Geophysical Research Abstracts Vol. 19, EGU2017-1161, 2017 EGU General Assembly 2017 © Author(s) 2016. CC Attribution 3.0 License.



## Understanding soil health by capitalizing on long-term field studies

Ehsan Tavakkoli, Zhe Wang, Lukas VanZweieten, and Michael Rose NSW DPI, Wagga Wagga, Australia (ehsan.tavakkoli@dpi.nsw.gov.au)

Microbial biodiversity in Australian agricultural soils is of paramount importance as it plays a critical role in regulating soil health, plant productivity, and the cycling of carbon, nitrogen, and other nutrients. Agricultural practices strongly affect soil microbial communities by changing the physical and chemical characteristics of the soil in which microorganisms live, thereby affecting their abundance, diversity, and activity. Despite its importance, the specific responses of various microbial groups to changing environmental conditions (e.g. increased/decreased carbon in response to land management) in agricultural soils are not well understood. This knowledge gap is largely due to previous methodological limitations that, until recently, did not allow microbial diversity and functioning to be meaningfully investigated on large numbers of samples. We sampled soils from a field trial on the effect of strategic tillage in no-till systems to examine the potential impact of tillage and stubble management on soil microbial composition. To determine the relative abundance of bacteria and fungi, we used quantitative PCR (qPCR), and to analyze the composition and diversity of the bacterial and fungal communities, we used bar-coded high-throughput sequencing. Bioinformatics of the sequencing generated data was performed using a previously scripted and tested pipeline, and involved allocation of the relevant sequences to their samples of origin according to the bar-code. In parallel, changes in soil quality and microbial functionality were determined using multi-enzyme activity assay and multiple substrate-induced respiration. The extracellular enzyme activities that were measured include:  $\beta$ -1,4glucosidase,  $\beta$ -D-cellobiohydrolase,  $\beta$ -Xylosidase, and  $\alpha$ -1,4-glucosidase which are all relevant to the C cycle;  $\beta$ -1,4-N-acetylglucosaminidase and L-leucine aminopeptidase which are both relevant to the N cycle associated and associated with protein catabolism. In this presentation, analyses of soil health and functionality in relation to its response to various agronomic practices and implications for C sequestration and nutrient cycling will be discussed.