

Bacterial and fungal community composition and functioning of two different peatlands in China

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Peatlands are important carbon sinks which store one third of the global soil carbon (~550 Gt) with only 3% of the land surface. The slow rate of organic matter decomposition associated with low microbial diversity and limited functioning under cold, acidic and anoxic condition is of critical importance in controlling biogeochemical cycles in northern peatlands. To evaluate the variation in microbial community composition and functionality can advance our understanding of the underlying mechanisms of the biogeochemical processes and interactions. However, there is still a lack of information for Chinese peatlands. Here, we sampled peat profiles at three different depths (10-20, 30-40 and 60-70 cm) from two typical peatlands in China: a rich fen in Qinghai-Tibet Plateau (QTP) and a poor fen in the Changbai Mountains (CBM). We investigated the bacterial (16S rRNA) and fungal (ITS2) community composition and diversity with high-throughput sequencing and predicted the metagenome functioning with PICRUSt (Phylogenetic Investigation of Communities by Reconstruction of Unobserved States).

The results showed that Proteobacteria, Acidobacteria and Actinobacteria were the most abundant bacterial phyla in the upper peat layer (10-20 cm) for both sites, with increasing abundance of Chloroflexi and Bacteroidetes down to the saturated zone (60-70 cm in CMB; 30-40 and 60-70 cm in QTP). For fungi, Ascomycota, Ciliophora and Basidiomycota were the most abundant phyla in both sites, with decreasing Ciliophora abundance down to the saturated zone. The α -diversity of both bacterial and fungal showed a decreasing trend with depth in QTP, with the largest diversity occurring at the depth of 30-40 cm in CMB. Regardless of sampling sites, the bacterial communities at the depth of 60-70 cm were more similar than the other depths. The fungal community was clustered into two groups, corresponding to two sampling sites. The variation in fungal community with depth was larger in QTP than in CBM. The predicted abundances of KEGG orthologs (KOs) assigned to the metabolism of amino acid, lipid and xenobiotics, as well as environmental adaptation, were decreased with depth in CBM, with energy metabolism showing the opposite trend. In contrast, the KO abundances of amino acid and lipid metabolism and environmental adaptation were the highest in the middle layer (30-40 cm) in QTP, where the KO abundance of energy metabolism was the lowest. In general, the difference in predicted metagenome functioning between sites was less obvious than between depths.

These results highlight the important role of hydrology in shaping the microbial community in minerotrophic peatlands. The effect of environmental drivers on microbial diversity and functioning may be mediated by shifting in hydrological dynamics (e.g. land use change and desiccation) which should be considered under future global change condition.