Do Management Regimes of Organically and Conventionally Managed Golf Course Soils Influence Microbial Communities and Relative Abundance of Important Turf Pathogens?

University of Massachusetts

Elisha Allan and Geunhwa Jung

We believe the preliminary results of our study show success in characterizing the nematode and microbe community among golf course management types and areas for the first time in turf. In addition to the broader results that we have reported, we have seen some species-specific differences in important turf pathogens as well as potential beneficial microbes. For example, Glomus sp., a common mycorrhizae fungus, was significantly more abundant on the conventional putting green than the organic putting green. Microdochium nivale, the causal agent of pink snow mold, was significantly more abundant on the organic course than the conventional or hybrid courses. However, the results of sequence based studies reporting species differences must always be analyzed with caution. It is possible to get false positive and negative results if the DNA sequences of closely related species are not present in the database. Additionally we were surprised to find that Sclerotinia homoeocarpa was not detected in any of our soil samples. Therefore, we conducted species-specific qPCR for this pathogen on samples from the soil and thatch of the courses taken in the Spring and Fall of 2014. We found that there was highly significantly more S. homoeocarpa in the thatch (mean 3.00 pg/µl) than in the soil (mean 0.02 pg/ul, not detected in 36 of 54 samples) and no significant differences in the abundance of this pathogen among courses. We are preparing the manuscript of these results to be submitted to the journal Plant Disease later this month.

The purpose of our project extension was to complete the originally proposed sequencing replicates. Our current funds will allow us to replicate the pyrosequencing once. Any extension funds will allow us to pyrosequence the fall of 2013 and 2014 samples. This additional data will allow us to 1) determine if there is any seasonal variation between spring and fall for microbes, which we hypothesize there will be, and could have implications for timing future management strategies and 2) having two replicates for each season will allow us to verify that our results are consistent over time. The need for the additional funds was due to an increase in pyrosequencing cost since the original proposal and a miscommunication with our collaborator on the cost of one of the sequencing reagents. We are currently sequencing the Spring 2013 samples and will report the results when possible.