

A road map to finding microbiomes that most contribute to plant and soil health

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ABSTRACT

The human eye does not have sufficient resolution to unravel the mysteries of soil and plant health. Corn is one of the major grains grown in Canada. The proposed maximum theoretical yield of corn is 450-500 bu/acre, but average growers are producing 150 bu/acre. The main aim of this study is to understand the factors associated with soil health and plant productivity beyond the cropping system and practices. We measure the aspects of soil physical, chemical properties and differences in microorganism communities will be related to yield responses collected from plants harvested from 40 diverse sites across Ontario using aerial infrared photography to identify sections of fields where plants appear healthy or stressed (as we discovered that when corn plants were randomly selected for testing, their microbiomes were quite similar). In this way, we hope to identify some of the primary reasons that confer the unevenness in crop yield seen across the same field when the same farm inputs had been applied. Such findings will be used to improve low production sites, thereby increasing overall yields significantly. Based on results from our previous studies we hypothesized that the difference in the plant productivity at different sites are due the abundance and diversity of microbial communities, and the impacts of their specific activities such as nitrogen fixation, phosphorous solubilisation, root growth promotion, and suppression of plant pathogens. The ratio of different soil chemical parameters affects microbial community richness and diversity in many ways. The study results will be integral in our understanding of the microbial community structures that influence crop productivity either negatively or positively. We expect to find out who are the key microorganisms and their roles in corn growth and productivity. Our initial analysis of data generated through TRFLP and next generation based sequencing of microbial communities showed, the endophytic microbial communities were distinct between low and high producing sites across most of the field sites tested. The high producing area had significantly higher bacterial richness and less diversity than the low producing area. Initial correlation analysis revealed potential positive interactions between the general fertility index, potassium to magnesium ratio, the gram negative and nitrogen fixer bacterial communities with yield and yield related parameters. Taken together, the corn sap bacterial community composition and richness was greatly influenced by soil chemical properties, which may indicate shifts in their functionality despite equal levels of total bacterial loads. The talk will identify factors associated with high and poor yielding sites and how this relates to soil and crop health.

INTRODUCTION

Microbiology studies for the most part have focused on the impacts of microorganisms as pathogens or for their use in industrial production of valuable commodities. Today however, the primary focus is on identifying their role in ecosystem health and ecology. The very significant reduction in the cost and speed for molecular tools and sequencing continues to significantly increase our abilities to examine whole microbial communities and to identify their potential functions. In agriculture sector, results from such studies have considerably improved our knowledge to comprehend plant-microbe interactions and have provided revolutionary information as to the role these microbiomes play in plants' health. The plant microbiome could potentially help its host by providing nutrients, producing phytohormones, synthesizing vitamins, detoxifying toxic compounds, stimulating plants' induced systemic resistance, and protecting them from a variety of biotic and abiotic stresses, etc.

The unravelling of the plant microbiome is changing agriculture practice and the concept of what is a "healthy plant". The agromicrobial revolution primarily focuses on the optimal use of

existing plants' microbial companion in order to improve plant performance and agricultural ecosystem functioning. Agricultural production systems must be examined from an ecological approach, with crop productivity being related to ecosystem services. Plant-associated microorganisms are fundamental for plant health and productivity as they affect plant nutrition, metabolism, physiology and performance. While the negative impacts of microorganisms on agroecosystem performance remains important, a greater focus on their beneficial impacts deserves closer attention. However, it must be emphasized that such benefits are going to be realized slowly. Here we provide three examples of how plant-microbe interactions have been utilized over millions of hectares and why it took decades for their utility to be realized. Suggestions that we can change agroecosystems overnight will only lead to disappointments in the research results.

The most well understood and exploited trait in the plant-microbial interaction catalogue is nitrogen fixation by *Rhizobium* species. The ability of *Rhizobia* to make atmospheric nitrogen available to plants and significantly increase their yields has been known for over 150 years. It has been estimated that nitrogen fixation by legumes

in natural ecosystems is in the range of 25-75 lb of nitrogen per acre per year whereas, in cropping systems it may be several hundred pounds per acre. Commercially available *Rhizobium* inocula have a nominal cost by comparison to their yield and environmental benefits. The nodules formed on legumes remains the only plant-microbial interaction that breeders recognize as being critical to the success of any new cultivar they aim to generate. While plant-microbe interactions of similar significance likely occur with many other crop species, the lack of any obvious phenotypic indicator likely could have resulted in the loss of genetic traits in the plants required for a successful outcome of the interaction with a designated partner. Who knows how many of such genetic functions have been deleted through the millennia of breeding processes? Studies of the interactions between Rhizobia and their hosts have revealed that there is an exchange of numerous chemical signals and this is a form of molecular dialogue. Hundreds of genes are likely involved in regulating the interactions of the two main groups of molecules that are required for a successful interaction. These are the nod gene-inducing flavonoids from the plant and the lipochito-oligosaccharide Nod factors from the Rhizobia. We have no idea of the traits that regulate microbial associations in corn, wheat, or rice in old or modern cultivars. The finding that Rhizobia can also form endophytic associations with rice and are able to colonize all the internal tissues of plant suggests that such interactions can have a major role in plant fitness and productivity. Surprisingly, the interactions proved to be strain and variety specific indicating that the growth responses are indeed heritable traits. Large-scale field trials evaluating five rice varieties and seven Rhizobia strains over five seasons showed that bacterial treatments increased yield by up to 47% in farmers' fields, with an average increase of 19.5%. This study exemplifies the critical importance for selection of appropriate isolates and specific crop cultivars for optimizing yield benefits. We need to appreciate the growers of the Nile Delta who had the wisdom to recognize that intercropping rice with legumes contributed to yield increases of their rice crop. However, it was the selection of this site for study by

the researchers that allowed them to discover that the build up of the selected Rhizobia populations provided the critical benefit to the agroecosystem functions in this area.

Conclusion:

A diverse group of fungi in the Basidiomycota, the Serendipitaceae encompasses endophytes and lineages that repeatedly evolved ericoid, orchid and ectomycorrhizal types. Accordingly, in many natural ecosystems these fungi form mycorrhizal symbioses with an astounding variety of host plants – every mycorrhizal type, in fact, except for arbuscular. Previous research performed in our lab with a strain of this group, *Serendipita vermifera*, demonstrated plant growth-promoting properties in a variety of plants. Unfortunately, the agronomic utility of these fungi is hampered by the paucity of strains available, the large majority isolated from Australian orchids. We have begun to address this constraint by isolating the first North American strain of *Serendipita*, named *Serendipita vermifera* subsp. *bescii* NFPB0129, from the roots of a switchgrass plant in Ardmore, Oklahoma. Soil-dwelling microorganisms are critical components of soil health, itself a determinant of plant productivity and stress tolerance. Deploying microbes to improve agriculture productivity is an extremely attractive approach that is non-transgenic and can be viewed collectively as the extended plant genome. Because these same microbes can contribute to restoring soil health and productivity, they have a bright future in low-input, sustainable agriculture that extends beyond more classically defined plant-microbe symbioses.