

protein, were also located near the biomarkers included that may be involved in papaya tolerance to *P. palmivora*. This study highlights specific functional R genes' and resistance related genes' segregation reflected by *P. palmivora*-resistance related AFLP markers were dominated those candidates pathogen resistance genes from tens/hundreds others members in the gene families.

Radar observations of the migration of *Nilaparvata lugens* S. (Delphacidae) in southern China

C. JIANG (1), D. Cheng (1)

(1) State Key Laboratory of Biology of Plant Diseases and Insect Pests, Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing, PRC PEOPLES REP OF CHINA
Phytopathology 101:S83

The brown planthopper, *Nilaparvata lugens* S., is one of the most serious pests of rice in both temperate and tropical regions of east and south Asia. It cannot overwinter in China. The migration regularity and flight behavior of *N. lugens* were studied by using an 8.8 mm wavelength scanning entomological radar, a searchlight trap and a ground light-trap, field cages, systematic field survey and dissection of female ovarian in 2007 and 2009. *N. lugens* took off at dusk and dawn. The dusk take-off with area density peaking 45 mins later can last 1 h, while the dawn take-off can last 30 mins. After mass take-off, *N. lugens* climbed up high altitude rapidly. In spring and autumn the flight altitude can reach 2200 and 1800 m respectively. *N. lugens* formed 3 dense layers which were at heights of 400 to 700 m, 700 to 1000 m and 1100 to 1700 m in spring and 300 to 500 m, 600 to 700 m and 900 to 1100 m in autumn. The thickness of autumn layer was thinner than spring layer. Wind shear was the main reason causing *N. lugens* forming dense layer, while heavy rainfall caused mass descent. Collective orientations of *N. lugens* with the typical "dumbbell" echo often at the height of 800 to 1200 m on the PPI were observed in the autumn migration. The orientation direction was $159.4 \pm 15.14^\circ$ with an acute angle $53.4 \pm 13.74^\circ$ to the wind direction.

Mycoviruses that infect plant pathogen *Sclerotinia sclerotiorum*

D. JIANG (1), X. Yu (1), H. Liu (1), B. Li (1), J. Xie (1), R. Liu (1), L. Liu (1), X. Sun (1), J. Xie (1), J. Cheng (1), Y. Fu (1), G. Li (1)

(1) Huzhang Agricultural University, Wuhan, PRC PEOPLES REP OF CHINA
Phytopathology 101:S83

Sclerotinia sclerotiorum is a ubiquitous inhabitant of soil in many parts of the world. The potential of hypovirus for biological control of chestnut blight (*Cryphonectria parasitica*) has attracted much interest, and led to discovery of new hypovirulent strains in other fungi. In our lab, five mycoviruses were characterized from *S. sclerotiorum*. A ssDNA virus, named as SsHADV-1, isolated from debilitated strain DT-8, is phylogenetically related to plant geminiviruses. This DNA virus could protect plants against infection of *S. sclerotiorum*. Two ss (+) RNA viruses, namely SsDRV and SsRV-L, co-infect debilitated strain Ep-IPN. SsDRV is associated with the debilitation. SsRV-L belong to Rubi-like subfamily, and relates to Hepatitis E virus phylogenetically, while SsDRV relates to plant Potexvirus. These two viruses have only one ORF, coding for RNA replicase. Two dsRNA mycoviruses, namely totivirus-like virus SsTV-L and partitivirus SsPV-S, co-infect strain Sunf-M which shows normal phenotypes. Surprisingly, SsPV-S CP has the highest similarity to ILR2 of *Arabidopsis thaliana*, thus, there was a gene horizontal transfer between SsPV-S like virus and ancestor of *A. thaliana*. Following this clue, we found that the horizontal gene transfer between dsRNA viruses and eukaryotes were common. Besides the five characterized viruses, 19 new viruses were identified from other *S. sclerotiorum* strains, suggesting that there is a rich diversity of mycoviruses in *S. sclerotiorum*.

Phylogenetic relationships among *Verticillium dahliae* vegetative compatibility groups based on IGS and polymorphic sequences

M. JIMENEZ-GASCO (1), G. M. Malcolm (1), M. Berbegal (2), J. Armengol (2), R. M. Jimenez-Diaz (3)

(1) Pennsylvania State University, University Park, PA, U.S.A.; (2) Universidad Politécnica de Valencia, Valencia, SPAIN; (3) Universidad de Cordoba and Instituto de Agricultura Sostenible (CSIC), Cordoba, SPAIN
Phytopathology 101:S83

Verticillium wilts caused by the soilborne fungus *Verticillium dahliae* are amongst the most challenging diseases to control. Populations of this pathogen comprise a few clonal lineages that correlate with vegetative compatibility groups (VCGs) and most genetic markers used to date have been unable to resolve diversity within clonal lineages. The objective of this study was to determine the phylogenetic relationships that might exist among VCGs and their subgroups. For this purpose, we analyzed sequences of the intergenic spacer region of the ribosomal DNA (IGS) and six anonymous polymorphic sequences in *V. dahliae* isolates representing the main VCGs and subgroups (VCGs 1A, 1B, 2A, 2B, 3, 4A, 4B, and 6) from different geographic origins and hosts. IGS alignments revealed a complex structure

with numerous large indels. Phylogenetic analysis indicated that certain subgroups (e.g., VCGs 1A and 1B) are closely related and share a common ancestor; however, other subgroups (e.g., VCG 4A) are related more closely to members of a different VCG (e.g., VCG 2B) than to subgroups of the same VCG (VCG 4B). Furthermore, our analyses indicate that VCG 2B is polyphyletic with members placed in at least three distinct phylogenetic lineages. These results raise questions concerning the significance of VCG groups and subgroups, the need for reassessment of VCGs in *V. dahliae*, and the adequacy of using current VCG analysis for assessing genetic diversity in *V. dahliae* populations.

Genetic diversity and temporal dynamics of *Venturia inaequalis* populations following two Apple scab epidemics in Pennsylvania

M. JIMENEZ-GASCO (1), L. Zhang (1), H. K. Ngugi (2)

(1) Pennsylvania State University, University Park, PA, U.S.A.; (2) Pennsylvania State University, Biglerville, PA, U.S.A.
Phytopathology 101:S83

Apple scab, caused by *Venturia inaequalis*, is one of the most important diseases in apple production with increasing management challenges. Pathogen populations have developed resistance to nearly every fungicide used, and there is a limited availability of resistant cultivars with agronomic characteristics that are commercially accepted. In this study we analyzed how populations of *V. inaequalis* changed during Apple scab epidemics in PA in the absence of chemical control. Sampling was done from two cultivars differing in their resistance to Apple scab: 'Golden Delicious' (susceptible) and 'Rome Beauty' (highly susceptible), at the beginning (May) and near-end (September) of two epidemic years, 2008 and 2009. Eight populations of *V. inaequalis* (765 isolates) were analyzed using seven microsatellite markers. Overall, in 2008 we observed a significant reduction of genotypic diversity and a dramatic shift in genotype composition from May to September in 'Rome Beauty', whereas populations from 'Golden Delicious' maintained the same level of diversity throughout the epidemic. However, populations in both cultivars remained stable and did not change significantly in 2009. These results suggest that fitness competition between individuals is more intense on highly susceptible cultivars than on cultivars carrying some resistance genes. We also hypothesize that the pathogen population structure in a given year may be highly influenced by weather and disease pressure during the preceding year.

Dynamic monitor of physiological race variation for wheat stripe rust in Gansu province in China

S. JIN (1), Q. Jia (1), S. Cao (1)

(1) Institute of Plant Protection, GAAS, Lanzhou, PRC PEOPLES REP OF CHINA
Phytopathology 101:S83

South Gansu is a variable physiological-race area of wheat stripe rust in China, from where a lot of dominant races are developed and prevail. In Gansu, the race monitoring of wheat stripe rust can provide advanced information for disease forecast and rust-resistance breeding. During the period of 2008~2010, there are 977 samples from 30 Gansu counties are monitored and in which 36 races are detected by Chinese differentials. The analysis to virulent gene indicates that the proportion rates of virulent strains to Yr-9, Yr3b+Yr4b, Yr-Su are respectively for 92.0%, 21.9% and 97.5%. CYR32 is firstly dominant race in the monitored 36 races, with the frequencies of 26.6%. While the second populated race is CYR31 with the frequencies of 16.9%. And those races such as CRY21, CRY23, CYR25, CRY27, CYR28, CYR29, CYR31, are not the main races, and only with the frequency of 0.1%~1.7%. It's notable that in 2010, there are 20 pathogenic strains are monitored to variety Guinong 22, Zhong 4, Chuanmai 42, 92R137 and T. spelta album. At present, Guinong 22, 92R137 and T. spelta album are all immune to CYR31, CYR32 and CYR33, which are used as resistant resources in many breeding plans. The occurrence of these new strains might be a potential threat and should be paid more attention.

Studies on viability of sclerotia collected from *Sclerotinia stem rot* infected soybean plants in Iowa during 1995–2010

L. Jing (1), S. NAVI (1)

(1) Iowa State University, Ames, IA, U.S.A.
Phytopathology 101:S83

Sclerotinia stem rot of soybean is caused by an ascomycetous fungus *Sclerotinia sclerotiorum*. In severe cases, this disease can cause up to 50% yield reduction in commercial fields. In developing management approaches of the disease, sclerotial viability plays an important role. Therefore, we studied viability of sclerotia collected during 1995–2010 from naturally infected soybean plants, northeast research and demonstration farm, Iowa and were stored in clear glass vials with screw caps at lab temperature. Viability of sclerotia was tested following germination test on PDA and apothecia production on sterilized vermiculite (20 g vermiculite +10 ml DSW). In

2011 APS • IPPC
Joint Meeting
August 6–10
Honolulu, Hawaii



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, Thielaviopsis, 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, buckwheat, 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. Hom (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.

The abstracts are published as submitted. They were formatted but not edited at the APS headquarters office.