Effect of tillage and cover crops on the cotton rhizosphere

Thomas F. Ducey* and Phillip J. Bauer
Agricultural Research Service-USDA, Florence SC

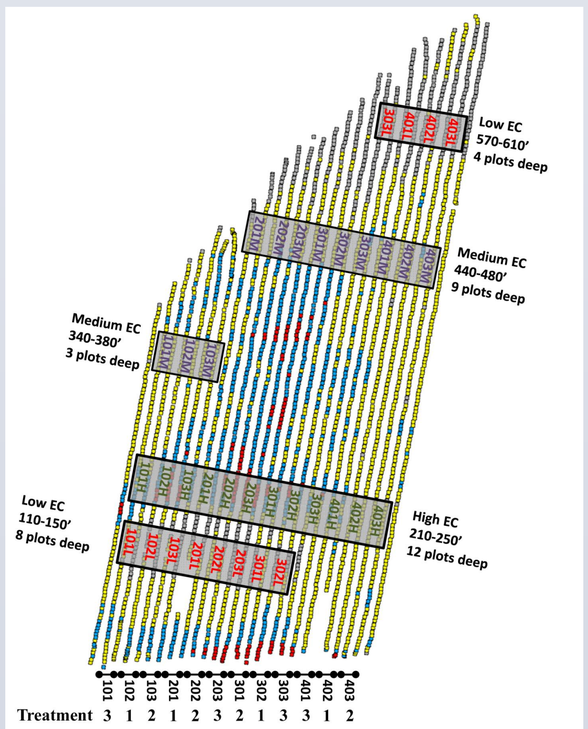
Background

Cover crops and conservation tillage management are frequently used to reduce erosion and improve soil physical, chemical, and biological properties. These management practices can also have significant impacts on soil microbial communities. Since these microbial communities (both bacterial and fungal) can both directly and indirectly provide plants with nutrients and water, understanding their response to agricultural manipulations may help us optimize management practices such that they spur microbial activity beneficial to cotton production. We report the response of the cotton rhizosphere to both tillage managements with or without winter cover crop additions. Soil enzymatic assays demonstrate an influence on microbial populations by both tillage and cover crop.

Methodology

This study has been conducted on two sets of plots located at the Clemson University Pee Dee Research Extension Center. The first totals twenty plots (see below), with 10 plots each under conservation or conventional tillage, and have been held under those management practices since 1978. Plots were planted with either corn (*Zea mays* L.) or cotton (*Gossypium hirsutum* L.), for five reps of each crop under each tillage practice. Crimson clover (*Trifolium incarnatum* L.) was introduced in the winter of 2014, in a split plot manner, with half the plot remaining fallow.

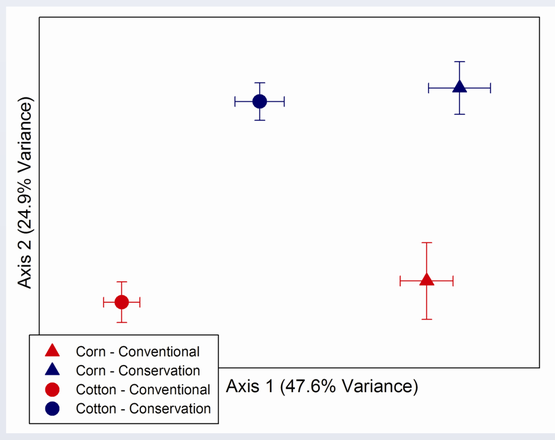
Given the long term, established nature of the first set of plots, a second set of plots (created in 2016) were placed on fields naïve to conservation tillage and cover cropping. The field was analyzed with a Veris Soil EC 3100 to provide an apparent soil conductivity (ECa) map (see right panel), and the field was partitioned into areas of high (> 1.5 dS m^{-1}), medium, and low (< 0.75 dS m^{-1}) ECa. Cover crops were planted in the winter of 2016, and bulk soil samples (0-2") were taken for fluorescent soil enzyme analysis in the Spring of 2017. Cover crops included a mixture of cereal rye (*Secale cereale*), crimson clover (*Trifolium incarnatum*), and radish (*Raphanus sativus*). Continued management will assess the "maturation" of the soils under both conservation tillage, and conservation tillage with cover crop management (as compared to a conventional tillage control).

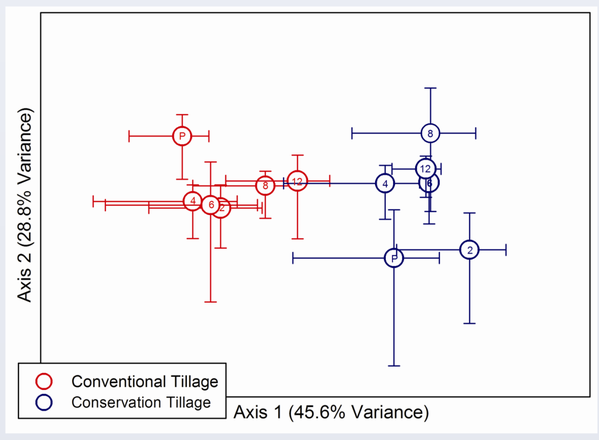


Soil samples were collected by uprooting three cotton plants in random positions within each plot, removing the above-ground biomass, and bagging the root system - complete with soil – on ice, and brought back to the lab. Bulk soil was shaken off of the roots, and the roots were washed twice with ddH_2O. Soil recovered from the washes was considered rhizosphere soil and used for downstream analysis. DNA was extracted from rhizosphere soil samples using a Zymo Research ZR Soil Microbe DNA Kit. Bacterial communities were "fingerprinted" and analyzed using terminal restriction fragment length polymorphism (T-RFLP). The 16S rRNA gene was amplified from soil DNA with primers (27F and 519R) and digested with AluI. Fragment analysis was performed on an ABI 3370 at the Cornell Institute of Technology's Biotechnology Resource Center (Ithaca, NY). For bulk soil analysis, a panel of enzymes – ß-1-4 glucosidase, ß-N-acetylglucose aminidase, acid phosphatase, and esterase were measured using a microtiter plate protocol and analyzed using a BioTek FLx800 fluorometer.

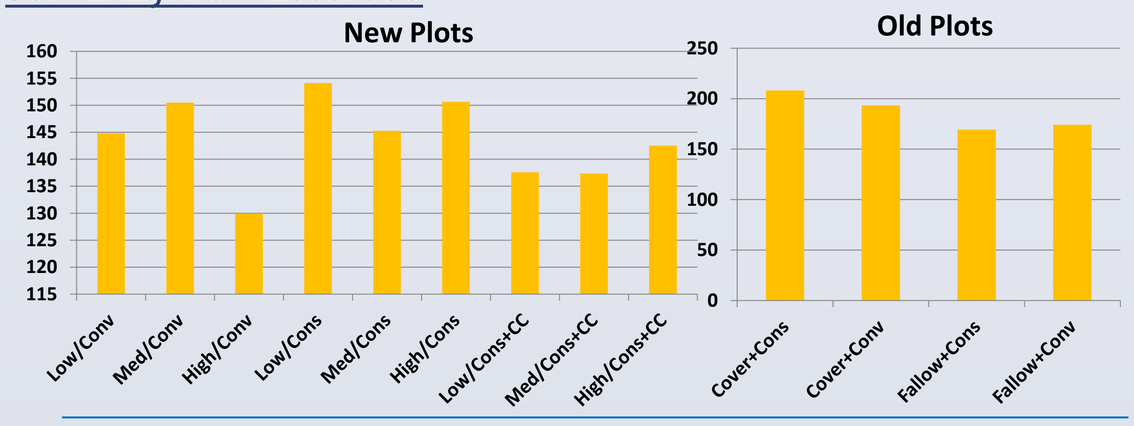
Results

Non-metric multidimensional scaling (NMS) ordination revealing significant differences between soil microbial populations, as determined by T-RFLP, under differing tillage practices and crop species (left panel). Right panel shows NMS ordination of cotton rhizosphere microbial communities. Designations inside circles indicate sampling time (pre-plant, 2, 4, 6, 8, or 12 weeks post emergence). Data points indicate significantly different soil microbial communities at all time points between the two tillage practices, as well as distinct rhizosphere communities by week 2 (conventional) and week 4 (conservation).

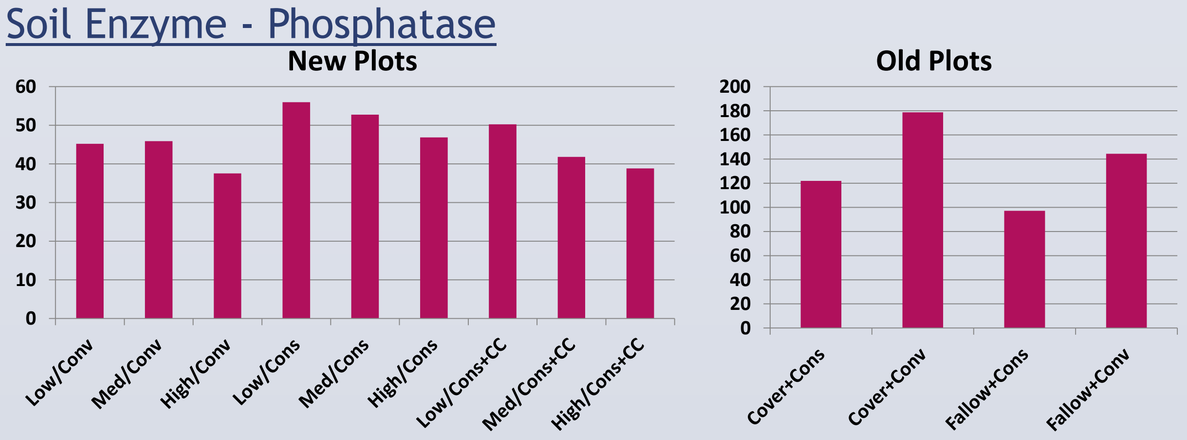




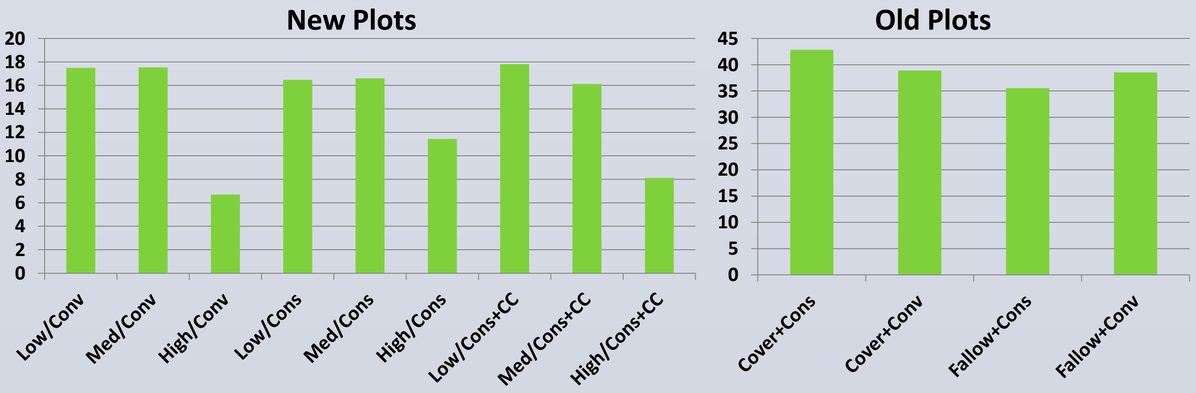
Soil Enzyme - Esterase



Soil Enzyme - Phosphatase



Soil Enzyme – ß-glucosidase



Conclusion

T-RFLP of soil microbial communities in the long term study plots demonstate distinct populations influenced by both tillage management and crop. "Maturation" of these communities during the growth stages of cotton are also different between the management practices. Soil enzyme patterns differed based on length of time between establishing treatment and sampling, management practice, and presence of cover crop. In a majority of all assays, high soil ECa correlated with lower enzyme activity.

Acknowledgements

The authors would like to thank Cotton Incorporated for funding that supported this project, as well as Hannah Rushmiller for her technical expertise.