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Peatlands in a latitudinal gradient: links between microbial composition and organic matter degradation

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Microbial breakdown of organic matter (OM) is slowed down by different environmental conditions in peatlands, such as low pH, low oxygen availability and presence of phenolic compounds, leading to their recognized carbon storage function (Freeman et al. 2001, Kang et al. 2018). Peatlands are worldwide distributed with environmental conditions and biogeographical legacy varying among regions, which determine different controlling factors of microbial OM degradation and affect carbon cycling and greenhouse gas (GHG) emissions from peat soils. Here, we present the results of a study aimed at investigating the structure and function of microbial communities involved in the OM decomposition in moss-dominated peatlands of tropical (Andes-Paramo, Colombia), temperate (Wales, UK), and arctic (Svalbard, Norway) regions. Prokaryote community, extracellular enzyme activity, and GHG (carbon dioxide, methane, and nitrous oxide) production were assessed in peat soil (first 10 cm depth) collected in one sampling campaign by region (summer north hemisphere). Results showed contrasting prokaryote communities among regions and a clear link between microbial composition and OM degrading metabolism. Arctic peatlands in Svalbard were shallow, circumneutral, with the highest prokaryote diversity (aerobic and anaerobic), an active lignin degradation, production of carbon dioxide, and nitrous oxide. In Wales, peatlands exhibited the lowest pH, an intermediate diversity of prokaryotes, with aerobic and anaerobic groups, and very low OM degrading activity and GHG production. Finally, in the Paramo's peatlands, the oxygen level was the lowest and consequently prokaryote community was dominated by anaerobic groups with an active anaerobic OM degradation and methane production. Our study is the first, to the extent of our knowledge, giving a comparative view of microbial OM decomposition in peatlands from contrasting and remote regions. Our results highlight the great global diversity of prokaryotes and microbial metabolism and give new lights on the relationship between microbial composition and microbial carbon cycling in peatlands.

References

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