Geophysical Research Abstracts
Vol. 20, EGU2018-12791, 2018
EGU General Assembly 2018

Effect of energy crop cultivation on genetic potential of methanogenesis in an abandoned peat extraction area

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Peatlands, which store ca 1/3 of the world's soil carbon, are mainly situated in the boreal and temperate zones, although these ecosystems exist also in tropics and Arctic regions. The area of peatlands has been decreasing rapidly over the last century due to peat extraction, among several other economic purposes. Extracted peat is in demand largely as an energy source or as a growing medium and soil conditioner in horticulture. The modern large-scale peat mining is conducted using vacuums to remove recently dried peat, which inevitably leads to the problem of abandoned peat extraction areas. These areas emit greenhouse gases (CH4, CO_2, and N2O) into the atmosphere for decades if restoration action is not implemented. All methanogens belong to the domain of archaea and possess mcrA gene, which encodes the alpha-subunit of the methyl coenzyme M reductase — the enzyme that catalyses the last step in the CH4 synthesis.

The purpose of this study was to assess the impact of energy crop (Phalaris arundinacea L.) cultivation and fertilisation on bacterial and archaeal and methanogenic community abundance in residual peat on an abandoned peat extraction area, and link these changes to methane emission from the peat. 12 plots were established in 2012 (two-year experiment) and a total of 216 peat samples were collected from three depths (0–20, 20–40, and 40–60 cm) at the vegetation period. Peat pHH_2O, DOC, total N, NH4-N, NO_3-N, total P, PO4-P, total S, SO4-S, Ca and K values were determined. Bacterial and archaeal 16S rRNA genes and methanogenic archaeal marker gene mcrA in peat were quantified by using quantitative PCR method. CH4 emissions from the plots were measured using a closed static chamber method. Besides the widely used statistical methods, linear mixed effects modelling was used to test relationships between gene parameter values and chemical variables and treatments in different soil layers.

The bacterial abundance was the highest in the top layer of peat and the archaea as well as the methanogens were more abundant in the deeper layers. The archaeal proportion was up to 40% in the prokaryotic community and the methanogens proportion was up to 2% in the archaeal community. Phalaris cultivation increased significantly the bacterial abundance, but did not affect the archaeal abundance. Archaeal and methanogen abundances were affected by fertiliser in the deeper layer of Phalaris cultivated peat. The mcrA abundance and CH4 emission were positively correlated in the deeper layers of the uncultivated peat, while in case of Phalaris cultivation these two parameters were not related. Phalaris cultivation mitigated CH4 emission, although methanogen abundance varied little in different layers of residual peat under cultivated sites over time.