REVEALING SOURCES OF BIOLOGICAL METHANE PRODUCTION IN BOREAL UPLAND FORESTS

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BACKROUND

Boreal upland forests are considered as a sink for the greenhouse gas methane (CH_4) due to methanotrophic microbes that oxidize CH_4 in soils. Recently, several studies have confirmed that emissions of CH_4 from vegetation can occasionally overcome the sink strength of the soil, and the forest ecosystems may then act as a source of CH_4. However, the origin and the production mechanisms of CH_4 emitted from trees still remain controversial. Our aim was to assess whether methane producing microbes (methanogens) in different compartments of the forest could account for CH_4 emissions within a boreal forest.

CH4 FLUX MEASUREMENTS

CH_4 flux measurements were conducted in southern Finland, in an ICOS forest site surrounding the SMEAR II station (Fig. 1). Above canopy measurements were conducted with flux gradient method from the 127 m tall mast (Fig. 1a and b). Forest floor CH_4 flux was measured by static chamber method with 54 soil chamber collars (Fig. 1a and c). The tree stem CH_4 emission rates were measured from three plots with different mean soil volumetric water content from three pine, spruce and birch trees (Fig. 1a and d).

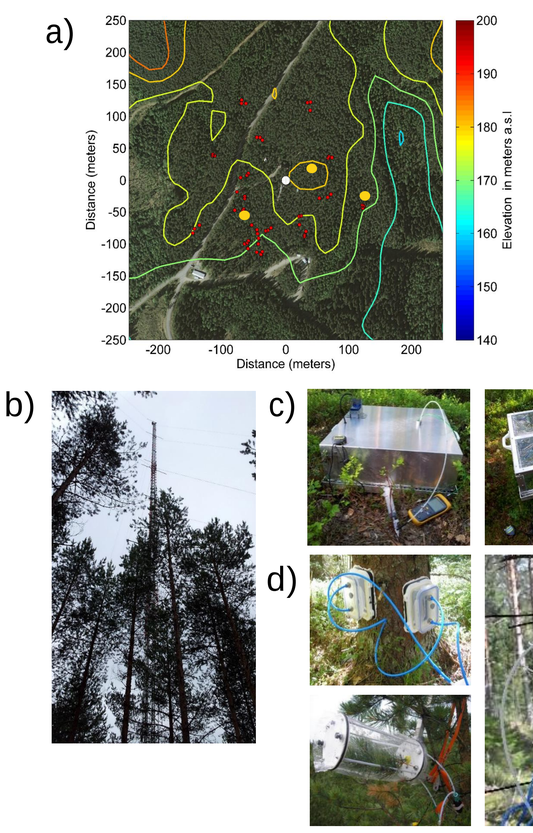

Figure 1. CH4 flux measurement site at Hyytiälä SMEAR II Station, Finland. a) White dot - tall mast; red dots - forest floor flux measurement sites; yellow dots - tree stem measurement sites b) tall mast for the above canopy measurements c) dark and transparent chambers for the forest floor measurements d) different types of chambers for the tree stem and canopy flux measurements.

Based on the above canopy measurements, boreal forest canopies acted as an occasional source of CH_4 in 2012-2014 (Fig. 2).

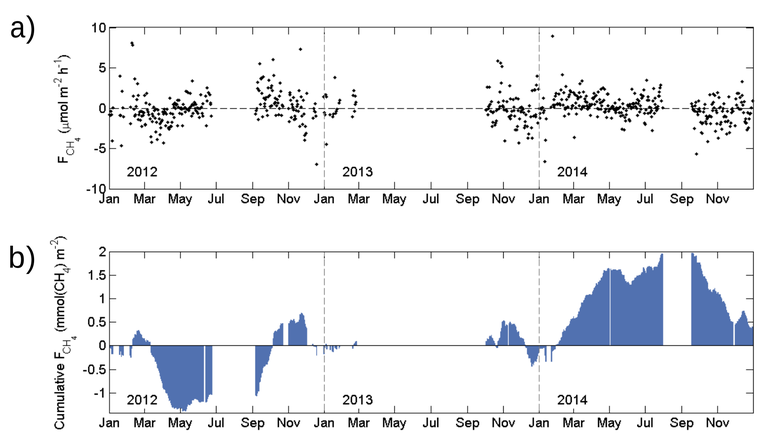

Figure 2. Above canopy fluxes a) daily means b) cumulative flux from 2012-2014. The data from 2013 is partly missing due to technical difficulties.

CH_4 flux measurements confirmed that forest floor acted as a sink of CH_4 for most of the year; however, some emissions were recorded mostly from the wet sites of the forest, from May to July in 2013 and 2014 (fig. 3).

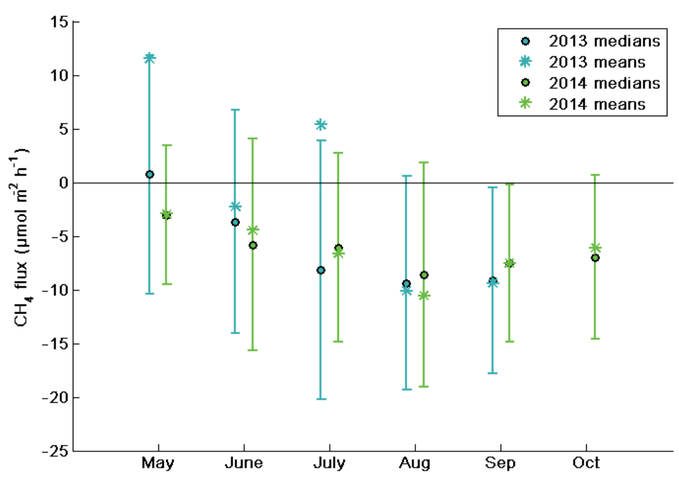

Figure 3. Forest floor CH4 fluxes per month in year 2013 and 2014. Flux is calculated as µmol m^{-2} h^{-1} and determined as means and medians with interquartile range lines.

Tree stems and shoots emitted small amounts of CH_4 throughout the year, with the highest emission rates coming from trees growing on the wet sites of the forest (Fig. 4).

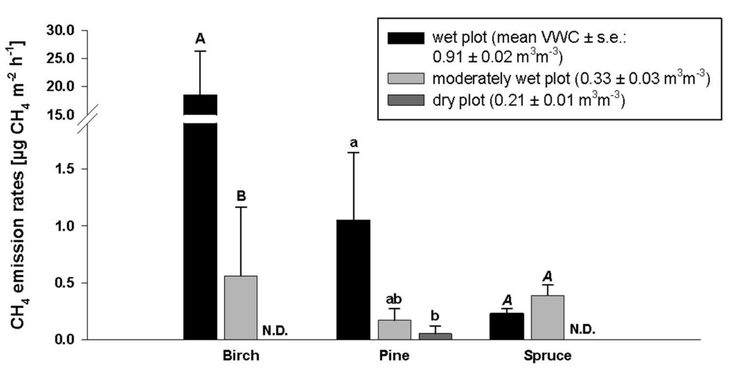

Figure 4. Stem emission rates of CH_4 from wet, moderately-wet and dry plots. VWC – soil volumetric water content. Emission rates are expressed per m^2 of stem surface area and determined as mean (± s.e.) of measurements on 3 trees per tree species and experimental plot, with 3 replicates per each chamber. Statistically significant differences at $p<0.05$ among experimental plots for each tree species are indicated by different letters above bars (Mann-Whitney Rank Sum test).

METHANOGENS

To detect the abundance of methanogens, samples of the most prevalent plant and tree species, soil and decaying wood were taken in June 2014 and 2015. Five replicate samples from each material were divided into different compartments: shoots, stem and roots, or upper and lower layer of soil. Samples were freeze-dried and grounded and DNA was extracted. qPCR analysis of the *mcr*A-gene was performed to quantify the methanogenic community.

From the paludified wet sites of the forest floor, high number of *mcr*A gene copies were detected (Fig 5). Few *mcr*A gene copies were also detected from decaying wood and some parts of the understory vegetation (Fig. 5). No *mcr*A gene copies were detected from humus and litter.

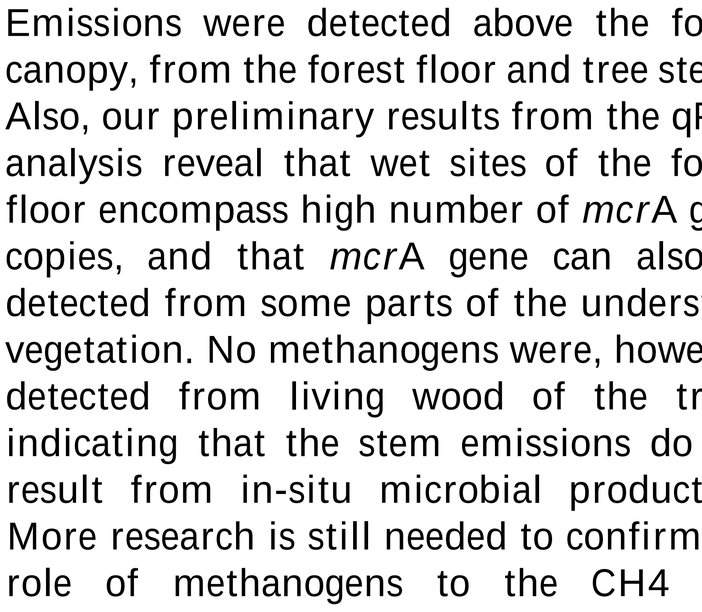

Figure 5. Detected *mcr*A gene copy number per g of dry weight (DW). Only positive samples are shown.

CONCLUSIONS

Our results demonstrate that boreal forests can occasionally act as a source of CH4. Emissions were detected above the forest canopy, from the forest floor and tree stems. Also, our preliminary results from the qPCR analysis reveal that wet sites of the forest floor encompass high number of *mcr*A gene copies, and that *mcr*A gene can also be detected from some parts of the understory vegetation. No methanogens were, however, detected from living wood of the trees, indicating that the stem emissions do not result from in-situ microbial production. More research is still needed to confirm the role of methanogens to the CH4 flux dynamics in boreal upland forests.

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