

Diversity and biogeography of microorganisms in microbial mats of Antarctic lakes

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The BelSPO project CCAMBIO aims to study the biogeographical distribution of microorganisms (bacteria, cyanobacteria, microeukaryotes) in lacustrine microbial mats using a combination of techniques including microscopic observations, strain isolation and genetic characterisation, and molecular diversity assessments using High Throughput Sequencing of environmental DNA. The samples were collected in different Antarctic and sub-Antarctic biogeographical regions.

Preliminary multivariate analysis of >130 samples revealed strong bioregionalisation patterns in microbial eukaryotes, which are in agreement with the classical subdivision of the Antarctic Realm into Maritime Antarctica, Continental Antarctica and the Sub-Antarctic Islands generally observed in plants and animals. The biogeographic structuring was less strong between the continent and Maritime Antarctica in prokaryotes suggesting more regular dispersal events between these two regions. The Sub-Antarctic assemblages harboured more complex foodwebs, with arthropods, nematods, rotifers, flatworms and annelids as main metazoan groups. Lakes on the continent, however, were characterised by fewer metazoan groups and a greater importance of microbial herbivores and secondary consumers, including a relative high diversity of ciliates and tardigrades. A first study of the biogeography of cyanobacteria was performed on samples from microbial mats collected in 13 Antarctic lakes with different ecological features and situated in 4 distinct ACRs. Biogeographic patterns appeared unrelated to geographic location but rather linked to lake physicochemical composition, mainly conductivity and DOC. Most OTUs (77.0%) were related to cyanobacterial lineages (defined at $\geq 99.0\%$ sequence similarity) restricted to the cold biosphere. 21,4% were associated to lineages currently restricted to Antarctic biotopes. The results suggest a constant dispersal of cyanobacterial propagules at the regional, intracontinental level, 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, especially those making up the rare fraction of the communities.

In the coming months, the molecular diversity data will be deposited into the "Microbial Antarctic Resource System (MARS)" presently developed into the webportal 'biodiversity.aq'. Better knowledge of the diversity and distribution of microorganisms will contribute to a better assessment of their resilience and local/regional responses to global change.