063A - The core microbiome of permafrost-affected arctic peatlands is stable over decades but sensitive to hydrological differences

Fabian Horn[1], Stine Holm[1], Lars Ganzert[1], Andre Friese[1], Julia Boike[2], Paul Overduin[2], Dirk Wagner[1], Susanne Liebner[1], Matthias Winkel*[1]

[1]GFZ German Research Centre for Geosciences, Germany, [2]Alfred Wegener Institute Helmholtz Centre for Polar and Marine Research, Germany

Global climate change will affect the microbial degradation of organic matter in arctic peatlands, which are sensitive to temperature changes. It is assumed that rising temperatures will raise microbial activity followed by increased production of greenhouses gases. However, the factors that control microbial communities in these rapidly changing environments and the effect on community composition in regard to organic matter degradation have not been studied in detail.

In this study, we analyzed the depth distribution of microbial communities (16S rRNA gene sequencing) from the rim and center of three low-centered polygon active layers with different hydrological regimes, one with a permanent standing water body and two with more fluctuating water bodies. We measured soil chemical
parameters (CHNS, anion, cation and gas concentrations, pH, and conductivity) as well as seasonal water levels.

Bacterial communities could be separated into bottom and top soil horizons reflecting water levels with clear oxygen regime shift and a decreasing diversity trend in the rim sites. In contrast, archaeal diversity and distribution over depth did not differ at any site. Besides hydrology and oxygen, none of the measured environmental parameters could explain the variation in the microbial distribution. Comparing our results with previous data from the same location showed a stable
core microbiome over decadal timescales that is not affected by rising temperatures in the soil.

Our study suggests that in the course of Global Change shifting hydrological regimes rather than increasing temperatures will alter microbial community composition in Arctic permafrost affected wetlands.