plants and soybean discoloration compared to the influence of bean leaf beetles.

A novel cell wall degrading enzyme in the plant parasitic nematode *Meloidogyne incognita*. M. DAUTOVA (1), H. Overmars (1), A. Schots (2), F. J. Gommers (1), J. Bakker (1), and G. Smant (1). (1) Laboratories of Nematology; (2) Monoclonal Antibodies, WUR, Binnenhaven 10, 6709 PD Wageningen, The Netherlands. Phytopathology 91:S21. Publication no. P-2001-0146-AMA.

Single pass 5-prime end sequencing of approximately 1,000 clones from a cDNA library constructed of preparasitic *M. incognita* J2 has revealed a partial sequence with a homology to xylanases of various bacterial origin. This expressed sequence tag was used to obtain a full-length transcript of 1220 nt encoding an open reading frame (*Mi-xyl1*) of 34,9 kDa. Hydrophobic cluster analysis classified the putative xylanase as a type 5 glycosyl hydrolase. Whole mount in situ hybridization showed specific labeling of the *Mi-xyl1* in the subventral esophageal glands of second stage juveniles. DNA blot hybridization indicated the presence of two homologues in *M. incognita* whereas no hybridization was found on genomic DNA fragments of *C. elegans* and cyst nematodes. Recombinant *Mi-xyl1* protein exhibited hydrolytic activity on xylan and carboxymethyl cellulose. Conclusively, root knot nematodes (*Meloidogyne* spp.) make use of a suite of cell wall degrading enzymes with overlapping activities to facilitate plant invasion.

Spatial patterns of antibiotic inhibition and resistance among Streptomycetes from prairie soils. A. L. DAVELOS, L. L. Kinkel, and D. A. Samac. Dept. Plant Pathology, University of Minnesota, St. Paul, MN 55108. Phytopathology 91:S21. Publication no. P-2001-0147-AMA.

Antibiotic activities of indigenous microbes have been implicated in the development of disease suppressive soils, and may play a role in pathogen inhibition in non-agricultural systems. However, little is known of the frequency, intensity, and diversity of antibiotic inhibition and resistance among indigenous microbes in prairie soil. The ability of Streptomyces isolates from prairie soil to inhibit and resist 10 standard Streptomyces isolates from a disease suppressive soil was evaluated. Analysis of antibiotic inhibition and resistance for individual isolates among 3 locations and 4 depths within a 1 m × 1 m plot revealed wide variation in inhibition and resistance. Fewer than 10 percent of isolates could inhibit or resist all ten standards. One third of isolates were unable to inhibit any of the standards while no isolate was susceptible to all of the standards. The frequency and intensity of inhibition of the standards by indigenous Streptomyces isolates varied among locations and tended to increase with increasing depth. Resistance was highly variable among locations and depths but no clear trends were evident.

Characterization of *Phytophthora phaseoli* isolates collected on Delmarva. C. R. DAVIDSON, R. B. Carroll, T. A. Evans, R. P. Mulrooney, and M. Sedegui. Department of Plant and Soil Sciences, University of Delaware, Newark, DE 19717-1303. Phytopathology 91:S21. Publication no. P-2001-0148-AMA.

With the appearance of new races of *Phytophthora phaseoli*, (cause of downy mildew on lima bean) and the lack of resistant cultivars, epiphytotics could lead to devastation of Delmarva's lima bean industry. Rapid and accurate identification of new races is essential for an effective disease management program. Work in our laboratory prior to 1999 indicated that race D was the prevalent genotype of *P. phaseoli* in the Delmarva region. New races of *P. phaseoli* were implicated as a result of recent downy mildew outbreaks on previously resistant cultivars. An investigation of these new races began with the collection of 132 field isolates from the Delmarva region. The use of cultivar differentials, involving systematic inoculation of known resistant (R) and susceptible (S) cultivars confirmed the presence of a new variant, which was designated as race F. Race E was determined to be the prevalent genotype in the region in 2000. DNA fingerprinting through AFLP, along with allozyme analysis using both GPI and PEP overlays was utilized to genetically characterize the races of this pathogen.

Nonfunctional tRNA gene in an unusual example of rRNA interoperon sequence heterogeneity in phytoplasma. R. E. DAVIS and E. L. Dally. Molecular Plant Pathology Laboratory, USDA-Agricultural Research Service, Beltsville, MD, USA 20705. Phytopathology 91:S21. Publication no. P-2001-0149-AMA.

Loofah witches' broom (LfWB) phytoplasma is the only described member of phylogenetic group 16SrVIII. For analysis of the rRNA operons of LfWB phytoplasma, 1.8 kbp DNA sequences containing most of the 16S rRNA gene, the 16S-23S rRNA spacer region, and the 5'-end of the 23S rRNA gene were cloned and subjected to RFLP and nucleotide sequence analyses. The results showed that the LfWB phytoplasma genome contained two sequence-heterogeneous rRNA operons, which we termed rrnA (GenBank no. AF248956) and rrnB (GenBank no. AF353090), respectively. The spacer region of operon rrnA contained a complete tRNA-Ile gene. In contrast, operon rrnB was characterized by 43 base deletions and a single base substitution in the tRNA-Ile gene and a 10-base deletion in the spacer region immediately upstream of the tRNA-Ile gene. This altered structure of operon rrnB is probably due to recombination and base misincorporation. The tRNA-Ile gene of LfWB rrnB is the first known example of a partially deleted, nonfunctional gene in a phytoplasma genome.

Mechanisms of harpin-induced resistance against blue mold of apples. G. de CAPDEVILLE (1), S. V. Beer (1), C. L. Wilson (2), and J. R. Aist (1). (1) Dept. Plant Pathology, Cornell Univ., Ithaca, NY 14853; (2) USDA-AFRS, Kearneysville, WV 25430. Phytopathology 91:S21. Publication no. P-2001-0150-AMA.

We studied mechanisms by which harpin, a protein produced by *Erwinia amylovora* and involved in its pathogenesis of apple, induces resistance in apple fruits to blue mold caused by *Penicillium expansum*. Light microscopy, SEM and TEM were used to determine possible resistance responses. A molecular study also is under way to evaluate the expression of pathogenesis-related genes. Light microscopy showed that mycelial growth occurred by 72 h after inoculation in the control tissue, but only after 144 h in the harpin-treated tissue. Numerous tannin vacuoles and wall appositions were observed in the epidermal cells of inoculated harpin-treated tissues, but not in the control tissue. SEM study of wound surfaces showed that the fungus grew within 48 h after inoculation of the control tissue, but only after 96 h in the harpin-treated tissue, where invasion attempts appeared thwarted by materials deposited at the penetration sites. The results suggest that the fungus may trigger resistance responses in harpin-treated apples even prior to penetration and colonization.

Pre- and postharvest application of antagonistic yeasts for the control of gray and blue mold: Efficacy and monitoring. D. De Clercq, C. Dickburt, P. Lepoivre, and M. H. JIJAKLI. Plant Pathology Unit, Gembloux Agricultural University, 5030 Gembloux, Belgium. Phytopathology 91:S21. Publication no. P-2001-0151-AMA.

Golden Delicious apples were treated either with *Pichia anomala* strain K or *Candida oleophila* strain O (10^7 cfu/ml), 12 or 2 days before harvest by spraying or one day after harvest by dipping. Whatever the treatment, apples were wounded and inoculated with both *Botrytis cinerea* (10^6 spores/ml) and *Penicillium expansum* (10^5 spores/ml) 2 days after harvest. Similar biocontrol efficacy was observed for both antagonists. The highest protection level was achieved on pre-harvest treated fruits with infection percentage ranged from 11 to 29% compared to 67% on untreated apples. Post-harvest treatments showed a significantly lower biocontrol efficacy than pre-harvest treatments. These results were related to monitoring experiments assessed by plated fruit washes on a semi-selective medium: population densities on field treated fruits reached at least 10^4 cfu/cm2 just before cold storage, whereas this threshold level was never observed on post-harvest treated apples.

Spore gradients of *Gibberella zeae* from overwintered inoculum in wheat fields. L. de Luna (1), I. Bujold (2), O. Carisse (2), and T. C. PAULITZ (3). (1) Macdonald Campus of McGill University; (2) Agriculture and Agrifoods Canada, St. Jean sur Richelieu, Quebec and (3) USDA-ARS, Pullman, WA. Phytopathology 91:S21. Publication no. P-2001-0152-AMA.

Ten-meter long plots of wheat at Macdonald Campus (MAC) and L'Acadie (LAC), Quebec were spray inoculated with macroconidia of *F. graminearum* in summer, 1998. Infected wheat stubble was left on the plots to overwinter. Perithecia of *G. zeae* were produced in the fall and spring. In May 1999, 50-m transects of rotorod volumetric spore samplers (one trap every 10 m) were established downwind from the plots and sampled daily. At MAC, ascospore concentrations >100 spores/m^3 occurred on 34 nights from June 1-August 30, in 16 separate release events that lasted 1-3 nights each. Spore gradients were modeled with the inverse power (IP), exponential (EX) and a generalized model (GEN) incorporating the IP, EX, and Gaussian models. The GEN model outperformed the other two models at both sites, fitting 66% and 82% of the gradients at LAC and MAC. The EX model fit 50% and 42% of the gradients at LAC and MAC. The distance at which spore concentrations declined 50% (D(50)) and 90% (D(90)) were calculated from the EX model. At LAC, D(50)=20 m, D(90)=66 m, and at MAC, D(50)=18 m, D(90)=60 m.