AGU FALL MEETING
San Francisco | 14 – 18 December 2015

# B11J-0581: Microbial Community Responses to Glycine Addition in Kansas Prairie Soils

**Monday, 14 December 2015**
**08:00 - 12:20**
*Moscone South - Poster Hall*

Advances in sequencing technologies are rapidly expanding our abilities to unravel aspects of microbial community structure and function in complex systems like soil; however, characterizing the highly diverse communities is problematic, due primarily to challenges in data analysis. To tackle this problem, we aimed to constrain the microbial diversity in a soil by enriching for particular functional groups within a community through addition of “trigger substrates”. Such trigger substrates, characterized by low molecular weight, readily soluble and diffusible in soil solution, representative of soil organic matter derivatives, would also be rapidly degradable. A relatively small energy investment to maintain the cell in a state of metabolic alertness for such substrates would be a better evolutionary strategy and presumably select for a cohort of microorganisms with the energetics and cellular machinery for utilization and growth. We chose glycine, a free amino acid (AA) known to have short turnover times (in the range of hours) in soil. As such, AAs are a good source of nitrogen and easily degradable, and can serve as building blocks for microbial proteins and other biomass components. We hypothesized that the addition of glycine as a trigger substrate will decrease microbial diversity and evenness, as taxa capable of metabolizing it are enriched in relation to those that are not. We tested this hypothesis by incubating three Kansas native prairie soils with glycine for 24 hours at 21 degree Celsius, and measured community level responses by 16S rRNA gene sequencing, metagenomics, and metatranscriptomics. Preliminary evaluation of 16S rRNA gene sequences revealed minor changes in bacterial community composition in response to glycine addition. We will also present data on functional gene abundance and expression. The results of these analyses will be useful in designing sequencing strategies aimed at dissecting and deciphering complex microbial communities.

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