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## **Divergent drivers of the microbial methane sink in temperate forest and grassland soils**

Running title: Drivers of soil microbial methane oxidation

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## **Abstract**

Aerated topsoils are important sinks for atmospheric methane ( $\text{CH}_4$ ) via oxidation by  $\text{CH}_4$ -oxidizing bacteria (MOB). However, intensified management of grasslands and forests may reduce the  $\text{CH}_4$  sink capacity of soils. We investigated the influence of grassland land-use intensity (150 sites) and forest management type (149 sites) on potential atmospheric  $\text{CH}_4$  oxidation rates (PMORs) and the abundance and diversity of MOB (with qPCR) in topsoils of three temperate regions in Germany. PMORs measurements in microcosms under defined conditions yielded approximately twice as much  $\text{CH}_4$  oxidation in forest than in grassland soils. High land use intensity of grasslands had a negative effect on PMORs (-40%) in almost all regions and fertilization was the predominant factor of grassland land use intensity leading to PMOR reduction by 20%. In contrast, forest management did not affect PMORs in forest soils. USC- $\alpha$ , was the dominant group of MOB in the forests. In contrast, USC- $\gamma$  was absent in more than half of the forest soils but present in almost all grassland soils. USC- $\alpha$  abundance had a direct positive effect on PMOR in forest, while in grasslands USC- $\alpha$  and USC- $\gamma$  abundance affected PMOR positively with a more pronounced contribution of USC- $\gamma$  than USC- $\alpha$ . Soil bulk density negatively influenced PMOR in both, forests and grasslands. We further found that the response of the PMORs to pH, soil texture, soil water holding capacity and organic carbon and nitrogen content differ between temperate forest and grassland soils. pH had no direct effects on PMOR, but indirect ones via the MOB abundances, showing a negative effect on USC- $\alpha$ , and a positive on USC- $\gamma$  abundance. We conclude that reduction in grassland land-use intensity and afforestation has the potential to increase the  $\text{CH}_4$  sink function of soils and that different parameters determine the microbial methane sink in forest and grassland soils.

**KEYWORDS**

potential methane oxidation rates, Upland soil cluster, methanotrophs, soil, greenhouse gas, land-use intensity, methane

## Introduction

The tropospheric concentration of methane ( $\text{CH}_4$ ) has increased by 150% since the beginning of the industrial era and its warming potential is 28 times higher than that of  $\text{CO}_2$  (Ciais et al., 2013). More than one-third of global  $\text{CH}_4$  emissions derive from methanogenesis in soils under anoxic conditions, which occur, for example, in wet rice cultivation and permanent or temporary wetlands (Ciais et al., 2013; Conrad, 2009). In contrast, well aerated soils typically function as net sinks for atmospheric  $\text{CH}_4$  due to the consumption of  $\text{CH}_4$  by methanotrophic bacteria (Le Mer and Roger 2001; Tate 2015; Kolb 2009).  $\text{CH}_4$  oxidation is primarily considered to be aerobic and is catalyzed by bacteria within the *Alphaproteobacteria*, *Gammaproteobacteria*, and *Verrucomicrobia*, but also the anaerobic candidate phylum NC10 (Knief 2015). The key enzyme for atmospheric methanotrophy is the particulate  $\text{CH}_4$  monooxygenase (pMMO) (Knief et al. 2015, Baani and Liesack 2008). Studies targeting the gene encoding the alpha subunit of pMMO (*pmoA*) as a functional marker have found that  $\text{CH}_4$  oxidizing bacteria (MOB) are highly diverse; additionally, several major soil lineages are currently poorly characterized or even missing cultured representatives, such as the Upland Soil Cluster (USC)  $\gamma$  (Knief 2015). Methanotrophs solely dependent on atmospheric  $\text{CH}_4$ , however, have resisted cultivation until very recently, when the atmospheric  $\text{CH}_4$  oxidizer *Methylocapsa gorgona* was isolated (Tveit et al., 2019). *M. gorgona* is a member of USC- $\alpha$  that has been detected in many different soils, such as forest and permafrost soils with mostly neutral to acidic pH (Kolb 2009, Degelmann et al. 2010; Kolb et al. 2005, Pratscher et al. 2017, Tveit et al. 2019). Other MOB assumed to be involved in atmospheric  $\text{CH}_4$  oxidation are members of USC- $\gamma$ , which was detected in neutral to alkaline upland soils and have recently been identified as the main methanotrophs in alpine grassland soils (Knief 2015; Deng et al. 2019).

Whether a soil acts as source or sink for  $\text{CH}_4$  is strongly controlled by soil environmental parameters such as oxygen, substrate availability, temperature, and N status, all of which are known to change the habitat and living conditions for methanogens as well as for MOB (Bodelier, 2011; Lyu, Shao, Akinyemi, & Whitman, 2018).

Land use change and management practices influence these soil environmental parameters and may therefore alter soil  $\text{CH}_4$  fluxes (Tate, 2015). A recent global meta-analysis revealed that the conversion from a natural to any anthropogenic land use increases  $\text{CH}_4$  emissions (McDaniel, Saha,

Dumont, Hernández, & Adams, 2019). However, the effects of land-use intensity and its mediating drivers on CH<sub>4</sub> emissions have not yet been resolved. It is generally assumed that fertilizers, especially ammonium-based fertilizers, decrease CH<sub>4</sub> oxidation rates due to competitive inhibition of the methane monooxygenase. In grassland soils, different management practices and intensities have been shown to influence atmospheric CH<sub>4</sub> uptake. For example, heavy livestock grazing reduces CH<sub>4</sub> uptake by 24–31% (Chen et al., 2011) and N fertilization can negatively affect CH<sub>4</sub> oxidation in cultivated soils (Mosier, Schimel, Valentine, Bronson, & Parton, 1991). In a more recent study on three Swiss grassland sites with different management intensities and elevations, highest CH<sub>4</sub> uptake was found at the least intensively and lowest CH<sub>4</sub> uptake at the most intensively managed site (Imer, Merbold, Eugster, & Buchmann, 2013). A meta-analysis by Liu and Greaver (2009), which found CH<sub>4</sub> uptake reduced when upland grassland soils were N-fertilized, further indicates that CH<sub>4</sub> uptake by grassland soils can be influenced by land-use intensity.

CH<sub>4</sub> uptake rates by forest soils were typically more pronounced than those of grassland soils with deciduous forests the strongest sinks for atmospheric CH<sub>4</sub> (Degelmann, Borken, & Kolb, 2009; Liu & Greaver, 2009). Similar to grassland management, forest management also influences atmospheric CH<sub>4</sub> uptake. The conversion of natural hardwood forests to spruce and pine forests reduced its CH<sub>4</sub> sink potential by about two-thirds (Borken, Xu, & Beese, 2003; Maurer, Kolb, Haumaier, & Borken, 2008). Other forest management effects, such as soil disturbance, compaction during clear-cutting and thinning, or N-deposition, have also been found to negatively affect the CH<sub>4</sub> sink function of forest soils (Frey, Niklaus, Kremer, Lüscher, & Zimmermann, 2011; Steudler, Bowden, Melillo, & Aber, 1989; Teepe, Brumme, Beese, & Ludwig, 2014). However, a general negative effect of N fertilization on CH<sub>4</sub> oxidation in both forest and upland grassland soils has also been questioned as it seems to depend on the amount of N present in soil (Bodelier, 2011; Bodelier & Laanbroek, 2004).

To date, few studies have linked atmospheric CH<sub>4</sub> oxidation to the abundances of the methanotrophic groups and the environmental factors influencing their abundances. It has been found for different soils that the proportion of USC- $\alpha$  was positively correlated with CH<sub>4</sub> uptake (Nazaries et al., 2013) and thus might be a key group of MOB contributing to the global atmospheric CH<sub>4</sub> sink. Malghani et al. (2016) also linked the abundance of USC- $\alpha$  methanotrophs to CH<sub>4</sub> oxidation rates. However, environmental factors can differentially influence CH<sub>4</sub> oxidation and the methanotrophic community.

For example, increasing soil moisture has been shown to lower CH<sub>4</sub> oxidation while stimulating MOB abundance in forest soils (Shrestha, Kammann, Lenhart, Dam, & Liesack, 2012). Recently, USC-γ has been identified as a dominant group in grassland soils (Zhao, Wang, Cheng, Yun, & Qiu, 2018), but it is not clear how the abundances of different MOB groups relate to CH<sub>4</sub> oxidation in soils or how they respond to land use and land-use intensity.

To investigate the relationship between MOB abundance, CH<sub>4</sub> oxidation, land use type (grassland and forest) and intensity of land use in more detail, we sampled topsoils of 150 grassland and 150 forest sites that differ in their grassland land-use intensity and in the type of forest management, respectively, in three temperate regions in Germany (Schwäbische Alb (ALB), Hainich-Dün (HAI) and Schorfheide-Chorin (SCH) region). We measured potential CH<sub>4</sub> oxidation rates, soil physico-chemical properties, and determined the abundances of the methanotrophic bacterial groups USC-α and USC-γ, which are assumed to be involved in CH<sub>4</sub> oxidation at atmospheric concentrations. We hypothesized that in grasslands, high management intensity (fertilization and/or frequent grazing and mowing) will reduce CH<sub>4</sub> oxidation rates due to higher availability of ammonium in soils and to greater soil compaction by machinery use and/or livestock trampling. In forests, intense management will reduce CH<sub>4</sub> oxidation rates due to soil compaction resulting from forest machinery. Further, soils with a higher abundance of MOB will have higher potential CH<sub>4</sub> uptake rates. In addition, we assume that soil environmental properties drive both CH<sub>4</sub> uptake and the abundance of MOB in soils.

## **Materials and methods**

### **Experimental design**

The study was conducted within the framework of the Biodiversity Exploratories project for long-term functional ecosystem research (Fischer et al. 2010, [www.biodiversity-exploratories.de](http://www.biodiversity-exploratories.de)). The Biodiversity Exploratories are located in three different climate regions of Germany: Schwäbische Alb (southwest, annual mean precipitation: 700–1000 mm, annual mean temperature 6–7 °C, abbreviated as ALB), Hainich-Dün (central Germany, annual mean precipitation: 500–800 mm, annual mean temperature 6.5–8 °C, abbreviated as HAI), and Schorfheide-Chorin (northeast, annual mean precipitation: 500–600 mm, annual mean temperature 8–8.5 °C, abbreviated as SCH). In each region 50 grassland (50 m x 50 m) and 50 forest sites (100 m x 100 m) were selected (Table S1). Soil

types varied between sites and were classified according to WRB (IUSS Working Group WRB, 2015). The grasslands were managed as meadows, pastures, or mown pastures. Grazing intensity, fertilization, and mowing frequency were monitored annually and a land-use intensity index (LUI) was calculated for each site for 2016 (Blüthgen et al., 2012). The LUI was calculated for the year 2016 for each plot as the square root of the sum of the standardized grazing intensity (livestock units days of grazing ha<sup>-1</sup> year<sup>-1</sup>), mowing frequency per year and the amount of nitrogen applied on the plot per year (kg nitrogen ha<sup>-1</sup> year<sup>-1</sup>). The values were standardized according to its mean within all plots.

In the forest sites, dominant tree species were beech, spruce, pine, or oak. A forest management index (ForMI) was calculated based on the proportion of non-native tree species, the proportion of harvested tree biomass, and the proportion of dead wood showing signs of saw cuts (Kahl & Bauhus, 2014).

### **Soil Sampling and soil properties**

All 299 sites were sampled in May 2017. In each plot, one composite soil sample was prepared consisting of 14 soil cores (upper 10 cm of mineral soil) that were taken along two intersecting transects (20 m in grasslands; 40 m in forest). The organic layer (forests) and vegetation above the soil (grasslands) had been removed before sampling. Samples were sieved (< 5 mm) and stored at 4 °C for measurements of potential CH<sub>4</sub> oxidation and at -20 °C for DNA extraction and measurements of soil properties.

Gravimetric soil water content was determined by drying 3–6 g of soil at 105 °C to constant weight. Soil pH was measured by mixing 10 g of air-dried sieved soil with 25 ml 0.01 M CaCl<sub>2</sub> solution and measuring the pH of the suspension with a glass electrode (pH meter 538 and pH glass electrode SenTix 61, WTW, Weilheim, Germany). An aliquot of the soil sample was dried at 105°C to determine the bulk density based on the sample volume and mass. The proportion of sand (2–0.063 mm), silt (0.063–0.002 mm), and clay (< 0.002 mm) in the soil samples was determined by sieving and sedimentation (DIN-ISO 11277). Samples for the determination of soil texture were taken in May 2011 as described above. Soil texture was classified according to the German 'Standortserkundungsanweisung' (VEB Projektierung Potsdam, 1974). For total carbon and total nitrogen measurements, samples were sieved (< 2 mm) and air-dried, ground in a ball mill (RETSCH

MM200, Retsch, Haan, Germany) and analyzed in an elemental analyzer (VarioMax, Hanau, Germany) at 1100 °C. Inorganic carbon was determined with the same elemental analyzer after the organic carbon had been removed by combustion of soil samples at 450 °C for 16 h. Organic carbon concentrations were calculated as the difference between total carbon and inorganic carbon. Ammonium ( $\text{NH}_4^+$ ) and nitrate ( $\text{NO}_3^-$ ) were extracted with 0.5 M  $\text{K}_2\text{SO}_4$  (soil to extractant ratio (w/v) of 1:4), shaken on a horizontal shaker for 30 min at 250 r.p.m. and centrifuged for 30 min at 4400 g. The concentrations of  $\text{NH}_4^+\text{-N}$  and  $\text{NO}_3^-\text{-N}$  were measured on an autoanalyzer using UV spectroscopy (Bran & Luebbe, Norderstedt, Germany).

### **Potential methane oxidation rates (PMORs)**

Potential  $\text{CH}_4$  oxidation rate (PMOR) was measured under atmospheric mixing ratios (2 ppm  $\text{CH}_4$ ) in microcosms of all 299 soil samples in triplicate. For this, an equivalent to 40 g soil dry weight (organic soils) and 70 g (mineral soils) fresh soil was weighed into plastic vessels (average diameter 6.8 cm). The water content was adjusted to 34% of the maximum water holding capacity of the respective soil, since 34% of maximum water holding capacity has been previously identified as the mean optimum for  $\text{CH}_4$  oxidation in different soils (Gulledge & Schimel, 1998). The water content was adjusted by gently air-drying the soil at 4 °C (for three to 72 hours) or adding deionized water to the soil. The soil was compacted in the plastic vessels to a bulk density of  $0.7\text{--}0.8\text{ g cm}^{-3}$  and pre-incubated at 20 °C for 5 days. The plastic vessels with the soils were put into glass jars (500 ml Weck Gläser, J. Weck GmbH u. Co. KG, Wehr-Öflingen, Germany) which were closed with airtight lids and incubated the soil samples at 20 °C in the dark. After airtight closing of the microcosms the headspace was over-pressurized by adding 50 ml of ambient air. Gas samples (12 ml) were taken from the headspace immediately, 1 hour, 2 hours, and 6 hours after closing with an airtight syringe through a three-way stopcock and transferred into pre-evacuated exetainers (5.9 ml, Labco Lt, UK). Gas concentrations were measured with an Agilent 7890 gas chromatograph equipped with a flame ionization detector (for  $\text{CH}_4$ ) coupled with a methanizer (for  $\text{CO}_2$ ) (Agilent Technologies Inc., Santa Clara, CA, USA). Gas flux rates were calculated by the slope of the regression line of a linear regression of the gas concentration against time.

### **DNA extraction and qPCR**



DNA was extracted from the soil (stored at -20 °C) with the Qiagen DNeasy PowerSoil Kit according to manufacturer's instructions, and stored at -20 °C until further use. DNA concentrations were measured on a NanoDrop™ 8000 (Thermo Fischer Scientific, Waltham, MA, USA). A preselection of 30 soils from all regions and land-use types were screened for the presence of *pmoA/mmoX* genes of specific methanotrophic taxa (general *pmoA*, USC- $\alpha$ , USC- $\gamma$ , Verrucomicrobia and *Methylocella*, (Costello and Lidstrom 1999; Kolb et al. 2003, 2005; Sharp, Stott, and Dunfield 2012; Rahman et al. 2011, Table S2). For the preselection, five samples with different PMOR (highest, lowest and from each region and land use type) were chosen. Three groups of methanotrophic bacteria were quantified with three different quantitative PCR assays in a 7500 Fast Real-Time PCR System (Applied Biosystems, USA). A general *pmoA* assay was used to detect a broad spectrum of MOB (Costello & Lidstrom, 1999), the FOREST assay (Kolb et al., 2003) to quantify USC- $\alpha$  specific *pmoA*, and the GAM assay to amplify a USC- $\gamma$  specific *pmoA* (Kolb et al., 2005). The qPCR reactions (20  $\mu$ l) were performed in 96-well plates with SensiFAST™ Sybr Lo-ROX master mix (Bioline (Meridian Life Science), Inc., Memphis, TN, USA) using a three-step thermal profile with denaturation at 95 °C for 25 s, annealing at assay specific temperature (Table S2) for 20 s, and elongation at 72 °C for 45 s. Bovine Serum Albumine was added to the master mix (final concentration 2 ng/ $\mu$ l).

## Statistics

All statistical analyses were carried out in R (Version 3.5.1, R Core Team 2018). Data were checked for normal distribution and homogeneity of variance and transformed if necessary. Significant differences between groups were tested with a two-sample t-test for normally distributed data and a Mann-Whitney test for non-normally distributed data. Linear regression analysis was used to assess the relationship between PMORs and physico-chemical and land-use parameters. The significance levels reported were based on Pearson's coefficient. Grasslands were grouped into high and low LUI and into heavily and weakly grazed using the k-means algorithm (Hartigan & Wong, 1979). Since PMORs were region-specific (especially in grasslands), PMORs were normalized to be able to compare the effects of land-use among all regions. The PMOR norm was calculated by dividing the PMOR of each plot by the mean PMOR of the respective region. qPCR measurements that were below detection limit were set to 100 for correlation analyzes and structural equation modelling.

Structural equation modelling (SEM) was used to unravel direct and indirect effects on PMORs. For this an a-priori model was set up. It was hypothesized that soil parameters (bulk density, pH and sand content) and land-use intensity in forest and grassland have a direct influence on PMORs and also an indirect effect via MOB abundances. Bulk density was chosen as a representative for other soil factors (water holding capacity, organic carbon and total nitrogen content) with which it covariate strongly. pH was chosen since it is an important factor for microbial activity (Lauber, Hamady, Knight, & Fierer, 2009). Also sand content was included in the model to represent the soil texture. The variables were transformed to normal distribution according to Templeton (2011). The model was fit with maximum-likelihood estimation (“sem” function in lavaan (Rosseel, 2012)). Since multivariate normality was not met in every model we used Satorra-Bentler correction to obtain robust fitting statistics (estimator = “MLM”). In the forest model, the path coefficient of pH to PMOR was constrained to zero since this improved model fit. In the forest models of the single regions the path coefficient of USC- $\gamma$  to PMOR was constrained to zero since USC- $\gamma$  was absent in many forest soils.

## Results

### Influence of land use, soil type, and soil texture on PMORs

Uptake of atmospheric CH<sub>4</sub> was detected in all 299 topsoils. Potential CH<sub>4</sub> oxidation rates (PMORs) varied between 0.006 and 1.695 ng CH<sub>4</sub> g<sup>-1</sup> DW h<sup>-1</sup> and were significantly higher in forest than in grassland soils (mean<sub>forest</sub> = 0.60 ng CH<sub>4</sub> g<sup>-1</sup> DW h<sup>-1</sup>, mean<sub>grassland</sub> = 0.31 ng CH<sub>4</sub> g<sup>-1</sup> DW h<sup>-1</sup>,  $p < 0.001$ , Figure 1a). This difference between forest and grassland soils was significant in all regions ( $p_{ALB} < 0.001$ ,  $p_{HAI} < 0.001$ ,  $p_{SCH} < 0.01$ , Figure 1b). In the forest soils PMORs did not vary among regions, but in grassland soils PMORs were highest in ALB, lowest in HAI and highly variable in SCH, presumably due to the high diversity of soil types and textures in this region.

In the forest soils, PMORs did not differ with respect to soil texture (Figure S 1a), but in grasslands PMORs were highest in loamy clay and loamy silt and lowest in loamy sand, silty clay and sandy loam soils (Figure S 1b). However, in the silty clay and loamy sand textures of the forest soils' PMORs were higher than in in grassland soils of similar texture. High clay content appeared to have a generally negative effect in the ALB region (both forest and grassland sites) but a positive effect in the SCH region (grasslands only, Figure S 2). Sand content therefore resulted in opposite trends in

these two regions. Sand content was mostly high in SCH and typically low in the ALB region grasslands (Figure S 2c, f).

### **Influence of forest management, tree species, and grassland land-use intensity on PMORs**

PMORs in forest soils were neither correlated to the ForMI nor to its components (proportion of non-native tree species, harvested tree biomass, and proportion of dead wood showing signs of cut, Figure S 3). However, the dominant tree species did significantly affect PMORs, with lowest CH<sub>4</sub> oxidation in oak, and highest in beech and spruce forests (Figure 2). Oak were only in slightly loamy sand soils in SCH region. However, when only this soil texture and region was considered PMORs were still significantly lower in oak than beech forests ( $p < 0.05$ ).

In contrast to forests, where management showed no influence, the LUI in grasslands was negatively correlated with PMORs when all regions were included ( $r_{LUI} = -0.27$ ,  $p < 0.001$ , Figure S 4a). When grasslands of all regions taken together were categorized into low and high LUI, PMORs were reduced by about 40% in high as compared to low LUI grassland soils (Figure 3a). With respect to the single components of LUI, fertilization decreased PMORs by about 20% (Figure 3b). Considering all grassland sites, grazing intensity and mowing frequency had no significant effect on PMORs (Figure 3c, d). Grassland management also affected the concentrations of NH<sub>4</sub><sup>+</sup> in soil, which were higher in non-fertilized compared to fertilized grasslands (Figure S 5b), while NO<sub>3</sub><sup>-</sup> concentrations were higher in fertilized than in non-fertilized soils (Figure S 5f).

### **Correlations of soil properties with PMORs**

Considering all forest soils, PMORs were neither correlated with water holding capacity nor with organic carbon and total nitrogen content (Figure S 6a-c). PMORs were, however, negatively correlated with bulk density across all forest soils ( $r_{bd} = -0.17$ ,  $p < 0.05$ , Figure S 6e). In ALB and HAI, pH was negatively correlated with PMORs, while in SCH pH was positively correlated with PMORs (Fig S 6d). However, pH was generally lower in SCH than in ALB or HAI (pH<sub>ALB</sub>: 3.3 – 6.9, pH<sub>HAI</sub>: 3.85 – 7.15, pH<sub>SCH</sub>: 3.2 – 3.77). The thickness of the organic layer measured in the natural habitat, but which was not included in the PMOR measurements in the microcosms, had an effect on

PMORs only in the HAI region, with a positive correlation between PMORs and the thickness of the organic layer ( $r_{bd} = 0.34$ ,  $p < 0.05$ , Figure S 6g).

In contrast to the forest soils, PMORs in grassland soils were positively correlated with soil organic carbon and total soil nitrogen content ( $r_{OC} = 0.60$ ,  $r_{N_{tot}} = 0.67$ ,  $p < 0.001$ , Figure S 7a, b). PMORs increased with increasing soil water holding capacity, but decreased with increasing bulk density ( $r_{whc} = 0.80$ ,  $r_{bd} = -0.77$ ,  $p < 0.001$ , Figure S 7c, e) when all grasslands were considered together, but not for the HAI region alone. Concentrations of both,  $NH_4^+$  and  $NO_3^-$  were positively correlated with PMORs in the grasslands ( $r_{NH_4} = 0.38$ ,  $r_{NO_3} = 0.40$ ,  $p < 0.001$ , Figure S 7g, h) and this was most pronounced in the SCH region. The effects of the mentioned soil physico-chemical conditions were usually most pronounced in the SCH region.

### **Influence of land use, soil type and soil texture on MOB**

In a preselection of 30 topsoil samples, no methanotrophs belonging to *Verrucomicrobia* or *Methylocella* (*Alphaproteobacteria*) were detected with specific PCR assays; hence, these assays were not performed for all 299 soils (data not shown). The primer pair A189f/mb661 (which targets a broad range of proteobacterial methanotrophs) yielded specific PCR products only in grassland soils from SCH, while no specific products were detected in the other regions (data not shown). In contrast, we detected methanotrophs belonging to USC- $\alpha$  and USC- $\gamma$  clades in most soils but with land-use type (forests versus grasslands) and region-specific abundance distributions (Figure 4). USC- $\alpha$  abundance varied widely, from  $2.8 \times 10^4$  to  $8.7 \times 10^8$  *pmoA* gene copies per gram dry soil and occurred in all forest soils, but in only 56% of the grassland soils (Figure 4). USC- $\gamma$  abundance ranged from  $2.8 \times 10^3$  to  $3.8 \times 10^6$  *pmoA* gene copies per gram dry soil and was detected in almost all grassland soils, but present only in approximately 30% of the forest soils (Figure 4). The median abundance of USC- $\alpha$  *pmoA* gene was almost 100 times higher in the forest than in the grassland soils in all regions ( $p < 0.001$ ). In forest soils, USC- $\alpha$  *pmoA* gene abundance was about 50-fold higher in SCH than in either HAI or ALB. In contrast to USC- $\alpha$  *pmoA*, gene abundance of USC- $\gamma$  was about 100 times higher in grassland than in forest soils. However, trends differed between the exploratories. In the ALB region, for example, USC- $\gamma$  abundance was only twice as high in forest than in grassland sites.

## **Influence of forest management, tree species, and grassland land-use intensity on MOB**

USC- $\alpha$  gene abundance was higher in oak and pine dominated forests compared to spruce and beech forests, while USC- $\gamma$  gene abundance was higher in beech and spruce forests (Figure S 8). USC- $\alpha$  did not correlate with ForMI, but there was a negative correlation between harvested tree biomass and USC- $\alpha$  (Figure S 9c). USC- $\gamma$  positively correlated with ForMI, non-native tree species and harvested tree biomass (Figure S 9a-c). In the grasslands there was no correlation between abundances of USC- $\alpha$  or USC- $\gamma$  and LUI (Figure S 10) and there was also no difference in USC- $\alpha$  and- $\gamma$  copy numbers between high and low LUI or its components (Figure S 11).

## **Correlations of MOB abundance with soil properties and with PMORs**

USC- $\alpha$  and USC- $\gamma$  *pmoA* gene copy numbers responded differently to abiotic soil properties (Figure S12-15). In forests for instance, USC- $\alpha$  gene copy numbers per g soil were negatively correlated to organic carbon ( $r_{\text{Corg}} = -0.70$ ,  $p < 0.01$ , Figure S 12a), whereas USC- $\gamma$  abundance was positively correlated with organic carbon and nitrogen content ( $r_{\text{Corg}} = 0.70$ ,  $p < 0.001$ , Figure S 14a). Overall, USC- $\alpha$  and USC- $\gamma$  abundances were differentially correlated with pH, while USC- $\alpha$  abundance was negatively correlated with pH ( $r_{\text{for}} = -0.70$ ,  $r_{\text{gras}} = -0.32$ ,  $p < 0.001$ , Figure S 12d and S 13d), USC- $\gamma$  abundance was positively correlated with pH ( $r_{\text{for}} = 0.54$ ,  $r_{\text{gras}} = 0.39$ ,  $p < 0.001$ , Figure S 14d and S 15d).

USC- $\alpha$  abundance was negatively correlated with  $\text{NH}_4^+$  content, whereas USC- $\gamma$  abundance was positively correlated in the SCH region only ( $r_{\text{USC}\alpha} = -0.32$ ,  $r_{\text{USC}\gamma} = 0.47$ ,  $p < 0.05$ , Figure S 13g, S 15g). USC- $\alpha$  and USC- $\gamma$  *pmoA* gene abundances were not correlated with  $\text{NO}_3^-$  content in the grassland soils (Figure S 13h, S 15h).

In the forests, USC- $\alpha$  *pmoA* abundance correlated positively with PMORs including all regions, as well as in each of the three regions ( $r_{\text{for}} = 0.18$ ,  $p < 0.05$ ;  $r_{\text{ALB}} = 0.57$ ,  $r_{\text{HAI}} = 0.51$ ,  $r_{\text{SCH}} = 0.68$ ,  $p < 0.001$ , Figure 5a). In the forests there were no positive correlations between USC- $\gamma$  *pmoA* abundance and PMORs (Figure S 16a) and in the grasslands there were no positive correlations between PMORs and USC- $\alpha$  abundance (Figure S 16b). However, in grasslands USC- $\gamma$  *pmoA* copy numbers were positively correlated with PMORs when all grasslands were taken together, and also in each of the three regions (soils  $r_{\text{gra}} = 0.44$ ,  $r_{\text{ALB}} = 0.53$ ,  $r_{\text{HAI}} = 0.53$ ,  $r_{\text{SCH}} = 0.59$ ,  $p < 0.001$ , Figure 5b).

When related to MOB abundance, PMOR was lower in forest than in grassland soils (Figure S 17a). Within the forest soils, PMOR related to MOB was lowest in SCH region while in grasslands it was highest in SCH region (Figure S 17b).

### **Direct and indirect effects of soil parameters and land use intensity on PMOR**

Generally, a larger part of PMOR variance could be explained in grasslands compared to forests (Figure 6). Bulk density had strong direct negative effects on PMOR in both, forests and grasslands (Figure 6a, b). pH had no direct effects but indirect effects on PMOR via the MOB abundances, with a negative effect on USC- $\alpha$  abundance and a positive effect on USC- $\gamma$  abundance. Sand content had an overall positive effect on PMOR in grasslands and an indirect positive effect via abundance of USC- $\alpha$  in forest. However, when looking at the regions separately, the soil sand content had only a positive effect on PMOR in the ALB forest region (Figure S 18a). While the forest management had no effect on PMOR, land use intensity of grasslands had a direct negative effect on PMOR but an indirect positive effect via USC- $\gamma$  abundance. However, the overall effect was negative and when looking at the regions separately there was only a direct negative effect (Figure S 19a, b). Only in SCH grasslands LUI had no direct effect on PMOR. MOB abundance had a direct effect on PMOR almost all regions. In forests, USC- $\alpha$  abundance had a strong direct positive effect on PMOR, whereas USC- $\gamma$  showed no direct effect on PMOR (Figure 6a, Figure S 19a-c). In grasslands, both USC- $\alpha$  and USC- $\gamma$  had direct positive effects on PMOR and here the effect of USC- $\gamma$  was stronger than that of USC- $\alpha$  (Figure 6b, Figure S 19a-c). Only in grasslands of the SCH region MOB abundance had no influence on PMOR.

## **Discussion**

### **Potential methane oxidation rates and soil parameters**

Potential CH<sub>4</sub> oxidation rates (PMORs) were generally about two times higher in forest than in grassland soils. This accords with meta-analyses of CH<sub>4</sub> oxidation rates in different habitats (ecosystem level measurements) that identified 2.5 fold higher CH<sub>4</sub> oxidation rates in forests than in other ecosystems and about two times higher in forest than in herbaceous ecosystems (Dutaur & Verchot, 2007; McDaniel et al., 2019). Compared to these studies, our PMORs were 1.5–2 times

higher than the in situ CH<sub>4</sub> fluxes. This may be due to the fact that we analyzed soil only from the layer with the highest potential for CH<sub>4</sub> oxidation (Kolb, 2009) and adjusted the water content to its optimal value for CH<sub>4</sub> oxidation (Gulledge & Schimel, 1998). Our measurements did not include deeper soil layers, which may be a source of CH<sub>4</sub>. However, by standardizing moisture we reduced variation found in the field, permitting better analyses of the influence of drivers such as soil properties or MOB on PMORs. We consider the measured abundances of MOB and the standardized PMORs as proxies that integrate CH<sub>4</sub> uptake and MOB activity dynamics over time.

Temperature and precipitation can influence methane oxidation. For instance, Van den Pol et.al. (1998) found highest methane uptake in soils with high temperature and intermediate soil moisture content (Van Den Pol-van Dasselaar, Van Beusichem, & Oenema, 1998). In our study, PMORs vary between the different regions in grassland but not in forest soils. As the overall climate is rather similar between grassland and forest sites within the same region this indicates that climatic differences cannot explain much of the differences of PMOR in grasslands between the three regions. In addition, the differences in mean temperature between the regions are relatively small. In a meta study, mean annual temperature and annual rainfall had only a weak correlation with atmospheric methane oxidation (Dutaur & Verchot, 2007). So, the differences in temperature and precipitation might be too small between the regions to induce large differences in PMORs. The variation of PMOR in grasslands was likely caused by other factors, as for example differences in soil properties between the three regions. In SCH, soil texture is sandier than in the other two regions where silty, loamy and clayey soil textures dominate. In HAI grasslands, PMORs were 4.5–5.5-fold lower than in the other grasslands. The soils of this region are generally denser, which may be a limiting factor for PMORs. The SEM indicated a general negative effect of bulk density in forests and grasslands. The high variability in SCH region might be explained by high variability in OC content of the soils.

Interestingly, many factors that correlated with PMORs in grasslands did not correlate with PMORs in forests. Within the grasslands, the PMORs increased with increasing water holding capacity but in the forest soils, water holding capacity did not have a significant effect on PMORs. Also, soil textures that were associated with low PMORs in grasslands were associated with higher PMORs in forests. These findings suggest that ecosystem type is an important driver of PMORs and that a response to soil physico-chemical conditions is specific to the type of ecosystem. The high PMORs in loamy

grassland soils of the SCH, however, could also be a result of their high OC concentrations. The organic layer of forest soils has been reported to reduce CH<sub>4</sub> oxidation in soils, probably acting as a diffusion barrier for CH<sub>4</sub> (Saari, Heiskanen, & Martikainen, 1998). However, we found no negative effect of the thickness of the organic layer (determined at each forest site during sampling, but the organic layer material itself was not included in the PMOR measurement) on PMORs. To the contrary, in the HAI region the organic layer thickness had a slight positive effect on PMORs. It may be that canopy cover and the presence of an O horizon is responsible for the different responses of PMORs to soil factors in forests and grasslands. Canopy cover and O-horizon inhibit the increase in water content of the upper mineral soil layers after rainfall events (Qian, Qing, Jinsen, Kaihua, & Guishan, 2014). Lower water content could in turn hamper gas diffusive transport in soils.

Bulk density and pH had an influence on PMORs in almost all grassland and forest soils of all three regions. PMOR generally decreased with increasing bulk density. Higher bulk density indicates low soil porosity and pronounced soil compaction which, considered together, may result in lower diffusion capacity of atmospheric gases into the soils. This in turn could lead to lower CH<sub>4</sub> availability in the soil and thus lower the CH<sub>4</sub> oxidation rates (Malghani et al., 2016). It is worth noting that the original bulk density in the field had an effect on CH<sub>4</sub> oxidation even after sieving and re-compaction of the soil, indicating a legacy effect of the former natural conditions. Also Sitaula et al. (Sitaula, Hansen, Sitaula, & Bakken, 2000) reported that soil compaction led to decreased CH<sub>4</sub> uptake even after compaction was removed by sieving of the soil samples. The response of PMORs to pH differed between forests and grasslands. While in forest soils PMORs had an optimum at around pH 4, in grasslands PMORs increased with increasing pH in two out of three regions. Soils have been shown CH<sub>4</sub> oxidation over a wide range of pH values and incubation of forest soils demonstrated CH<sub>4</sub> oxidation from pH 3–7.5 even though the optimal pH for CH<sub>4</sub> oxidation ranged from 4 to 7.5 (Amaral, Ren, & Knowles, 1998; Benstead & King, 2001; Saari, Rinnan, & Martikainen, 2004). Sitaula et al. (1995) observed an increase in CH<sub>4</sub> oxidation when soil from a pine forest was irrigated with acidic water (Sitaula, Bakken, & Abrahamsen, 1995). In contrast, CH<sub>4</sub> oxidation has been reported to decrease with lower pH in grasslands (Hütsch, Webster, & Powlson, 1994), which is in accordance with our results. Also in arable soils, strong inhibition of CH<sub>4</sub> oxidation was reported when the soil pH was lowered from 8 to 7.1 (Hütsch, 2001). Thus, our findings underline, that pH has



a substantial impact on CH<sub>4</sub> oxidation; however, its influence differs between different ecosystem types. While in forests CH<sub>4</sub> oxidation is favoured by slightly acidic conditions, in grasslands CH<sub>4</sub> oxidation is higher in neutral soils. We found that the effect of pH was direct only in forest sites in the ALB region, while in the other cases the observed effects of pH were indirect via the abundances of the two types of methane oxidising bacteria. This indicates that there are different MOB communities with different pH optima in forests and grasslands.

We note that the variation in PMORs was far greater within the grasslands than in the forests and was region-dependent within the grasslands. PMORs were generally higher in forest than in grassland soils, indicating that forest soils act as robust sinks for CH<sub>4</sub> over a wide range of different physico-chemical soil conditions.

### **Drivers of MOB abundances and relationship with PMOR**

We measured MOB abundances in nearly 299 different soils, thus yielding a comprehensive dataset to connect MOB with soil physico-chemical soil properties and PMORs. The composition and importance of the MOB seems to be ecosystem type- and region-specific. USC- $\alpha$  *pmoA* abundances were positively correlated with PMORs in forests of all regions, but USC- $\alpha$  was absent in many grasslands. In contrast, USC- $\gamma$  *pmoA* were consistently present in the grasslands and were positively correlated with PMORs in all of the grasslands but in none of the forest regions. This indicates the far greater importance of USC- $\alpha$  MOB for CH<sub>4</sub> oxidation in forest soils and that of USC- $\gamma$  MOB for CH<sub>4</sub> oxidation in grasslands. In some grasslands USC- $\alpha$  abundance might be an additional driver of CH<sub>4</sub> oxidation, even though it has a smaller effect on CH<sub>4</sub> oxidation than USC- $\gamma$  abundance. USC- $\alpha$  MOB have been previously detected in forest soils and 16S rRNA gene amplicon datasets demonstrate that they occur in forest soils (Tveit et al., 2019). A recent study found that USC- $\gamma$  was dominant in upland grassland soils from a region in China (Deng et al., 2019). In combination with their wide occurrence also in our samples provides evidence that USC- $\gamma$  is an important MOB in grassland soils in different regions of the world.

Soil pH was the most important predictor of USC- $\alpha$  and - $\gamma$  gene abundances, with USC- $\alpha$  preferring more acidic and USC- $\gamma$  preferring neutral soils. The lower pH of the forests and more neutral pH in the grasslands may therefore explain, in part, the distribution patterns of the two USC groups.

However, USC- $\alpha$  were also present in neutral soils. This confirms results of former studies (Kolb, 2009; Kolb et al., 2003). However, the negative correlation of USC- $\alpha$  abundance and pH is also surprising, given the latest findings on the physiology of atmospheric MOB belonging to the USC- $\alpha$  *M. gorgona*. The optimal pH for growth of *M. gorgona* is at an almost neutral pH of 6.5 to 7, but other *Methylocapsa* strains that were able to grow at atmospheric CH<sub>4</sub> concentrations had a lower pH optimum of 5-6.2 (Tveit et al., 2019).

PMOR per unit biomass was generally lower in forest than in grassland soils. This might be due to the different microbial communities in these land use type which might have a different specific activity. In forests, PMOR per unit biomass was lowest in SCH region that was also the region with the highest bulk density among forest soils. The PMOR per unit biomass might thus be influenced by gas diffusive transport which is lower in soils with high bulk density and thus a higher abundance of MOBs might be needed to oxidize similar amounts of CH<sub>4</sub>.

### **Effects of grassland land-use intensity and forest management**

We found that grassland land-use intensity had a negative effect on PMORs, which supports our initial hypothesis. Structural equation modelling showed a direct negative effect of LUI across all regions. Only in SCH region, no effect on PMOR was detectable. This region is less intensively managed in terms of fertilization compared to the other two regions. This may explain why there was no effect of LUI on PMORs in SCH region since fertilization in particular negatively influenced PMORs, with 20% lower rates in fertilized compared to non-fertilized soils. Ammonium ions, that are a component of fertilizers, are known to inhibit methane monooxygenase (Schnell & King, 1994). However, we could not detect higher ammonium concentrations in the fertilized soils. Since we do not know the exact date of fertilization, and as the ammonium concentration in soils is highly dynamic, the concentration at our sampling date may not have reflected the mean ammonium concentrations over the year. There may also be a legacy effect of formerly high ammonium concentrations from fertilization that negatively influences the MOB community over the long-term. Interestingly, fertilization had no effect on the abundances of MOBs but it did have an effect on PMORs. With respect to the other two components of grassland land-use intensity, we could not detect any significant effect of either grazing or mowing on PMORs. However, a high land-use

intensity index, which integrates fertilization, grazing, and mowing, reduced PMORs by 40% in comparison to grasslands with low land use intensity. Hence, the latter two factors did have an additive negative effect on PMORs. The reduction of PMORs by grazing and mowing may have been due to soil compaction as caused to animal trampling and mowing machines. However, only in combination with N-fertilization did soil compaction lead to a reduction in CH<sub>4</sub> oxidation in these soils. Heavy grazing reduces water infiltration into soil (Abdel-Magid, Schuman, & Hart, 1987) and thus also alters gas diffusive transport into soil.

Our study investigated PMORs over many different grasslands and land-use intensities and we can confirm that fertilization has a negative effect on PMORs over different soil types over a regional gradient of more than 800 km, in contrast to previous studies reporting somewhat contradictory effects of fertilization on CH<sub>4</sub> oxidation (Imer et al., 2013; Liu & Greaver, 2009). We thus conclude that by a reduction of land-use intensity, especially N-fertilization, the CH<sub>4</sub> sink function of temperate grasslands could be improved or the other way around, an intensification of grassland land use bears the risk of the reduction of methane uptake in grassland soils.

Within the investigated 149 forest soils, we did not observe any effect of forest management on PMORs. This suggests that the ability of temperate forest soils to serve as CH<sub>4</sub> sinks is not substantially affected by commonly applied forest management practices. Homogenisation of the soils prior to measuring PMOR may have partly removed negative effects that were consequences of forest management practices, such as soil compaction due to forest machinery. However, we still see a legacy effect of the natural bulk density. Hence, it is unlikely that forest management effects were completely eliminated by the treatment of the soil before PMOR measurements. It is likely that inhibition of PMORs is most prevalent in the logging trails, which were excluded from soils sampling in our study. A closer sampling of the forest soils may be necessary to better understand the influence of management in forests. However, based on our data, we must reject our initial hypothesis of a negative effect of forest management on PMORs.

We found that the dominant tree species had some effect on PMORs. Even though the literature indicates that spruce forest soils exhibit a lower capacity to oxidize CH<sub>4</sub> than beech forest soils (Borken and Beese, 2006; Degelmann *et al.*, 2009), we could not detect significant differences between beech dominated and coniferous forests (pine or spruce) across all forest sites. However,

PMORs were lower in oak than in beech dominated forests. In oak dominated forests USC- $\alpha$  abundance and soil respiration rates were also reduced, indicating the presence of inhibitory substances in the soil that hamper microbial activity. Bárcena et al. (2014) also found that CH<sub>4</sub> oxidation rates were higher in spruce than in young oak forests. However, others have reported that oak forests have higher rates than spruce and pine forests (Reay, Nedwell, McNamara, & Ineson, 2005). It is likely that tree species alone is not the most important factor impairing PMORs. Soil physico-chemical conditions can differentially influence CH<sub>4</sub> oxidation with respect to different tree species. For example, while higher water content increased CH<sub>4</sub> oxidation in spruce soils, it decreased CH<sub>4</sub> oxidation in scots pine and larch soils (Menyailo & Hungate, 2003). Possibly, there are optimal soil types and textures for a certain tree species and thus, a specific main tree species could maximize CH<sub>4</sub> oxidation in a particular soil.

Our results clearly demonstrate that forest soils are an important sink for atmospheric CH<sub>4</sub> and that this is largely stable over different physico-chemical conditions and forest management practices. Since PMORs were higher in forests than in grasslands, afforestation has the potential to enlarge the global CH<sub>4</sub> sink of soils and thus, help mitigate global warming by decreasing atmospheric CH<sub>4</sub> concentrations.

## **Conclusions**

PMORs are differentially controlled in forest and grassland soils. Our survey demonstrates that forests are an important and robust sink for CH<sub>4</sub> over a wide range of different physico-chemical soil conditions while in grasslands PMORs are clearly more influenced by site-specific soil properties. Additionally, we detected a negative effect of grassland land-use intensity, especially fertilization, while the different forest management practices did not affect PMORs. Thus, reduction in grassland management intensity as well as afforestation may increase the capacity of soils to serve as CH<sub>4</sub> sinks. Furthermore, our results strongly suggest that USC- $\alpha$  and USC- $\gamma$  have land-use type specific distributions, with USC- $\alpha$  the dominant group in forests and USC- $\gamma$  the dominant group in grasslands. Also, the direct positive correlations between PMORs and USC- $\alpha$  in forests and between PMORs and mainly USC- $\gamma$  in grasslands indicate that USC- $\alpha$  is the major microbial group responsible for the CH<sub>4</sub> sink capacity in forests and USC- $\gamma$  is the major group responsible for the CH<sub>4</sub> sink capacity of

grasslands. Finally, the study also revealed that different sets of site parameters control the microbial methane capacity sink in forests and grasslands.

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## References

- Abdel-Magid, A. H., Schuman, G. E., & Hart, R. H. (1987). Soil Bulk Density and Water Infiltration Grazing Systems as Affected by Grazing Systems. *Journal of Range Management*, 40(4), 307–309.
- Amaral, J. A., Ren, T., & Knowles, R. (1998). Atmospheric Methane Consumption by Forest Soils and Extracted Bacteria at Different pH Values. *Applied and Environmental Microbiology*, 64(7), 2397–2402.
- Bárcena, T. G., D’Imperio, L., Gundersen, P., Vesterdal, L., Priemé, A., & Christiansen, J. R. (2014). Conversion of cropland to forest increases soil CH<sub>4</sub> oxidation and abundance of CH<sub>4</sub> oxidizing bacteria with stand age. *Applied Soil Ecology*, 79(April), 49–58. Retrieved from <https://doi.org/10.1016/j.apsoil.2014.03.004>
- Benstead, J., & King, G. M. (2001). The effect of soil acidification on atmospheric methane uptake by a Maine forest soil. *FEMS Microbiology Ecology*, 34(3), 207–212. Retrieved from [https://doi.org/10.1016/S0168-6496\(00\)00096-9](https://doi.org/10.1016/S0168-6496(00)00096-9)
- Blüthgen, N., Dormann, C. F., Prati, D., Klaus, V. H., Kleinebecker, T., Hölzel, N., ... Weisser, W. W. (2012). A quantitative index of land-use intensity in grasslands: Integrating mowing, grazing and fertilization. *Basic and Applied Ecology*, 13(3), 207–220. Retrieved from <https://doi.org/10.1016/j.baae.2012.04.001>
- Bodelier, P. L. E. (2011). Interactions between nitrogenous fertilizers and methane cycling in wetland and upland soils. *Current Opinion in Environmental Sustainability*, 3(5), 379–388. Retrieved from <https://doi.org/10.1016/j.cosust.2011.06.002>
- Bodelier, P. L. E., & Laanbroek, H. J. (2004). Nitrogen as a regulatory factor of methane oxidation in soils and sediments. *FEMS Microbiology Ecology*, 47(3), 265–277. Retrieved from [https://doi.org/10.1016/S0168-6496\(03\)00304-0](https://doi.org/10.1016/S0168-6496(03)00304-0)
- Borken, W., & Beese, F. (2006). Methane and nitrous oxide fluxes of soils in pure and mixed stands of European beech and Norway spruce. *European Journal of Soil Science*, 57(5), 617–625. Retrieved from <https://doi.org/10.1111/j.1365-2389.2005.00752.x>
- Borken, W., Xu, Y. J., & Beese, F. (2003). Conversion of hardwood forests to spruce and pine plantations strongly reduced soil methane sink in Germany. *Global Change Biology*, 9(6), 956–

966. Retrieved from <https://doi.org/10.1046/j.1365-2486.2003.00631.x>
- Chen, W., Wolf, B., Zheng, X., Yao, Z., Butterbach-Bahl, K., Brüggemann, N., ... Han, X. (2011). Annual methane uptake by temperate semiarid steppes as regulated by stocking rates, aboveground plant biomass and topsoil air permeability. *Global Change Biology*, 17(9), 2803–2816. Retrieved from <https://doi.org/10.1111/j.1365-2486.2011.02444.x>
- Ciais, P., Sabine, C., Bala, G., Bopp, L., Brovkin, V., Canadell, J., ... Thornton, P. (2013). IPCC. In T. F. Stocker, D. Qin, G.-K. Plattner, M. Tignor, S. K. Allen, J. Boschung, ... P. M. Midgley (Eds.), *Climate Change 2013: The Physical Science Basis. Contribution of Working Group I to the Fifth Assessment Report of the Intergovernmental Panel on Climate Change*. Cambridge University Press, Cambridge, United Kingdom and New York, NY, USA.
- Conrad, R. (2009). Minireview The global methane cycle : recent advances in understanding the microbial processes involved. *Environmental Microbiology Reports*, 1(5), 285–292. Retrieved from <https://doi.org/10.1111/j.1758-2229.2009.00038.x>
- Costello, A. M., & Lidstrom, M. E. (1999). Molecular characterization of functional and phylogenetic genes from natural populations of methanotrophs in lake sediments. *Applied and Environmental Microbiology*, 65(11), 5066–5074.
- Degelmann, D. M., Borken, W., Drake, H. L., & Kolb, S. (2010). Different atmospheric methane-oxidizing communities in european beech and norway spruce soils. *Applied and Environmental Microbiology*, 76(10), 3228–3235. Retrieved from <https://doi.org/10.1128/AEM.02730-09>
- Degelmann, D. M., Borken, W., & Kolb, S. (2009). Methane oxidation kinetics differ in european beech and Norway spruce soils. *European Journal of Soil Science*, 60(4), 499–506. Retrieved from <https://doi.org/10.1111/j.1365-2389.2009.01138.x>
- Deng, Y., Che, R., Wang, F., Conrad, R., Dumont, M., Yun, J., ... Wang, Y. (2019). Science of the Total Environment Upland Soil Cluster Gamma dominates methanotrophic communities in upland grassland soils. *Science of the Total Environment*, 670, 826–836. Retrieved from <https://doi.org/10.1016/j.scitotenv.2019.03.299>
- Dutaur, L., & Verchot, L. V. (2007). A global inventory of the soil CH<sub>4</sub> sink. *Global Biogeochemical Cycles*, 21(4), n/a-n/a. Retrieved from <https://doi.org/10.1029/2006GB002734>
- Fischer, M., Bossdorf, O., Gockel, S., Hänsel, F., Hemp, A., Hessenmöller, D., ... Weisser, W. W.

- (2010). Implementing large-scale and long-term functional biodiversity research: The Biodiversity Exploratories. *Basic and Applied Ecology*, 11(6), 473–485. Retrieved from <https://doi.org/10.1016/j.baec.2010.07.009>
- Frey, B., Niklaus, P. A., Kremer, J., Lüscher, P., & Zimmermann, S. (2011). Heavy-Machinery Traffic Impacts Methane Emissions as Well as Methanogen Abundance and Community Structure in Oxic Forest Soils. *Applied and Environmental Microbiology*, 77(17), 6060–6068. Retrieved from <https://doi.org/10.1128/aem.05206-11>
- Gulledge, J., & Schimel, J. P. (1998). MOISTURE CONTROL OVER ATMOSPHERIC CH<sub>4</sub> CONSUMPTION AND CO<sub>2</sub> PRODUCTION IN DIVERSE ALASKAN SOILS. *Soil Biology and Biochemistry*, 30(8/9), 1127–1132.
- Hartigan, J. A., & Wong, M. A. (1979). A K-Means Clustering Algorithm. *Journal of the Royal Statistical Society*, 28(1), 100–108. Retrieved from <https://doi.org/10.9756/bijdm.1106>
- Hütsch, B. W. (2001). Methane oxidation, nitrification, and counts of methanotrophic bacteria in soils from a long-term fertilization experiment ('Ewiger Roggenbau' at Halle). *Journal of Plant Nutrition and Soil Science*, 164(1), 21–28. Retrieved from [https://doi.org/10.1002/1522-2624\(200102\)164:1<21::AID-JPLN21>3.0.CO;2-B](https://doi.org/10.1002/1522-2624(200102)164:1<21::AID-JPLN21>3.0.CO;2-B)
- Hütsch, B. W., Webster, C. P., & Powlson, D. S. (1994). Methane oxidation in soil as affected by land use, soil pH and N fertilization. *Soil Biology and Biochemistry*, 26(12), 1613–1622. Retrieved from [https://doi.org/10.1016/0038-0717\(94\)90313-1](https://doi.org/10.1016/0038-0717(94)90313-1)
- Imer, D., Merbold, L., Eugster, W., & Buchmann, N. (2013). Temporal and spatial variations of soil CO<sub>2</sub>, CH<sub>4</sub> and N<sub>2</sub>O fluxes at three differently managed grasslands. *Biogeosciences*, 10(9), 5931–5945. Retrieved from <https://doi.org/10.5194/bg-10-5931-2013>
- Kahl, T., & Bauhus, J. (2014). An index of forest management intensity based on assessment of harvested tree volume, tree species composition and dead wood origin. *Nature Conservation*, 7, 15–27.
- Knief, C. (2015). Diversity and habitat preferences of cultivated and uncultivated aerobic methanotrophic bacteria evaluated based on pmoA as molecular marker. *Frontiers in Microbiology*, 6, 1346. Retrieved from <https://doi.org/10.3389/fmicb.2015.01346>
- Kolb, S. (2009). The quest for atmospheric methane oxidizers in forest soils. *Environmental*



*Microbiology Reports*, 1(5), 336–346. Retrieved from <https://doi.org/10.1111/j.1758-2229.2009.00047.x>

Kolb, S., Knief, C., Dunfield, P. F., & Conrad, R. (2005). Abundance and activity of uncultured methanotrophic bacteria involved in the consumption of atmospheric methane in two forest soils. *Environmental Microbiology*, 7(8), 1150–1161. Retrieved from <https://doi.org/10.1111/j.1462-2920.2005.00791.x>

Kolb, S., Knief, C., Stubner, S., & Conrad, R. (2003). Quantitative Detection of Methanotrophs in Soil by Novel pmoA -Targeted Real-Time PCR Assays. *Applied and Environmental Microbiology*, 69(5), 2423–2429. Retrieved from <https://doi.org/10.1128/AEM.69.5.2423>

Lauber, C. L., Hamady, M., Knight, R., & Fierer, N. (2009). Pyrosequencing-based assessment of soil pH as a predictor of soil bacterial community structure at the continental scale. *Applied and Environmental Microbiology*, 75(15), 5111–5120. Retrieved from <https://doi.org/10.1128/AEM.00335-09>

Le Mer, J., & Roger, P. (2001). Production, oxidation, emission and consumption of methane by soils: A review. *European Journal of Soil Biology*, 37(1), 25–50. Retrieved from [https://doi.org/10.1016/S1164-5563\(01\)01067-6](https://doi.org/10.1016/S1164-5563(01)01067-6)

Liu, L., & Greaver, T. L. (2009). A review of nitrogen enrichment effects on three biogenic GHGs: the CO<sub>2</sub> sink may be largely offset by stimulated N<sub>2</sub>O and CH<sub>4</sub> emission. *Ecology Letters*, 12(10), 1103–1117. Retrieved from <https://doi.org/10.1111/j.1461-0248.2009.01351.x>

Lyu, Z., Shao, N., Akinyemi, T., & Whitman, W. B. (2018). Methanogenesis. *Current Biology*, 28(13), R727–R732. Retrieved from <https://doi.org/10.1016/j.cub.2018.05.021>

Malghani, S., Reim, A., von Fischer, J., Conrad, R., Kuebler, K., & Trumbore, S. E. (2016). Soil methanotroph abundance and community composition are not influenced by substrate availability in laboratory incubations. *Soil Biology and Biochemistry*, 101, 184–194. Retrieved from <https://doi.org/10.1016/j.soilbio.2016.07.009>

Maurer, D., Kolb, S., Haumaier, L., & Borken, W. (2008). Inhibition of atmospheric methane oxidation by monoterpenes in Norway spruce and European beech soils. *Soil Biology and Biochemistry*, 40(12), 3014–3020. Retrieved from <https://doi.org/10.1016/j.soilbio.2008.08.023>

McDaniel, M. D., Saha, D., Dumont, M. G., Hernández, M., & Adams, M. A. (2019). The Effect of

- Land-Use Change on Soil CH<sub>4</sub> and N<sub>2</sub>O Fluxes: A Global Meta-Analysis. *Ecosystems*, 22, 1424–1443. Retrieved from <https://doi.org/10.1007/s10021-019-00347-z>
- Menyailo, O. V., & Hungate, B. A. (2003). Interactive effects of tree species and soil moisture on methane consumption. *Soil Biology and Biochemistry*, 35(4), 625–628. Retrieved from [https://doi.org/10.1016/S0038-0717\(03\)00018-X](https://doi.org/10.1016/S0038-0717(03)00018-X)
- Mosier, A., Schimel, D., Valentine, D., Bronson, K., & Parton, W. (1991). Methane and nitrous oxide fluxes in native, fertilized and cultivated grasslands. *Nature*, 350(6316), 330–332. Retrieved from <https://doi.org/10.1038/350330a0>
- Nazaries, L., Pan, Y., Bodrossy, L., Baggs, E. M., Millard, P., Murrell, J. C., & Singh, B. K. (2013). Evidence of Microbial Regulation of Biogeochemical Cycles from a Study on Methane Flux and Land Use Change. *Applied and Environmental Microbiology*, 79(13), 4031–4040. Retrieved from <https://doi.org/10.1128/aem.00095-13>
- Qian, L., Qing, Z., Jinsen, Z., Kaihua, L., & Guishan, Y. (2014). Soil Moisture Response to Rainfall in Forestland and Vegetable Plot in Taihu Lake Basin , China. *Chinese Geographical Science*, 25, 426–437. Retrieved from <https://doi.org/10.1007/s11769-014-0715-0>
- R Core Team. (2018). R: A Language and Environment for Statistical Computing. Vienna, Austria: R Foundation for Statistical Computing. Retrieved from <https://www.r-project.org>
- Rahman, M. T., Crombie, A., Chen, Y., Stralis-Pavese, N., Bodrossy, L., Meir, P., ... Murrell, J. C. (2011). Environmental distribution and abundance of the facultative methanotroph *Methylocella*. *ISME Journal*, 5(6), 1061–1066. Retrieved from <https://doi.org/10.1038/ismej.2010.190>
- Reay, D. S., Nedwell, D. B., McNamara, N., & Ineson, P. (2005). Effect of tree species on methane and ammonium oxidation capacity in forest soils. *Soil Biology and Biochemistry*, 37(4), 719–730. Retrieved from <https://doi.org/10.1016/j.soilbio.2004.10.004>
- Rosseel, Y. (2012). lavaan: An R Package for Structural Equation Modeling. *Journal of Statistical Software*, 48(2), 1–36.
- Saari, A., Heiskanen, J., & Martikainen, P. J. (1998). Effect of the organic horizon on methane oxidation and uptake in soil of a boreal Scots pine forest. *FEMS Microbiology Ecology*, 26(3), 245–255. Retrieved from [https://doi.org/10.1016/S0168-6496\(98\)00040-3](https://doi.org/10.1016/S0168-6496(98)00040-3)
- Saari, A., Rinnan, R., & Martikainen, P. J. (2004). Methane oxidation in boreal forest soils: Kinetics

and sensitivity to pH and ammonium. *Soil Biology and Biochemistry*, 36(7), 1037–1046.

Retrieved from <https://doi.org/10.1016/j.soilbio.2004.01.018>

Schnell, S., & King, G. M. (1994). Mechanistic Analysis of Ammonium Inhibition of Atmospheric Methane Consumption in Forest Soils. *Applied and Environmental Microbiology*, 60(10), 3514–3521.

Sharp, C. E., Stott, M. B., & Dunfield, P. F. (2012). Detection of autotrophic verrucomicrobial methanotrophs in a geothermal environment using stable isotope probing. *Frontiers in Microbiology*, 3(AUG), 1–9. Retrieved from <https://doi.org/10.3389/fmicb.2012.00303>

Shrestha, P. M., Kammann, C., Lenhart, K., Dam, B., & Liesack, W. (2012). Linking activity, composition and seasonal dynamics of atmospheric methane oxidizers in a meadow soil. *ISME Journal*, 6(6), 1115–1126. Retrieved from <https://doi.org/10.1038/ismej.2011.179>

Sitaula, B. K., Bakken, L. R., & Abrahamsen, G. (1995). CH<sub>4</sub> uptake by temperate forest soil: Effect of N input and soil acidification. *Soil Biology and Biochemistry*, 27(7), 871–880. Retrieved from [https://doi.org/10.1016/0038-0717\(95\)00017-9](https://doi.org/10.1016/0038-0717(95)00017-9)

Sitaula, B. K., Hansen, S., Sitaula, J. I. B., & Bakken, L. R. (2000). Methane Oxidation Potentials and Fluxes in Agricultural Soil : Effects of Fertilisation and Soil Compaction. *Biogeochemistry*, 48(3), 323–339.

Steudler, P. A., Bowden, R. D., Melillo, J. M., & Aber, J. D. (1989). Influence of nitrogen fertilization on methane uptake in temperate forest soils. *Nature*, 341(6240), 314–316. Retrieved from <https://doi.org/10.1038/341314a0>

Tate, K. R. (2015). Soil methane oxidation and land-use change - from process to mitigation. *Soil Biology and Biochemistry*, 80, 260–272. Retrieved from <https://doi.org/10.1016/j.soilbio.2014.10.010>

Teepe, R., Brumme, R., Beese, F., & Ludwig, B. (2014). Nitrous Oxide Emission and Methane Consumption Following Compaction of Forest Soils. *Soil Science Society of America Journal*, 68(2), 605. Retrieved from <https://doi.org/10.2136/sssaj2004.6050>

Templeton, G. F. (2011). A two-step approach for transforming continuous variables to normal: Implications and recommendations for IS research. *Communications of the Association for Information Systems*, 28(1), 41–58. Retrieved from <https://doi.org/10.17705/1cais.02804>

Tveit, A. T., Hestnes, A. G., Robinson, S. L., Schintlmeister, A., Dedys, S. N., Jehmlich, N., ... Svenning, M. M. (2019). Widespread soil bacterium that oxidizes atmospheric methane. *Proceedings of the National Academy of Sciences*, 116(17), 8515–8524. Retrieved from <https://doi.org/10.1073/pnas.1817812116>

Van Den Pol-van Dasselaar, A., Van Beusichem, M. L., & Oenema, O. (1998). Effects of soil moisture content and temperature on methane uptake by grasslands on sandy soils. *Plant and Soil*, 204(2), 213–222. Retrieved from <https://doi.org/10.1023/A:1004371309361>

VEB Projektierung Potsdam. (1974). Anweisung für die forstliche Standortserkundung in der DDR (Standortserkundungs-Anweisung /SEA 74). Potsdam.

Zhao, R., Wang, H., Cheng, X., Yun, Y., & Qiu, X. (2018). Upland soil cluster  $\gamma$  dominates the methanotroph communities in the karst Heshang Cave. *FEMS Microbiology Ecology*, 94(12), 1–13. Retrieved from <https://doi.org/10.1093/femsec/fiy192>

## Figure Captions

**Figure 1** Potential methane oxidation rates (PMORs) in forests and grasslands. PMORs (a) including all regions separated into forests and grasslands, and (b) in the regions Schwäbische Alb (ALB), Hainich (HAI) and Schorfheide (SCH) in forests and grasslands, significance codes:  $p < 0.01$  (\*\*),  $p < 0.001$  (\*\*\*),  $n = 299$ .

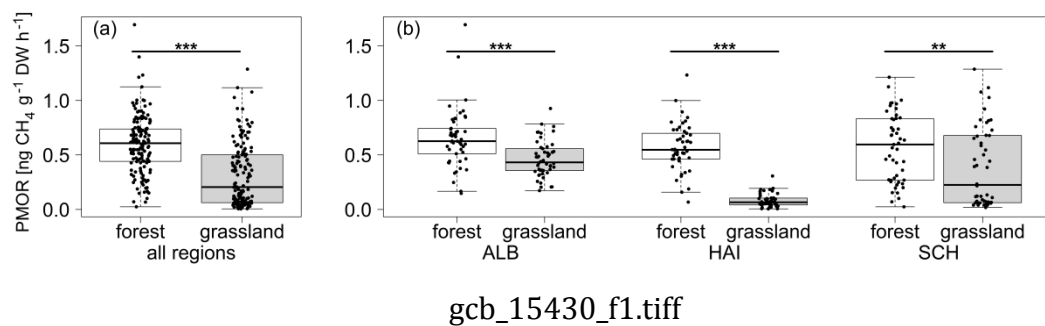
**Figure 2** Effect of tree species (Be = beech, Oa = oak, Sp = spruce and Pi = pine) on potential methane oxidation rates (PMORs) in the forests including all regions. Colored points indicate soil texture,  $n = 149$ .

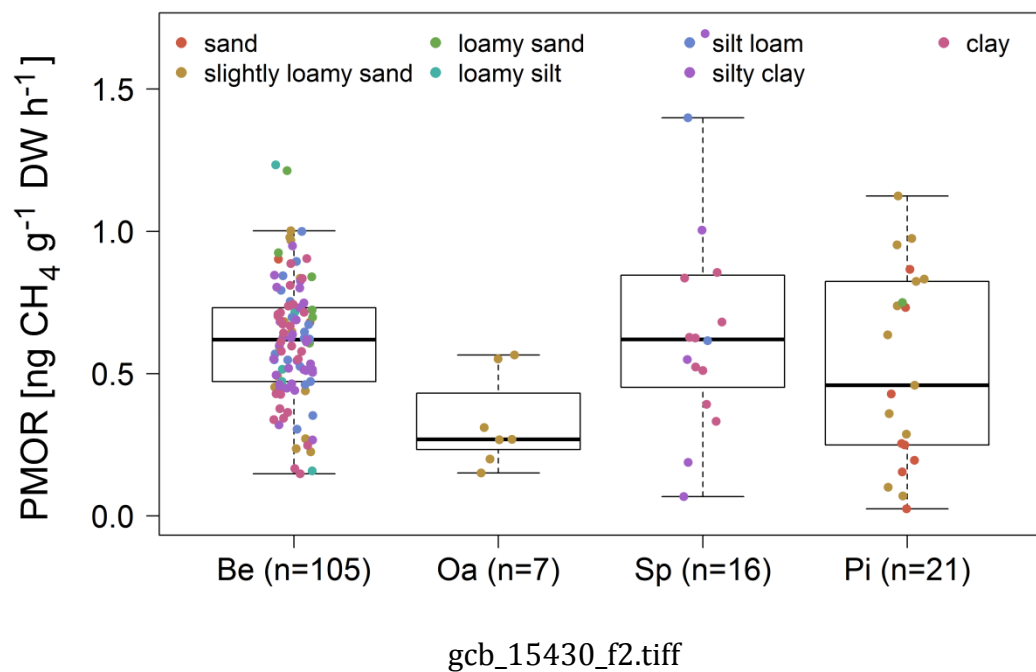
**Figure 3** Effects of (a) land-use intensity index (LUI), (b) without (no) and with (yes) fertilization, and low and high intensity of (c) grazing and (d) mowing on normalized potential methane oxidation rates (PMORs norm) in the grassland soils. PMORs norm was calculated by dividing the PMORs of each plot by the mean PMORs of the respective region; significance codes:  $p < 0.05$  (\*),  $p < 0.01$  (\*\*),  $n = 150$ .

**Figure 4** Abundance of *pmoA* copies of Upland soil cluster- $\alpha$  (USC- $\alpha$ ) in (a) all regions (b) in the regions Schwäbische Alb (ALB), Hainich (HAI) and Schorfheide (SCH) in forest (white) and grassland (grey) soils. Abundance of Upland soil cluster- $\gamma$  (USC- $\gamma$ ) in (c) all regions (d) in the regions Schwäbische Alb (ALB), Hainich (HAI) and Schorfheide (SCH). Abundances below detection limit were set to 100.  $p < 0.001$  (\*\*\*),  $n = 295$ .

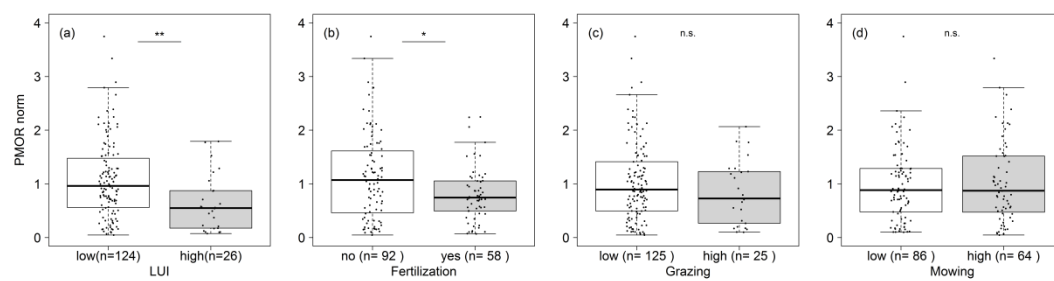
**Figure 5** Correlation of potential methane oxidation rates (PMORs) with (a) Upland soil cluster- $\alpha$  (USC- $\alpha$ ) abundance in forest soils and with (b) Upland soil cluster- $\gamma$  (USC- $\gamma$ ) abundance in grassland soils. The colors represent the different regions Schwäbische Alb (ALB), Hainich (HAI) and Schorfheide (SCH). The significance levels reported are based on Pearson's coefficient.

**Figure 6** Results of structural equation modellings showing the direct and indirect effect of soil properties and land use intensity on PMOR for (a) all forest and (b) all grassland soils. The numbers at the lines show the standardized path coefficients. Significant ( $p < 0.05$ ) paths are shown as black (positive effect) or red (negative effect) lines. Non-significant ( $p > 0.05$ ) paths are shown in dashed grey lines. BD = bulk density, sand = sand content [%], ForMI = forest management index, LUI = land use intensity index, USC- $\alpha$  = abundance of Upland soil cluster  $\alpha$  copy numbers per soil, USC- $\gamma$  = abundance of Upland soil cluster  $\gamma$  copy numbers per soil. Amount of variance explained by the model ( $r^2$ ) is listed for the response variables.  $\chi^2 = 1.079; 0.255$ ,  $df = 2; 1$ ;  $p(\chi^2) = 0.583; 0.628$ , CFI = 1; 1, RMSEA = 0; 0, SRMR = 0.011; 0.006 in (a) and (b) respectively.

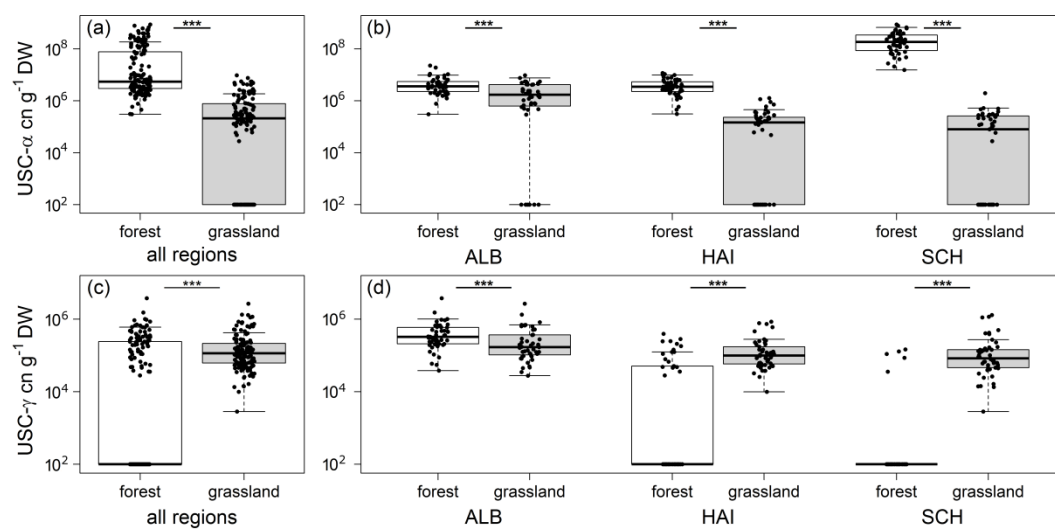




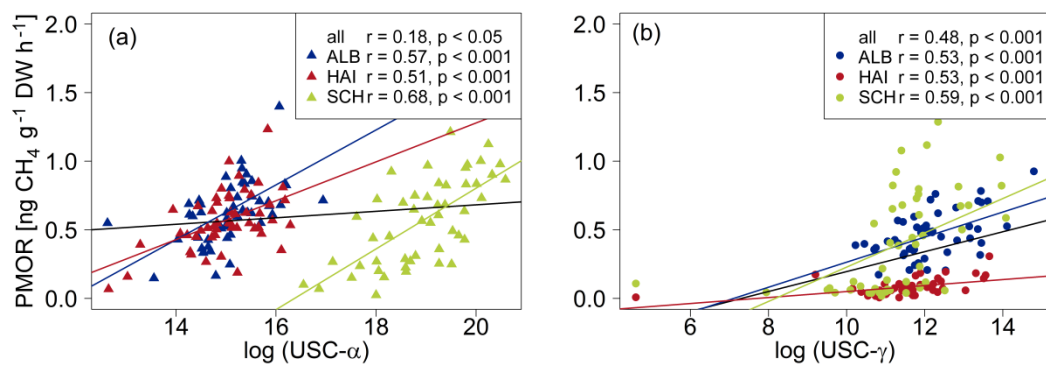




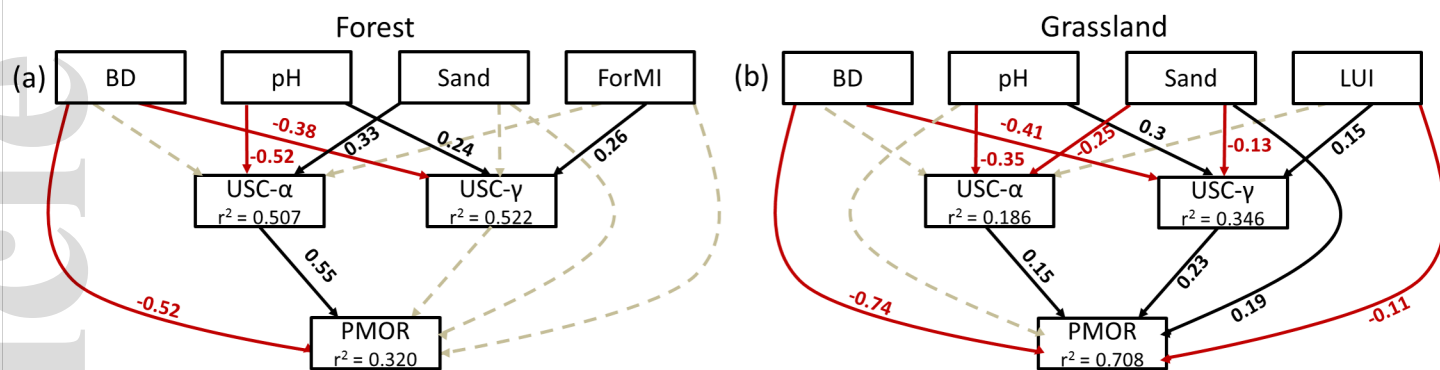
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