present on associated plants; The enormous biomass, mainly made up of 217 neutral arthropods for R idaeus, is composed of indirect auxiliairies because they act as additional food to the 8 direct auxiliairies; 13 associated plants contribute to maintaining the auxiliary populations.

Influence of *Maize mosaic virus* on the fitness and wing morphology of *Peregrinus maidis* (Hemiptera: Delphacidae)
C. H. HIGASHI (1), A. Bressan (1)
(1) University of Hawaii, Honolulu, HI, U.S.A.
Phytopathology 101:S72

Maize mosaic virus (MMV; Rhabdoviridae) is a corn virus transmitted propagatively by the corn planthopper, *Peregrinus maidis* (Hemiptera: Delphacidae). We examined the fitness of *P. maidis* developing on MMV-infected or healthy corn leaves; however, our results showed no significant differences in mean developmental time, mean fecundity, and mean longevity. Delphacid planthoppers can differentiate wing dimorphic forms called either macropters (long wing forms) or brachypters (short wing forms). Since the abundance of these forms may vary in response to the physiological status of the host plant, we examined the effect of MMV on the wing morphology of *P. maidis*. Our results showed that planthoppers that developed on young (21–28 days old) infected plants produced 17% more of brachypters than planthoppers that developed on healthy plants of the same age. Conversely, planthoppers that developed on old (42–49 days old) infected plants produced 16% more of macropters than planthoppers that developed on healthy plants of the same age. Our results suggest that MMV infection may modulate the density and dispersal of planthoppers according to the stage of plant infection. At early stage, the virus may increase the vector population by producing more brachypters; however, at late stages of plant infection the virus may promote vector dispersal by triggering larger production of macropters.

Nuclear magnetic resonance for non-destructive imaging of belowground damage caused by *Heterodera schachtii* and *Rhizoctonia solani* on sugar beet
C. Hillnhütter (1), R. SIKORA (1), E. Oerke (1), D. van Dusschoten (2)
(1) Institute of Crop Science and Resource Conservation (INRES), Bonn, GERMANY; (2) ICG-3: Phytosphere, Jülich, GERMANY
Phytopathology 101:S72

Belowground symptoms of sugar beet caused by the beet cyst nematode (BCN) *Heterodera schachtii* include the development of compensatory secondary roots and beet deformity that can be assessed only following destructive removal of entire root systems from the soil. Infections by the soil-borne basidiomycete *Rhizoctonia solani* cause brown or black decay on beet and roots (*Rhizoctonia* crown and root rot, RCRR). Nuclear magnetic resonance imaging was applied for the detection of belowground symptoms caused by BCN and/or RCRR on sugar beet. Excessive lateral root development and beet deformation of plants infected by BCN was obvious 28 days after inoculation (dai) on resonance images when compared to non-infected plants. Three dimensional resonance images recorded 56 dai gave insight on BCN cysts attached to the roots in the soil. *Rhizoctonia* crown and root rot was visualized by lower intensity of the NMR signal at sites where rotting occurred. The disease complex of both organisms together resulted in RCRR development on the site of nematode penetration. Analysis of damage of sugar beet plants indicated to synergistic activity of both pathogens in combination which may result from direct and indirect interactions. Nuclear magnetic resonance imaging of plants can give new insights into the development of pathogens infecting belowground (and aboveground) plant parts because of the non-destructive nature and high spatial resolution of the method and may be also valuable in plant breeding.

Effect of soil-incorporated cover crops and Actinovate biocontrol on suppression of Fusarium wilt of watermelon
J. HIMMELSTEIN (1), K. Everts (2), J. Maul (3)
(1) University of Maryland, College Park, MD, U.S.A.; (2) University of Maryland, College Park and University of Delaware, Salisbury, DE, U.S.A.; (3) Sustainable Agriculture Systems Lab. USDA-ARS, Beltsville, MD, U.S.A.
Phytopathology 101:S72

Fusarium wilt, caused by *Fusarium oxysporum* f. sp. *niveum* (FON) has resurfaced as an economically important watermelon disease due to the loss of the use of methyl bromide fumigant, and the increase in production of triploid cultivars that lack resistance. Cover crops and biocontrol products have shown promise in reducing Fusarium wilt. For example the soil-incorporated cover crop *Vicia villosa* has suppressed Fusarium wilt of watermelon, but the mechanism of suppression is not known. We measured soil respiration following incorporation of a *V. villosa* cover crop to determine if it conferred general suppression. We also evaluated cover crops *V. villosa*, *Trifolium incarnatum*, *Secale cereale*, and *Brassica juncea*, and no cover, alone and in combination with Actinovate biocontrol (*Streptomyces lydicus*) for induction of suppression. In 2009 Actinovate significantly increased marketable fruit yield in plots inoculated with FON compared to plots without Actinovate, or plots with no inoculation; however in 2010 this effect was not seen. Fusarium wilt incidence was not significantly different among treatments in 2009 or 2010. Measurements in both years indicated that incorporation of *T. incarnatum* residue significantly increased the rate of soil respiration at the beginning of the field season compared to *V. villosa* and other cover crops. Because wilt suppression has been reported for *V. villosa* but not *T. incarnatum*, this may imply that disease suppression is not general.

The identification and characterization of genes involved in foliar infection of maize by *Cercospora zeae-maydis*
R. L. HIRSCH (1), B. H. Bluhm (1)
(1) University of Arkansas, Fayetteville, AR, U.S.A.
Phytopathology 101:S72

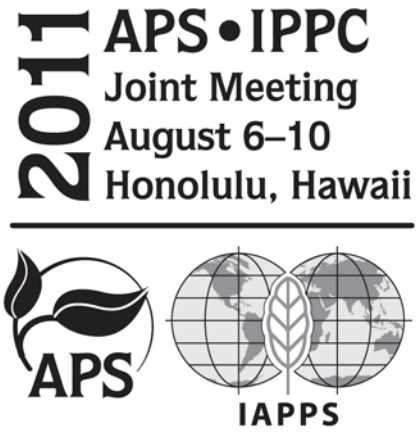
Gray leaf spot, caused by *Cercospora zeae-maydis*, is one of the world's most devastating foliar diseases of maize. Despite the impact of this disease, little is known about the interaction between *C. zeae-maydis* and maize at the molecular level. The recent discovery and characterization of *CRP1*, a putative ortholog of the White collar-1 family of fungal blue-light photoreceptors, established a linkage between the perception of light and the infection of the pathogen through stomata. To further dissect pathogenesis at the molecular level, laser-capture microdissection is being utilized to isolate fungal tissue during infection, specifically hyphae approaching stomata, nascent appressoria, and mature appressoria. From these samples, the transcriptome of the pathogen is being obtained with next-generation sequencing technologies (RNA-seq) and analyzed to identify genes associated with specific stages of the infection process, such as stomatal tropism and appressorium formation. Candidate genes will be disrupted through targeted mutagenesis to determine their specific roles in pathogenesis. Regulatory genes characterized in this study will further elucidate the genetic mechanisms underlying foliar infection in *C. zeae-maydis* and related filamentous fungi.

Incursion of Myrtle rust in Australia caused by *Uredo rangelii*
M. HIRSCH (1)
(1) Australian Government, Canberra, AUSTRALIA
Phytopathology 101:S72

On April 25 2010 a new rust of Myrtaceae was detected in a nursery on the central east coast of New South Wales, Australia. The pathogen was subsequently identified as *Uredo rangelii* belonging to the 'guava rust complex'. Given the wide host range of pathogens in this complex and the large number of Eucalyptus and other native Myrtaceae in Australia, an extensive campaign was established to slow down the spread of the disease. However, it has been found on many properties and in the bush in NSW and Queensland to the point that it is now not technically feasible to maintain this campaign. Governments and industry are now in the process of transitioning to long term disease management to mitigate the impact on the natural environment, including endangered species and industries that rely on Myrtaceae. The knowledge of this disease and its potential impact in Australia is very limited. Taxonomic studies are underway to determine the exact relationship of this pathogen within the guava rust comples. It has now been identified on 55 species of Myrtaceae but further seedling testing suggest that most Myrtaceae might be susceptible to the disease although there are some indications of useful sources of host plant resistance. Other studies focus on modelling environmental impact based on current data. We are seeking international science collaborations to broaden our understanding of the ecology and behavior of this disease relative to other members of the guava rust complex.

Biocontrol of bacterial wilt of tobacco via induced resistance by endophytic bacteria
H. HOANG (1), N. Furuya (1), M. Takeshita (1), K. Tsuchiya (1)
(1) Kyushu University, Fukuoka, JAPAN
Phytopathology 101:S72

Plant growth-promoting endophytic bacteria, *Pseudomonas* spp., significantly reduced the disease incidence and severity of bacterial wilt of tobacco caused by *Ralstonia solanacearum*. By means of real-time quantitative polymerase chain reaction (qPCR) using specific primers targeted 16S rDNA region of *Pseudomonas* spp., the bacterial population in tobacco plants was quantified. *Pseudomonas* spp. colonized the plant root up to 10^6 cfu per gram fresh weight. Real-time quantitative reverse transcription-PCR (qRT-PCR) analysis on the expression of defense-regulatory genes *Coi1*, *NPR1* and *EREBPs* and on the down-stream defense genes *PR1* (*PR-1a* and *PR-1b*) and *PDF1.2* in the tobacco leaves was carried out to determine the nature of the resistance induced by *Pseudomonas* spp. The expression of *PR1* gene, related to the salicylic acid (SA) dependent pathway, was highly up-regulated in the leaves after dipping the roots in the suspension of *Pseudomonas* spp. at the concentration of 10^8 cfu per ml for 24 h. However, no significant change in the expression of the *PDF1.2* gene, related to the SA independent pathway



2011 APS-IPPC Joint Meeting
Abstracts of Presentations

Abstracts submitted for presentation at the APS-IPPC 2011 Joint Meeting in Honolulu, Hawaii, August 6–10, 2011 (including abstracts submitted for presentation at the 2011 APS Pacific Division Meeting). The abstracts are arranged alphabetically by the first author's name.

Prioritizing cover crops for improving root health and yield of vegetables in the Northeast

G. S. ABAWI (1), C. H. Petzoldt (1), B. K. Gugino (2), J. A. LaMondia (3)
(1) Cornell University, Geneva, NY, U.S.A.; (2) The Pennsylvania State University, University Park, PA, U.S.A.; (3) CT Agric. Exp. Station, Windsor, CT, U.S.A.
Phytopathology 101:S1

Cover crops are used increasingly by growers to improve soil quality, prevent erosion, increase organic matter, and suppress root pathogens and pests. However, limited information is available on their use for suppressing pathogens (Rhizoctonia, Pythium, Fusarium, Thieloviopsis, Pratylenchus, and Meloidogyne) of vegetables grown in the Northeast. Thus, a collaborative project was initiated in 2009 to assess the efficacy of selected cover crops in suppressing root pathogens of vegetables and improving soil health in research and on-farm field trials in New York, Pennsylvania and Connecticut. In NY, strips (4.5 X 60 M) of 9 cover crops (rye grain + hairy vetch, oat, sudex, forage radish, red clover, rapeseed, buchwheat, wheat, and a fallow check) were randomized in 4 fields with 3 replications (3.2 ha total). The fields had different management histories resulting in varied levels of pathogen pressure and soil quality. In 2010, cover crop biomass was measured and collected soil samples were assessed for root health (greenhouse bean bioassay), nematode diversity and density, and selected soil health parameters (Cornell Soil Health Test). In general, root rot severity was lowest and yield of snap bean was highest in the field with the highest soil quality. After one year, the cover crops greatly affected root health and bean yield in this trial as well as the microplots and/or on-farm trials conducted in CT and PA. Another cycle of evaluations is in progress.

Reduction of aflatoxins, cyclopiazonic acid and fumonisins in corn by biocontrol strains of non-aflatoxigenic *Aspergillus flavus*

H. ABBAS (1), B. Horn (2), M. Weaver (3), X. Jin (3), C. Abel (4), W. T. Shier (5)
(1) USDA ARS CG & PRU, Stoneville, MS, U.S.A.; (2) National Peanut Research Laboratory, USDA, ARS, Dawson, GA, U.S.A.; (3) USDA ARS, Biological Control of Pests Research Unit, Stoneville, MS, U.S.A.; (4) USDA-ARS Corn Insects and Crop Genetics Research Unit, Ames, IA, U.S.A.; (5) Department of Medicinal Chemistry, University of Minnesota, Minneapolis, MN, U.S.A.
Phytopathology 101:S1

Non-aflatoxigenic biocontrol strains of Aspergillus flavus were examined for ability to reduce, production in corn of aflatoxins and cyclopiazonic acid (CPA) by A. flavus and fumonisins (FBs) by Fusarium verticillioides. The ability of non-aflatoxigenic strains to prevent aflatoxin production by subsequent challenge with toxigenic A. flavus strains was assessed in 4 experiments. Non-aflatoxigenic strain K49 effectively prevented toxin production at various inoculation levels in 3 experiments. K49 also was evaluated alongside the widely used biocontrol strains NRRL 21882 (Afla-Guard®) and AF36 for prevention of aflatoxin and CPA production by strains K54 and F3W4. K49 and NRRL 21882 were superior to AF36 in reducing aflatoxins. K49 and NRRL 21882 produced no CPA, and reduced CPA and aflatoxin production in a subsequent challenge with F3W4 and K54 by 84–97% and 83–98%, respectively. In contrast, AF36 inoculation and subsequent challenge with F3W4 reduced aflatoxins by 20% and 93% with K54, but showed no CPA reduction with F3W4 and only 62% CPA reduction with K54. Because AF36 produces CPA, high CPA accumulated in corn with AF36 alone. Pin-bar wounding and pin-bar inoculation with F. verticillioides NS-2 resulted in FBs levels of 253 and 1087 ppm, respectively. Inoculation with K49 alone or a mixture of K49 and NS-2 reduced FBs level to 0.1 and 27 ppm, respectively. AF36 and NRRL 21882 showed similar FBs reduction trends to K49. NRRL 21882 and K49 are effective in reducing aflatoxins, CPA and FBs in corn.

Managing potato scab and enhancing tuber yield with low rates of fish emulsion applied as a pre-plant soil amendment

P. A. ABBASI (1)
(1) Agriculture & Agri-Food Canada, London, Ontario, CANADA
Phytopathology 101:S1

Fish emulsion (FE) is an excellent organic soil amendment to enrich soil microbes and generate disease suppressive conditions against soil-borne diseases such as seedling damping-off, potato scab, and verticillium wilt. However, the rates (20,000 L/ha) of FE that provided effective control of potato scab can be too costly for commercial use. The aim of this 3-year field study was to see if much lower rates of FE could suppress potato scab and increase tuber yield. Diluted FE (1000 and 2000 L/ha or 0.05 and 0.1%) was applied to the field plots twice a year before planting and after harvesting potatoes starting in fall of 2007. The high rate of FE (2000 L/ha) consistently reduced scab severity by 42% in 2008, 57% in 2009, and 44% in 2010; reduced the percentage of tubers with deep-pitted scab by 30% in 2008, 51% in 2009, and 66% in 2010; and increased the percentage of marketable tubers by 21% in 2008, 55% in 2009, and 12% in 2010. Both rates of FE increased total tuber yield by 16–19% in 2008, 14–20% in 2009, and 7–11% in 2010. FE soil amendment enhanced the numbers of soil bacteria including those of potential bio-control agents belonging to the genera *Pseudomonas* and *Bacillus*. These results suggest that economically feasible rates of FE applied more frequently can provide disease suppression and enhance tuber yield. Next step is to monitor the lasting impact of these disease suppressive conditions on continuous potatoes without any further FE application.