

S05: Large scale analyses of spatial diversity patterns

Biogeography and macroevolution in the Arctic and Antarctic lacustrine microbiomes

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Despite similar contemporary environmental conditions, the Arctic and Antarctic regions have a different tectonic, glacial and paleoclimatic history. Combined with interhemispheric differences in spatial configuration of landmasses, these past events exerted strong constraints on the present-day patterns in the diversity and distribution of polar plants and animals. In contrast, little is known about the diversity and biogeography of microorganisms in polar lake and terrestrial habitats, though they play a considerable role in nearly all the ecosystem functions in these habitats. We performed a continental-scale inventory of benthic microbial mats in 223 (sub)Arctic and (sub)Antarctic lakes to study bipolar differences in the community structure and biodiversity of bacteria and eukaryotes by using high-throughput amplicon sequencing (Illumina MiSeq), of parts of the 16S (V1-V3) and 18S (V4) small subunit ribosomal RNA genes. Distinct biogeographic zones in both eukaryotes and bacteria emerged, with a clear differentiation between the Northern and Southern hemisphere communities. The Antarctic food-webs appeared to be less complex and truncated, with particular functional groups being absent (e.g. Annelida) while others were comparably diverse (e.g. ciliates) as their Arctic counterparts. Moreover, local OTU-richness of both eukaryotes and bacteria was significantly lower in Antarctica compared with the Arctic and decreased with increasing latitude in the Southern Hemisphere. Generalized linear models revealed that this interhemispheric diversity-asymmetry in bacteria diversity could be significantly explained by environmental properties of the lakes and differences in energy availability, while in eukaryotes, the lack of connectivity appeared to put additional constraints on OTU-richness. Also at the higher taxonomic level interhemispheric difference in diversity patterns emerged; the Arctic communities appeared to be more diverse in all eukaryotic groups (except Cercozoa) based on OTUs clustered at sequence similarities ranging between 90 and 97%. Although diversity unique to Antarctica was consistently much lower at these different OTU-clustering similarities, each OTU harboured a markedly higher amount of sequence diversity compared to those unique to the Northern hemisphere. Combined, for eukaryotes this suggests the survival of diverse and complex lacustrine food webs in glacial refugia during ice ages, probably facilitated by high dispersal rates between well-connected Northern hemisphere landmasses. In Antarctica, on the other hand, glacial-interglacial cycles and the isolation of the continent resulted in regional extinction events in some groups and selective survival or possibly radiations in others. Conversely, most bacterial groups did not exhibit these interhemispheric differences, which might indicate better dispersal and/or lower extinction rates.