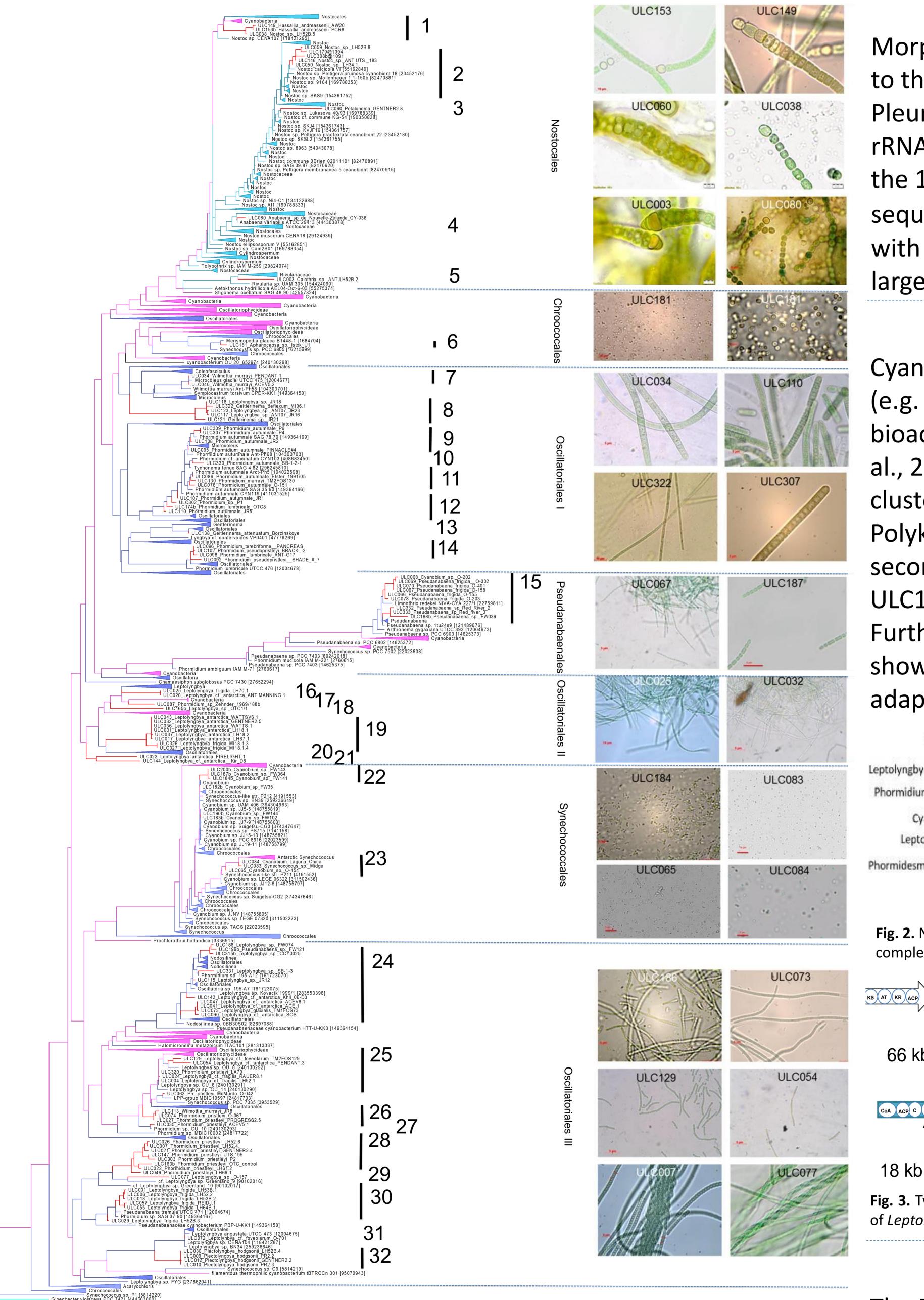
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Introduction

The aim of the BCCM/ULC public collection is to gather representatives of the polar cyanobacterial diversity from different ecological origins as limnetic mats, soil crusts, cryoconites or endoliths. Currently, it harbors 224 cyanobacterial strains, with 140 being of Antarctic origin. Continuous maintenance of living cultures, most of which are also cryopreserved (as back-up), ensure the preservation and the rapid delivery of strains to clients for fundamental and applied research.

The collection is funded by the Belgian Science Policy Office since 2011 and certified by ISO 9001 for the public deposition and distribution of strains. All available strains can be found on the catalogue: http://bccm.belspo.be/catalogues/ulc-catalogue-search.



Biodiversity

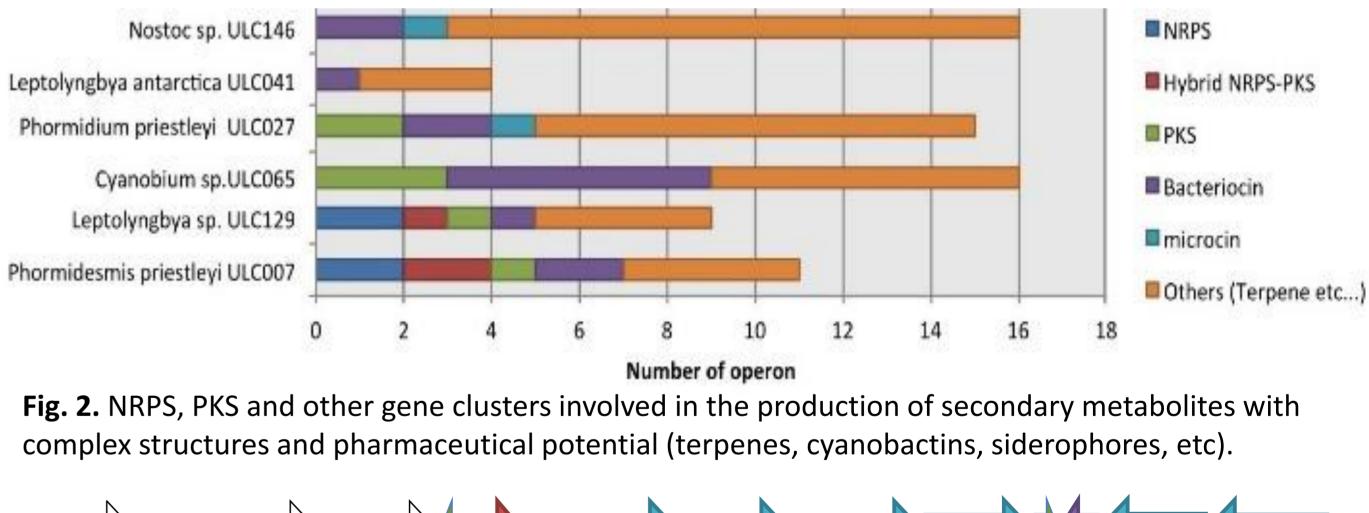
Morphological identification showed that the strains belong to the orders Synechococcales, Oscillatoriales, Pleurocapsales, Chroococcidiopsidales and Nostocales. 16S rRNA and ITS of the strains are gradually sequenced. For now, the 159 BCCM/ULC strains, for which the 16S rRNA sequences are available, correspond to 69 OTUs (sequences with > 99 % 16S rRNA similarity), and thus, represent a quite large diversity (Fig. 1).

Bioactive compounds

Cyanobacteria produce a wide range of secondary metabolites (e.g. alkaloids, cyclic and linear peptides, polyketides) with bioactive potential. Genome sequencing of 15 strains (Lara et al., 2017; Cornet et al., 2018) revealed the presence of gene clusters for Non-Ribosomal Peptide Synthetases (NRPS), Polyketide Synthases (PKS), hybrid clusters and other types of secondary metabolites in the strains ULC007, ULC065 and

ULC129 (Fig. 2, Fig. 3).

Furthermore, comparison of polar and non-polar genomes showed that protein encoding genes (PEGs) involved in cold adaptation mechanisms are more abundant in the polar ones.



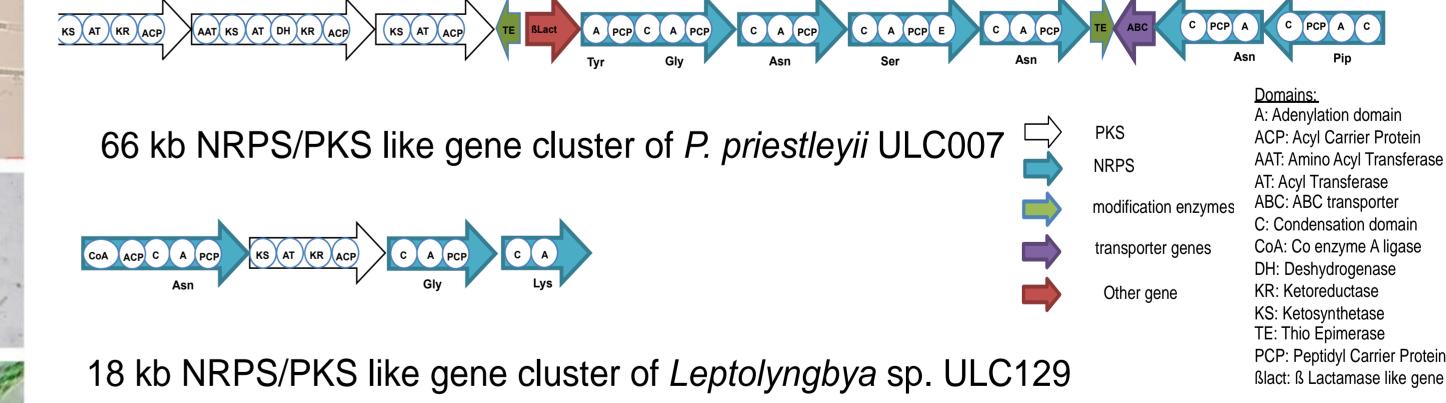


Fig. 3. Two hybrid NRPS-PKS like clusters found in the genome of *P. priestleyii* ULC007 and metagenome of Leptolyngbya spp. ULC129.

Conclusions

The BCCM/ULC public collection serves as a Biological Resource Centre to conserve ex situ and to describe the biodiversity of polar cyanobacteria, as well as a resource for the discovery of novel bioactive compounds.



Fig. 1. Phylogenetic tree based on 1140 16S rRNA sequences of cyanobacteria (1273 positions) with branches of

BCCM/ULC strains marked in red. The tree was inferred using RaxML under a GTR-GAMMA model and 100

References: Cornet et al. (2018) Microbial genomics 4, DOI 10.1099/mgen.0.000212; Lara Y, et al. (2017) Genome Announcement 5:e01546-16.

bootstrap pseudo-replicates. Lineages were numbered and illustrated by microscopic pictures.

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