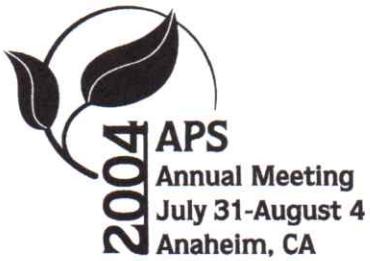

2004 APS Annual Meeting Abstracts of Presentations

Abstracts submitted for presentation at the APS 2004 Annual Meeting in Anaheim, California, July 31–August 4, 2004 (including abstracts submitted for presentation at the 2004 Pacific Division Meeting). The abstracts are arranged alphabetically, by first author's name.

Integrating morphological and molecular characterization for the identification of *Pythium* species: The case of *Pythium christmatum* from fraser fir and *Pythium pseudointermedium* from corn. Z. G. ABAD (1,2), J. Phillips (1,2), and J. A. Abad (2). (1) Plant Pathogen Identification Laboratory; (2) Dept. Plant Pathology, North Carolina State University, Raleigh, NC. Phytopathology 94:S1. Publication no. P-2004-0001-AMA.

The Genus *Pythium* with over 200 reported species is an exceptional group of straminipiles in terms of ecology and plant pathology. Many *Pythium* spp. occupy a high level of niche diversity that cannot be surpassed by any other straminipile or fungi. From our collection of isolates, two heterothallic putative new species have been identified. *Pythium christmatum*, isolated from fraser fir, produces sporangia spherical, pyriform, ellipsoid, terminal and intercalary. *Pythium pseudointermedium*, isolated from corn, produces spherical, terminal and intercalary sporangia as well as cylindrical intercalary sporangia. Most morphological features of both species do not fit with descriptions of any described taxa. The phylogenetic analyses of the ITS rDNA region from our two isolates along with 120 other *Pythium* spp. (PPIL data base) support that both organisms are in fact different species. *Pythium christmatum* is in the same cluster with *P. macrosporum* and *P. abappressorium*. *Pythium pseudointermedium* groups with *P. intermedium*. Sequences of the ITS rDNA region of both species are different and have been deposited at the GenBank. Based on the integration of morphological and ITS rDNA sequence analyses, we conclude that these are putative new species.

Comparison of sequences amplified by N gene and universal *Tospovirus* primers. J. A. ABAD (1), J. Speck (1), A. M. Harness (2), M. D. Bandla (2), and J. W. Moyer (1). (1) Dept. of Plant Pathology, North Carolina State University, Raleigh, NC; (2) Agdia Inc., Elkhart, IN. Phytopathology 94:S1. Publication no. P-2004-0002-AMA.

Tospoviruses (Genus *Tospovirus*, Family *Bunyaviridae*) have emerged as one of the most important causes of viral diseases in cultivated plants worldwide. Precise identification of viruses is vital for disease diagnosis to impede dissemination and to prevent epidemics. Most assays utilize RT-PCR targeting the N gene for detection and genotyping of tospoviruses. We investigated the use of universal Tospoprimers (AGDIA, Elkhart, IN), which amplify a 415 nt fragment of the viral RNA-dependent RNA polymerase gene (L RNA), and determined that they equally differentiate *Tospovirus* species when compared with the use of N gene (S RNA) specific primers. Phylogenetic analyses of the L RNA segment (130 deduced amino acids from 35 sequences generated by Tospoprimers in this work and 5 from databanks) and the N gene segment (255 deduced amino acids from 35 sequences from this work and 20 from databanks) revealed seven clusters corresponding to seven different *Tospovirus* species including *Tomato spotted wilt virus*, *Impatiens necrotic spot virus*, *Iris yellow spot virus*. The amino acid sequence identities ranged from 59% to 84% and 30% to 85% for the L RNA and N gene segments, respectively. The variability within species is being analyzed. In conclusion, identical grouping of species by using both primer sets shows the suitability of Tospoprimers to identify tospoviruses to the species level.

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

Assessing root health by a soil bioassay with beans as an indicator of soil health. G. S. ABAWI (1), J. W. Ludwig (1), and C. H. Petzoldt (2). (1) Plant Path. Dept.; (2) IPM Program, NYSAES, Cornell Univ., Geneva, NY 14456. Phytopathology 94:S1. Publication no. P-2004-0003-AMA.

The emerging concept of soil health deals with integrating the soil physical, chemical and biological properties for improving soil quality and crop productivity in a sustainable and environmentally friendly manner. Practical and informative assessments of soil biological properties remain a challenge. Healthy and productive soils are expected to contain high populations of diverse beneficial microbial communities and low populations and diversity of parasitic soil organisms. We have successfully used a soil bioassay with snap beans as a measure of a general soil suppressive capacity of soils to root pathogens. The latter was conducted in collaboration with the Soil Health Program Work Team for vegetable production systems at Cornell. The protocol involves thoroughly mixing each composite soil sample, placing the soil in 2 or more 10-cm clay pots, planting 7 seeds/pot and growing for 4-6 weeks in a greenhouse. Washed roots were then rated for root rot severity (RRS, root health) on a scale of 1 (no visible disease symptoms) to 9 (>75% of roots are affected, reduced in size and at different stages of decay). For example, the RRS ratings of bean roots grown in soils from 9-year-old plots maintained under conventional, organic, present-IPM, and future-IPM vegetable production systems (IPM Program, Cornell) averaged 7.3, 4.1, 3.3, and 2.7, respectively in 2002. Similar results were obtained in 2003. Observed differences in root health status in the large number of soils tested will be related to other soil properties as well as crop yield and quality.

Effect of heat stress on aflatoxin and fumonisin production in corn (maize, *Zea mays*) in Arkansas. H. K. ABBAS (1), W. T. Shier (2), and R. D. Cartwright (3). (1) USDA-ARS, CG&PRU, Stoneville, MS; (2) College of Pharmacy, University of Minnesota, Minneapolis, MN; (3) Cooperative Extension Service, University of Arkansas, Little Rock, AR. Phytopathology 94:S1. Publication no. P-2004-0004-AMA.

A severe infestation by aflatoxin-producing fungi diminished the food quality of the southern US corn (maize) crop in 1998. Commercial corn hybrids planted at the same and other locations in Arkansas (21 in 1998; 29 in 1999; 15 in 2001; some planted multiple years) were evaluated for resistance to mycotoxin contamination from natural infection by *Fusarium* spp. and *Aspergillus* spp. At harvest, kernel corn samples were evaluated for the presence of aflatoxins and fumonisins. In 1998, samples from all hybrids exceeded 20 ppb aflatoxin (range: 21-699 ppb) and 2 ppm fumonisins (23-79 ppm), the maximum levels permitted for some uses by United States Food and Drug Administration guidelines. In 1999 aflatoxin levels ranged from none detected in most hybrids to 255.3 ppb, and fumonisin levels from 0.3-8.1 ppm. In 2001 the fumonisin levels were very high in all hybrids (range: 8-83.6 ppm), whereas aflatoxin levels were low (<5 in most hybrids, ranging up to 131 ppb). The presence of aflatoxin (AFB1 and AFB2) in samples was confirmed by TLC and LC/APCI/MS and fumonisins (FB1, FB2, FB3, FB4 and FC4) by LC/ESI/MS. Arkansas experienced unusually high day and nighttime temperatures in 1998, but nearly normal temperatures in 1999 and 2001. The results are consistent with heat stress having an important affect on mycotoxin production in corn by *A. flavus* and *Fusarium* spp.

Against these isolates, the background polygenic resistance was inadequate to prevent severe disease. These results indicate that sole reliance upon this single dominant gene-based resistance is not sustainable.

Fusarium stem rot of vanilla in North Sulawesi. E. C. Y. LIEW (1), F. Rondonuwu (2), A. Pinaria (2), D. T. Sembel (2), B. A. Summerell (3), and L. W. Burgess (1). (1) Faculty of Agriculture, Food & Natural Resources, The University of Sydney, NSW 2006, Australia; (2) Department of Pests & Diseases, Faculty of Agriculture, Sam Ratulangi University, North Sulawesi, Indonesia; (3) Royal Botanic Gardens, Sydney, NSW 2000, Australia. Phytopathology 94:S61. Publication no. P-2004-0409-AMA.

Vanilla is an important and popular cash crop offering high economic returns to smallholder farmers in North Sulawesi. However, the production of vanilla in this region is greatly constrained by Fusarium stem rot. Although the disease is most severe on the stem of the vanilla vine, it is also found on the leaves and roots. On the stem internode, small brown water-soaked spots or lesions initially appear, which enlarge and become necrotic, eventually girdling and shriveling up the stem. The lesion often expands to adjacent internodes and develops along the vine. In a recent disease survey of vanilla farms on 12 sites throughout North Sulawesi, the disease was detected at incidences of 20-78% on each site. Several *Fusarium* species were isolated from various plant parts of diseased vines. Only *F. oxysporum* was shown to be pathogenic in greenhouse experiments. *Colletotrichum* was also isolated from diseased tissue but at a lower frequency.

***Ceratocystis* associated with clove decline in North Sulawesi.** E. C. Y. LIEW (1), B. Assa (2), M. J. Wingfield (3), D. T. Sembel (2), B. A. Summerell (4), and L. W. Burgess (1). (1) Faculty of Agriculture, Food & Natural Resources, The University of Sydney, NSW 2006, Australia; (2) Department of Pests & Diseases, Faculty of Agriculture, Sam Ratulangi University, North Sulawesi, Indonesia; (3) Forestry & Agricultural Biotechnology Institute (FABI), University of Pretoria, Republic of South Africa; (4) Royal Botanic Gardens, Sydney, NSW 2000, Australia. Phytopathology 94:S61. Publication no. P-2004-0410-AMA.

Clove decline is the most serious of clove diseases in North Sulawesi, Indonesia. Despite its devastating impact on one of the most important cash crops in this region, the aetiology of this disease has yet been established until recently. Infected trees show symptoms of wilt and defoliation, which often lead to the death of whole trees. In a recent disease survey of 17 sites and more than 100 farms throughout North Sulawesi, clove decline was observed on all sites, with disease incidence of greater than 90%. A fungus, closely resembling the wilt pathogen, *Ceratocystis fimbriata*, was consistently isolated from wood tissues of infected trees. This fungus appears to be associated with a wood-boring beetle, *Hexamitodera semivelutina*. The larvae bore into trees forming extensive galleries within the trunks. All isolates of this fungus were obtained from stained wood tissue adjacent to these wood-borer galleries. Multiple pathogenicity tests confirmed the pathogenicity of this fungus on both seedlings and mature clove trees. Molecular studies are being conducted on these isolates to confirm their identity.

Expression of *Soybean mosaic virus* (SMV) HC-Pro in transgenic soybean plants enhances SMV symptoms. H. S. LIM (1), T. S. Ko (2), L. L. Domier (1,3), H. G. Kim (4), and G. L. Hartman (1,3). (1) University of Illinois Urbana, IL; (2) University of Minnesota, St. Paul, MN; (3) USDA-ARS Urbana, IL; (4) Chungnam National University, Daejeon, Korea. Phytopathology 94:S61. Publication no. P-2004-0411-AMA.

Transgenic soybean lines expressing the helper component-protease (HC-Pro) coding region of SMV G5 were produced by *Agrobacterium*-mediated transformation of immature soybean cotyledons. Homozygous transgenic lines were recovered with single copy insertions that expressed SMV HC-Pro mRNA at levels ranging from 5 to 34% of that found in SMV-infected plants. Ten days after inoculation with SMV, all HC-Pro transgenic lines had symptoms more severe than *uidA* transgenic plants. Symptom severity was related to HC-Pro expression levels in the transgenic lines, but SMV RNA titers did not differ among the lines. Similar levels of small interfering RNAs were detected in SMV-infected HC-Pro and *uidA* transgenic plants. Starting at 20 days after inoculation, new leaves of the transgenic line that expressed the highest level of HC-Pro mRNA no longer showed symptoms, and SMV RNA titers were drastically reduced. The titers of coat-protein and HC-Pro coding regions declined at similar rates suggesting that the HC-Pro coding region was not preferentially targeted. In soybean lines that expressed lower levels of HC-Pro, symptoms remained severe at all sampling dates and no reductions in SMV RNA titers were observed. These results show that HC-Pro enhances SMV symptom severity in transgenic plants and that even potyvirus HC-Pro transgenes are susceptible to virus-induced gene silencing when expressed at high levels.

Characterization of two new strains of grapevine rupestris stem pitting associated virus. M. F. LIMA (1), R. Alkowni (2), D. Golino (1), J. K. Uyemoto (1), and A. Rowhani (1). (1) Department of Plant Pathology, University of California, Davis, CA; (2) Arab American University, Jenin, Palestine. Phytopathology 94:S61. Publication no. P-2004-0412-AMA.

Grapevine rupestris stem pitting associated virus (GRSPaV) is graft-transmissible and associated with rupestris stem pitting disorder. GRSPaV is detected by indexing on *Vitis rupestris* cv. St. George, in which it induces pittings below the graft union. GRSPaV belongs to the genus *Foveavirus* in the family *Flexiviridae*. In field surveys in California, two new strains of GRSPaV from a *V. vinifera* cv. Syrah (SY-RSP) and cv. Pinot Noir (PN-RSP) were identified. CDNA libraries were made from dsRNA, using random primers. Selected cDNA clones were sequenced and specific primers were designed and used in RT-PCR to fill the gaps. Sequences were compared with the published sequences of GRSPaV. Both isolates showed similar genome organization, comprising six ORFs. Nucleotide and amino acid analysis showed 76-89% and 85-96% (SY-RSP), and 79-89% and 83-93% (PN-RSP), respectively, to published isolate. Specific detection primers for both isolates were designed for a survey to determine their rate of spread in the field.

Genotyping and assessing genetic diversity in the PD strains of *Xylella fastidiosa* by simple sequence repeat (SSR) DNA markers. H. LIN (1), M. Francis (2), S. Barros (2), R. Hu (2), E. L. Civerolo (1), and A. M. Walker (2). (1) ARS-USDA, 9611 S. Riverbend Avenue, Parilier, CA 93648; (2) Department of Viticulture & Enology, University of California, Davis, CA 95616. Phytopathology 94:S61. Publication no. P-2004-0413-AMA.

The insect-transmitted bacterium, *Xylella fastidiosa* (Xf), causes diseases in many economically important plants, including Pierce's disease in grape. Understanding the genetic diversity and population structure of the pathogen are critical steps in managing disease outbreaks. With the recently available genomic sequencing of four Xf strains, Pierce's disease of grapevine (PD), citrus variegated chlorosis (CVC), almond leaf scorch (ALS), and oleander leaf scorch (OLS), identification of repeated sequence loci is facilitated. A genome wide search was performed for identifying Simple Sequence Repeat (SSR) motifs among the all four strain sequence databases, and 60 SSR loci were selected for primer design. These simple repeat motifs consist of 2-8 bp repeat units and were distributed across the whole genome. We evaluated these SSR primers with 21 Xf isolates collected from Napa Valley, San Joaquin Valley and southern California vineyards. Seventy percent of these SSR primers were highly polymorphic and distinguished genetically close strains. This PCR-based SSR marker is a precise and repeatable marker system. The power of this polymorphic detection system makes it a useful tool for population structure, genetic diversity and epidemiological risk assessment analyses.

Formulating locally effective integrated management packages for tomato bacterial wilt. C.-H. Lin and J.-F. WANG. AVRDC-The World Vegetable Center, Tainan, Taiwan. Phytopathology 94:S61. Publication no. P-2004-0414-AMA.

Bacterial wilt, caused by *Ralstonia solanacearum*, is an endemic and important tomato disease worldwide. Efficacy of reported control methods, including tolerant cultivars, resistant rootstocks, and soil amendments, could be variable over strains, locations or soils. A case study was conducted on formulating effective management packages for a production area in Taiwan. First 52 local strains were profiled based on their aggressiveness. Representative strains were selected for evaluating commercial tolerant cultivars and resistant rootstocks. Eggplant and tomato varieties, EG203 (mean percent wilting 0%) and Hawaii7996 (mean percent wilting 21%), were selected as potential rootstocks. All tolerant cultivars tested were susceptible. Local soil samples were collected to evaluate the efficacy of a soil amendment consisting urea (825 kg/ha) and slaked lime (3993 kg/ha). The amendment could reduce the pathogen density from 7.0 to 4.7 log (cfu/g dry soil) and the disease incidence from 60% to 3% at 28°C in the greenhouse. A field trial was conducted in fall 2003 consisting of 6 treatments combining the soil amendment and 3 planting materials (ASVEG10, ASVEG10 grafted on EG203 or on Hawaii7996). At 105 days after transplanting, about 90% of ASVEG10 was wilted, while treatments with eggplant rootstock showed only 1 to 3% wilting. The soil amendment effect was only observed on the treatments with tomato rootstock, which provided additional 29% reduction of incidence. The results show that applying a pre-selection scheme could ensure the success of local integrated management package.

Rice bacterial blight resistance genes *Xa7*, *xa5*, and *Xa4* confer resistance during all developmental stages. K. M. LINHOLM (1,2), E. Garcia (2), C. M. Vera Cruz (2), and J. E. Leach (1). (1) Kansas State University, Manhattan, KS; (2) International Rice Research Institute, Manila, Philippines. Phytopathology 94:S61. Publication no. P-2004-0415-AMA.