

C07-P06

CYANOBACTERIAL DIVERSITY ALONG A LATITUDINAL ARCTIC GRADIENT

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Cold environments constitute ~85% of the biosphere, with most of the aquatic life being microbes (Margesin et al., 2011). Low temperature (<5°C) not only controls which organisms exist (i.e. biodiversity), but is likely to have affected how life evolved on Earth (Bada et al., 2002). Very little is known about the cellular microbes in cold environments and how they could interact each other. This is an important gap in our knowledge because microbes are central to life on the planet—they perform processes no other living organisms can do – and we have little idea about how they respond to environmental cues, or how they may respond to future global ecosystem changes (Quesada & Velázquez, 2012). Cyanobacteria are the oldest oxygenic phototrophic microorganisms on Earth, the origins of most of the historic primary production and oxygenation of the planet and promote inclusion of the atmospheric nitrogen into biological nutrient cycling. Cyanobacteria have achieved a considerable morphological complexity and functional differentiation for a prokaryotic organism, including separation of cells depending on their function. The remains of some of these structures could be recognized in up to 3.5 billion years old deposits (Schopf, 2000). Cyanobacteria show little change in cellular structure and function over extended spans of geological time and continue to dominate today in extreme environments, including those that deteriorated by anthropogenic impacts (pollution, eutrophication). Consequently, their study in modern extreme environments serves for interpretation of their fossil record and also to investigate the possible impacts on the biosphere. Ecosystem processes are sensitive to climate variability (natural or anthropogenic, spatial or temporal) and community composition. In that purpose, we sampled different lakes and ponds at three different locations in the high Canadian Arctic (Ward Hunt Island, Ellesmere Island and Cornwallis Island/Resolute Bay) (Figure 1) covering a latitudinal gradient. Cyanobacteria diversity was investigated *in vivo* along the latitudinal gradient of Arctic freshwater ecosystems and then analysed by high throughput tools —by using Illumina MiSeq Next Generation Sequencing technology. A set of environmental variables was correlated to community's composition by a multivariate approach, the high-throughput results pointed out the ecological and taxonomical differences in cyanobacterial assemblages. Apparently, there were not any single environmental variable explaining such differences, but a selection of sub-sets of variables may act as proper proxies to communities' composition attending to the cyanobacterial fraction. New insights on biodiversity and organisms interactions in such communities will advance our knowledge about microbial ecology and possible effects of environmental change endangered Arctic landscapes.



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