The effect of compost carbon cycling and the active soil microbiota

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**Abstract**

Rangelands cover an estimated 40-70% of global landmass, approximately one-third of the landmass of the United States and half of California. The soils of this vast land area have high carbon (C) storage capacity, which makes it an important target ecosystem for the mitigation of greenhouse gas emission and effects on climate change, in particular under land management techniques that favor increased C sequestration rates. While microbial communities are key players in the processes responsible for C storage and loss in soils, we have barely shed light on these highly complex processes in part due to the tremendous and seemingly intractable diversity of microbes, largely uncultured, that inhabit soil ecosystems.

In our study, we compare Mediterranean grassland soil plots that were amended with greenwaste compost in a single event 6 years ago. Subsampling of control and amended plots was performed in depth increments of 0-10 cm. We present data on greenhouse gas emissions and budgets of carbon, nitrogen, phosphorus, and micronutrients in dependence of compost amendment. Changes in the active members of the soil microbial community were assessed using a novel approach combining flow cytometry and 16S tag sequencing disclosing “who is active”. This is the first study revealing the nature of actively metabolizing microbial community members linked to the geochemical characteristics of compost-amended soil.

**Objectives**

- Distinguish the redox-active from the bulk microbial population
- Compare community structures between control and composted soil
- Identify major microbial taxonomic groups stimulated by a composting event

**Materials and Methods**

**Conclusions**

FACS helps reduce complexity of soil microbial communities

- Compost changes the microclimate in surface soil for years after the composting event
- Long-term effects on soil organic carbon content and microbial community structure and activity

Compost-treated plots generally cluster together:
- Community richness
- Dominant microbial groups

Metagenome sequencing will reveal functional potential of redox-active microbes

**Results**

Total: 177 genera

**References**


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