Plant Input Effects on the Biodiversity and Function of Grassland Bacterial Communities

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INTRODUCTION

The structure and activity of rhizosphere bacterial communities is thought to be dependant on the quality and quantity of root C input into the soil. Specifically the presence of plants in soil should select for competitive species generating more dominantly structured communities.

What is less clear is how these plant mediated effects affect the functioning of soil bacterial communities. An understanding of these relationships is required to predict the effects of different land uses on carbon cycling and C-storage in soils.

Whilst soils are known to be highly diverse, It is difficult to directly relate the diversity of soil bacterial communities to functional ability in terms of carbon cycling. This is due to the belief that functional redundancy exists in soils due to high biodiversity and an overlap in the functional capacities of different species.

AIMS

To test the effects of rhizodeposition on bacterial communities, by examining whether the presence or absence of plants impacts on the functional and taxonomic responses of the bacterial community to substrate additions.

Specifically:

1) ***Do plant induced alterations of bacterial community structure affect bacterial functioning?***
2) ***Does the presence or absence of plants select for different active populations involved in either labile or recalcitrant carbon decomposition pathways?***

METHODS

Grassland soil samples were collected from triplicate plots at the Sourhope field site, Scottish borders, UK. Each plot contained two experimental treatments; 1) native grassland flora (foliated), and 2) where all vegetation had been removed and soil covered to prevent re-growth (defoliated). Soil cores were taken to the laboratory and sieved where incubations were established at 15 ºC with either glucose, glycine, cellulose (4.0 mg C per g dry soil) or water as a control. Soil respiration was measured by GC to assess function. The bacterial community was examined both before and 3-weeks after substrate addition by PCR of total nucleic acids and subsequent DGGE.

	Foliated	Defoliated	*P* value
% moisture	42.33	41	0.743
pH	4.39	4.57	0.394
C g g soil^{-1}	0.136	0.098	0.243
N g g soil^{-1}	0.010	0.008	0.256
C:N	13.71	12.66	0.328
Extractable RNA (ng/µl)	79.47	86.94	0.639

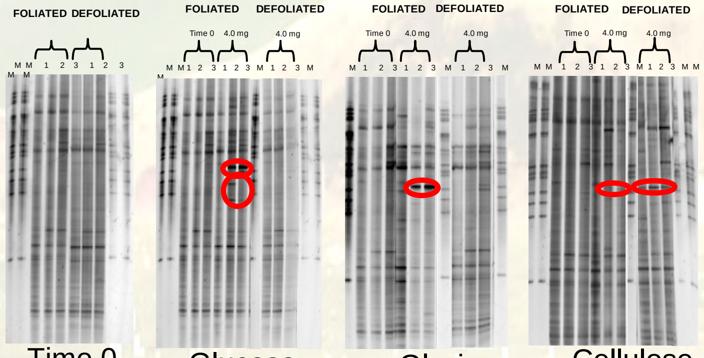
Table of mean values (n=3) of foliated and defoliated soil properties prior to substrate addition. No significant differences between soil properties.

RESULTS

Community Analysis

DGGE gels of bacterial communities from both foliated and defoliated soil show that prior to substrate addition, community compositions were seemingly identical, though foliated profiles contained certain bands of higher relative abundance. 3-weeks after substrate addition DGGE analysis revealed community differences between soil types.

1) Glucose and glycine addition resulted in the competitive outgrowth of certain species (ringed) but only in the foliated soils. 2) Conversely Cellulose addition caused outgrowth only in the defoliated soils.



Time 0 Glucose Glycine Cellulose

16S rDNA DGGE profiles of PCR amplified nucleic acids extracted from foliated and defoliated soil before substrate addition (Time 0) and 3 weeks after the addition of either glycine, glucose or cellulose at 4.0 mg C per g dry soil. Numbers 1-3 represent replicates, whilst M denotes marker lanes.

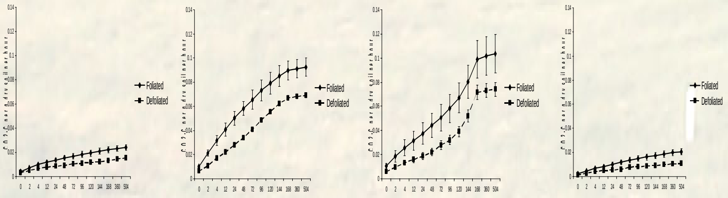
RESULTS

Functional Responses

1) Basal soil respiration was higher in foliated soil compared to defoliated soil (see water control).

2) Respiration was also highest in foliated soils following the addition of each of the substrates.

3) Labile substrates (glucose and glycine) were more readily metabolised than cellulose.



No Substrate Glucose Glycine Cellulose

Cumulative soil respiration rates at 15 ºC (mg CO2-C / g dry soil) over time after the addition of water (control), glucose, glycine and cellulose. Error bars are standard error of the mean (n=3).

RESULTS

Net Respiration

	Glucose	Glycine	Cellulose
Foliated	**0.072**	**0.083**	0.0035
Defoliated	0.058	0.063	**0.0046**
P	0.019	0.039	0.035

Table of mean (n = 3) final cumulative respiration amount (mg CO_2-C / g dry soil) minus basal respiration derived from the water control.

1) Higher net respiration was observed in the foliated soils following glucose and glycine addition.

2) However, higher net respiration was observed following cellulose addition in the defoliated soil.

3) Significant differences existed between foliated and defoliated soil respiration for all substrate additions.

CONCLUSIONS

1. **The presence of plants selects for a bacterial community more active in the degradation of labile substrates *i.e.* glycine and glucose.**
2. **Soil bacterial communities in defoliated soils were more able to respire recalcitrant substrates such as cellulose.**
3. **In both cases the effect was manifested by both a community response (outgrowth of certain species) and a functional response (increased respiration of the added substrate).**
4. **The functional capacity of soil bacterial communities cannot be addressed simply by assessing the molecular biodiversity present. Apparently similar communities can invoke different functional and taxonomic responses to substrate addition, according to the life history of that community. This is most likely explained by the communities possessing pre-adapted active subsets of populations not visible in total bacterial community profiles**

FUTURE WORK

The use of stable-isotope-labelled compounds at ecologically relevant concentrations to unequivocally identify substrate utilising bacteria by sequence analysis and to provide a detailed C balance