

Multi-domain evidence for fine-scale bioregionalisation patterns in the Antarctic lacustrine microbiome

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The geological, climatic and glacial history of Antarctica has highly influenced its terrestrial biodiversity and resulted in disjunct distributions of taxa, impoverished communities and clear bioregionalisation patterns. The Antarctic Realm is traditionally subdivided into three regions: Continental, Maritime and Sub-Antarctica. Recent meta-analyses, mainly based on the inventory of multicellular, macroscopic organisms, further allowed the recognition of more fine-scaled biogeographic entities, namely the Antarctic Conservation Biogeographic Regions (ACBRs). Although the Antarctic is dominated by microbial communities, it is unclear whether these subdivisions effectively hold true for bacteria and single-celled microeukaryotes. Such region-wide studies were mainly hampered by the absence of methods that enabled to characterize entire microbial communities with a consistent taxonomic resolution and at a relatively low cost. Here we used a large scale high-throughput sequencing approach to target the V1-V3 and V4 variable regions of the 16S (Bacteria) and 18S rRNA genes (Eukarya) in 138 lakes from 8 ACBRs and 2 Sub-Antarctic islands, in combination with morphology-based enumerations of diatom morphospecies in 453 lakes (7 ACBRs and 6 Sub-Antarctic islands or archipelagos. Clear biogeographic and macroecological patterns in both eukaryotes and bacteria emerged, including a significant latitudinal diversity gradient. In the diatoms, the incidence of endemism appeared to be high and increased with latitude, which could be significantly explained by variation in summer-winter temperature, time since deglaciation, and isolation from the nearest continent other than Antarctica. In Bacteria, biogeographical patterns were present, with a clear separation between Sub-Antarctica and the continent, but also between Continental and Maritime Antarctica. Nevertheless, also on smaller geographical scales did lakes in close proximity show higher similarities in bacterial community composition, although in particular electric conductivity was an important forcing environmental variable. In microeukaryotes were biogeographical patterns more pronounced, with much less OTUs shared between different regions. Multivariate analyses revealed that these patterns could be significantly explained by a combination of differences in environmental properties and historical factors (including the time of deglaciation and the amount of isolation), with the relative importance of both sets of predictors being different between Bacteria and the main Eukaryotic phyla. Historical factors being more important in the latter. Our results confirm that microbes exhibit patterns congruent to those found in multicellular organisms, which urges the application of effective conservation measures to prevent the admixing and homogenization of microbial communities in the Antarctic Realm.