

Poster #58

Coupling Changes in Soil Respiration and Nutrient Cycling with Community Structure and Function in Long-Term Soil Warming Experiments

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In a twenty-six year soil warming experiment in a mid-latitude hardwood forest, we documented changes in soil carbon cycling to investigate the potential consequences for the climate system. We show that soil warming results in a four-phase pattern of soil organic matter decay and carbon dioxide fluxes to the atmosphere, with phases of substantial loss of soil carbon alternating with phases of no detectable loss. Several factors combine to affect the timing and magnitude of soil carbon loss and thermal acclimation. These include depletion of microbially-accessible carbon pools, reductions in microbial biomass, a shift in microbial carbon use efficiency and changes in microbial community composition. Our results support projections of a long-term, self-reinforcing carbon feedback from mid-latitude forests to the climate system as the world warms.

To test changes in community composition and activity, DNA and RNA were extracted from soil samples taken from three soil warming experiments at Harvard Forest, including the 26-year experiment, and submitted to the Department of Energy's Joint Genome Institute (JGI) for phylotyping (16S rRNA and ITS), metagenomics, and metatranscriptomics. The population of most abundant bacteria in our warming plots has declined by fourfold, yet the bacteria biomass has remained unchanged as fungal biomass has declined. Different views of the soil community structure were observed between DNA and RNA samples. Eukaryotic sequences comprise ~30% of the mRNA sequences in the organic layer and are an order of magnitude more prevalent than in metagenomic samples. The metatranscriptomic sequencing results included a diverse representation of the soil organismal community including RNA viruses, archaea, bacteria, protists, fungi, invertebrates and plants, a view of a canonical soil food web illustration. Significant decreases were detected in viral, fungal and invertebrate clades, while several bacterial clades increased. The number of differentially abundant taxa and expressed genes increased over the three age-staggered long-term forest soil warming experiments, suggesting an ongoing change in community structure and ecosystem function. Cellular and ecosystem functions have been effected with respect to warming, including those related to protein stability, selfish genetic elements, toxin resistance, and biogeochemical cycling (C, N, P, S, Fe).

Continued changes in soil respiration and nutrient cycling coupled with progressive changes in soil community structure and function with long-term experimental warming suggest the effects of rising global temperatures are unlikely to be ephemeral and will produce complex ecological feedbacks.