

## Genome sequencing of an endemic filamentous Antarctic cyanobacterium

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The strain *Phormidium priestleyi* ULC007 was isolated from a benthic mat located in a shallow freshwater pond in the Larsemann Hills (69°S), Western Antarctica. This strain belongs to a cyanobacterial cluster that appeared as potentially endemic (Taton et al. 2006). After obtaining an axenic isolate, we sequenced the genome of this strain in the frame of the BELSPO CCAMBIO project, in order to better understand the functioning, metabolism and adaptative strategies of cyanobacteria to the extreme Antarctic environment.

Genomic DNA was extracted using the GenElute Bacterial genomic DNA kit (Sigma). The genome was sequenced with 100-paired end reads via Illumina sequencing technology (1.5 Gb data). Sequences from the Illumina run were assembled using Velvet and SPAdes software packages. The genome sequences were annotated using glimmer3 and a reference database composed of cyanobacterial genomes previously annotated by RAST taking the SEED approach with subsystems and FIGfams technology.

The Illumina run generated 4,404,753 reads. Preliminary assembly of the dataset yielded 152 contigs (5,696,987 bp) from 1036 bp to 312,036 bp (48,8% GC content). Further bioinformatic analyses are in progress. In a preliminary analysis, we observed the presence of genes involved in nitrogen fixation, oxidative stress, circadian clock, polyketide synthases, non-ribosomal peptide synthases, as well as gene encoding putative bacteriocins. The genome sequence of this endemic cyanobacterium from an extreme environment will allow unravelling its strategies to cope with stresses and hostile life conditions.