

Biogeographic patterns and genomic adaptation of benthic cyanobacteria in Antarctic lakes

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Cyanobacteria are a major component of Antarctic lacustrine ecosystems, usually forming conspicuous complex benthic communities known as microbial mats (Singh & Elster 2007; Vincent & Quesada 2012). Despite their importance as the dominant phototrophs, a comprehensive understanding of the ecology, function and biogeography of Antarctic cyanobacteria is far from being achieved. The present study assessed (a) the biogeographic patterns of benthic cyanobacterial communities in 13 Antarctic lakes and (b) the genomic make-up of the strain *Phormidesmis priestleyi* ULC007, which belongs to a widely distributed Antarctic lineage. Community-level profiling using 454 pyrosequencing of the 16S rRNA revealed communities largely dominated by phylotypes ascribed to the order Pseudanabaenales. Biogeographic patterns were unrelated to geographic location and highly connected to lake physicochemical composition, mainly conductivity and DOC content. The vast majority of phylotypes (79 OTUs, 77.0%) were related to cyanobacterial lineages (defined at $\geq 99.0\%$ sequence similarity) restricted to the cold biosphere (i.e. polar and alpine biotopes). These results suggest that cyanobacteria are widely distributed within Antarctica, resulting in communities mostly arranged according to environmental gradients. At the global level, on the other hand, barriers to dispersal appear to exist for some cyanobacterial lineages, resulting in a high degree of endemism within the Antarctic continent. In order to gain further insights on the functional diversity and adaptation of Antarctic cyanobacteria, the genome of *P. priestleyi* ULC007 was sequenced. This strain was isolated from Lake Bruehwiler in the Larsemann Hills (Taton et al. 2006; Lara et al. 2017) and, according to our pyrosequencing analysis, appears restricted to Antarctic lakes with low TOC content. Duplication patterns of genes involved in stress response (e.g. *dnaI*, *dnaK*, *recF*, *cspA*) and circadian clock (e.g. *kaiA/B/C*, *cikA*, *pex*, *sasA*) were investigated and compared with other publicly available genomes. Preliminary analysis grouped *P. priestleyi* ULC007 with other extremophilic strains, giving further support to the role of gene duplication in the adaptation to extreme environmental conditions. Additional analyses on evolutionary mechanisms (e.g. horizontal gene transfer, genome rearrangements) are being carried out and characterisation of other genomes is in progress, including cyanobacterial strains isolated from hypersaline Antarctic lakes. This will provide a better understanding of the survival strategies developed by mat-forming cyanobacteria in harsh conditions, contributing to the better understanding of the ecological and biogeographic ranges of Antarctic cyanobacteria and potential impacts of environmental changes.

References

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