

# Forage Crops & Soil Microbes Promote Soil Health

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The United Nations General Assembly has declared 2015 the International Year of Soils (IYS 2015). IYS 2015 aims to increase awareness and understanding of the importance of soil for food security and essential ecosystem functions. Often taken for granted, soils are key to human civilization. Throughout history, civilizations have prospered or declined as a function of the availability and productivity of their soils.

Soil is composed of minerals, organic matter, gases, liquids, and living organisms that together support plant life. The number and diversity of organisms in soil is truly astounding. About a quarter of the diversity of life on earth resides in soil.

Microorganisms are most numerous with an estimated 100 billion bacteria in each cubic centimeter of soil. Until recently, the identification and study of most of these were out of reach because only a fraction could be grown in laboratory isolation. Development of inexpensive and high throughput DNA sequencing methods is opening the door to a greater understanding of the microorganisms that are a key component of soils. New research projects in the USDA-ARS-Plant Science Research Unit are focused on understanding the role of soil microbes in the rotation effect with the goal of enhancing and stabilizing the yield gains provided by crop rotation.

Although used for millennia, crop rotations are the “black box” of agronomic science. The response is measured but it is unknown how and why it occurs. Long-term replicated studies have demonstrated that growing corn after 2+ years of alfalfa increases corn grain yields by 5-15% over corn grown with the equivalent amount of nitrogen fertilizer that is provided by alfalfa.

Various studies suggest the rotation effect is due to beneficial soil microbe activity. Long-term studies in Wisconsin and Iowa assessed alfalfa/corn/soybean rotation effect on soil quality indicators. The most significant effect of the alfalfa component was on the amount of soil microbial carbon. Highest amounts were measured in soil with continuous alfalfa followed by the 5-year rotations including 2 years of alfalfa, and lowest amounts were in the corn/soybean rotation, continuous soybean, and continuous corn. In most cases the same trend was observed for soil aggregates. Total organic carbon was also highest in the 5-year rotation after alfalfa growth, but was also high in the corn/soybean rotation and third year corn. Thus, rotation with alfalfa increases microbial biomass and soil aggregation, which is not correlated with total soil organic matter. Microbes are a critical component of soil aggregates. However, their identity and roles in the process of soil aggregation are unknown. Better understanding of the soil aggregation process would allow management methods to be designed to maximize their effectiveness for improving soil structure and soil health.

Our goal is to identify microbes associated with alfalfa roots and how communities differ with location, soil fertility, and root system structure. In previous research, an alfalfa variety was developed with numerous fine roots and a variety with very few fine roots. Plants were grown at three sites with different levels of potassium and phosphorus fertility. Currently microbes associated with alfalfa roots under each condition are being identified.

To understand which organisms are present in soils and whether they contribute to plant fertility or disease, we are applying a technique known as ‘metagenomics’ involving the extraction and sequencing of soil DNA to determine which species are present and what functions they are capable of. While some initial investigations have concentrated on prairie grassland and forest soils, new focus has been applied to agroecosystems and effects of using different management practices. A recent study associated with the roots of different corn varieties revealed different corn genotypes harbor unique microbial assemblages, which in turn might augment plant health or disease resistance. This finding has sparked interest into which plant-microbe interactions are heritable and can be influenced by plant breeding.

Another advantage metagenomic techniques have over traditional assessments is the ability to screen for organisms that are difficult to grow outside of their native soil habitat. We will apply metagenomics to better understand which microbes contribute to disease resistance and soil fertility in association with alfalfa and other forage crops.



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