



# Can plant – soil interactions be a controller on GHG emissions from soils?



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## Introduction

Plant-soil interactions play an important role in regulating greenhouse gas emissions (CO<sub>2</sub> and N<sub>2</sub>O) and in the storage of carbon (C) as soil organic matter (SOM) creating the potential for crop selection to be a tool for mitigating climate changing and improving soil health. This is relevant across all crops and cropping systems but is of particular importance in grassland soils which are known to be important stores of C. However, there is still a need to understand which plant traits drive differences in the rates and products of C cycling and how this is regulated by the soil microbiome which mediates all soil nutrient cycling processes.

Microbial communities are central to the regulation of soil functions consequently, soil communities influence greenhouse gas (GHG) emissions, soil C storage and nutrient availability by regulating the biogeochemical processes that determine the fate of C in soils. Understanding the structure and function of soil communities associated with plant roots is therefore critical to understanding how crop selection can help soils be managed for multiple benefits.

The aim of this research is therefore to characterise plant-driven soil microbial community selection across a range of agricultural grasses, and to assess the extent to which distinct microbial community compositions were predictive of CO<sub>2</sub> emissions from soil.



## Methods

A microcosm experiment was used to investigate the interaction between grass variety, microbial communities and CO<sub>2</sub> emissions. Microcosms (Fig 1.) were planted with one of 10 different grass varieties, representing 5 different grass species (Table 1) and fertilised with NH<sub>4</sub>NO<sub>3</sub> at an agriculturally relevant rate (60 kg N ha<sup>-1</sup>).



Fig. 1. Microcosm design and CO<sub>2</sub> collection. Table 1. List of the 5 different grass species and 10 different grass varieties used in this study.

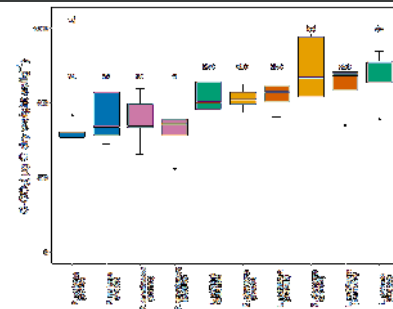
Grass Species	Grass variety
<i>Lolium perenne</i>	Seagoe
<i>Lolium perenne</i>	Solomon
<i>Phleum pratense</i>	Presto
<i>Phleum pratense</i>	Comer
<i>Festuca arundinacea</i>	Barelite
<i>Festuca arundinacea</i>	Borneo
<i>Dactylis glomerata</i>	Sparta
<i>Dactylis glomerata</i>	Donata
<i>Lolium multiflorum</i>	Muriello
<i>Lolium multiflorum</i>	Barmultra

When the grass had germinated, microcosms were sampled weekly for CO<sub>2</sub> over a 6-week period. CO<sub>2</sub> efflux was measured from grass free headspaces using an Environmental gas monitor (PP systems, Amesbury, USA).

At 6 weeks, microcosms were destructively sampled and microbial communities characterised using next generation sequencing. 16SrRNA amplicon libraries were created and sequenced using the Illumina Miseq. Qiime2 with DADA2 plugin was used to determine amplicon sequence variants (ASV). Differences in community composition was visualised using PCoA and associations with CO<sub>2</sub> tested using Canonical analysis of principal coordinates (CAP).

## Results

Cumulative CO<sub>2</sub> emissions differed between grass varieties (p<0.001) (Fig.2a), with all grasses except Barelite producing more CO<sub>2</sub> than the control. There was a linear relationship between cumulative CO<sub>2</sub> emissions and grass biomass (r<sup>2</sup> = 0.21, P < 0.001).



Across all samples a total of 13991 unique ASVs were detected of which 5182 were found in more than one microcosm. Structure of microbial communities differed both between grass species (p < 0.001) and grass varieties (p < 0.05) (Fig 2b.).

CAP found that microbial community structure was associated with a small but significant proportion of CO<sub>2</sub> emissions independent of the effects of grass variety (9%, p<0.05). This increased to 10% (p<0.05) when DOC concentrations were included in the model with communities associated with high DOC concentration associated with low CO<sub>2</sub> emissions (Fig 2c.).

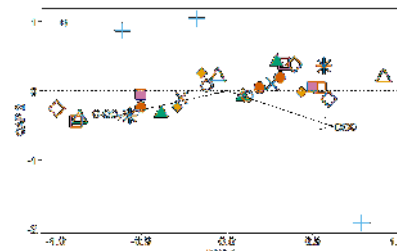
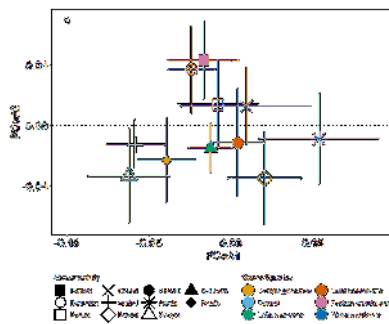


Figure 2 a) Cumulative CO<sub>2</sub> emissions for each of the 10 different grass varieties included in this study and the unplanted control. Grasses with the same letter are not significantly different from each other (p> 0.05). b) PCoA using relative abundance sequence data. c) CAP analysis of relative abundance data with grass variety as a conditional variable and CO<sub>2</sub> emissions and DOC as constraining variables.

## Conclusions

- The selection of grass variety for cultivation has the potential to be an important tool for managing soil C storage and CO<sub>2</sub> emissions in grassland soils.
- Different grasses selected for their own unique microbial communities and the composition of these communities had a small but significant effect on CO<sub>2</sub> emissions from soils.
- This provides insight into the potential mechanisms by which grass selection may control the partitioning of C into soil, plant and atmospheric pools and highlights the important role crop selection may play in mitigating climate change and improving soil health.

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