Molecular Analysis of Turfgrass Rhizosphere Bacterial Communities

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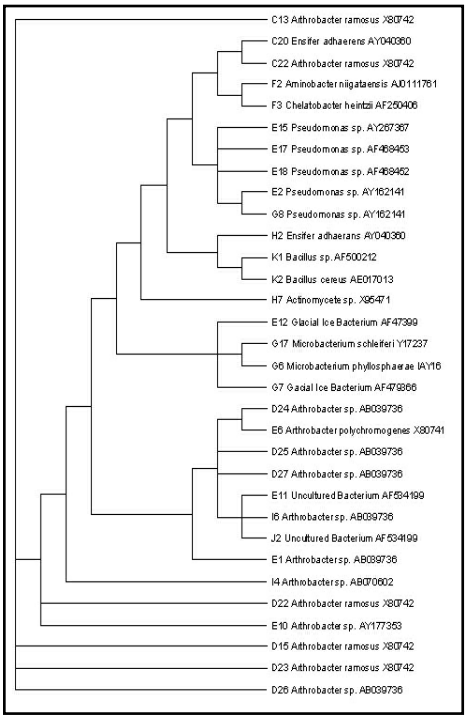
Objectives:

1. To determine the bacterial taxa associated with turfgrass soils in an attempt to correlate soil quality parameters with particular microbial taxa.

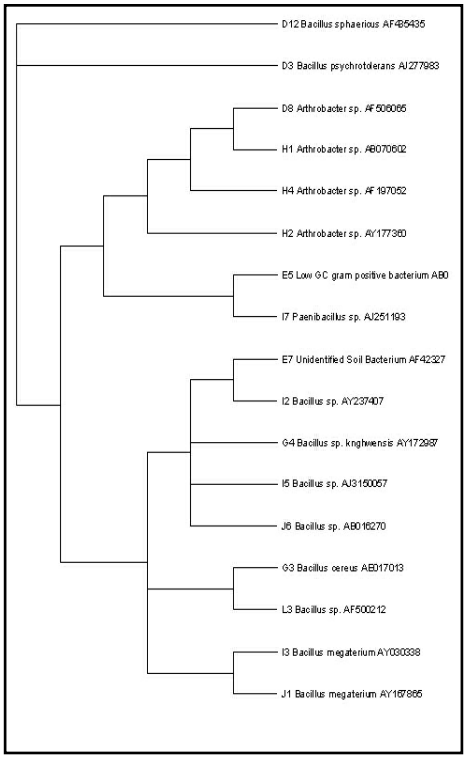
Start Date: 2001
Project Duration: three years
Total Funding: $90,000

Microbial characteristics of soils and plant rhizospheres are being viewed increasingly as sensitive indicators of soil health since there are clear beneficial relationships between microbial diversity, soil and plant quality, and ecosystem sustainability. In turfgrass management, soil health issues are becoming more important as golf course superintendents are forced to manage turfgrasses under less-than-ideal agronomic practices.

Research at Cornell University is combining traditional culturing methods with new molecular methods for characterizing microbial communities. An advantage of the combined approach is that many nonculturable microorganisms known to exist in all soils can now be studied. Some of these non-culturable microorganisms may have major impacts on soil quality and impacts on turfgrass quality.



Phylogenetic tree of aligned 16S rDNA sequences amplified from sand rootzones under L-93 bentgrass



Phylogenetic tree of aligned 16S rDNA sequences amplified from soil rootzones under L-93 bentgrass

The goal of this research is to understand which microorganisms inhabit turfgrass soils so that we can correlate soil quality parameters with specific microbial taxa. This work is following new molecular approaches for studying microbial communities. Such a strategy is being used widely in microbial ecology and revealing novel microorganisms and microbial associations with plants.

This work involves the extraction of microbial DNA from microbial cells in soil, the amplification of specific DNA sequences from this DNA that serve as signatures for particular microorganisms, and matching the signatures with known sequences that have been studied in the past. Our work is focusing on rhizosphere microbial communities inhabiting soil-based and sand-based rootzone profiles under L-93 creeping bentgrass.

Questions to be answered from this work are: 1) Do the bacterial communities from the two rootzones differ?, 2) Are their particular species that dominate in one root zone over the other?, 3) What proportion of species that we find in culture are present in rootzone microbial communities?, and 4) Can we infer functionality to groups of microorganisms recovered from each of the two rootzones?

So far, our work is revealing dramatic differences in the microbial communities associated with the two rootzone types. Furthermore, there are also significant and rather large differences between the organisms recovered by conventional dilution plating procedures and those obtained by direct DNA extractions. Many new and poorly described and uncultured species are being discovered in these turfgrass rootzones.

Summary Points

- Sequences obtained from direct DNA extractions reveal a different picture of the rhizosphere microbial community than do isolations on 0.1X TSA plates.
- Sand rootzones posses a different bacterial community than do soil rootzones. This is reflected in both the culturable strains, as well as the direct DNA extractions
- Many of the sequences from DNA directly extracted from soil and sand rootzones reveal a large number of unknown or previously undescribed species. This is commonly encountered in studies of soil microbial communities.
- A greater diversity of bacterial species appears to exist in sand rootzones than in soil rootzones. This has yet to be verified statistically, yet the tree topology indicates that those sequences from soil are more closely related than those from sand.
- Culturing biases samples in favor of *Bacillus*, *Arthrobacter*, and *Pseudomonas* species.