The impact of precipitation and nitrogen deposition changes on the microbial community and greenhouse gas cycles of a Southern California grassland

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Project Goals: The overall project goal is to describe the impact of changes in precipitation regimes and nitrogen deposition levels, predicted by regional and global models for Southern California, on grassland leaf litter decomposition and associated microbial community. In this presentation we describe a piece of the project, the goals of which are to investigate the impact of these treatments on the structure and function surface soil microbial composition, with specific focus on greenhouse gas fluxes. Further, this project seeks to strengthen the connection between microbial community structure and function, and potentially enhance our understanding of the biospheric role in greenhouse gas cycles.

Fluctuations in greenhouse gas (GHG) concentrations in the atmosphere can lead to profound climatic and environmental changes. Likewise, environmental changes can influence variation in soil consumption and release of key greenhouse gases. Carbon dioxide (CO_2), methane (CH_4), and nitrous oxide (N_2O) are currently increasing in the atmosphere at high rates due to human activities. Accurately understanding natural and anthropogenic roles in ever-changing greenhouse gas cycles is necessary for a more complete understanding of biosphere-atmosphere interactions. It is only with this understanding that decisions can be made at local, national and international levels to mitigate potentially harmful climatic changes. This project examines the biological mechanisms behind the response and resilience of soil microbial communities to change. This is examined in both community composition as well as function, in terms of production and consumption of CH_4, CO_2 and N_2O, thereby enhancing our understanding of the biospheric role in greenhouse gas cycles.

Southern California provides an excellent natural laboratory for investigating the relationships between climate, plant composition, net primary production, soil microbial ecology, and ecosystem function. California's coastal climate is Mediterranean, with a mild wet winter, a warm or hot dry summer, and extreme inter-annual precipitation variation associated with ocean currents. Soil trace gas fluxes may be variable in this ecosystem due to this high climatic variability on seasonal and inter-annual scales, with intense pulses of precipitation and extensive drought. This region is likely to experience profound environmental change in the next 50 years, due to high densities of fossil fuel combustion, NOx emission, and nitrogen deposition (Fenn et al. 2003). Total nitrogen deposition is 2.5 to 4.0 gN $m^{-2}yr^{-1}$ in many regions of the San Gabriel and San Bernardino Mountains, and increasing (Fenn et al. 2003). Global Circulation Model (GCM) and Regional Climate Model (RCM) runs almost uniformly project significant warming in California (IPCC 2007), which can lead to increased drought conditions. Projections of future precipitation are less certain, with many GCMs projecting increased winter precipitation, and some models predicting a dramatic change (IPCC 2007). Hence the study of the impacts of increased N deposition within the context of both increased and decreased precipitation is relevant to understanding the response of this system to projected changes in this environment.

This experiment, performed at Loma Ridge in the Irvine Ranch Conservancy, manipulates N and

rainfall in a grassland community in a factorial combination of replicated plots. Nitrogen is added in fall and mid-spring as slow-release granular ammonium nitrate (osmocote) pellets at 6 gN m^{-2} yr^{-1}. This level of N addition in treatment plots is comparable to the higher levels of nitrogen deposition in the region (Fenn et al. 2003) and is similar to that used in other studies. The 50% precipitation increase and decrease treatments, which have been in place since 2007, are achieved by manipulating both the average size and number of storms (Hanson 2000), to simulate anticipated precipitation shifts. The experiment uses rainout shelters with clear polyethylene retractable roofs to remove ~50% of the annual precipitation from the low water plots by selective closure during a subset of the winter storms. The water draining off the shelters is collected with metal gutters and PVC pipe, stored and applied to increased precipitation plots.

Gas flux rates of N_2O, CH_4 and CO_2 have been measured across the start of the rainy season of 2011-2012. All gases are measured monthly using static vented chambers and gas chromatography. In addition, CO_2 is measured constantly using automated flow-through chambers. The initial data show some striking trends. As predicted, decreased rainfall is associated with lower ecosystem respiration across plots, but increased rainfall was also shown to coincide with lower respiration rates than controls. Increased N deposition was found to correlate with increase N_2O release, as expected. No trends have yet been observed in CH_4 flux, but both consumption and release have been observed in the site.

Concurrent with gas flux measurements, *in situ* soil moisture and temperature data are being collected. Soil cores are removed from each plot when gas flux measurements are performed. Cores are frozen immediately and returned to the lab where DNA and/or RNA are extracted. Pyrosequencing (454) analysis of the microbial community has been performed on a subset of samples using the same 16S primers and bioinformatics pipeline currently employed to examine litter microbial communities. The initial data from this subset of samples will be presented.

This research has only just started, with several molecular techniques to be employed later on on samples across time and treatments. Changes in the relative abundances the functional genes *pmoA* (for methanotrophy), *nirS*, *nirK* and *nosZ* (for denitrifiction), and *amoA* (for nitrifiction), along with associated mRNA activity, will be measured by qPCR and rt-qPCR, respectively. Also, samples of pooled replicate plots are being analyzed by a full meta-genomic Illumina sequencing protocol, with data forthcoming.

References:

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