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100. Molecular detection and quantification of disease suppressive microbial inoculants and *Pythium ultimum* in soil-less potting mixes. Pasura, A. and Elliott, G. C. *Phytopathology* 97(7)Suppl:S90. 2007.

surface. Experimental plots were established to monitor the response of nitrogen fixing bacterial populations to different turf-grass management systems. Tall Fescue was planted directly into topsoil (T), subsoil (S), or compost amended treatments of each (TC and SC, respectively). After the establishment of the turf-grass, nitrogen fertilizers were added at 0, 2 or 4 lbs N per 1000ft². Prior to seeding, the abundance of nifH genes detected by quantitative PCR was significantly greater in both topsoil-containing treatments (T and TC) than in the two subsoils. ($P < 0.060$). After growing turf-grass for three months, nifH copy number was significantly higher in TC and SC soils ($P < 0.001$) indicating positive influence of compost amendment on nitrogen fixing bacteria in both top and sub soils. Preliminary analysis of nifH sequences obtained from the initial sampling using LIBSHUFF indicated that the population structure of nitrogen-fixing bacteria may differ in the topsoil and subsoil ($P = 0.146$). Thus, quantitative PCR and preliminary diversity study of nifH indicated potentially unique nitrogen fixing bacterial group in the subsoil. Impact of additional nitrogen fertilizer input and changes in nitrogen fixing bacterial community over time will be further studied.

Protein profile changes in soybean leaves upon *Phakopsora pachyrhizi* infection

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Soybean rust, caused by *Phakopsora pachyrhizi*, originally occurred in eastern Asia. It now has spread to South America and the Continental United States. Sixteen states have reported soybean rust disease on soybean or kudzu in 2006. This disease has the potential to cause severe economic losses to the U. S. soybean growers, especially in the South, where the environmental conditions are more conducive to the disease. No commercial varieties are resistant to this disease. Many countries such as Brazil are relying solely on the costly fungicide applications to control the soybean rust. As a first step toward the development of resistant soybean varieties, we investigated the host-fungus interactions between soybean and *Phakopsora pachyrhizi* during the infection. Soybean leaf protein profiles from inoculated and non-inoculated soybean plants were compared using proteomics. The levels of protein expression between control and inoculated leaves were compared using Progenesis software. Six down-regulated and 4 up-regulated proteins were identified and then sequenced using LC-MS/MS. The resulting MS spectrums and peptide sequences are being compared to those in the NCBI, Swiss-Prot, and EST databases to identify their homologies.

A re-evaluation of phylogenetic relationships between the causal agents of carrot black rot, *A. radicina* and *A. carotiincultae*

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Phylogenetic relationship between *A. radicina* ($n = 20$) and *A. carotiincultae* ($n = 10$) were re-evaluated based upon morphology, sequence analysis of rDNA [ITS and mitochondrial small subunit (mtSSU)], protein coding genes [calmodulin, actin, beta-tubulin, chitin synthase, translation elongation factor (EF-1a), Alt a1, glyceraldehyde-3-phosphate dehydrogenase (gpd)], and RAPD and ISSR analysis of total genomic DNA. Although some morphological characters overlapped to a limited degree, with *A. radicina* isolates expressing moderate variation and *A. carotiincultae* isolates being highly uniform, *A. carotiincultae* could be statistically differentiated from *A. radicina* on the basis of average number of transverse septa per conidium. Sequences of rDNA and most protein coding genes were invariant between species. However, polymorphisms with the EF-1a and Alt a1 genes strictly separated the populations of *A. radicina* and *A. carotiincultae* as separate lineages, as did RAPD and ISSR analysis. The polymorphic gpd gene did not strictly separate the two species. However, isolates of *A. radicina* encompassed several haplotypes, one of which was the exclusive haplotype possessed by *A. carotiincultae* isolates, suggesting evidence of lineage sorting. These results suggest that the two species are closely related with *A. carotiincultae* a recent distinct lineage and separate species.

Long term effects of weed management practices and cover cropping on the culturable bacteria community in a commercial vineyard in Salinas Valley, California

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Little is known about the effect vineyard floor management practices have on culturable bacteria population in the berm or row middles. This investigation was undertaken to examine how soil-borne bacterial communities in vineyards are influenced by long term weed management and cover crop practices, and to determine the impact of row middle management on bacteria populations in

the berm. Six years after the establishment of weed management strategies in row middles (cultivation, pre-emergence herbicide, post-emergence herbicide) and cover crop treatments (rye and bare) in a conventionally managed vineyard, bacteria populations were examined. Bacteria were enumerated by serial dilution and plating of bulk soil from row middles, and rhizosphere soil/roots from berm samples on 10% trypticase soy broth agar (TSBA) and R2A. Sampling was conducted at three phenological crop stages, early berry formation, harvest, and dormancy. Row middle samples, despite lacking the influence of grapevine roots and irrigation, contained significantly greater ($P < 0.001$) culturable bacterial populations than the berm where roots and moisture are abundant. Furthermore, weed management practices had a significant effect on culturable bacteria populations with pre-emergent weed treatment having a significantly ($P < 0.01$) higher population than mechanical weed treatment when enumerated on TSBA.

Large-scale surveys for multiple pest species; the search for citrus canker and Huanglongbing in Florida

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The Florida citrus industry has faced a considerable challenge in recent years from the invasion of two economically destructive plant pathogens, Asiatic citrus canker (ACC) and Huanglongbing (HLB). ACC is well established across the state, and HLB, first discovered in 2005, is now common in citrus growing areas in the south. Obtaining updated information on the distribution of these diseases is critical for effective disease management. For this purpose a multi-pest survey program was recently initiated whereby survey teams inspect commercial plantings across the state for both diseases. A random weighted sampling protocol was designed to refine the survey effort for known biases. Information was collated on the host cultivar/species composition of every commercial plantation in the state and a software routine was written to perform a stratified random sample weighted toward more susceptible plantations. The surveys are performed in approximately 3 month cycles with up to 25% of the 750ha commercial citrus area in Florida surveyed each time. Similar surveys are planned for California and Texas. Data collection on this scale draws up many challenges (e.g. logistical and data management issues) but also presents many opportunities including improved understanding of epidemic development over geographic scales and the opportunity to validate simulation models.

Molecular detection and quantification of disease suppressive microbial inoculants and *Pythium ultimum* in soil-less potting mixes

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Microbial inoculants (MI) products are commercially available for management of soilborne pathogens in greenhouse crops. However, MI have not been consistently effective in reducing disease incidence in replicated greenhouse trials. This might be due to inadequate active populations of MI or overwhelming populations of pathogens in the rhizosphere. Traditional quantifying methods of both MI and pathogens use plate count on selective media. With some microbes, such culture-dependent methods yield high variability and have not proven useful in our trials. Strain-specific primers for detection of *S. lydicus* WYEC108 and species-specific primers for detection of *B. subtilis*, *T. harzianum*, and *Pythium ultimum* were designed for real-time polymerase reaction. Specificity of each primer set was confirmed by melting curves. Standard curves were generated for each of the species using SYBR Green dye for detection of amplification cycles. DNA was extracted from soil-less potting mixes (SPM) and standard curves were generated for each MI and for *P. ultimum* to correlate populations of each species in the SPM with quantities of DNA amplified from the same SPM. This molecular technique for quantification of MI and *P. ultimum* overcomes the limitation of culture-dependent methods and has been successfully tested in SPM with widely different components. The method allows rapid and accurate quantitative detection in studies of population dynamics of both MI and *P. ultimum* in SPM.

Relative efficacy of triazole-based fungicides for Fusarium head blight and deoxynivalenol control in wheat

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Fungicide efficacy against Fusarium head blight and deoxynivalenol (DON) in wheat has been highly inconsistent. Of the classes of fungicides most