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Abstract for ASM 2012

Long Term Elevated Atmospheric Carbon Dioxide and Tropospheric Ozone Affect Soil Bacterial and Fungal Community Structure in an Aspen Plantation

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Ten years of elevated atmospheric carbon dioxide (eCO₂) has resulted in 30% increase in aspen tree growth at the aspen free air carbon dioxide enrichment (FACE) experiment. However, soil organic matter accrual has lagged behind the ambient treatment despite higher litter production under eCO₂ (Zak *et al.* 2011 Ecol Lett). This suggests that eCO₂ has accelerated the decay of plant detritus. Ozone fumigation of ozone-resistant aspen has been shown to have little additional effect on the eCO₂ response. We are investigating the impacts of these two treatments on soil bacterial and fungal community biomass and structure to explore the possibility that this response results from a shift in bacterial and fungal composition. Soil biomass, and bacterial abundance, and fungal abundance were unchanged in aspen soils after ten years of eCO₂, ozone or a combined treatment when compared to the ambient controls. Using Sanger and 454 pyrotag ribosomal RNA gene sequencing we found that bacterial and fungal community richness increased with eCO₂ across multiple OTU levels, but that beta-diversity was unchanged. The composition of the bacterial community structure was more similar among field replicates and between field treatments than the composition of the fungal community. Shotgun metagenomes (454 titanium) were used to compare the relative abundance of functional traits by binning into SEED categories, and to determine the representation of certain bacterial taxa. Although they were each very different in sequence composition, the metagenomes were very similar when sequences were binned into broad functional groups. One consistent trend across all datasets was the depletion of *Acidobacteria* Group 1 members in soils from the eCO₂ treatment. Collectively, these results suggest that the additional soil C under eCO₂ treatment allows more community members to occupy particular soil niches, resulting in an increase in community richness. The observed community compositional changes may be due to altered resources and competition against slower growing, oligotrophic bacteria typified by some members the *Acidobacteria* phylum.