

14. Mapping soil carbon from cradle to grave #3: Plant-microbial interactions regulate soil C cycling

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Project Goals: Our project is focused on gaining a fundamental understanding of C cycling in soil, as mediated by soil microorganisms and their interactions with plants. Our work investigates how the interactions between roots and soil microorganisms affects transformation of root derived C, decomposition and loss as CO₂, as well as soil C sorption and stabilization at ambient and elevated levels of atmospheric CO₂.

Plants transfer atmosphere CO₂ into belowground soil C pools where soil microorganisms are primary mediators of C transformation and mineralization. Plant roots can strongly affect microbial transformation and mineralization of root-derived C but the molecular mechanisms underlying these plant-microbial interactions are poorly understood, as are the possible modulations caused by changing climate. We examined the effects of live *Avena fatua* roots (a common annual grass) on decomposition of ¹³C-labeled root litter in a California grassland soil over two simulated growing-seasons. The presence of live roots consistently suppressed rates of litter decomposition; however this effect disappeared with plant senescence. Presence of live roots significantly altered the abundance, composition and functional potential of microbial communities (assessed by qPCR, MiSeq 16S and ITS sequencing, and GeoChip 4, respectively). Two possible mechanisms (preferential substrate utilization and drying stress) were identified for explaining the reduced rates of litter decomposition in the presence of live plant roots.

We also investigated the influence of elevated CO₂ (eCO₂) on C cycling through plant-microbial interactions. Plants grown with eCO₂ (700 ppm, ¹³CO₂) increased both total C allocated belowground and the amount of root-derived ¹³C in the mineral-associated fraction, which is generally considered to be relatively stable soil C. Microbial communities associated with *Avena fatua* roots at different plant growth stages were analysed using Illumina 16S sequencing. Although eCO₂ caused little effect on the composition of bacterial communities in rhizosphere or bulk soil, the age of plant roots did play an important role in shaping rhizosphere microbial communities and driving their succession. Microbial diversity indices (richness, phylogenetic diversity, Shannon, Peilou's evenness) were significantly reduced in rhizosphere soil as compared to bulk soil, possibly due to bacterial responses to root carbon inputs and root-induced changes in soil microbial niches. Network analyses revealed successively greater complexity of microbial interactions in rhizosphere microbial communities compared to those in bulk soil. Understanding the mechanisms by which roots influence the assembly of rhizosphere microbiomes may allow delineation of generalizations useful in modelling terrestrial carbon processes.