2004 North Central Division Meeting Abstracts

Abstracts presented at the APS North Central Division meeting in St. Paul, Minnesota, June 23–25, 2004. The abstracts are arranged alphabetically, by first author's name.

Origin of virulence diversity in plant pathogen populations: Bean rust as a case study. M. ACEVEDO (1), C. Jochua (1), C. M. Araya (2), and J. R. Steadman (1). (1) Dept. Plant Pathology, University of Nebraska, Lincoln, NE 68583; (2) Phytopathology Laboratory, Heredia National University, Costa Rica. Phytopathology 95:S161. Publication no. P-2005-0001-NCA.

Virulence diversity in plant pathogen populations is a major constraint in the management of plant diseases. Determining of virulence variability in natural populations can give insights about the origin and evolution of pathogen virulence. The bean rust pathogen, *Uromyces appendiculatus* is characterized by high diversity of virulence phenotypes in natural and cropping systems. Characterization of the virulence of rust isolates from natural populations and agricultural fields from major bean production areas in Africa and the Americas suggests a coevolutionary relationship between host and pathogen.

Relative importance of the small oak bark beetle, in the overland transmission of *Ceratocystis fagacearum* in Minnesota. A. Ambourn (1), J. Juzwik (2), and J. Eggers (2). (1) Dept. Entomology, Univ. of Minnesota, St. Paul, MN 55108; (2) USDA Forest Service, 1561 Lindig St., St. Paul, MN 55108. Phytopathology 95:S161. Publication no. P-2005-0002-NCA.

The small oak bark beetle, *Pseudopityophthorus minutissimus* Zimm., is an implicated vector of the oak wilt fungus *Ceratocystis fagacearum* (Bretz) Hunt. Based primarily on anecdotal evidence, the insect's relative importance in the overland transmission of the pathogen in Minnesota is considered low. Field and laboratory studies were initiated in 2003 to test this hypothesis. Based on the number of beetles from window flight traps located in wilting oak canopies, peak abundance occurred 12 – 19 May (869 of 1,852 collected 17 April – 22 September). Assays of the beetles (5 per group) for viable *C. fagacearum* propagules were conducted. Only 2.1% in May (n = 280) and 6.6% in June (n = 120) of the groups assayed were carrying the fungus. Beetles were also found to colonize branches in the canopies of oak wilt killed trees, but no beetles emerging from these branches carried viable pathogen propagules. These data support the hypothesis that *P. minutissimus* is not an important vector in the state.

Use of force of infection to determine relative importance of two sap beetles species in the overland transmission of *Ceratocystis fagacearum*. A. AMBOURN (1), J. Juzwik (2), and R. D. Moon (1). (1) Dept. Entomology, Univ. of Minnesota, St. Paul, MN 55108; (2) USDA Forest Service, 1561 Lindig St., St. Paul, MN 55108. Phytopathology 95:S161. Publication no. P-2005-0003-NCA.

Sap beetles are considered the primary overland vectors of the oak wilt fungus *Ceratocystis fagacearum* (CF) in the north central region of the U.S. Recent studies have implicated *Colopterus truncatus* and *Carpophilus sayi* as the principal sap beetle vectors in Minnesota. Studies were conducted over 2 years to measure the abundance of dispersing adults and frequencies of their contamination with viable pathogen propagules. Force of infection (FOI = mean monthly beetle density × proportion of beetles carrying CF) was used as a measure of relative importance. Highest numbers of *C. truncatus* were found in April 2002 and May 2003. Although the highest contamination frequencies occurred in July - August, the numbers of beetles trapped were low. FOI for *C. truncatus* was highest in April - June. Highest numbers of *C. sayi* were found in October of both years. However, the highest contamination frequencies occurred in April-June and FOI was highest in June. Risk of pathogen spread by these insects is, thus, highest in the spring and *C. truncatus* may be a relatively more significant vector than *C. sayi*.

Catching the wave: Dealing with frogeye leaf spot in the north central region. J. P. BOND, M. E. Schmidt, J. S. Russin, Y. K. Goh, and C. M. Vick. Dept. of Plant, Soil and Agricultural Systems, Southern Illinois University, Carbondale, IL 62901. Phytopathology 95:S161. Publication no. P-2005-0004-NCA.

Cercospora sojina Hara, the causal agent of frogeye leaf spot of soybean recently has increased in distribution and importance in the north central region. The use of resistant varieties is the most effective method of managing *C. sojina*. However, the reaction of most soybean varieties developed for this region to *C. sojina* has not been determined. A regional project funded by the North Central Soybean Research Program has facilitated the selection of a set of host differentials, characterization of pathogen isolates, and the evaluation of soybean varieties. In 2003, over 30 isolates of the fungus were collected throughout Missouri and southern Illinois, and their relative virulence levels were determined. Over 600 public and private varieties were evaluated for resistance in fields either artificially or naturally infested with the pathogen. Of the 450 commercial varieties tested, 87 of these varieties did not express symptoms of frogeye leaf spot. In the public germplasm, 46 lines of the 150 tested did not express foliar symptoms.

Evaluation of disease predictors and scheduling the first fungicide spray for managing late blight of celery. R. S. BOUNDS and M. K. Hausbeck. Dept. Plant Pathology, Michigan State University, East Lansing, MI 48824. Phytopathology 95:S161. Publication no. P-2005-0005-NCA.

Late blight of celery, caused by *Septoria apiicola*, is managed by weekly fungicide applications initiated 1-3 weeks after transplanting. This study evaluated a *S. apiicola* predictor developed in MI, a *Cercospora apii* predictor, and the Tom-Cast predictor using 10, 15, or 20 disease severity value (DSV) thresholds. Azoxystrobin alternated with chlorothalonil or chlorothalonil alone was applied at 7-day intervals or according to disease predictors to 'Dutchess' celery in 2003. Petiole disease severity of untreated plants was >50%, while the *Septoria*, *Cercospora*, and Tom-Cast (10 DSV) predictors limited disease to <2% and prompted 2-5 fewer sprays when compared to the 7-day schedule. In a separate trial, a weekly fungicide program of azoxystrobin alternated with chlorothalonil initiated 4 weeks after transplanting was as effective as initiating sprays one week after transplanting. A 50% reduction in marketable yield resulted when weekly spray programs were initiated after disease symptoms developed.

Frequency of susceptibility to northern stem canker in soybean varieties from maturity groups 0 through II. T. E. CHASE and R. Geppert. Plant Science Department, South Dakota State University, Brookings, SD 57007. Phytopathology 95:S161. Publication no. P-2005-0006-NCA.

A total of 377 soybean entries submitted to the South Dakota State University crop performance testing program were assessed for susceptibility to northern

stem canker, caused by *Diaporthe phaseolorum* var. *caulivora* (DPC). Entries included conventional (CI, CII) and glyphosate-resistant (RR 0, RRI, RR II) varieties and lines from 32 private companies as well as the SDSU public breeding program. The study was conducted as a field trial in 2003. Ten plants at the flowering stage were inoculated per plot with DPC infested toothpicks. Plots were rated 5-6 weeks later. Varieties with 0% killed were classified as resistant (R); 10-30% killed were classified as moderately resistant (MR); 40-100% killed were classified as susceptible (S). The percentage of classes (R/MR/S) within each group was as follows: C I, 23/31/46; C II, 15/49/36; RR 0, 11/29/59; RR I, 8/26/65; RR II, 11/58/31. A group of 45 varieties was selected for a follow-up greenhouse study. Greenhouse inoculations gave higher levels of infection overall but did not correlate well with the results from the field study.

Seed inoculation with *Bradyrhizobium* and *Bacillus* spp. increases soybean yield. C. ESTEVEZ DE JENSEN, J. Kurle, and J. Percich. Dept. Plant Pathology, University of Minnesota, St. Paul, MN 55108. Phytopathology 95:S162. Publication no. P-2005-0007-NCA.

The effects of Yield Shield (*Bacillus pumilus*) GB34, Kodiak (*B. subtilis*) GB03, and Bio Yield (*B. amyloliquefaciens*) GB99, (*Paenobacillus macerans*) GB122, with or without inoculation of HiStick 2 (*Bradyrhizobium*), a liquid formulation of *Bradyrhizobium*, Apron Maxx RTA and an untreated control were evaluated. The combined application of *Bradyrhizobium* and *Bacillus* increased root and nodule dry wt. Average yields were increased 37% when inoculation with *Bradyrhizobium*, was compared to the untreated control (2,833 vs. 2,060 Kg/ha respectively). Yields were not significantly increased when the effect of seed application of Kodiak, Yield Shield, and Bio Yield was compared to the ApronMaxx seed treatment. However, average yields were increased over 56% when combined inoculation with *Bradyrhizobium* and seed application of Kodiak, Yield Shield and Bio Yield, were compared to application of *Bacillus* spp. alone (3,015 vs.1,921 Kg/ha respectively). These results are consistent with previous research and suggests that *Bacillus* is synergistic with *Bradyrhizobium*.

Histochemical and transcriptome analysis of the interactions between *Medicago truncatula* and the pathogens *Colletotrichum trifolii* and *Erisyphe pisi*. D. FOSTER-HARTNETT (1), S. Penuela (1), D. Danesh (1), N. Sharapova (1), K. A. VandenBosch (1), N. D. Young (1), and D. A. Samac (2). (1) University of Minnesota, St. Paul, MN 55108; (2) USDA-ARS, St. Paul, MN 55108. Phytopathology 95:S162. Publication no. P-2005-0008-NCA.

Medicago truncatula accessions were screened for reaction to *Colletotrichum trifolii*. Three basic phenotypes were observed by histochemical staining. Transcriptome analysis of a resistant accession 24 h post-inoculation with the fungus was carried out with microarray slides (6,000 EST set). In response to infection, 84 ESTs were up-regulated and two were down-regulated (more than 2-fold change). Up-regulated genes are involved in flavonoid, stilbene, lignin, and phytoalexin production and regulation of cell-death, consistent with the phenotype observed. A similar transcriptome analysis was performed on an accession resistant to *E. pisi* (powdery mildew). Of the 84 ESTs up-regulated in response to *C. trifolii*, 63 were also up-regulated in response to powdery mildew infection, indicating that the response pathways to a hemi-biotrophic/necrotrophic and a biotrophic pathogen overlap significantly.

A genetic map of *Gibberella zeae* using sequence-tagged sites and AFLPs. L. R. GALE (1), J. D. Bryant (2), H. Giese (3), T. Katan (4), K. O'Donnell (5), H. Suga (6), T. R. Usgaard (5), T. J. Ward (5), and H. C. Kistler (1). (1) CDL, USDA, St. Paul, MN; (2) University of Minnesota, St. Paul, MN; (3) Royal Veterinary and Agricultural University, Copenhagen, Denmark; (4) Volcani Center, Bet Dagan, Israel; (5) NCAUR, USDA, Peoria, IL; (6) Gifu University, Gifu, Japan. Phytopathology 95:S162. Publication no. P-2005-0009-NCA.

A genetic map of *Gibberella zeae* (anamorph *Fusarium graminearum*) was constructed using a cross between nitrate-nonutilizing (*nit*) mutants of strain PH-1 and a Minnesota field strain, 00-676. A total of 111 ascospore progeny were analyzed for segregation in 237 loci. Genetic markers consisted of SNPs (detected as dCAPs, n = 86 or CAPs, n = 47), AFLPs (n = 71), SSRs (n = 27), and six other markers. While 213 markers exhibited Mendelian inheritance, segregation distortion was observed for 17 markers at four genomic locations. A linkage map was generated using JoinMap 3.0 and a LOD threshold value of 4.0. Eleven linkage groups were obtained, covering 1154 cM and anchoring 99.8% of the sequence assembly. All linkage groups and anchored supercontigs were assembled into four chromosomes, leaving only 11 smaller supercontigs (76,055 bp total) of the nuclear DNA not anchored.

Detection and quantification of *Fusarium solani* f. sp. *glycines* in soybean roots with real-time PCR. X. Gao (1), T. A. Jackson (1), K. N. Lambert (1), S. Li (1), G. L. Hartman (2), and T. L. Niblack (1). (1) Department of Crop Sciences, University of Illinois, Urbana, IL 61801; (2) USDA-ARS, Urbana, IL 61801. Phytopathology 95:S162. Publication no. P-2005-0010-NCA.

Fusarium solani f. sp. *glycines* (Fsg) causes soybean sudden death syndrome (SDS). A novel real-time quantitative polymerase chain reaction (QPCR) assay based on detection of the mitochondrial small subunit rRNA gene was developed for absolute quantification of Fsg. The QPCR protocol detected all four isolates of Fsg tested, and did not detect DNA from five isolates of *F. solani*, one isolate of *F. oxysporum*, or one of *F. equiseti*. DNA of Fsg was detected in 14 root samples from field plots of soybean plants with and without SDS foliar symptoms, while Fsg was detected in 35.7% of the samples using a modified Nash and Snyder semi-selective medium. Assays testing PCR amplification efficiency were performed to ensure DNA extracts were inhibitor-free. The quantities of Fsg DNA in root samples from field plots ranged from 1.1 to 221.7 ng/mg root. The QPCR protocol is specific and more sensitive than the traditional bioassay on a selective medium, and is useful to detect and quantify the fungus in soybean roots.

***Phytophthora capsici* isolated from snap beans is pathogenic to cucumber fruit and soybean.** A. J. GEVENS and M. K. Hausbeck. Department of Plant Pathology, Michigan State University, East Lansing, MI 48824. Phytopathology 95:S162. Publication no. P-2005-0011-NCA.

In August 2003, water-soaked foliage, stem necrosis, and overall plant decline was observed along the surface water drainage pattern in two commercial snap bean fields in Oceana County, MI. Both fields have a history of *Phytophthora capsici* infestation. Diseased tissue from stems, petioles, and leaves collected from the two fields yielded 52 isolates of *P. capsici*. This is the first documentation of *P. capsici* on snap beans in MI. Isolates were primarily of the A1 compatibility type (CT) (63%) and were sensitive to the fungicide mefenoxam (85%). One isolate was fully insensitive to mefenoxam and 13% were intermediately sensitive. All isolates were pathogenic to cucumber fruit. Six isolates were used to inoculate 11 bean species and all were pathogenic, causing localized water-soaked lesions. Virulence of the 6 *P. capsici* isolates to soybean plants was determined by rating (0 = healthy, 5 = dead) disease development for 6 days post inoculation. Disease ratings averaged ≥4.0 and differences in virulence between the two fields were observed. Rotating beans with other susceptible hosts is not currently recommended.

First detection of the perfect stage of sugar beet powdery mildew in Wyoming and Montana. G. D. GRANC (1) and B. J. Jacobsen (2). (1) Dept. of Plant Sciences, University of Wyoming, Laramie, WY 82071; (2) Dept. of Plant Science and Pathology, Montana State University, Bozeman, MT 59717. Phytopathology 95:S162. Publication no. P-2005-0012-NCA.

Powdery mildew of sugar beet (*Beta vulgaris* L.) is frequently observed in the High Plains of Wyoming and Montana. The perfect stage of the fungus [*Erysiphe polygoni* DC (syn. *E. betae* {Vanha} Welzien)] was observed for the first time in southeastern Wyoming in 2002 and southeastern Montana in 2003. Infected leaves collected from field-grown sugar beet were viewed microscopically. Immature ascocarps were observed during early September and mature ascocarps did not appear until early October. The first detection of the perfect stage in Idaho and Colorado in 2001 (Gallion, J. J., and L. E. Hanson. 2003. Plant Dis. 87:200) followed by its successive appearance in Wyoming and Montana as reported herein, suggests the eastward and northward migration of a new mating type(s). The ascocarp's role in disease epidemiology is not known. However, the increased potential for genetic recombination has important implications for fungicide resistance management and the development of resistant cultivars.

Improving the relationship between IKONOS satellite image intensity and soybean yield as affected by SCN using geostatistics. J. GUAN (1), M. S. Kaiser (2), P. C. Caragea (2), G. L. Tylka (1), and F. W. Nutter, Jr. (1). (1) Dept. Plant Pathology, Iowa State Univeristy, Ames, IA 50011; (2) Dept. Statistics, Iowa State University, Ames, IA 50011. Phytopathology 95:S162. Publication no. P-2005-0013-NCA.

A field experiment was conducted in 2000 at the Iowa State University Woodruff Research Farm to establish the relationship between satellite image intensity and soybean yield in a SCN-infested field divided into 995 2 m × 3 m quadrats. IKONOS satellite images in 4 m resolution with red, green, blue, and near infrared bands were obtained on three dates. Yield was determined by harvesting the center two rows of each quadrat. Continuous soybean yield and satellite image intensity maps were generated using geostatistics by overlaying a 30 × 25 grid on the continuous maps. Soybean yield and satellite image intensities were then averaged for each grid cell. Linear regression was performed to relate satellite image intensities to soybean yield. The use of geostatistics greatly improved the relationship between satellite image

intensity and soybean yield by explaining up to 29% more of the variation in soybean yield compared to traditional regression methods.

An inoculation method to induce Sclerotinia stalk rot in field-grown sunflowers. T. J. GULYA (1), M. Draper (2), and R. Henson (3). (1) USDA-ARS Northern Crop Science Laboratory, Fargo, ND 58105; (2) Dept. of Plant Science, South Dakota State University, Brookings, SD 57007; and (3) North Dakota State University, Carrington Research Extension Center, Carrington, ND 58421. Phytopathology 95:S163. Publication no. P-2005-0014-NCA.

The efficacy of *Sclerotinia sclerotiorum* sclerotia or mycelia (grown on either oats or millet) to induce Sclerotinia stalk rot in field-grown sunflower plants was tested in a two-year study at two locations. Grain-based inoculum was superior to sclerotia in inducing disease at all inoculation dates. The lowest rate of grain/mycelia inoculum (40 g/6 m row) produced significantly more disease (37%) than even the highest rate of sclerotia (80/row), which produced 12% stalk rot. The optimal inoculation technique consisted of digging a 4-cm deep furrow 15-cm from the plants at the V-6 stage and uniformly placing the mycelial-colonized grain in the furrow. Using the millet/mycelia inoculum, twenty hybrids were evaluated at four locations for tolerance to Sclerotinia stalk rot. Rankings were similar at all four locations, despite differences in climate and disease severity at each location. Averaged over four locations, stalk rot reaction ranged from a low of 17% to a high of 53%.

The national plant diagnostic network at age two. R. HAMMERSCHMIDT. Dept. Plant Pathology, Michigan State University, East Lansing, MI 48824. Phytopathology 95:S163. Publication no. P-2005-0015-NCA.

The National Plant Diagnostic Network (NPDN) was established in 2002 by the Secretary of Agriculture through the USDA/CSREES. The NPDN mission is to enhance nationwide agriculture security by quickly detecting, diagnosing, and reporting high consequence plant pathogens and pests that were deliberately or accidentally introduced. This is being achieved by creating a network of land grant universities based on a cohesive, distributed system. The NPDN is divided into five regions. Each region has a center to coordinate and support regional diagnostic activities. Some activities of the NPDN and its centers include: developing educational programs for first detectors; running scenario exercises to test the networks ability to handle a high consequence pathogen or pest; establishing web-based communication, sample submission, and data handling; and providing diagnosticians with protocols and infra-structure support. Specific examples of the accomplishments of the network will be described along with future objectives.

Relationship between weather and white mold of dry bean in North Dakota. R. HARIKRISHNAN and L. del Rio. Dept. of Plant Pathology, North Dakota State University, Fargo, ND 58105. Phytopathology 95:S163. Publication no. P-2005-0016-NCA.

Understanding how weather affects white mold [*Sclerotinia sclerotiorum* (Lib.) de Bary; WM] development is critical for disease prediction and management recommendations. Data collected in a disease survey of 90 fields during 2003 growing season was used to assess WM development (prevalence and incidence) in dry beans. Weather data for the growing season (May 15-August, 2003), collected from 10 North Dakota Agriculture Weather Network stations within the surveyed areas were sub-divided into 15 d intervals to understand the association between weather and WM development. Single degree-of-freedom contrasts were used to study variability of WM prevalence and incidence. Association between weather and WM was evaluated using stepwise regression. Results indicate variability in WM development across the region surveyed during the season. WM prevalence ranged from 57 to 80%, while incidence ranged from 9 to 26%. WM development was significantly associated with daily mean rainfall in July second half and August, and daily mean minimum temperature in August.

Targeted gene replacement of candidate pathogenicity genes in *Fusarium graminearum*. K. L. B. HILBURN (1), J.-R. Xu (2), and H. C. Kistler (1). (1) USDA-ARS CDL, St. Paul, MN 55108; (2) Dept. Botany and Plant Pathology, Purdue Univ., West Lafayette, IN 47907. Phytopathology 95:S163. Publication no. P-2005-0017-NCA.

Fusarium graminearum infection of cereals (Fusarium head blight) results in serious losses in crop yield and quality throughout the world. Genes potentially affecting pathogenicity may be predicted from EST databases and annotation of the *F. graminearum* genomic sequence. Candidate pathogenicity genes can then be studied by gene deletion and observation of resultant phenotypes. A PCR-based approach was utilized whereby sequences upstream and downstream of the targeted gene were amplified and ligated to a gene for hygromycin phosphotransferase (hph), conferring hygromycin resistance. Transformation of *F. graminearum* strain PH-1 with the construct results in replacement of the targeted gene with the hph gene by homologous recombination (double crossover event). Transformant strains were identified using PCR. So far, two candidate pathogenicity genes have been deleted and pathogenicity studies of the transformant strains are being conducted.

Characterization of *Phytophthora cactorum* isolated from American ginseng. S. N. HILL and M. K. Hausbeck. Department of Plant Pathology, Michigan State University, East Lansing, MI 48824. Phytopathology 95:S163. Publication no. P-2005-0018-NCA.

Foliar blight and root rot on ginseng caused by *Phytophthora cactorum* are significant disease problems that have been managed with frequent use of the fungicide mefenoxam. In the spring of 2003, a ginseng garden for the IR-4 residue program was established at Michigan State University using 2- to 3-year-old roots from Wisconsin. Following a period of cool, wet weather, symptoms including reddening of leaflets, root rot, and plant wilting and death were observed. *Phytophthora cactorum* was isolated from diseased plants. Disease progressed rapidly despite several applications of mefenoxam so isolates were screened for sensitivity to the fungicide by measuring radial mycelial growth on 100 ppm mefenoxam-amended V8 agar. Nineteen isolates were recovered from the MSU garden and the majority (79%) were resistant to mefenoxam. Additional isolates (95) were recovered from 35 ginseng gardens in Wisconsin and Michigan and most (76%) were resistant to mefenoxam. All isolates were tested for pathogenicity using an apple fruit bioassay and all were virulent. This is the first report of mefenoxam resistance in *P. cactorum* on ginseng.

Induced resistance in potato to common scab. E. C. HOLLISTER (1), R. Hammerschmidt (1), W. W. Kirk (1), and D. S. Douches (2). (1) Dept. Plant Pathology; (2) Dept. Crop and Soil Sciences, Michigan State University, East Lansing, MI 48824. Phytopathology 95:S163. Publication no. P-2005-0019-NCA.

Potato common scab, caused by *Streptomyces scabies*, is an important disease with two control measures: host resistance and soil moisture maintenance. Other disease management tools are critically needed because most cultivars are scab-susceptible and precise irrigation is not always possible. The successful use of resistance activators in other pathosystems implies that this method may be useful in managing common scab. The objective of this study was to investigate the effects of four compounds and application timing on common scab incidence and severity. Field experiments were conducted using a common scab-susceptible cultivar to evaluate the effects of the resistance activators and different application methods on common scab development and PR protein production. In 2001, in-furrow and foliar treatments of harpin and chitosan produced more than 30 percent of harvested tubers in the disease free category. In 2002, chitosan in-furrow treatments produced slightly more disease free tubers than the control and in 2003 no treatments were effective in reducing infection.

Screening for resistance to *Phytophthora sojae* in early maturing soybean plant introductions from the USDA soybean germplasm collection. H. JIA and J. E. Kurle. Dept. of Plant Pathology, University of Minnesota, St. Paul, MN 55108. Phytopathology 95:S163. Publication no. P-2005-0020-NCA.

Phytophthora sojae, the causal agent of Phytophthora root and stem rot (PRR), causes significant soybean yield loss in the United States. Planting resistant cultivars has proven to be the most effective measure of controlling PRR. Single dominant *Rps* genes resistant to *P. sojae* have been incorporated into soybean cultivars for control of PRR. Early maturing plant introductions (PIs) are a potential source of *Rps* genes for use in cultivars adapted for planting in northern Minnesota. We have screened a selection of 113 early maturing PIs (Maturity Groups 000, 00, 0, and I) from the USDA Soybean Germplasm Collection for the presence of the *Rps* genes and for the presence of partial resistance. *P. sojae* races 4, 7, 17, 25, and 28 are being used to determine if *Rps1c*, *Rps1k*, or *Rps6* is present in these PIs by the hypocotyl inoculation method. Six out of 113 early maturing PIs exhibited resistance to both race 17 and race 28, indicating that they may have *Rps1c* alone or multiple *Rps* genes.

Pathogenic variability of populations of the bean rust pathogen within individual bean fields. C. N. JOCHUA and J. R. Steadman. Plant Pathology Dept., University of Nebraska, Lincoln, NE 68583. Phytopathology 95:S163. Publication no. P-2005-0021-NCA.

Uromyces appendiculatus, cause of bean rust, is known to be highly variable, with over 300 races reported. However, pathogenic variation of this fungus in a single field has not been studied. Ten leaf samples with rust were collected at random in each of four fields in Honduras, Dominican Republican (DR), Nebraska (NE) and Michigan (MI). A total of 243 isolates (67 from Honduras,

50 from DR, 56 from NE and 70 from MI) were analyzed for virulence. The SAHN program of NTSYS was used to group the isolates based on disease reaction similarity on 12 bean differential lines with different rust resistance genes. Each group was considered a different rust pathotype. In Honduras, DR, NE and MI fields, 25, 18, 7, and 2 different pathotypes were identified, respectively. The number of pathotypes in each single sample from each field varied from 1 to 7. In the Honduras field, two samples had seven pathotypes, three samples had five pathotypes while other two samples had only two pathotypes out of the 25 identified in that field. Thus, multiple rust samples should be collected in each field to represent the diversity of *U. appendiculatus* pathotypes in a field.

Evaluation of high pressure spray inoculation of *bean pod mottle virus* on yield and test weight of soybean. M. A. C. LANGHAM, C. L. Cihlar-Strunk, and A. E. Hoberg. South Dakota State University, Plant Science Dept., Brookings, SD 57007. Phytopathology 95:S164. Publication no. P-2005-0022-NCA.

Bean pod mottle virus (BPMV) (Genus: *Comovirus*; Family: *Comoviridae*) was inoculated to soybean (Prairie 2141 RR) in two-row plots (6 m) at three dates (three replications per date) with five different inoculation methods (hand inoculation or air pressure inoculation at 172, 345, 517, or 690 kPa) during 2003. An uninoculated control was included for comparison. Yield loss at the early inoculation date was significantly greater ($P = 0.001$) than yield loss in the groups inoculated at the middle and late dates. Yield losses were also significantly different ($P = 0.001$) for inoculation method. Greatest yield losses were observed with hand inoculation followed closely by air pressure inoculation at 690 kPa. Inoculation at 172 and 345 kPa was not significantly different from the control. Test weights of the soybeans followed an opposing pattern with test weight for the early inoculation date being significantly greater (0.01) than the test weights for the middle and late dates.

Effects of two genotypes of *Phialophora gregata* on soybean growth and yield. D. MALVICK and E. Grunden. Dept. of Crop Sciences, Univ. of Illinois at Urbana-Champaign, Urbana, IL 61801. Phytopathology 95:S164. Publication no. P-2005-0023-NCA.

Two genotypes of *Phialophora gregata* cause brown stem rot (BSR) of soybean. Typically, genotype A causes leaf symptoms and internal stem browning, whereas genotype B causes internal stem browning only. This study was conducted to determine the effects of each genotype on soybean growth and yield in replicated greenhouse and field experiments. Four to six cultivars with different levels of BSR resistance were inoculated by stem injection with genotypes A and B in replicated greenhouse and field experiments. Internal stem browning developed in all inoculated plots. In greenhouse experiments, both genotypes reduced fresh biomass and number of pods per plant 5%-50% relative to controls at the R7 stage. In field experiments in 2002, both genotypes reduced yields of four cultivars tested, although the only significant ($P = 0.05$) yield reduction (12%) occurred in one cultivar inoculated with the B genotype. Field inoculations in 2003 had no consistent effect on yields of the five cultivars tested. Preliminary results suggest both genotypes of *P. gregata* can reduce growth and yield of soybeans in greenhouse and field studies.

Evaluation of crops common to Minnesota for management of the soybean cyst nematode. D. R. MILLER (1), S. Y. Chen (1), P. M. Porter (2), G. A. Johnson (1), and D. L. Wyse (2). (1) Southern Research and Outreach Center, University of Minnesota, Waseca, MN 56093; (2) Dept. of Agronomy and Plant Genetics, University of Minnesota, St. Paul, MN 55108. Phytopathology 95:S164. Publication no. P-2005-0024-NCA.

In the north central region of the U.S., corn is almost exclusively used as a non-host rotation crop with soybeans for management of the soybean cyst nematode (SCN). This study was conducted to determine if other crops commonly grown in Minnesota were effective in reducing SCN populations when rotated with soybeans. SCN population changes were monitored at mid-season and at harvest in 2001 and at planting, mid-season, and at harvest in 2002 for sixteen crops along with two soybean controls (SCN resistant and susceptible) and 6 fallow controls near Waseca, Lamberton, and Morris, Minnesota. Compared to the hand-weeded fallow control, SCN populations were not consistently lower due to any previous crop. However, to identify and screen crops for future research, the SCN population change factors were combined over locations and sampling times. Sugarbeets, canola, sorghum, alfalfa, pea, corn with rye, and wheat had lower SCN populations than corn while potato, hairy vetch, flax, oats, red clover, barley, sunflower, and buckwheat were higher. These crops are currently being evaluated under greenhouse conditions.

PVY$^{OC\ \&\ N}$ expression in advanced potato breeding lines. D. S. MOLLOV (1), D. C. Hane (2), and C. A. Thill (1). (1) Dept. Horticultural Science, University of Minnesota, St. Paul, MN 55108; (2) Hermiston Exp. Station, Oregon State University, Hermiston, OR 97838. Phytopathology 95:S164. Publication no. P-2005-0025-NCA.

PVY symptoms vary widely and asymptomatic (ASM) cultivars lead to erroneous acceptance of certified seed and inefficient selection during breeding. This research was designed to: 1) detect potential ASM clones in advanced U.S. breeding populations, and 2) determine the utility of multi location selection for this trait. Seventy five breeding lines from 8 programs were planted in 2003 in 2 disease transmission nurseries; Oregon (OR) and Minnesota (MN). Following infection, genotypes were evaluated in a 03/04 winter nursery and disease severity was scored visually from 1 (no readable symptoms) to 5 (severe symptoms), then tested for PVY$^{OC,\ N}$ by ELISA. A clone scoring 1, but positive by ELISA was considered ASM. PVY$^{OC,\ N}$ infection frequency was 77 and 8% in MN, and 93 and 4% in OR, respectively. This research supports that multi location testing was necessary. Nine genotypes were identified as being potentially PVY ASM after exposure at MN, 13 at OR and 17 after combining locations. Early generation selection should be applied to reduce the number of asymptomatic clones in breeding.

Use of remote sensing, geographic information systems, and spatial statistics to assess soybean yield and soybean cyst nematode (SCN) populations in soybean fields. A. J. A. MOREIRA, J. Guan, G. L. Tylka, and F. W. Nutter, Jr. Dept. Plant Pathology, Iowa State University, Ames, IA. Phytopathology 95:S164. Publication no. P-2005-0026-NCA.

SCN-susceptible soybean varieties were planted in two SCN-infested fields divided into 995 and 613 (2 m × 3 m) quadrats at the ISU Woodruff and Bruner Research Farms from 2000 to 2002. SCN population densities were determined for each quadrat prior planting and after harvest. Reflectance from soybean canopies was recorded every 7 to 14 days throughout seasons, and soybean yield was obtained from each quadrat. Spatial dependence of SCN populations varied within and between seasons in both fields. Environmental factors seem to affect spatial structure of SCN populations, and severe winters decreased the distance that spatial dependence was observed in SCN populations. The best relationships between reflectance and yield occurred when reflectance was assessed in late July/early August, when soybean plants were at R5 growth stage. Although the relationships between reflectance and yield were affected by the environment, vegetation indices that combined infrared with red or green wavelength bands provided the best relationships with yield.

Characterization of infection of two soybean genotypes by *Sclerotinia sclerotiorum*. B. D. NELSON. Dept. Plant Pathology, North Dakota State University, Fargo, ND 58105-5012. Phytopathology 95:S164. Publication no. P-2005-0027-NCA.

Characterization of infection of a partially resistant (NKS 1990) and a susceptible (MN 0301) soybean (*Glycine max* (L.) Merr.) cultivar by *Sclerotinia sclerotiorum* was examined with light and scanning electron microscopy. Petioles of plants at R1-R2 growth stages were inoculated in a humid chamber at 22°C with infested tissue paper placed directly on the petioles. Tissues were examined at 24, 48, 30, 72 and 110 h post inoculation. Infection occurred directly through the walls of the trichomes and the epidermal cells. Infection hyphae were generally swollen at the ends and often there were clusters of infection hyphae originating from one hypha. Infections began between 24 to 30 h post inoculation. Hyphae in the cortex were observed as early as 48 h, but in some inoculated plants there were no hyphae after 72 h. Intracellular hyphae were observed in host tissue before there was any gross evidence of host tissue degradation by the pathogen. There were no apparent differences between NKS 1990 and MN 0301 in observations made up to 110 h post inoculation. In nature, trichomes are most likely the primary site of infection on petioles.

Soybean virus survey in North Dakota. B. D. NELSON and G. A. Danielson. Department of Plant Pathology, North Dakota State University, Fargo, ND 58105-5012. Phytopathology 95:S164. Publication no. P-2005-0028-NCA.

Soybean (*Glycine max* (L.) Merr.) is the principal oilseed in North Dakota with 1.3 million ha planted in 2003. To benchmark current soybean viruses, surveys were conducted in 2001 and 2002. In August 2001 leaves were collected arbitrarily from 124 soybean fields from 13 eastern counties. In 2002, leaves from plants showing virus-like symptoms were collected from 84 fields in Cass, Grand Forks, Richland, and Traill counties. All leaves were frozen at –80°C until processed. Sap was extracted in 0.02 M phosphate buffer and samples were tested for presence of viruses with DAS ELISA kits from Agdia (Elkhart, IN). Leaf samples from 2001 were tested for presence of Bean pod mottle virus (BPMV) and Soybean mosaic virus (SMV) while samples from 2002 were tested for BPMV, SMV, Alfalfa mosaic virus

(AMV) and Tobacco streak virus (TSV). Also, food grade seed was collected from 21 seed lots grown in the Red River Valley in 2001. Seeds were hydrated in distilled water, seed coats were removed and ground in buffer and samples tested for BPMV. All leaf and seed samples were negative for viruses. These results indicate that BPMV, SMV, AMV and TSV are not yet problems in North Dakota soybean production.

Evaluation of the Iowa State Model to predict the seasonal risk for Stewart's disease of corn. F. W. NUTTER, JR. and P. E. Esker. Dept. Plant Pathology, Iowa State University, Ames, IA 50011. Phytopathology 95:S165. Publication no. P-2005-0029-NCA.

The presence of Stewart's disease of corn in seed corn fields has severe economic implications in that seed corn harvested from fields found to have Stewart's disease cannot be exported to many countries due to phytosanitary regulations. The predictive model is based upon the number of months during Dec., Jan., and Feb. that the mean monthly air temperature was ≥24 F; 0 months represents no risk, 1 month ≥24 F represents moderate-to-high risk, and 3 months ≥24 F represents a high risk for Stewart's disease. Risk predictions may be up or downgraded based upon the presence of snow cover that maintained 4" soil temperatures ≥30 F during periods when air temperatures were very low. In 2001, the predicted seasonal risk was low (<2% prevalence) and the actual prevalence was 2.9%. In 2002, the predicted seasonal risk was moderate (10% prevalence) and the actual prevalence was 4.9%. In 2003, the predicted risk for Stewart's disease prevalence was low for 2/3 of Iowa and moderate-to-high for 1/3 of the state. Therefore, the predicted risk for 2003 was 5% and the actual prevalence was 8.9%.

Resistance to wheat leaf rust and stem rust in Sharon goat grass (*Aegilops sharonensis*). P. OLIVERA (1), B. Steffenson (1), and Y. Anikster (2). (1) Dept. of Plant Pathology, University of Minnesota, St. Paul, MN. (2) Plant Science Dept., Tel Aviv University and Institute for Cereal Crops Improvement, Tel Aviv, Israel. Phytopathology 95:S165. Publication no. P-2005-0030-NCA.

Leaf rust, caused by *Puccinia triticina*, and stem rust, caused by *Puccinia graminus* f. sp. *tritci*, are important diseases of wheat in many production areas. Wild relatives can be rich sources of resistance genes for cultivated wheat. We tested 102 accessions of *Aegilops sharonensis*, a diploid relative of wheat endemic to Israel, to identify potential sources of resistance to leaf rust and stem rust for use in wheat improvement. Over 50% of the accessions were highly resistant leaf rust as seedlings, and >70% were highly resistant in the adult stage, suggesting that additional resistance genes were expressed during the later developmental stages. The frequency and level of resistance in accessions was higher in southern Israel (Zikim and Nizzanim) than in northern and central Israel. Over 85% of the accessions were resistant to stem rust race QCCJ, but only 54% were resistant to the more virulent race TPMK. These results indicate that *Ae. Sharonensis* may be a valuable source of resistance genes for wheat improvement.

***Sclerotinia sclerotiorum* does not detectably modify or metabolize lignin in mature soybean stems.** A. J. PELTIER (1), R. D. Hatfield (2), and C. R. Grau (1). (1) Dept. Plant Pathology, Univ. of WI; (2) USDA-ARS, Dairy Forage Res. Ctr.; Madison, WI 53706. Phytopathology 95:S165. Publication no. P-2005-0031-NCA.

Sclerotinia sclerotiorum (*Ss*) secretes various cell wall degrading enzymes to establish a pathogenic relationship with soybean. Cellulases and poly-galacturonases are involved but the activity of lignin peroxidase is not known. The objective of this study was to determine if *Ss* degrades or modifies lignin in soybean stem tissues. *Ss* was seeded onto moist, sterile, ground mature soybean stems in watch glasses (WG). WG were sealed in glass Petri dishes to maintain humidity. After 6, 12 or 23 days of incubation, the contents of each WG was dried, weighed and subjected to nitrobenzene oxidation and gas chromatography. Oxidized lignin components were quantified in each sample and included *p*-hydroxybenzaldehyde, vanillin, syringaldehyde, and vanillic, syringic, coumaric, and ferulic acids using isovanillin as the internal standard. Assayed compounds were of equal concentration for all treatments (P = 0.36 - 0.98). *Ss* did not degrade or modify lignin in mature soybean stems. Results justify further investigating the role of lignin in resistance to *Ss*.

Using a general disease development model to assess rust incipient times in a season: Implications for soybean rust. S. PIVONIA and X. B. Yang. Dept. Plant Pathology, Iowa State University, Ames, IA 50011. Phytopathology 95:S165. Publication no. P-2005-0032-NCA.

Soybean rust (*Phakopsora pachyrhizi*) is a threat to U.S. soybean production. Previous risk assessments showed that weather conditions during a growing season are suitable for disease development in the U.S. Previous studies assumed availability of inoculum early in a season and assessment of rust appearance time during a season is critical to determine yield loss potential. Comparative epidemiology was used to assess rust incipient times in 4 sites across the U.S. soybean production area. The effects of temperature on development of 4 rusts were evaluated using a general disease model. The relationships between modeling results, infections multiplication rate, and the expected rusts incipient times were examined. Among the rusts studied, early-appearing rusts had suitable conditions for development earlier in the season. However, a lag of several weeks to 3 months was found between the time suitable for rust development and the time when rust is detected in fields. The lags differed among the rusts examined. Implications of modeling results to soybean rust expected incipience in a growing season are discussed.

Statewide monitoring and sensitivity shifts to azoxystrobin in *Alternaria solani* in WI. N. ROSENZWEIG (1), G. Olaya (2), and W. R. Stevenson (1). (1) Dept. of Plant Pathology, University of Wisconsin, Madison, WI 53706; (2) Syngenta Crop Protection, Vero Beach, FL 32967. Phytopathology 95:S165. Publication no. P-2005-0033-NCA.

Azoxystrobin (AZ) was released in the U.S. in 1999 and initially provided outstanding control of potato early blight. Disease progression in AZ potato treated field plots during 1997 was effectively suppressed, compared to chlorothalonil (CH) and untreated plots. After six years of AZ commercial use, the level of early blight control is declining. Disease progress curves in plots treated with AZ (3 sprays)/CH (6 sprays), from 1999-2003, progressively resembled those from CH treated plots. *Alternaria solani* isolates with decreased *in vitro* sensitivity to AZ were first detected in the U.S. in WI in 2001. During 2002 and 2003 statewide monitoring of *A. solani in vitro* response to AZ revealed a sensitivity decrease correlated with site-specific mutations in the cytochrome b gene. Mean EC_{50} (mg/L) values increased by more than 20 fold between the 1998 (0.03 mg/L) baseline and 2003 (0.7 mg/L).

Linking soil properties to root rot suppression by organic amendments in the field. D. ROTENBERG (1), L. R. Cooperband (1), and R. M. Goodman (2). (1) Dept. of Soil Science; (2) Dept. of Plant Pathology, University of Wisconsin, Madison, WI 53706. Phytopathology 95:S165. Publication no. P-2005-0034-NCA.

Paper mill residuals (PMR), an industrial by-product of the paper making process, and PMR composts have been applied successfully to agricultural soils to improve soil quality. A vegetable cropping systems study in Wisconsin's Central Sands was initiated to evaluate the effects of annual additions of fresh PMR and two PMR composts on soil properties and naturally occurring diseases. All PMR amendments reduced severity of common root rot of bean in the field and greenhouse in 2002. Our objective was to identify soil properties associated with root rot suppression. Soil measures included total carbon (TC), particulate organic matter carbon (POM-C), volumetric moisture, nitrate-N, total microbial activity (FDA), and rhizosphere bacterial community composition (T-RFLP analyses). High microbial activity correlated with increased amounts of TC and POM-C in all amended plots. Multiple regression (MR) analysis revealed that TC and microbial activity together explained 70 percent of the variation in root rot severity, while community composition and soil nitrate-N played minor roles in the MR model.

Detection of brown root rot of alfalfa in Minnesota and Wisconsin. D. A. SAMAC (1) and C. R. Hollingsworth (2). (1) Dept. of Plant Pathology, University of Minnesota and USDA-ARS, St. Paul, MN 55108; (2) Dept. of Plant Pathology, University of Minnesota, Crookston, MN 56716. Phytopathology 95:S165. Publication no. P-2005-0035-NCA.

Brown root rot of alfalfa, caused by *Phoma sclerotioides*, is associated with stand decline and reduced yield of forage legumes in western Canada and the western U.S. A survey was conducted in the fall of 2003 to determine the distribution of the disease in the upper midwest. Alfalfa plants were submitted from Iowa, Illinois, Minnesota, Wisconsin, and Ontario from 104 locations. DNA extracted from roots was used in PCR reactions with *P. sclerotioides*-specific primers. In Wisconsin, the pathogen was found in Shawano, Columbia, and Oconto County. In Minnesota, plants from seven counties tested positive for the pathogen including: Marshall, Otter Tail, Pennington, Red Lake, Sherburne, Wabasha, and Washington County. No positive plants were found in samples submitted from Illinois, Iowa or Ontario. Samples submitted in the spring of 2004 from fields with winter injury in Pierce Co. and St. Croix Co., WI and Winona Co., MN tested positive for the pathogen. This study suggests that the disease is found throughout Minnesota and may be associated with winter kill.

Invasive species: The view from a containment facility. N. SHISHKOFF. Foreign Disease/Weed Science Research Unit, ARS/USDA, Fort Detrick, MD 21702-5023. Phytopathology 95:S166. Publication no. P-2005-0036-NCA.

The biosafety level 3 containment facility at Fort Detrick, MD, is currently used to study organisms with the potential to spread to the United States, or which have already gained a foothold in some parts of the country. A "virtual tour" of the containment facility will point out its key features, then some of the organisms currently being studied will be discussed, including soybean rust, soybean dwarf virus, karnal bunt of wheat, and "sudden oak death". These will serve as examples as to how decisions are made of what organisms to study, how a disease is studied in preparation of its introduction, and what happens if the organism is then introduced. Recent technological advances promise to improve methods of detection, breeding for resistance, and understanding of disease, all of which will increase the need for BSL-3 facilities.

Evaluation of azoxystrobin and fludioxonil for management of corn seedling diseases in Illinois. C. D. SOLORZANO, W. L. Pedersen, and D. K. Malvick. Dept. of Crop Sciences, University of Illinois, Urbana, IL 61801. Phytopathology 95:S166. Publication no. P-2005-0037-NCA.

Seedborne fungi are causal agens of corn seed rots and seedling blights. The fungicides azoxystrobin (AZ), fludioxonil (FL) and mefenoxam (MF) were evaluated in replicated field trials for management of seedborne pathogens. These fungicides were applied to seed of seven corn hybrids infected with various combinations of *Fusarium moniliforme*, *Aspergillus flavus*, *Aspergillus niger*, *Penicillium* spp., *Stenocarpella maydis* and *Trichoderma* spp. Seed of hybrid W-A was infected with all of the fungi except *S. maydis* and *Trichoderma* spp. Plants of WA grown from seed treated with AZ, FL + MF, FL, or AZ + FL + MF yielded significantly more than plants grown from untreated controls (UC) ($P < 0.05$). Hybrid FRG was infected with *Stenocarpella maydis* and *Fusarium moniliforme*, and when treated with AZ + FL + MF treatment resulted in the highest increase in emergence and yield for the seven hybrids combined, and they were greater ($P < 0.05$) than the AZ and UC treatments. Results suggest fungicidal seed treatments can improve stand and yield of corn hybrids produced from seed infected with fungi.

Effects of co-inoculation of ectomycorrhizal fungi and *Streptomyces* bacteria on the growth of *Pinus resinosa* and on the biological control of root pathogens. J. L. STOLZE and D. M. Becker. Dept. Biology, Northern Michigan University, Marquette, MI 49855. Phytopathology 95:S166. Publication no. P-2005-0038-NCA.

Co-inoculation of roots with proper bacterial-fungal combinations can potentially improve plant growth and reduce plant disease. Interactions between 16 strains of potential mycorrhizal helper bacteria (MHB) (*Streptomyces* spp.), two ectomycorrhizal (ECM) fungi, three root pathogenic fungi, and *P. resinosa* were studied. A physiological profile of the bacteria was developed using Biolog SF-P2 microplates with 95 carbon sources to determine which MHB might be the most efficient at colonizing and persisting in the rhizosphere. Co-plate bioassays were performed between MHB and ECM fungi and MHB and pathogenic fungi. After two weeks of growth, 50% of the MHB significantly ($P < 0.05$) enhanced the growth of both ECM fungi; 43% and 81% of the MHB significantly ($P < 0.05$) inhibited the growth of two pathogenic fungi. Growth chamber studies of *P. resinosa* seedlings inoculated with MHB, ECM and a pathogenic fungus were also performed. These MHB and ECM represent a promising method to improve plant growth and are an important alternative to the use of chemical pesticides.

Evaluation of stratified sampling strategies to access maximal genetic diversity from crop plant genebank collections. R. L. SYVERSON and J. M. Bradeen. Dept. of Plant Pathology, University of Minnesota, St. Paul, MN 55108. Phytopathology 95:S166. Publication no. P-2005-0039-NCA.

Wild germplasm is a frequently accessed source of genes for crop improvement. For potato, the wild species *Solanum bulbocastanum* is a source of late blight and *Verticillium* resistance. We seek a plan germplasm sampling strategy to maximize genetic diversity with minimal resource input. We used AFLP estimates of genome diversity to evaluate stratified sampling methodologies based on subspecies affiliations, geographic origin, and intra- vs. inter-population relationships for more than 200 *S. bulbocastanum* genotypes from the USDA Potato Genebank. Included were 2-5 *S. bulbocastanum* genotypes from each of 42 populations representing 3 morphologically defined subspecies and the entire geographic range of the species. Genotypes were analyzed with 1-3 AFLP primer pairs. Dendrograms do not support defined subspecies. Genetic distance between genotypes correlates poorly with geographic distance between populations. Considerable genetic variation occurs both within and between populations. Our results will be interpreted relative to sampling strategies for crop plant germplasm utilization.

Rust fungi-shifty pathogens: Molecular methods for rapid detection and identification. L. J. SZABO and C. Barnes. USDA ARS Cereal Disease Laboratory, Dept. Plant Pathology, University of Minnesota, St. Paul, MN 55108. Phytopathology 95:S166. Publication no. P-2005-0040-NCA.

In recent years, there has been a growing interest in the development of molecular methods for the rapid detection and identification of rust fungi. In part, this has been driven by an increased concern about crop biosecurity and the recent spread of economically important rust pathogens. Real-time PCR assays using TaqMan probes have been developed for cereal and grass rusts including stem rust (*Puccinia graminis*), stripe rust (*P. striiformis*), crown rust (*P. coronata*) and leaf rust (*P. recondita* and *P. triticina*). These assays are species specific and work with either isolated spores or infected plant material. Assays are linear over four orders of magnitude and can detect DNA levels equivalent to 10 urediniospores. A rust specific internal standard has been developed as an internal control. In addition, this technology provides new tools for properly identifying rust samples, when the characteristic spores (teliospores) and hosts information are not available.

Investigations of manganese oxidation by two plant pathogenic fungi. I. A. THOMPSON (1), J. R. Xu (1), D. M. Huber (1), and D. G. Schulze (2). (1) Dept. of Botany and Plant Pathology; (2) Dept. of Agronomy, Purdue University, West Lafayette, IN. Phytopathology 95:S166. Publication no. P-2005-0041-NCA.

Manganese oxidation is hypothesized to influence fungal virulence in two pathosystems, take all of wheat caused by *Gaeumannomyces graminis* var. *tritici* (Ggt) and blast of rice caused by *Magnaporthe grisea*. Manganese oxidation activity in crude culture extracts from Ggt was inhibited by phenanthroline, a copperchelating compound, suggesting the involvement of a multicopper oxidase such as laccase in Mn oxidation. Deletion of genes with homology to manganese peroxidase (MnP), a lignolytic enzyme containing a heme prosthetic group, altered but did not abolish Mn oxidation by *M. grisea*. Compared to wild-type isolates, deletion mutants with non-wild type Mn oxidation phenotypes induced smaller lesions on susceptible rice line CO-39. This evidence supports a link between Mn oxidation and virulence and suggests that two enzymes influence Mn oxidation for these plant pathogenic fungi.

Efficacy of propiconazole for preventative and therapeutic control of oak wilt in Minnesota. K. WARD, J. Eggers, and J. Juzwik. North Central Research Station, USDA Forest Service, St. Paul, MN. Phytopathology 95:S166. Publication no. P-2005-0042-NCA.

Systemic injection of the fungicide propiconazole (PPZL) is one of several measures used in the management of oak wilt caused by *Ceratocystis fagacearum* (Bretz) Hunt. Efficacy data for PPZL use in northern U.S. states, however, is lacking. Operational treatments for preventative and/or therapeutic control of oak wilt in red and white oak species were performed by commercial arborists in 1998 and evaluated over 5 years; experimental trials with red oaks began in 2002. Over one third of the red oaks and only one white oak became infected after operational treatments with PPZL to prevent spread of the pathogen through root grafts,. When PPZL was injected 2 weeks prior to experimental crown inoculation of northern pin oaks with the pathogen, only limited wilting occurred. In contrast, when the pathogen was introduced 2 weeks prior to PPZL treatment, 79% of inoculated trees died. Therapeutic treatment with PPZL of infected wilting red oaks failed to arrest symptom development in experimental trials. In the operational evaluation, very few of the infected white oaks exhibited new wilt symptoms after treatment and none of the trees had died.

***Tomato spotted wilt virus* glycoprotein G(N) binds larval thrips midguts and inhibits virus acquisition.** A. E. WHITFIELD (1), D. E. Ullman (2), and T. L. German (1). (1) Dept. Entomology, University of Wisconsin, Madison, WI 53706; (2) Dept. Entomology, University of California, Davis, CA 95616. Phytopathology 95:S166. Publication no. P-2005-0043-NCA.

Tomato spotted wilt virus (TSWV), the prototypic member of the genus *Tospovirus*, is transmitted from plant-to-plant by thrips. The envelope glycoproteins, G(N) and G(C), are essential for virus infection of thrips. Thus it is assumed that the envelope glycoproteins play important roles in the entry of TSWV into the insect midgut. To directly test the hypothesis that G(N) plays a role in TSWV acquisition by thrips, we expressed and purified a soluble, recombinant form of G(N) (G(N)-S). We detected specific binding to thrips midguts when purified G(N)-S was fed to thrips in an *in vivo* binding assay. TSWV N protein and HCMV glycoprotein B did not bind to thrips midguts indicating that the G(N)-S/thrips midgut interaction is specific. TSWV-acquisition inhibition assays revealed that thrips fed concomitantly on purified TSWV and G(N)-S had reduced amounts of virus in their midguts when compared to thrips fed TSWV alone. Our findings provide evidence that G(N) serves as a viral ligand that mediates attachment of TSWV to thrips midguts.

Competitive selection of *Phytophthora infestans* in the U.S. and Northern Ireland. G. K. YOUNG (1,2), W. W. Kirk (1), L. R. Cooke (2), and P. Tumbalum (1). (1) Dept. Plant Pathology, Michigan State University, East Lansing, MI 48824; (2) Dept. of Applied Plant Science, Queen's University of Belfast, Newforge Lane, Belfast, BT9 5PX, UK. Phytopathology 95:S167. Publication no. P-2005-0044-NCA.

Distinct clonal lineages of *Phytophthora infestans* have evolved in the U.S. and across Europe. Knowledge of competitive interactions between genotypes will allow better understanding of the role of the cultivar in population selection. Representative isolates were chosen from both Michigan and N. Ireland for inoculation onto two separate field trials in 2003. Isolates were characterized using common genotypic and phenotypic tests. Cultivars with differing levels of resistance were planted for comparison. Single-lesions were removed from the field at 1 percent infection, re-characterized and re-assigned to their respective groupings. In N. Ireland selection by cultivar was evident with fewer isolates infecting the more resistant cultivars. By contrast, in the U.S. the highly aggressive US-8 dominated infection of all cultivars regardless of resistance to foliar late blight.

Kernel infection by *Fusarium graminearium* in spring wheat germplasm. X. Zhang (1), Y. JIN (2), and D. Dykes (3). (1) Dept. Agronomy and Plant Genetics, University of Minnesota, St. Paul, MN 55108; (2) Cereal Disease Laboratory, USDA-ARS, St. Paul, MN 55108; (3) College of Pharmacy, South Dakota State University, Brookings, SD 57006. Phytopathology 95:S167. Publication no. P-2005-0045-NCA.

This study investigated infection of wheat kernels by *Fusarium graminearum*, by comparing kernel infection with Fusarium damaged kernel (FDK), amount of DON, and level of kernel discoloration and shriveling. Seed samples of 14 lines, with three replicates over two years in a *F. graminearium* inoculated nursery were used. Two hundred seeds per experiment unit were grouped into four classes: plump normal color, plump bleached, shriveled normal color, and shriveled discolored. Kernel infection was evaluated on acidic PDA. Correlation of seed infection with FDK was significant, and correlation with DON was not. Highest frequency of infection occurred on the discolored and shriveled kernels. Correlation analysis of seed infection between classes and regression analysis of percentage of seed infected in the four classes to total percentage of seed infected indicated that bleached plump kernels and shriveled normal color kernels may not be caused by fungal infection.