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METHANE TURNOVER BEFORE AND AFTER RESTORATION OF YOUNG FORESTRY-DRAINED FENS

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SUMMARY

Restoration of forestry-drained peatlands has been studied relatively widely using traditional physicochemical methods and vegetation follow-up. Restoration affects especially the carbon cycle, which is, above all, a microbiological process. Still, these key organisms and their response to restoration are poorly characterized. We studied the microbiological impacts of restoration on young forestry-drained fens. Our main focus was on the methane cycle.

KEY WORDS: peatland restoration, methane turnover, microbial communities

INTRODUCTION

Large proportion of northern peatlands has been drained for forestry, which drastically changes their carbon dynamics. Restoration aims to bring back pristine-like, water-saturated ecosystems that generally work as sinks for carbon dioxide (CO_2) and sources of methane (CH_4). It has been shown that restoration of forestry-drained peatlands affects substantially both CO_2 and CH_4 emissions (Komulainen *et al*., 1998, Komulainen *et al*., 1999). Although this effect originates from changes in the underlying microbial communities and processes, these microbiological aspects have received surprisingly little attention (Urbanová *et al*., 2011 one of the few). A recent, wide-ranging meta-analysis on wetland restoration included no microbial community data (Moreno-Mateos *et al*., 2012).

We aimed to analyse how disturbing and restoring the peatland ecosystem affects microbes and their functions in the carbon cycle. In relation to the likely increase in CH_4 production activity caused by water level rising, we expected to see changes in the community composition of the CH_4 producing and oxidizing microbes. In order to help to further develop restoration strategies, we evaluate the potential of microbial variables as indicators for restoration success.

MATERIAL AND METHODS

Study sites were young fens located in Siikajoki, on the eastern coast of the Gulf of Bothnia, Finland (64°45´N, 24°42´ E). Sites include two drained areas to be restored, two drained areas without restoration measures and two pristine control sites. Drained areas included areas with reasonable tree growth (named "trees") and areas that remained open after drainage (named "open") (Fig. 1). Characteristics of the pristine control sites have been described in Leppälä *et al*. (2011) (the youngest sites 1 and 2).

First samples were taken in July 2008 before restoration i.e. rising of the water table (WT) level. Sampling was repeated two years after restoration in August 2010. Methane producing archaea were examined with terminal restriction fragment length polymorphism (T-RFLP) -analysis based on methanogen-specific *mcrA* genes and methane-oxidizing bacteria by denaturing gradient gel electrophoresis (DGGE) based on methanotroph-specific *pmoA* genes. Both *mcrA* and *pmoA* and also sulphate reducing bacteria (SRB)-specific *dsrA* genes were quantified using quantitative PCR (qPCR). Phospholipid fatty acid analysis (PLFA) was used to reveal more general changes in the bacterial and fungal communities and biomass. Potential CH_4 and CO_2 production together with CH_4 oxidation were measured in laboratory incubations shortly after sampling. Microbial data is compared with the changes in vegetation and hydrology.

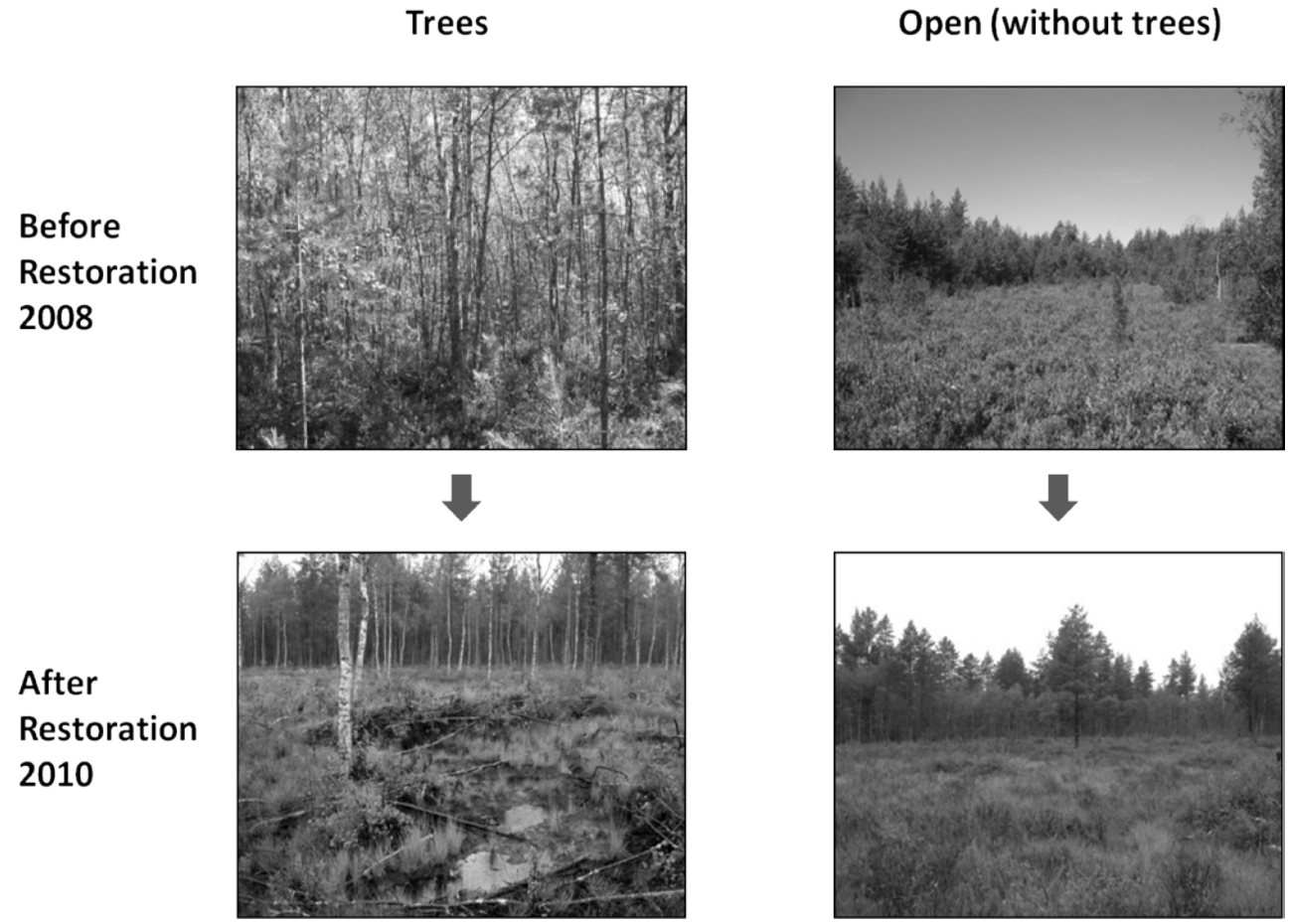

Figure 1. Restoration sites at the times of sampling. In addition to these sites, samples were taken also from drained "trees" and "open" sites left unrestored and from pristine control sites.

RESULTS AND DISCUSSION

Before the restoration event (2008), both CH_4 production and oxidation potentials were clearly highest in the pristine control sites and lowest in the sites with tree growth. After restoration (2010) the CH_4 production potential of the restored open site was almost similar to that of the pristine sites and higher than that of the unrestored drained open site. Both restored and still drained open sites had higher CH_4 oxidation potentials than the pristine sites. CH_4 production and oxidation potentials remained low on sites with a tree stand, even on the restored tree site. CO_2 production potentials were several times higher on every sampling site on the second sampling year (2010) and no clear effects of restoration were detected based on this variable. On the whole, differences between sampling years were higher than the effects of restoration in all measured activity potentials. Reason for this result is found on the weather conditions. During the first sampling, WT levels were higher than normal due to heavy rainfall and during the second sampling WT levels were lower than normal due to drought. This weather situation can be expected to affect especially the potential activity measurements that represent the conditions at that time of sampling.

Quantitative PCR analysis showed an increase with restoration in both methanogens and methanotrophs on the site with a tree stand. In contrast, in the unrestored drained sites (open and with tree stand) numbers of the indicator genes were smaller during second sampling in 2010 than in 2008. Compared to the potential activity measurements, qPCR appears to illustrate more long-term changes of the microbial community as DNA-based analysis includes also dormant and dead organisms whose DNA may remain intact for long periods of time (Nielsen *et al.*, 2007), and as such seems to be better suited as an indicator of restoration.

Based on all the data analysed thus far, effects of restoration were most clearly seen in the general microbial community level. PLFA data showed clear restoration effects especially in the site with a tree stand and also on the open site (Fig. 2). Changes in phospholipid fatty acid compositions between sampling years were smaller in the drained and pristine control sites. PLFA also showed statistically significant biomass increase only on the restored tree site. Although WT was on a low level during the second sampling, in the long run restoration seemed to turn the peat more anoxic. This can be seen in the decreased amount of fungi compared to bacteria, which is consistent with a previous study where, in reverse, water-level drawdown increased the relative amount of fungi in a fen environment (Jaatinen *et al.*, 2007). It should be noted that in another study conducted on a restored cut-away peatland PLFA alone did not provide enough resolution to distinguish between different restoration stages (Andersen *et al*., 2010). This could be the case also on our forestry-drained sites if restoration succession would be followed in a longer time-scale.

Analysis of the methanogen and methanotroph community data (T-RFLP and DGGE) and the SRB-qPCR is in progress. The whole set of microbiological data will be compared to the changes in vegetation, WT and pH.

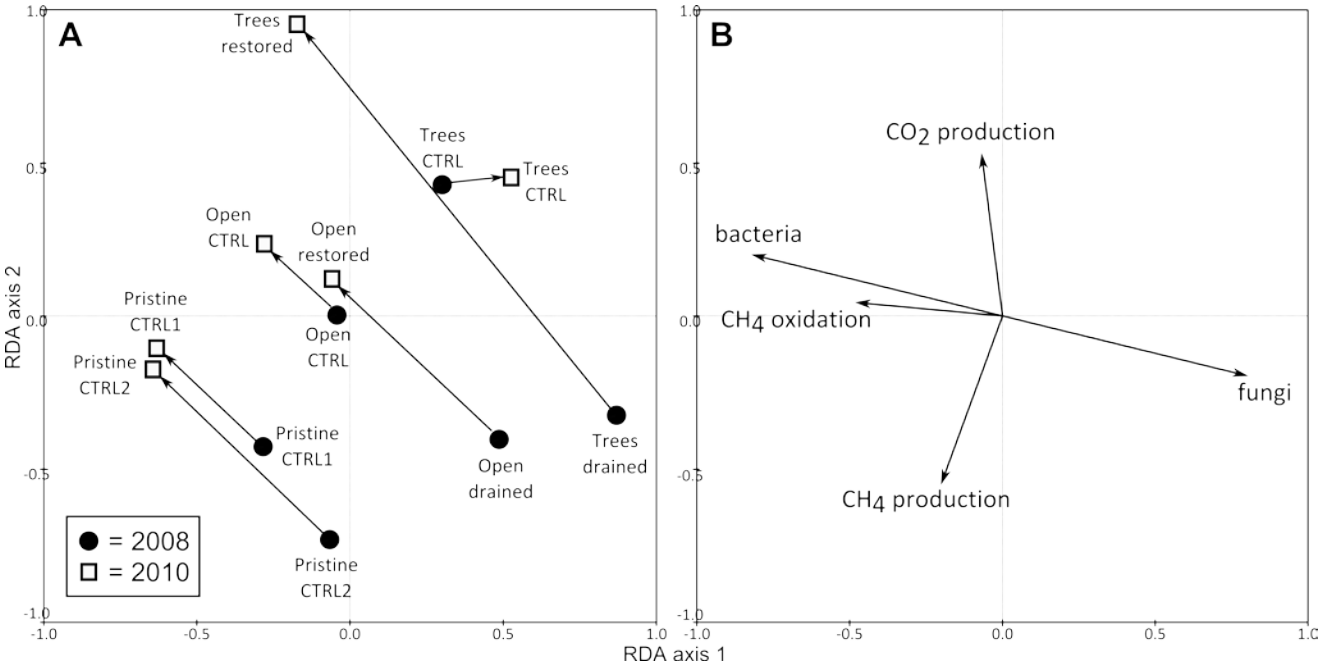

Figure 2. Redundancy analysis (RDA) on the PLFA data showing (A) sampling sites from the two different years 2008 and 2010 (arrows indicating the change between the years) and (B) relation of potential activities and functional groups (mol% sum of phospholipid fatty acids previously linked to bacteria and fungi (grouped similarly as in Jaatinen *et al*., 2007)) to sampling sites. While sites per year were used as active environmental variables, potential activities and functional groups were included as passive in the analysis. RDA axis 1 and 2 explained 39 and 7 % of the variation, respectively.

CONCLUSIONS

Restoration induced a change in the microbial communities that was most evident in the general microbial community level. The open sampling sites were more similar to the pristine sites before and after restoration. The largest changes were seen in the restored site with tree stand i.e. that had been successfully forested after drainage. Based on this experiment, PLFA could be a suitable tool in the follow-up of the restoration process. Also DNA-based methods could be used as an indicator of restoration succession. Potential activity measurements were tied to the conditions prevailing at the sampling time and as such were not that suited to reflect the long-term changes occurring on the sites. To reliably link our microbiological data to the changes of currently used restoration indicators like vegetation, a third sampling in a few years time should be conducted.

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