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## **Captured metagenomics reveals high spatial variability in functional potential in CH<sub>4</sub> producing and consuming microorganisms in a temperate Swedish peatland.**

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Microbial communities of methane producing methanogens and consuming methanotrophs play an important role for the earth's atmospheric methane budget. Despite their global significance, the functional potential of these communities is poorly understood. To investigate this, we applied the molecular technique, captured metagenomics, to identify the variability in functional diversity of microorganisms involved in the metabolism of methane in an environmentally controlled laboratory study. Nine plant-peat mesocosms dominated by the sedge *Eriophorum vaginatum*, with varying coverage, were collected from a temperate natural wetland in Sweden and subjected to a simulated growing season. Samples for analysis of captured metagenomes were taken from the top, bottom and root adjacent zone at the end of the experiment. In addition, over the simulated season, measured gas fluxes of carbon dioxide (CO<sub>2</sub>) and CH<sub>4</sub>,  $\delta^{13}\text{C}$  of emitted CH<sub>4</sub> and the pore water concentration of dissolved methane and low molecular weight organic acids were recorded. The functional genes resulting from the captured metagenomes had a higher Shannon  $\alpha$ -diversity in the root zone when compared to the bottom and top. Sequences coding for methane metabolism were significantly more diverse in the root and bottom zones when compared to the top. However, the frequency of Acetyl-CoA decarboxylase and methane monooxygenase subunit A were significantly higher in the high emitting methane flux category when compared to the medium and low emitting mesocosms. We conclude that captured metagenomic analyses of functional genes provides a good measure of the functional potential of methanogenic and methanotrophic microbial communities. This technique can be used to investigate how methanogens and methanotrophs function in peatlands and thus, contribute to the concentration of atmospheric methane.