

Structure and function of the global peatland microbiome

SIMON M. K. CHEUNG, RICHARD D. PANCOST AND
CASEY BRYCE

University of Bristol

Peatlands are important carbon sinks but can also be sources of greenhouse gases, including methane and nitrous oxide. This balance depends on environmental factors and climate conditions, which influence microbial processes in peatlands. To date, the structure, function, and ecological drivers of peatland microbial communities (microbiomes) have been examined primarily at the local scale. In this study, by leveraging 109 publicly available metagenomes from 20 near-natural peatland sites worldwide, we aimed to identify global patterns and elucidate the main drivers of microbial composition and function in peatlands. Our results showed that peatland type and peat depth determined both the taxonomic and functional diversity of the peatland microbiome. Variation and hierarchical partitioning analysis revealed that dominant vegetation type and peatland type were the most important predictors of community taxonomy and function. Peat depth was also an important driver of community function, but not its taxonomic composition. In contrast, pH played a prominent role in controlling taxonomic community membership, but only had minor effects on community function.

The bog microbiome was dominated by the phyla Acidobacteria (26%), Proteobacteria (24%), and *Candidatus* Saccharibacteria (10%), the fen microbiome by Proteobacteria (48%), Euryarchaeota (11%), and Acidobacteria (9%), and the tropical peatland microbiome by Proteobacteria (47%), Acidobacteria (20%), and Actinobacteria (16%). CAZyme genes involved in the degradation of major plant cell wall components were recovered in all metagenomes, with most being more abundant in bogs compared with tropical peatlands. Functional marker gene analysis revealed a widespread metabolic potential for all three types of methanogenesis in tropical peatlands, whereas bogs and fens primarily relied on hydrogenotrophic and acetoclastic methanogenesis. Notably, a widespread potential for methane oxidation, denitrification, thiosulfate/polysulfide reduction, and iron reduction was also observed in tropical peatlands. The potential for denitrification and thiosulfate/polysulfide reduction was also prevalent in fens; however, the potential for all these processes was less common in bogs. Overall, our findings provide important insights into the structure, function, and ecological drivers of the peatland microbiome on a global scale, with implications for their biogeochemical function and carbon storage capacity.