Root x Microbial Community Interactions in Humification and Decomposition Processes

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Introduction

Soil microorganisms mediate decomposition and humification processes in soil (Fig. 1). Rates of decomposition have been shown to be increased and/or decreased by the presence of living roots, but little is known about the mechanisms through which living roots impact the soil microbial processes involved. Living roots also have been shown to promote the conservation or mineralization of native soil organic matter (SOM). Plant effects on soil water status and N availability may partly explain many of the contradictory results from greenhouse and field studies. The actual mechanisms involved, however, are still elusive.

A recent review of the effect of living roots on SOM turnover emphasized that the diversity of the microflora present at all stages of interaction comprise a critical unknown in the process (Dormaar, 1990). Our current understanding of how below-ground life (living roots/microbial communities and their activities) controls decomposition and humification processes remains extremely limited.

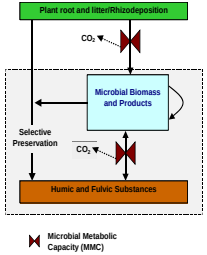


Fig. 1. Humification processes in soils begin after the initial phase of residue decomposition and transformation. Decomposition is driven by activity of microorganisms and their enzymes. The conceptual model depicts the microbial community control of humification processes through the incorporation of an array of microbial products as SOM precursors and their metabolic capacity (MMC), which we define as the utilization and resynthesis of C, turnover of the biomass, and loss of C via CO_2.

Research Questions

We propose that:

1) Living roots impact rates and products of the conversion of below-ground plant carbon into humic substances by affecting the composition and activity of the root-associated microbial community.
2) Living roots impact rates of plant litter decomposition by affecting the composition and activity of the root-associated microbial community.
3) The magnitude and net impact of living roots is partially dependent on N-availability.

Approach

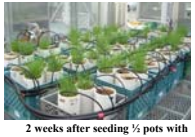
We are using a ^{13}C tracer approach to follow the fate of C in the root system of *Avena barbata* (slender wild oats) and to determine the effects of

√ Living roots (with and without subsequent crops of wild oats)

√ Nitrogen availability (with and without added N)

Experimental Design: 2 x 2 factorial design with 4 replicates
Soil moisture is continuously monitored using dielectric constant moisture probes and all treatments will be maintained at a constant water content during the treatment periods.

Initial ^{13}C labeling of below-ground system (Fall 2004) at UCB



2 weeks after seeding ½ pots with *Avena barbata* April 2005

- In Spring 2004, soil from the Schubert watershed at the Sierra Foothills Research and Extension Center, located 30 km east of Marysville, CA, was excavated from a Oak Woodland ecosystem. Wild oats are the dominant grass species (80%).
- The soil was sieved (6-mm screen) and packed into eighty-eight 10 cm x 30 cm PVC cylinders to a bulk density of 1.21 g cm^{-3}.
- *A. barbata* seeds were planted using a seed density of ~18,800 seeds m^{-2}, similar to field densities. Plant labeling with $^{13}CO_2$ began when plants were 3 weeks old, using 24-36 hr exposures to the labeled atmosphere 10 times during the development of the oats.

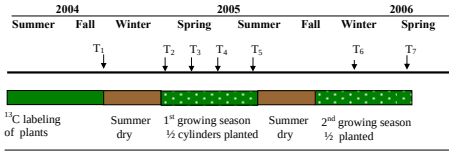


Fig. 2. Timeline of activities. After the production of ^{13}C-labeled belowground system, the above-ground biomass was removed and the pots were exposed to a dry, warm summer fallow. The initial treatments were applied in April 2005. The N treatment is a split application of urea-N added 3 and 8 weeks after germination (20 kg N ha^{-1} total). Pots will be excavated periodically and the soil analyses listed below will be conducted.

Soil Analyses

- Total ^{13}C in recognizable root debris (> 2 mm) and bulk soil (< 2 mm)
- Light fraction ^{13}C and N (density fractionation)
- Microbial biomass ^{13}C (CFE)
- Microbial ^{13}C in community groups (PLFA and DNA)
- C enzyme activities

Results

Table 1. Selected biochemical and physical soil properties of the Argonaut silt loam (Mollic Haploxeralf) used in this study (0-9 cm depth).

Soil property						
pH	Total C	Total N	Mineralizable C	Mineralizable N	Nitrification potential	Bulk density
	g kg^{-1}		kg ha^{-1}		mg N kg d^{-1}	g cm^{-3}
5.42	28	2.4	320	9.6	5.70	1.21

► Research from this site suggests that both microorganisms and wild oats are a significant sink for nitrate, leading to low extractable nitrate levels during the Fall and Winter grass growing season (Herman et al., 2003).

► During the grass growing season, N limitation may affect the efficiency of decomposers and reduce decomposition of the previously produced roots and/or increase native SOM N mineralization. The N fertilization treatment tested here, may shed light on this potentially regulating factor.

Table 2. Initial C and ^{13}C enrichment of plant and soil pools prior to the start of treatments in April 2005.

		Above-ground	Below-ground		
		Shoots	Roots	Soil < 2 mm	
Date		C	C	^{13}C	
		g m^{-2}			‰
Jan-05	end of ^{13}C labeling	1492	413 (55)	12.6 (2.5)	
Apr-05	end of summer	-	146 (16)	21.5 (2.9)	

- Uniformly ^{13}C–labeled *A. barbata* shoot biomass was highly enriched in ^{13}C (582 ‰) after soil dry-down in January 2005.
- Root biomass (> 2 mm) declined to 35% of its starting mass over the initial 3 month summer period (January to April).
- Bulk soil (< 2mm) was more enriched in ^{13}C (‰) after the fallow summer in April reflecting the contributed of ^{13}C from decaying roots.
- Microbial biomass C was more enriched than bulk soil (< 2 mm) in January 2005 (65 ‰).

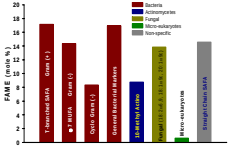


Fig. 3. Mole fraction of selected phospholipid fatty acids (PLFA) extracted from soil prior to establishment of wild oat crop.

- PLFA analysis will provide a quantitative measure of changes in the broad soil microbial community composition in the bulk soil due to the effects of living roots and N additions.
- In conjunction with ^{13}C determinations, ^{13}C-PLFA will enable the comparison of the activity of microbial groups. The amount of *A. barbata* root ^{13}C converted into microbial biomass and its turnover rate will be quantified among broad cell-type groups.

Discussion

√ Recent research showed no significant differences in microbial community composition between rhizosphere and bulk soil (i.e., TRFLP analysis) in *Avena* planted soils.

√ Gross N mineralization and cell numbers, however, were significantly higher in rhizosphere versus bulk soil (Herman et al., 2005).

√ In addition, ongoing work has demonstrated greater chitinase activity in *Avena* rhizosphere soil compared with bulk soil on a per cell basis.

This project will develop a quantitative road map of the flow of C from plant roots to soil microorganisms to humic materials. The impact of living roots on the pathways and outcomes of humification and the effects of microbial community composition and activity will be quantified. A better understanding of the mechanisms involved in the effects of living roots on C dynamics in soil will enhance the development of management strategies that increase C sequestration rates in grasslands and agricultural ecosystems.

References

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