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Soil microbial community response to buried crop residues is site-specific and depends on depth of burial

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Introduction

- Crop residues provide the main carbon (C) input in agricultural soils. Understanding their fate is important for optimizing nutrient cycling for plant growth and sustained soil productivity.
- Tillage practices can result in the burial of residues at different depths. How this affects their decomposition by microorganisms is unknown.
- As part of a broader network of projects, we are studying how management affects the fate of residue C in agroecosystems across Canada in order to promote practices that optimize C cycling in agricultural systems.

Objectives

The overall experimental objective is to determine how depth of burial affects the fate of crop residue C in different climates.

The specific objectives of this microbial profiling aspect of the study were:

- to determine whether the microbial response to fresh residue C varies at different depths in the soil profile
- to compare the response of microbial decomposer communities in a semi-arid vs. humid climate

Materials and Methods

In fall of 2009, an in-situ crop residue decomposition experiment was installed at two sites with different moisture regimes:

1.Ottawa, ON (humid; MAP 882 mm).

2.Lethbridge, AB (semi-arid; MAP 386 mm)

- Soil cores (38.1mm diam.) were excavated to the bottom of three depths:

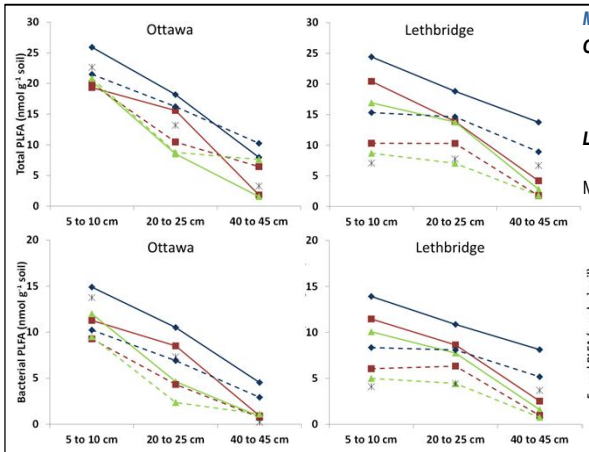
  10 cm; 25 cm; 45cm

- Barley residue was incorporated into the appropriate soil increment (e.g. 5-10 cm; 283 g C m^{-2}) in a fiberglass mesh bag. The bag was placed back into the tube, returned to its original depth and the remaining soil core replaced above it.

- Replicate cores (n=4) were installed in rows in nested sets of the 3 depths, 0.3 m apart.
- After 1 and 2 years, the soil within and surrounding the mesh bag was recovered by excavating to 5 cm above the mash bag, placing a PVC pipe (10 cm diam.) around the bag and then removing the larger soil sample within the pipe.

- 3 soil samples were obtained for each core:
  1. mesh bag contents
  2. below
  3. surrounding
- Microbial phospholipid fatty acid (PLFA) biomarkers were extracted from 4.0 g of lyophilized soil and quantified using an internal standard (19:0) with GC-FID and the MIDI™ system. Microbial abundance data were analyzed using ANOVA in SPSS v.20 and community profiles were subjected to NMDS ordination in PCOrd v.5.0.

Results and Discussion



Microbial dynamics responded differently in humid and semi-arid climates

Ottawa: total and bacterial biomass within the mesh bags had a depth-dependent response to residues after the first year, followed by a general increase at year 2. Fungi appeared to be dominant in decomposition, temporarily increasing at year 1 ($p<0.001$).

Lethbridge: microbial biomass increased within the mesh bags at all depths ($p<0.001$) and was sustained above background levels after 1 and 2 years.

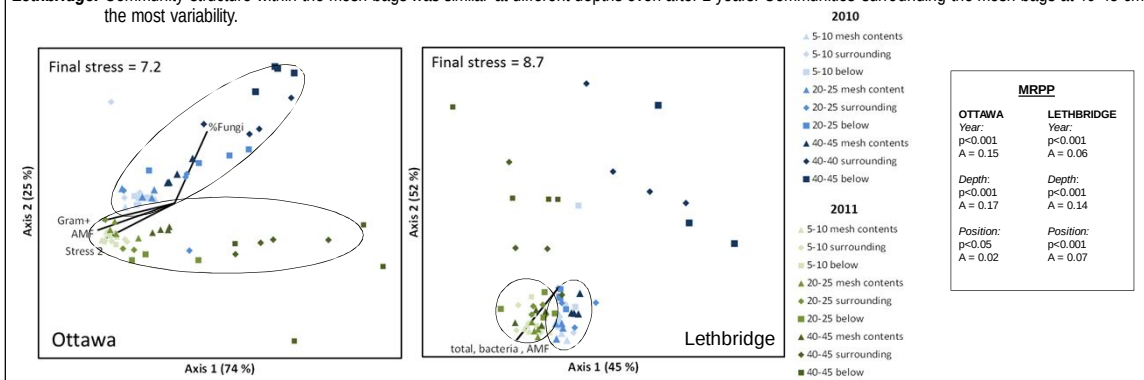
Microbial response surrounding and below the buried residues was more variable, and interacted with depth at both locations ($p<0.05$).

Figure 1. Total, bacterial and fungal biomass following addition of barley residues at 5-10, 20-25 and 40-45 cm depths at Ottawa and Lethbridge.

Addition of barley residues resulted in distinct microbial communities which was different at humid and semi-arid locations

Ottawa: Decomposition likely occurred at a faster rate due to increased soil moisture resulting in communities that were distinct at 1 and 2 years after residue addition. Similarly, community structure differed as a result of proximity to the residues and followed a strong depth gradient.

Lethbridge: Community structure within the mesh bags was similar at different depths even after 2 years. Communities surrounding the mesh bags at 40-45 cm showed the most variability.



MRPP

OTTAWA	LETHBRIDGE
Year:	*Year:*
p<0.001	p<0.001
A = 0.15	A = 0.06
Depth:	*Depth:*
p<0.001	p<0.001
A = 0.17	A = 0.14
Position:	*Position:*
p<0.05	p<0.001
A = 0.02	A = 0.07

Figure 2. Microbial community structure of soils within, surrounding and below mesh bags amended with barley residues at three different depths.

Discussion and Conclusions

Changes in microbial community structure were more responsive to depth of residue burial at Ottawa than Lethbridge.

- Dry conditions at Lethbridge likely limited microbial activity and transport of soluble substrates, resulting in the development of similar microbial consortia in response to residue additions. Greater activity and access to residue-derived substrates as a result of increased soil moisture at Ottawa produced a more dominant effect of soil depth and resulted in microbial communities which had greater divergence in structure.

These differences may ultimately influence the rate and pathways of residue incorporation into soil organic matter as a result of depth of incorporation.

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