

2009 NORTH CENTRAL DIVISION MEETING ABSTRACTS
JUNE 21-23, 2009 – AMES, IOWA

SYMPOSIUM: IMPLICATIONS OF CLIMATE CHANGE ON PLANT PATHOGENS

- S-1 Climate impacts on agriculture: Implications for crop management.** J. L. HATFIELD. National Soil Tilth Laboratory, Ames, IA.

Climate impacts on agriculture can be either direct or indirect in terms of affecting production or quality of the product. The direct impacts result from temperature, precipitation, or CO₂ effects on crop growth and development while the indirect impacts result from the climatic impacts on weed, insect, or disease populations which in turn affect crop production. Climate has changed, is changing, and will continue to change; however, the current state of the climate relative to agriculture is one in which there is increasing variability in temperature and precipitation and rising CO₂ concentrations. Increasing temperatures hasten plant development and can lead to plant stress when there are limited soil water supplies. One aspect of rising CO₂ concentrations is increased water use efficiency; however, this may not overcome plant stress induced by lack of soil water recharge by variable precipitation. Variations in climatic parameters will affect growth and development of weeds which will make weed management an increasing challenge. Changing temperature and precipitation patterns will affect the overwintering of insects and diseases and increase the range of pests. Development of management strategies to increase agricultural production will have to consider all aspects of climate on the agricultural systems and where the opportunities exist for improved efficiency in crop production and potential for enhanced crop protection strategies.

- S-2 Climate change and food security.** L. ZISKA. USDA Crop Systems and Global Change Lab, Beltsville, MD.

Documented and projected changes in atmospheric carbon dioxide are likely to alter agricultural productivity in two ways: directly, by supplying additional carbon for photosynthesis and growth; and, indirectly, by altering climate, specifically surface temperatures and precipitation. In this overview on the impact of carbon dioxide and climate change on food security, I will present data from a number of sources that document the likely changes in temperature, temperature and carbon dioxide and water availability on crop quality and production, and identify other biological interactions with pests, weeds, and diseases. In addition, I will discuss possible opportunities, focusing on exploitation of genetic and intra-specific variability within plant germplasm as a possible means to maintain agricultural production in the future.

- S-3 Forecasting weather and climate for plant disease models: A western perspective.** L. COOP and the Western Weather Workgroup Integrated Plant Protection Center. Oregon State University, Corvallis, OR.

Input requirements for many plant disease models currently challenge our ability to incorporate short and long term climate change effects. In the Western US, these challenges supplement ones incited by the mountain and coastal influenced terrain. The Western Weather Workgroup has addressed some of these needs via a series of meetings, grant projects, and on-farm field trials. Some helpful technologies that address the problems of scale in disease forecasting that we are using include PRISM climate mapping, mesoscale weather forecasts, online error analysis, ingest of real time public and private weather observations, and new methods for downscaling IPCC climate change

model projections. A proposed Swiss Needlecast model for PNW forests can benefit from these climate change model projections, and so can degree-day model forecasts by using modified climate "normals". Many of the technologies presented have been incorporated into a nationally focused website, <http://uspest.org/wea>, which addresses several IPM and plant biosecurity needs.

S-4 Modeling plant disease in a changing climate. J. RUSSO. ZedX, Inc., Bellefonte, PA.

Environment, along with host and pathogen, are the long-recognized key components for disease development. A changing climate impacts the environment component and, by their triangular relationship, host and pathogen. The challenge to plant epidemiological modelers is to incorporate the appropriate weather variables for quantifying the impact of a changing climate on disease development. Furthermore, modelers must be sensitive to the spatial and temporal scales represented by weather variable data and the uncertainty associated with the data in predicted disease behavior. Lastly, even after accounting for scale and uncertainty, the modeling of plant disease in a changing climate must be evaluated in the context of an ecosystem.

SYMPOSIUM: NEMATODE PESTS OF THE NORTH CENTRAL REGION

S-5 Insights into the mode of action of cyst nematode effector proteins. T. HEWEZI and T. J. Baum. Iowa State University, Ames, IA.

Plant-parasitic cyst nematodes secrete proteinaceous effectors, which play the central role in host infection and formation of their feeding sites. The majority of these proteins are novel and their putative functions can not be assigned due to the absence of significant sequence similarities to known proteins in sequence databases. Elucidation of the mechanism of action of these effectors is an absolute necessity for engineering resistance to these damaging plant pests. Remarkable progress has been made recently in understanding the mode of action of cyst nematode effectors. Two effectors targeting different subcellular compartments have been functionally characterized. The first effector is a cellulose binding protein (CBP) that acts in cell wall modification. Transgenic plants expressing CBP revealed its vital role in mediating plant susceptibility to cyst nematode infection. We identified pectin methylesterase 3 (PME3) as a strong and specific interactor of CBP. Our data indicate that CBP interacts with PME3 thereby activating and potentially targeting this enzyme to modulate the properties of the cell wall via modification of pectin, and subsequently affecting plant growth and pathogen susceptibility. The second effector is a cytoplasmic protein, which we term 10A06. 10A06 was found to affect plant morphology and nematode susceptibility when expressed in planta. 10A06 specifically interacts with a plant spermidine synthase (SPDS). Our results collectively indicate that 10A06 functions in modulating polyamine signaling to promote plant susceptibility.

S-6 Plant-parasitic nematodes in midwestern corn fields. T. A. JACKSON. University of Nebraska, Lincoln, NE.

Plant parasitic nematodes have historically been a costly challenge for corn production in some areas, but some common cropping practices helped to mitigate their impacts. During recent years, producers have utilized more pyrethroid insecticides and transgenic insect resistant corn hybrids, neither of which is as effective against nematodes as the organosphosphate and carbamate soil insecticides used in the past. The recent increase in the incidence of damage caused by nematodes, particularly in the Midwest has led to questions about the prevalence of nematodes in corn fields and the potential for further injury. In 2006, a preliminary survey, funded by Syngenta Seed Care, of corn fields in Nebraska was initiated and expanded to include other states in the corn belt during 2007.

Three fields were arbitrarily selected to represent each county with more than 20,000 acres of corn. Both soil and root samples were collected from the fields and submitted to one of six laboratories, five university and one private laboratory, for analysis. Results of the analyses indicated that plant parasitic nematodes were present in practically every field to varying degrees, with some population densities exceeding historic estimates of damage thresholds. Results also varied markedly by state, indicating that the efficiency of the nematode extraction procedures varied between laboratories. These results indicate that there is the potential for yield loss in corn caused by nematodes warranting further research.

S-7 *Pratylenchus penetrans* is a common and persistent pathogen of potato in the north central region. A. E. MACGUIDWIN. University of Wisconsin-Madison, Madison, WI.

Root lesion nematodes, *Pratylenchus spp.*, are the most common nematode problem in the North Central region. *Pratylenchus penetrans* is the species most damaging to a wide range of crops including potato. Surveys showed 9 of 102 potato fields in Wisconsin surpassed the threshold for nematode damage (200 per 100 cc soil). The same number of fields surpassed the damage threshold for *Verticillium dahliae* (10 propagules per gram soil). The majority of the remaining fields were infested with subthreshold densities of both pathogens and at risk for the potato early dying disease (PED) caused by the interaction of *V. dahliae* and *P. penetrans*. The potential for PED in the surveyed fields was verified by a bioassay and corroborated our laboratory research showing the interaction of these two pathogens. Historical data shows that population densities of *P. penetrans* have increased in Wisconsin over the last twenty years. One of the factors likely to have contributed to an increase in *P. penetrans* is a change in crop rotations. Rotation crops vary in their host status for reproduction by *P. penetrans*, but also important are root system characteristics that impact the quantity and quality of dead root fragments serving as reservoirs of nematode inoculum for the next crop. Our analysis of many historical data sets showed that a significant proportion of a *P. penetrans* population survives in detached root fragments when live hosts are not available. Growers recognize the importance of *P. penetrans* to potato, but are only beginning to appreciate the impact of *P. penetrans* on other crops and the role that crop rotation plays in the root lesion nematode disease of potato.

SYMPOSIUM: IMPLICATIONS OF PLANT DISEASES IN BIOFUEL PRODUCTION

S-8 Plant disease in *Miscanthus* and other cellulosic biomass crops. E. HEATON. Iowa State University, Ames, IA.

Cellulosic biomass crops are slated for production on roughly 30 million acres of U.S. farmland in the next 20 years but very little is known about the implications plant disease might have for these crops. To date, the acreage of dedicated energy crops is small, and disease issues have yet to cause concern. What issues might we expect? What has been observed in small stands? Reproductive growth is not important in cellulosic crops, therefore chief concerns are expected to be foliar blights that reduce carbon assimilation, and root and stalk rots that reduce harvestable yield. In the Midwest, sorghum (*Sorghum bicolor*), switchgrass (*Panicum virgatum*) and Miscanthus (*Miscanthus × giganteus*) are the leading herbaceous candidate biomass crops. Sorghum is a familiar crop now being bred for dedicated biomass production. Diseases currently problematic for forage sorghum, including downy mildew, (*Peronosclerospora sorghi*), *Fusarium spp.* and Anthracnose (*Colletotricum graminicola*), will become increasingly important for biomass sorghum. Switchgrass has been studied as a biomass crop for decades, but still little is known about its pests and pathogens. Principle diseases include rusts, smuts, root rots and *Panicum mosaic virus*. Generally, diseases have not caused major yield reductions and susceptibility varies among cultivars. Miscanthus is still new to the US but has been

studied and used in Europe for nearly 20 years. A relative of sugarcane, *M. × giganteus* is sterile and currently planted from rhizome pieces, leading to clonal fields with little or no genetic variation over large areas. Even so, no economically important diseases have emerged in *M. × giganteus*. In Europe, *Fusarium* rots and *Barley yellow dwarf virus* have been reported. A disease survey of *M. × giganteus* recently conducted across the Midwest has observed 1 virus, 5 fungal diseases and 10 different genera of plant parasitic nematodes present in fields.

S-9 Impact of diseases on biomass productivity in switchgrass. G. P. MUNKVOLD. Iowa State University, Ames, IA.

Switchgrass (*Panicum virgatum*) is widely considered as a preferred feedstock for lignocellulosic ethanol production, which could lead to a significant increase in area planted to this crop. Current switchgrass production is dominated by a few cultivars that have been developed for site adaptation but not specifically for disease resistance. Increased density of switchgrass in the landscape may exacerbate existing disease problems, which could present a significant obstacle to biomass productivity. The diseases with the greatest potential to suppress biomass yield are switchgrass smut, caused by *Tilletia maclaganii*, and switchgrass rust, *Puccinia emaculata*. The smut disease results in stunting, premature flowering, and replacement of seeds by fungal sori; it has been reported from several states spanning from Kansas to New York, and likely occurs elsewhere in the U.S. Studies in Iowa indicated that the disease occurred in over 50% of the area planted to switchgrass, and that it reaches high levels of incidence (up to 70%) in older stands. Smut incidence, stand density, and yield were determined in 10 fields differing in disease incidence (from 0.7 to 55.4%, mean 26%). Mean biomass/tiller was reduced by 38 to 82% in diseased tillers compared to healthy tillers. Yield loss estimates ranged from 1.7 to 40.1% among the fields. Disease incidence and yield loss had a linear relationship ($R^2 = 0.95$) and, based on regression modeling, yield loss for all sampled fields was estimated at 17.0%. Economically viable switchgrass production will require strategies to reduce the impact of smut and rust. Cultivar development is the most promising approach, and recent efforts include selection for *P. emaculata* resistance, but resistance to *T. maclaganii* has not been identified consistently in any current cultivars, and sources of resistance for use in breeding are not yet evident.

S-10 Concentration of *Fusarium* toxins in naturally contaminated corn and corn processing co-products derived from ethanol production. A. W. Schaafsma (1), V. LIMAY-RIOS (1), and J. D. Miller (2). (1) University of Guelph, Ridgetown, Ontario, Canada. (2) Carleton University, Ottawa, Ontario, Canada.

In north temperate areas such as Ontario, contamination by toxins from *Fusarium graminearum*, particularly deoxynivalenol (DON) and zearalenone, is common. Fumonisin contribution has been modest by comparison with other corn-producing areas. In this study, three matrices [corn meal, distiller's dried grains with solubles (DDGS), and condensed distiller's soluble (CDS)] were sampled in sequence from a continuous dry milling processing plant for the determination of mass balance of DON. LC-MS/MS was used as a confirmatory method for determination of DON and other *Fusarium* toxins. DON concentrations in the CDS and the final DDGS co-product were significantly higher ($P \leq 0.01$) than in the starting material (corn grain). Toxin concentration increased by a factor of 3 on a dry weight basis in DDGS compared to the starting corn, and by 4 in CDS. Mean concentration of DON in CDS was four times higher (7.1 mg kg^{-1}) than in corn grains (1.8 mg kg^{-1}) and 1.4 times higher than in DDGS (5.24 mg kg^{-1}). Mass balance calculations show that CDS is the main source of contamination of DON comprising ca. 70% of the toxin found in the final product (DDGS). Most DON (87%) was accounted for by this analysis. The presence of mycotoxins in DDGS and CDS affects their utility as animal feed supplements. Our data indicate that concentrations in the grain corn entering ethanol plants should be close to the dietary values recommended for swine in Canada and the United States for DON (1 mg kg^{-1}). Aside from DON, small amounts of acetyldeoxynivalenol, DON glucoside and zearalenone were found in corn, DDGS and CDS. Unlike the situation for DON,

the DON glucoside was not concentrated into DDGS and CDS. This indicates that some DON glucoside may have been hydrolyzed during the fermentation process.

S-11 Microbial characterization of distillers wet grains: Results and challenges. M. LEHMAN. USDA-ARS North Central Agricultural Research Laboratory, Brookings, SD.

Distillers grains are co-produced with ethanol and carbon dioxide during the production of fuel ethanol from the dry milling and fermentation of corn grain, yet there is little basic microbiological information on these materials. We have characterized the microbiology of distillers wet grains (DWG) over a nine-day period following their production at an industrial fuel ethanol plant. This freshly-produced DWG had a pH of about 4.4, a moisture content of about 53.5% (wet weight basis), and 4×10^5 total yeast cells/dry g, of which about 0.1% were viable. Total bacteria cells were initially below detection limits (ca. 10^6 cells/dry g) and then were estimated to be $\sim 5 \times 10^7$ cells/dry g during the first four days following production. Culturable aerobic heterotrophic organisms (fungi plus bacteria) ranged between 10^4 and 10^5 CFU/dry g during the initial four day period and lactic-acid bacteria (LAB) increased from 36 to 10^3 CFU/dry g over this same period. After nine days, total viable bacteria and yeasts/molds topped 10^8 CFU/dry g and LAB approached 10^6 CFU/dry g. Community phospholipid fatty acid analysis (PLFA) yielded limited data, but indicated a stable microbial community over the first four days of storage. Thirteen morphologically-distinct isolates were recovered of which ten were yeasts and molds from six different genera, two were strains of the lactic acid-producing *Pediococcus pentosaceus*, and only one was an aerobic heterotrophic bacteria, *Micrococcus luteus*. The microbiology of DWG is fundamental to assessment of spoilage, deleterious effects (e.g., toxins), or beneficial effects (e.g., probiotics) in its use as feed or in alternative applications. Significant challenges are encountered when applying culture-independent analyses (DNA-based, PLFA, total protein, and direct observation techniques) to characterize the microbiology of wet distillers grains.

SYMPOSIUM: POTENTIAL CROP BIOSECURITY RISKS THAT THREATEN AGRICULTURE IN THE NORTH CENTRAL REGION: STAYING AHEAD OF THE CURVE

S-12 Disease threats to natural and agricultural plant systems: Think locally, act globally. J. STACK. Kansas State University, Manhattan, KS.

Plant health is the foundation for human health and wellbeing. Plant-based agricultural systems are critical to the economies of many states in the Midwest and Great Plains regions of the United States and the exports from these regions contribute to global food security. Recurring and emerging diseases pose direct and indirect threats to sustainability of plant, animal, and human systems. Comprehensive plant biosecurity plans are necessary prerequisites to sustainable plant health in the face of the long list of general and specific threats that results from global trade, climate change, population growth, and biocrime. A plant biosecurity strategy that minimizes the impacts from plant diseases without compromising production efficiency and trade is essential. Among the challenges to plant biosecurity are: 1) the ability to accurately identify and prioritize pathogen threats and plant system vulnerabilities, 2) the ability to develop preparedness plans that are strong enough to protect plant systems from identified threats while robust enough to protect against unanticipated emerging disease threats, and 3) the development of resilience in natural and agricultural plant systems. We need to think locally (e.g., develop strong plant biosecurity plans and don't import uninspected plants or plant products) and act globally (e.g., support national and international phytosanitary regulations and don't export uninspected plants or plant products). While the threats from bioterrorism are often overstated, the threats from accidental introductions as a result of global trade in plants and plant products are often understated. The large number of existing disease threats to Midwest and Great

Plains plant systems, the potential for newly emerging yet unknown disease threats, and our poor ability to accurately prioritize those threats requires a more general approach to plant biosecurity. The uncertainty associated with the processes of threat identification, vulnerability assessment, and impact prediction should be cause for concern.

S-13 Regional and national efforts to enhance detection and diagnostics. R.

HAMMERSCHMIDT. Michigan State University, East Lansing, MI.

The threat of accidental and intentional introductions of new pathogens and pests along with the potential for re-emergence of older disease/pest problems illustrates the need for enhanced capacity diagnostics and detection. Two programs, the USDA-CSREES sponsored National Plant Diagnostic Network (NPDN) and ipmPIPE (Pest Information Platform for Extension Education), which is sponsored by several USDA agencies and other private and public groups, will be used to describe recent efforts to improve diagnostic and detection capacity. Since its inception in 2002, the NPDN has, for example: enhanced diagnostic capacity at land grant diagnostics labs; provided diagnostic training for new disease problems; assisted in the development of standard operating procedures for diagnostics; developed and deployed first detector training programs; and conducted disease detection and diagnostic exercises. Through these efforts, there has been an improvement in our ability to detect and diagnose as well as enhanced communication and cooperation among the land grant university diagnosticians, state departments of agriculture and USDA-APHIS. The ipmPIPE is a national warning system to help growers protect their crops from the diseases and pests. The program was initiated with funding from USDA and the soybean industry to assist in early detection and diagnosis of Asian soybean rust. There are now four additional ipmPIPE programs: soybean aphid, legumes, cucurbit downy mildew, and pecan nut casebearer. In each of the ipmPIPE programs, field observations and sampling are conducted by the land grant university in each state. Samples are examined by university NPDN labs or state specialists, and the results are entered into electronic databases. There is a public website that is available for use by growers and others for obtaining current information on disease/pest spread and management recommendations. For more information visit: www.NPDN.org and www.ipmpipe.org.

S-14 The role of the seed industry in crop biosecurity. W. E. DOLEZAL. Pioneer Hi-Bred International, Inc., Johnston, IA.

The North Central Region of the United States is a rich agricultural production region for several major commodities, including corn, soybean, wheat and sunflower. It is also a major region for seed production, especially for corn and soybean. The establishment and continued funding of the National Plant Diagnostic Network, with its regional networks and the Soybean, Legume and Soybean Aphid ipm-PIPE programs have greatly aided in the accurate identification and monitoring of major economic pests which threaten crops in the North Central Region. Efforts for building low cost, true partnerships with seed industry personnel in existing federal and state pest monitoring programs, plus a pilot public/private collaborative effort in monitoring *Puccinia polysora* will be discussed.

S-15 Meeting the challenges of U.S. crop biosecurity: Pre- and post threat introduction. F.W.

NUTTER, JR. (1), N. Holah (1), N. Van Rij (2), D. Wright (3), and J. Marois (3). (1) Iowa State University, Ames IA. (2) Cedara Department of Agriculture, Pietermaritzburg, South Africa. (3) University of Florida, Quincy, FL.

The global monitoring of exotic biotic plant pathogens, prior to their introduction into the U.S. by natural, accidental, or deliberate means, remains a key challenge in the effort to safeguard our nation's agricultural biosecurity. Remote sensing, GPS and GIS technologies are now being

integrated and utilized successfully to identify specific plant pathogens. This new paradigm replaces less successful attempts to find and apply unique spectral signatures for pathogen identification. Pathogen-specific temporal and spatial signatures for Asian soybean rust and *Cercospora* leaf spot epidemics affecting soybean crops grown in South Africa, Argentina, and the U.S. were extracted from high resolution (<1.0 m² per pixel) satellite images obtained by commercial satellites. Such approaches offer the means to detect and correctly identify biotic threats prior to (and after) introduction into the US, thereby serving as both an early (pre-introduction) warning system and as a tool for post-introduction response.

STUDENT ORAL PRESENTATIONS

O-1 **Genetic diversity of *Colletotrichum coccodes* vegetative compatibility groups using fluorescent amplified fragment length polymorphism markers.** K. M. ALANANBEH, N. Gudmestad. North Dakota State University, Fargo, ND.

Colletotrichum coccodes (Wallr.) Hughes, is a cosmopolitan pathogen that has a wide distribution and host range. *C. coccodes* is an imperfect fungus and vegetative compatibility serves as a means of genetic exchange and is useful for measuring genotypic diversity. Seven vegetative compatibility groups (VCG's) have been identified for this fungus using nitrate nit mutants. Vegetative incompatibility (*vic*) alleles present among continental populations prevents anastomosis from occurring among these populations, thereby limiting VCG as a method to evaluate diversity of the global population. The main objective of this study was to study the genetic diversity of the VCG's among the North American, European, and Middle Eastern isolates of *C. coccodes* using Fluorescent Amplified Fragment Length Polymorphism (AFLP) markers to obtain a better understanding of the genetic diversity of the global population. A total of 526 isolates of *C. coccodes* were used in this study, 311 were from North America (NA), 183 from the Middle East (Israel), and 32 isolates from Scotland. Three AFLP primer sets were used to generate amplified fragments. The *C. coccodes* isolates were compared with 62 isolates previously studied. All DNA fragments within the range of 100 to 620 bp were scored manually for the three primer sets. The bands were scored for presence or absence (1 = presence or 0 = absence). Binomial data was used to create a similarity matrix using the WINDIST application of the WINBOOT program and the DICE similarity coefficient. Analysis of the first primer set showed that the NA-isolates were assigned to VCG's 1, 2, 3, 4, 5, and 6. This is consistent with previous findings. Israeli isolates were assigned to VCG's 2 and 5, and Scottish isolates were assigned to VCG5. According to the banding pattern on AFLP gels VCG2 and VCG5 had the highest frequency compared to the other isolates in NA and Israeli isolates.

O-2 **Temporal fluctuations in plant parasitic nematode population densities in corn across various Nebraska cropping environments.** J. L. BEHN, T. Jackson. University of Nebraska-Lincoln, Lincoln, NE.

Behavioral differences have been observed among genera of plant parasitic nematodes with respect to movement within the soil profile. Nematode migration through the soil complicates recommendations for sampling strategies. It is not clear what environmental or biological conditions determine why and which nematode genera migrate. Samples were collected at monthly intervals, as weather permitted, from 8 locations with varying irrigation practices, cropping history, and nematicide use. All four Fullerton, NE sites showed ectoparasitic nematode genera population densities (*Xiphinema* spp., *Trichodorus* spp., and *Tylenchorynchus* spp.) that increased over the winter months from November 2008 to May 2009 in the absence of a host crop. At one Ewing, NE location, the *Xiphinema* spp. population density trends were similar to Fullerton, increasing over the winter months. However, at a second site in Ewing, the population densities of *Xiphinema* spp. decreased, while at the remaining

two sites in Ewing, *Xiphinema* spp. populations held steady over the winter. *Trichodorus* spp. were found in only locations 3 and 4 at the Ewing site, and the population densities decreased over the winter for both locations, contradictory to *Trichodorus* spp. at the Fullerton site. It is difficult to interpret the reasons for differences in these population density trends since these preliminary data are inconclusive. Continued sampling of the sites is planned over the next calendar year to identify the trends of the nematode genera so that sampling recommendations can be improved for nematodes of corn.

O-3 The inheritance of mefenoxam resistance in single-zoospore isolates of *Phytophthora erythroseptica*. V. CHAPARA, R. J. Taylor, J. S. Pasche, N. C. Gudmestad. Department of Plant Pathology, North Dakota State University, Fargo, ND.

Pink rot of potato, caused by a homothallic diploid Oomycete *Phytophthora erythroseptica*, is reported to be an economically important disease in the United States and known to vary markedly in its sensitivity to the phenylamide fungicide mefenoxam. Previous studies using single-zoospore populations of *P. erythroseptica* suggested that mefenoxam resistance was inherited quantitatively. A study was conducted with eight hundred single-zoospore isolates of *P. erythroseptica*, produced from the eight parental isolates having varying sensitivity (2 resistant, 4 intermediately resistant and 2 sensitive isolates) to mefenoxam. In vitro assays were conducted with mefenoxam concentrations of 0, 0.01, 0.1, 1.0, 10.0 and 100.0 µg/ml for isolates with sensitive and intermediate fungicide responses, for resistant isolates higher concentrations of 0, 1, 10, 100, 200 and 300 µg/ml were used. In all instances each isolate was tested twice. The progeny of sensitive (EC₅₀ < 1 µg/ml) isolates had the same phenotype as the parents, with no major shift towards increased insensitivity to the fungicide. Similarly, the progeny from resistant parents (EC₅₀ > 100 µg/ml) were also resistant to mefenoxam, however, the progeny from one parent were less insensitive to the fungicide and the progeny from the other parent were generally more insensitive. All of the single-zoospore progeny derived from the four intermediately resistant isolates (EC₅₀ values range from 1 to 99 µg/ml) had the same phenotype as the parental isolates with progeny of two parents trending towards increased insensitivity while the progeny of another parent generally had decreased insensitivity to the fungicide. These results on the inheritance of mefenoxam resistance using single-zoospore progeny of *P. erythroseptica* do not support the conclusions of previous studies that mefenoxam resistance is inherited quantitatively.

O-4 *Pantoea stewartii* subsp. *stewartii* carries two type III secretion systems required for adaptation to insect vector and plant hosts. V. R. CORREA (3), D. R. Majerczak (5), E. Ammar (2), M. Merighi (5), C. Exner (3), D. L. Coplin (5), R. C. Pratt (3), M. G. Redinbaugh (1), S. A. Hogenhout (4). (1) ARS, USDA Corn and Soybean Research, Plant Pathology, OARDC/The Ohio State University; (2) Entomology, OARDC/The Ohio State University; (3) Horticulture and Crop Science, OARDC/The Ohio State University; (4) John Innes Centre, Norwich, UK.; (5) Plant Pathology, The Ohio State University.

Animal and plant pathogenic bacteria interact with their hosts by injecting virulence proteins into host cells via type III secretion systems (TTSS). The Hrc-Hrp cluster of *Pantoea stewartii* subsp. *stewartii* (Pnss), the causative agent of Stewart's wilt in maize (*Zea mays* L.), was previously shown to be important for pathogenicity in plants. Pnss has a second TTSS (PSI-2), that is similar to the invasion-associated TTSS, typical of animal pathogens. We hypothesized that PSI-2 is required for Pnss colonization of its vector, the maize flea beetle, *Chaetocnema pulicaria*. The PSI-2's *psaN* gene, which encodes an ATPase essential for building the injectisome and secretion of effectors, was inactivated with transposon insertions and frame-shift mutations. Beetles were allowed to feed on plants infected with Pnss mutants or wild-type bacteria. Insect colonization by Pnss mutants and wild type bacteria was analyzed using immunofluorescence confocal microscopy of dissected insect organs

or using viable cell counts of insect homogenates. Pnss carrying transposon insertions and frame-shift mutations negated bacterial persistence in flea beetle guts and reduced subsequent transmission to maize. Complementation of mutants with plasmids carrying the *psaN+* gene partially restored bacterial persistence and transmission. Pnss *psaN* mutants were fully virulent on maize, indicating that PSI-2 was not required for plant pathogenicity. Our results demonstrate that the multiple TTSS in Pnss are functionally active and play different roles in adaptation of the bacterium to insect and plant hosts.

O-5 Assessment of soybean genotypes for resistance to *Pythium* spp.: Key to managing this seedling disease complex. M. L. ELLIS, P. A. Paul, A. E. Dorrance. Department of Plant Pathology, Ohio State University, OARDC, Wooster, OH.

Resistance to *Pythium* spp. is not well known in soybean cultivars, especially for those species most prevalent in Ohio soybean fields. The objective of this research was to begin screening for resistance to *P. irregulare* and *P. ultimum* var. *sporangiferum*. A greenhouse assay was used to evaluate 96 soybean lines for potential resistance to two isolates of *P. irregulare*, followed by an evaluation of the top performing lines with two isolates of *P. ultimum* var. *sporangiferum*. For both assays, data for seed germination, total weight, root weight, and a root rot score using an ordinal scale were collected. Based on the results from the two assays, there were no significant interactions between isolates within species and lines. There was a significant difference between the two isolates of *P. irregulare* and among lines for the initial screening. Thirty two lines were screened with *P. ultimum* var. *sporangiferum* and there was a significant difference between isolates for root weight. PI 424354 had the highest weight following inoculation with *P. irregulare*; however, it performed poorly, compared to the other lines, when inoculated with *P. ultimum* var. *sporangiferum*. Of the 32 lines screened, none were resistant to one of the *P. ultimum* var. *sporangiferum* isolates. These results suggest that there is potential resistance to both *Pythium* spp.; however, this resistance may not confer resistance to all isolates within and across species.

O-6 Characterization of two *Arabidopsis* bHLH transcription factors that are induced in cyst nematode syncytia. JING JIN, Tarek Hewezi, Thomas Baum. Department of Plant Pathology, Iowa State University, Ames, IA.

The soybean cyst nematode (SCN, *Heterodera glycines*) is a biotrophic endoparasite that annually causes an estimated one billion dollar loss to the United States soybean industry. The model system of *Arabidopsis thaliana* and the sugar beet cyst nematode (BCN, *Heterodera schachtii*), a close relative of SCN, has been used broadly to study the compatible interaction between a cyst nematode and a plant. Successful cyst nematode parasitism relies on the formation and maintenance of feeding sites (syncytia) in host roots through processes that are highly regulated by the interaction between the cyst nematode and the host. By using promoter::GUS fusion constructs, we have discovered that two basic Helix-Loop-Helix (bHLH) transcription factor promoters are induced in syncytia at 3 and 7 days after nematode inoculation and that the syncytium appears to be the only location of coexpression for both genes. We also detected that mRNA abundance of both transcription factor genes was up-regulated in *Arabidopsis* roots following BCN infection, corroborating our promoter data. Overexpressing bHLH genes in *Arabidopsis* altered root morphology and changed susceptibility to BCN. By using yeast-two-hybrid analyses and bimolecular fluorescent complementation assays, we determined that the two bHLH transcription factors studied here can form a heterodimer. We hypothesize that this heterodimer specifically forms in the developing cyst nematode feeding site and is involved in the reprogramming of root cells into syncytia. Expression analyses are under way to identify target genes regulated by both transcription factors.

O-8 Effect of sclerotial moisture content on carpogenic germination of *Sclerotinia sclerotiorum*. A. NEPAL, L. E. del Rio. North Dakota State University, Fargo, ND.

The effect of sclerotial hydration levels on *Sclerotinia sclerotiorum* carpogenic germination (CG) was studied under controlled environment. Sclerotia of *S. sclerotiorum* isolate WM031 was classified as large, medium or small by sieving. Sclerotial water uptake in plain water and in three soil textures set at four water content levels was characterized using four replications and ten sclerotia per replication. Sclerotia were placed on petri dish bottoms in moist chambers that kept them at 100%, 70–80%, 40–50%, and 20–30% of their maximum hydration level using cool mist humidifiers. Moist chambers were set at 18/14°C day/night for three months prior to CG quantification. The experiment was replicated three times with 15 sclerotia per replication. Water uptake rate by small sclerotia was significantly higher ($\alpha = 0.05$) than medium and large sclerotia in all moisture treatments. Small sclerotia were fully hydrated in <5 hours, medium sclerotia in <15 hours, and large sclerotia in <25 hours, irrespectively of the texture and saturation levels of the soil in which they were incubated. A significant interaction ($\alpha = 0.05$) between sclerotial hydration level and size was observed for both, CG and the average number of apothecia produced per sclerotium. At 100% hydration, large sclerotia had 1.7 and 2.9 times more CG and apothecia per sclerotium, respectively, than medium and small sclerotia. At 70 to 80% hydration, only 10% of medium and small sclerotia produced apothecia while large sclerotia did not produce any. Sclerotia at 50% hydration or drier did not produce apothecia irrespectively of size.

O-9 Is *Rps8* alone? Evidence for different genes for resistance to *Phytophthora sojae* on the chromosome 13 of soybean PI 399073. M. A. ORTEGA (3), D. Tucker (1), S. A. Berry (3), S. St. Martin (2), S. Maroof (1), P. Cregan (6), D. Hyten (4), R. Shoemaker (5), A. E. Dorrance (3). (1) Department of Crop and Soil Environ. Sciences, Virginia Polytechnic Institute and State University, Blacksburg, VA, USA; (2) Department of Horticulture and Crop Science, The Ohio State University, Columbus, OH, (3) Department of Plant Pathology, The Ohio State University, Wooster, OH; (4) SDA ARS, Soybean Genomics and Improvement Lab. BARC, Beltsville, MD; (5) USDA ARS, Department of Agronomy, Iowa State University, Ames, IA; (6) USDA ARS, Soybean Genomics and Improvement Lab. BARC, Beltsville, MD.

PI 399073, a plant introduction from South Korea, is the source of *Rps8*, one of the genes that confers resistance to *Phytophthora sojae*, the causal agent of Phytophthora root and stem rot in soybeans. Three Williams (*rps8/rps8*) × PI 399073 (*Rps8/Rps8*) BC₄F_{2,3} populations were evaluated for the introgression of *Rps8* by association of resistance to *P. sojae* race 25 (1a, 1b, 1c, 1k, 7) with 72 SSR and SNP markers from a region on chromosome 13 where *Rps8* was previously mapped. A PI 399073 (*Rps8/Rps8*) × PI 408211B (*Rps?/Rps?*) F_{3,4} population was used to map resistance to *P. sojae* isolate Butmu (1a, 1b, 1k, 2, 7), and was positioned below the introgression site found in the backcrosses. Williams (*rps8/rps8*) × PI 399073 (*Rps8/Rps8*) BC₄F_{4,5} lines, each line having different location and size of introgression in this region of chromosome 13, were inoculated with the isolates of race 1, 4, 7, 17, 25, and Butmu. The phenotypes of each line were different from each other for the same isolate, as well as to different isolates, this could be attributed to different *Rps* genes present in PI 399073 that were introgressed differentially in the lines tested. The position and size of the introgression on chromosome 13 in a particular BC₄F_{4,5} line could carry one or more *Rps* genes, the response to a different pathogen isolate could depend on which gene or genes were present in that line. These results suggest that PI 399073 could have two or more resistance to *Phytophthora sojae* genes on chromosome 13.

O-10 Comparison of molecular and mycelium assay for determining benzimidazole resistance in field populations of *Venturia inaequalis* in Indiana. K. L. QUELLO, K. Chapman, J. Beckerman. Purdue University, West Lafayette, IN.

Apple scab, caused by the fungus *Venturia inaequalis*, is the most destructive disease on apples in the Midwest, and is controlled primarily by fungicides. As a result, fungicide resistance has become a problem in orchards. Fungicide resistance testing requires pure cultures of the fungus. Unfortunately, isolating pure cultures of *V. inaequalis* after the end of spring is difficult due to the microflora on the apple leaf. The use of a molecular assay in situ could avoid this requirement. We developed a screen that utilizes PCR in situ to detect Topsin-M (thiophanate-methyl) resistance. *V. inaequalis* isolates collected from Indiana were screened with mycelium assays for thiophanate-methyl resistance. Isolates were found to range from sensitive (no growth at 0.5 µg active ingredient (a.i.) thiophanate-methyl /mL) to low resistance (growth at 0.5 µg a.i./mL but not 5 µg a.i./mL) to medium resistance (growth at 5 µg a.i./mL but not at 50 µg a.i./mL) to very high resistance (rapid growth at 50 µg a.i./mL). To test the accuracy of a molecular assay, concordance between known mutations in the beta-tubulin gene and phenotype was determined. DNA was extracted from pure cultures and the beta-tubulin gene was amplified and digested. Restriction enzyme BstUI was used to verify a restriction fragment length polymorphism (RFLP) at codon 198 that corresponded to very high fungicide resistance. 68% of resistant isolates were positive for the polymorphism. The remaining resistant isolates that did not contain the RFLP were sequenced. 100% of these isolates possessed a point mutation at codon 240 in the beta-tubulin gene. This mutation can be differentiated by PCR-RFLP using Cac8I. All resistant isolates could be identified with the two restriction enzyme digests. These two PCR-based RFLP detection methods could be used to rapidly detect thiophanate-methyl resistance isolates of *V. inaequalis* at any time.

O-11 Mapping multiple novel resistance genes against *Phytophthora sojae* in soybean PI 408211B. Z. ZHANG (2), S. A. Berry (2), R. Mian (3), S. K. St. Martin (1), A. E. Dorrance (2). (1) Department of Horticulture and Crop Science, The Ohio State University, Columbus, OH; (2) Department of Plant Pathology, The Ohio State University/OARDC, Wooster, OH; (3) USDA-ARS and Department of Horticulture and Crop Science, The Ohio State University/ORADC, Wooster, OH.

Fourteen *Rps* genes conferring resistance to *Phytophthora sojae*, which causes Phytophthora root and stem rot, have been identified in different soybean cultivars and plant introductions (PI). PI 408211B was proposed to have one novel dominant resistance gene against *P. sojae* race OH17 (*vir1b*, 1d, 2, 3a, 3b, 3c, 4, 5, 6 and 7) and three previously documented dominant resistance genes against race OH25 (*vir1a*, 1b, 1c, 1k and 7). Simple sequence repeat (SSR) and single-nucleotide polymorphisms (SNPs) markers tightly linked with the resistance to OH17 were identified. Using the soybean sequence assembly, new SSR and SNPs markers were developed to fine map this gene on a mapping population of 79 F4:5 recombinant inbred lines from a cross, 'Williams' X PI408211B. The gene was mapped between Scf260-027 and Satt530 with a map distance of 1.3cM and 4.9cM, respectively, on chromosome 3. The result was validated in an independent population of 48 F2:4 lines from a cross 'Sloan' X PI408211B. A population of 360 BC4:7 lines from backcrosses of 'Stressland' X PI408211B which does not have a locus for resistance to OH17 but maintained resistance to OH25 was used to map the resistance gene against OH25. Bulk segregant analysis (BSA) was used to screen 177 polymorphic SSR markers on twenty chromosomes with 10 to 20 cM intervals. None of the SSR markers previously linked with known *Rps* genes was associated with the resistance to OH25, which suggests that this resistance occurs at novel loci. BSA indicates that the resistance to OH25 is associated with chromosome 9 and upper part of chromosome 16. Single marker association analysis on 'Williams' X PI408211B F4:5 identified a region at lower half of chromosome 3 which was also associated with the resistance to OH25.

STUDENT POSTERS

- P-1 Progress Towards Generation of Plant Anti-FvTox1 Antibodies against a *Fusarium virguliforme* Toxin that Induces Sudden Death Syndrome in Soybean.** H. K. BRAR, M. K. Bhattacharyya. Dept. of Agronomy and Interdepartmental Genetics Program, Iowa State University, Ames, IA.

Sudden death syndrome (SDS), caused by *Fusarium virguliforme* (Fv), is a serious soybean disease. It is hypothesized that the foliar SDS symptoms are caused by a phytotoxin(s), released to the roots by the fungal pathogen. A low molecular weight protein (~13.5 kDa) has been shown to produce foliar SDS. The proteinaceous toxin was named as FvTox1. Mice monoclonal antibodies were generated against FvTox1. We have cloned two single chain variable fragment (scFv) antibodies from the hybridoma cell lines that express the mice monoclonal anti-FvTox1 antibodies. Through western blot analysis, we have shown that the recombinant scFv's anti-FvTox1 proteins expressed in *Escherichia coli* can bind to the *E. coli* expressed recombinant FvTox1 protein. Two recombinant scFv's anti-FvTox1 genes are currently being expressed in transformed soybean calli. We will investigate if any of the scFv's anti-FvTox1 proteins (plant anti-FvTox1 antibodies) expressed in transformed soybean calli can bind to the FvTox1 protein. If we can show successful expression of the plant anti-FvTox1 antibodies in transformed calli, stable transgenic soybean lines will be created to stably express the plant anti-FvTox1 antibodies. The transgenic lines expressing detectable levels of the plant anti-FvTox1 antibodies will be then investigated to determine if the plant anti-FvTox1 antibodies can suppress the development of foliar SDS.

- P-2 Corn ear insect damage, fungal infection severity, and mycotoxin concentrations across varying Bt resistance platforms in Nebraska corn fields with natural insect infestation.** K. BRAUER (2), R. Wright (1), T. Jackson (2). (1) Department of Entomology, University of Nebraska, Lincoln, NE. (2) Department of Plant Pathology, University of Nebraska Lincoln, Lincoln, NE.

Ear rotting fungi are common in field corn. While they may not drastically reduce yield directly, secondarily they can contaminate grain with mycotoxins, for which producers can be severely penalized. Ear feeding insects play an important role in fungal colonization of the corn ear by creating wounds that serve as infection points. Insects can be managed with the use of *Bacillus thuringiensis* (Bt) proteins in corn. Field trials with two planting dates were established at two locations in 2007 and 2008 to test this hypothesis under natural insect infestation that included western bean cutworm, corn ear worm, and European corn borer. Treatments consisted of similar corn hybrids with genes for cry proteins Cry1F and Cry1Ab, stacked with cry proteins for rootworm resistance, and their near isogenic line counterparts. At crop maturity, ears were manually harvested and the severity of insect injury and visible fungal infection was determined. Fungal infection rates were recorded from kernels cultured on PDA and fumonisin levels were analyzed with a competitive direct ELISA test. Insect damage severity in 2007 was minimal, but was greater in all later planting dates in both years. Variance between treatments was not significant, but positive correlations between insect damage, *Fusarium* ear rot and kernel infection, and fumonisin concentration were identified. When analyzed in classes, Bt hybrids, stacked Bt hybrids, and isogenic lines; Bt hybrids and stacked Bt hybrids provided significant ($P \leq 0.01$) reductions in the severity of insect damage, ear rot diseases, fungal kernel infection, and fumonisin concentration. Higher levels of insect damage were observed in 2008 than the previous year, but insect pressure was likely still not severe enough to detect a difference between cry protein treatments.

- P-3 Transient expression of MFSV genes in *Drosophila* S2 cells.** F. M. CISNEROS (4), C. Tsai (3), A. E. Whitfield (2), S. A. Hogenhout (1), M. G. Redinbaugh (5). (1) John Innes

Centre, UK. (2) Kansas State University, Manhattan, KS. (3) National Taiwan University, Taiwan. (4) The Ohio State University, Columbus, OH (5) USDA-The Ohio State University, Columbus, OH.

Maize fine streak virus (MFSV) is a member of the genus Nucleorhabdovirus that is transmitted by the leafhopper *Graminella nigrifrons*. The virus replicates in both its maize host and its insect vector. To determine whether *Drosophila* S2 cells support the production of full-length MFSV proteins, we inserted the open reading frames for the nucleoprotein (N), phosphoprotein (P) and replicase protein (L) of MFSV into the pMT/V5-His-Topo vector to produce V5 epitope/ 6X His tagged proteins. The S2 cells were transfected with these plasmid constructs. When analyzed by western blot, antibodies to the V5 epitope clearly reacted with proteins of ~55 and 43 kDa in cells transfected with plasmids carrying the N and P genes, respectively, the sizes expected for the full-length fusion proteins. No bands were detected in non-transfected *Drosophila* S2 cells. The expression of the N gene was also tested with antibodies raised against MFSV virions, which detects the N protein as well as several other viral proteins. MFSV virion antibodies detected a protein of ~55 kDa in S2 cell protein extracts. Antibodies raised against a peptide sequence from the deduced MFSV P protein reacted with a protein of ~ 43 kDa in transfected S2 cell protein extracts. The expression of the MFSV N and P genes were detected over a period of 4 days after induction of gene expression with CuSO₄, but were not detected in cells not exposed to CuSO₄. Experiments are underway to assess MFSV L gene expression in S2 cells. Our results indicate that *Drosophila* S2 cells can steadily express full-length N and P proteins for at least 4 days. This finding is important in order to optimize *Drosophila* S2 cell system conditions for construction of an infectious full-length clone of MFSV.

P-4 Interactions between lesion nematodes and fungal pathogens on maize seedlings. M. P. DA SILVA, G. P. Munkvold. Iowa State University, Ames, IA.

Lesion nematodes (*Pratylenchus penetrans*), are well known to have interactions with root rot pathogens on a wide variety of host plants. The objectives of this research were to measure the effects of *P. penetrans* infestation on seedling disease symptoms caused by fungal pathogens (*Rhizoctonia* and *Fusarium* spp.), assess the impact of nematode control with abamectin on above pathogens, and evaluate potential added seedling disease management benefit of abamectin combined with commercial fungicide seed treatment on maize. In a greenhouse experiment, 150 ml pots filled with autoclaved sand-soil mixture with a layer of fungal inoculum (colonized corn meal/sand mixture) on top of the seed. A suspension of 1000 *P. penetrans* (adults, juveniles and eggs) was added to the pots at the time of planting. A factorial experimental design was used including 8 seed treatments × 4 pathogen treatments × 4 reps. Experiments were harvested 30 days after planting. Emergence was evaluated at 8, 13 and 20 days after planting. Shoot lengths, fresh and dry shoot weights, fresh and dry root weights and root health were determined. Roots were scanned and image analysis conducted with WinRhizo software; root length, root volume and root branching were determined. The results suggest significant effects on root health with interactions between fungal pathogens/root-lesion nematodes and between seed treatment/fungal inoculation. Results also suggest significant effects on root length and root branching for fungal inoculation. *R. solani* had a greater effect on emergence than *F. verticillioides*. Further root health analysis will be conducted with WinRhizo.

P-5 De-acclimation and re-acclimation responses to sudden temperature shifts in *Lolium perenne*. J. D. FARRELL, U. Frei, S. Fei, T. Lubberstedt. Iowa State University, Ames, IA.

Climate change has resulted in a higher variability in climate patterns; exposing plants to frequent freeze thaw cycles especially during the late winter and early spring. Perennial ryegrass (*Lolium perenne*) was chosen as a model for investigating cold acclimation and freezing tolerance in relation to shifting temperatures. Perennial ryegrass is an important crop in Europe, Asia and Africa as both forage and turf grass. In the United States perennial ryegrass has the potential to become a cover crop

in maize fields where stover is removed. Recently, genomic resources have become available including ESTs, microarrays and BAC libraries. Preliminary frost tolerance assays, also known as ion leakage assay have revealed an interesting pattern between two Mediterranean cultivars. One cultivar acclimated quickly, however as the cold temperatures continued the frost tolerance decreased compared to the other cultivar, which acclimated slowly and was able to sustain frost tolerance. The objective of this study is to determine the frost tolerance of these two Mediterranean cultivars during cold acclimation, de-acclimation and re-acclimation, simulating the typical pattern of a late winter thaw cycle. In parallel mRNAs will be collected from each cultivar during normal, cold acclimation, de-acclimated and re-acclimation conditions for cDNA microarrays assays. Comparing gene expression between the two Mediterranean cultivars during different temperature conditions will help identify molecular mechanisms involved in acclimation, de-acclimation and re-acclimation. The long term goal of this project is to identify the candidate genes involved in these acclimation processes, to find the genomic location of these genes and to extract the full length gene and promoter sequence; in the hopes of expanding our knowledge to other crop species.

P-6 Evaluation of aggressiveness and host range of *Fusarium acuminatum* and *Fusarium redolens* associated with root rot of dry beans. A. GAMBHIR, R. S. Lamppa, J. B. Rasmussen, R. S. Goswami. North Dakota State University, Fargo, ND.

Dry bean (*Phaseolus vulgaris*), a favored rotational crop with high nitrogen fixing ability and food value, is affected by a large number of fungal diseases. Production of this crop in the US is primarily concentrated in the North Central region of the country, where *Fusarium* root rots are a major concern. *Fusarium solani* f. sp. *phaseoli* has been considered as the primary causal agent of this disease. However, our findings suggest the involvement of other *Fusarium* species. Among these, *Fusarium acuminatum* and *Fusarium redolens*, were detected for the first time in 2007 in North Dakota and Minnesota, on roots of dry bean plants collected from root rot afflicted fields. Roots of the infected plants exhibited reddish brown lesions or discoloration on hypocotyl and tap roots, characteristic of *Fusarium* root rot in dry beans. Koch's postulates were completed for these species. Variation in aggressiveness on dry beans among isolates and their ability to infect crops commonly grown in rotation with dry beans was evaluated in greenhouse trials. Isolates of *F. acuminatum* and *F. redolens* from dry beans exhibited pronounced differences in the ability to cause disease on a highly susceptible kidney bean cultivar. Some of the isolates evaluated were as aggressive as *F. solani* f. sp. *phaseoli*. Aggressive isolates from both species were able to infect barley, canola, chickpeas, corn, field pea, flax, lentils, potato, soybeans, sugarbeet, sunflower and wheat. But the disease severity and symptoms developed varied between hosts. These findings suggest a possible change in *Fusarium* species causing root rots of dry beans in this region and highlight the potential threat posed by them to production of dry beans and other crops grown in rotation.

P-7 Evaluation of extraction methods for detecting *Xanthomonas axonopodis* pv. *phaseoli* in common bean seed. Y. HE, G. Munkvold. Seed Science Center, Iowa State University, Ames, IA.

Xanthomonas axonopodis pv. *phaseoli* (Xap) and Xap var. *fuscans* are important seedborne pathogens of *Phaseolus vulgaris*. In order to maintain seed quality and meet phytosanitary requirements, accurate seed health testing methods are critical. Currently accepted methods for these pathogens include several variations on extraction methods; therefore our objective is to assess the influence of different extraction steps on the sensitivity of Xap detection in *P. vulgaris* seeds. Seeds were inoculated with Xap to reach inoculum levels from 10¹ CFU/seed to 10⁵ CFU/seed and mixed with clean and healthy *P. vulgaris* seeds. One contaminated seed was mixed into each 1000-seed subsample. Thirty 1000-seed subsamples were tested for each different extraction condition. Extraction methods tested included soaking whole seeds in sterilized saline phosphate buffer overnight at 4°C and at room temperature for 3h, soaking with and without vacuum, and concentrating

the seed extract by centrifuging. The seed extract dilutions were cultured on semi selective agar media MT and XCP1. The proportions of positive subsamples were recorded and compared to measure the effects of each extraction step on detection sensitivity. The results showed that vacuum extraction and centrifugation of seed extracts increased sensitivity, and soaking overnight at 4°C was more effective than soaking at room temperature for 3h. Our results suggest that a centrifugation step would be a valuable addition to the current method approved by the International Seed Testing Association (ISTA), but these results should be confirmed using naturally infected seedlots.

P-8 Optimizing extraction of *Fusarium virguliforme* DNA from crop residue and conidia. T. M. KOLANDER, D. K. Malvick, J. E. Kurlle. University of Minnesota, Minneapolis, MN.

Sudden death syndrome (SDS) of soybean (*Glycine max*), caused by *Fusarium virguliforme* (*Fv*), can cause severe yield losses. Crop rotation is not effective for managing SDS. One explanation is that *Fv* may survive and possibly grow on residue from crops rotated with soybean. We tested three methods for extracting *Fv* DNA from crop residue and *Fv* conidia for use in PCR. Residue of soybean, corn (*Zea mays*), alfalfa (*Medicago sativa*), and wheat (*Triticum aestivum*) was soaked in a suspension of *Fv* conidia. Residue was buried in pasteurized field soil maintained at ~23°C for 3 and 6 weeks. Modifications of the MoBio UltraClean™ Plant (UCP) kit, FastDNA® (FD) kit, and the MoBio PowerSoil™ (PS) kit were used for residue extractions and the latter two kits were used for extractions from 10⁴ to 10⁷ conidia. Standard PCR (sPCR) and quantitative PCR (qPCR) were completed using *Fv*-specific primers. The sPCR bands from residue were consistently more intense for the FD kit, especially at 3 weeks post-burial. At 3 weeks, mean qPCR Ct values for the FD kit were on average 0.9, 0.6, 2.8, and 6.5 cycles lower than the PS kit for corn, wheat, alfalfa, and soybean, respectively. At 6 weeks, Ct values resulting from the FD kit were lower only for alfalfa and soybean. The Ct values for soybean, resulting from the FD kit, were 6.3 and 7.3 cycles lower than the UCP kit after 3 and 6 weeks, respectively. Using sPCR and qPCR, quantities of *Fv* DNA obtained with the PS kit correlated with the number of conidia. *Fv* DNA from conidia was not detected with qPCR using the FD kit. The FD kit was generally more effective at extracting *Fv* DNA from crop residue, especially soybean and alfalfa, and the PS kit was superior for extracting DNA from conidia.

P-9 Quantifying and comparing the aggressiveness of *Pantoea stewartii* isolates from Iowa. L. LIU, C. C. Block, F. W. Nutter. Department of Plant Pathology, Iowa State University, Ames, IA.

Stewart's disease, caused by *Pantoea stewartii*, can cause severe economic damage to seed and sweet corn crops due to phytosanitary regulations that prevent the export of seed, as well as cause direct reductions in yield. The aggressiveness of thirteen *Pantoea stewartii* isolates was quantified and compared by measuring incubation period (day), rate of lesion expansion/day, and time to leaf death. Growth chamber experiments were conducted at the optimal temperature of 30°C. Sweet corn plants (variety "Jubilee") were inoculated at the V8 growth stage with 12 wild-type *Pantoea stewartii* isolates and a rifampicin-nalidixic acid resistant isolate, Rif 9A. Both sides of the mid-rib of 4 leaves per plant were inoculated with 1 of the 13 isolates (1 × 10⁸ CFU/ml). There were 5 corn plants for each isolate and 65 plants per replication. Experiments were performed twice for each isolate. Acropetal and basipetal lesion expansions were measured beginning when lesions were first visible. Measurements continued at 24-h intervals until no further lesion expansion was possible (leaves were dead). Our results to date show no statistical difference among lesion expansion rates of the 13 *Pantoea stewartii* isolates, which averaged 0.3984 cm/day acropetally and 0.4999 cm/day basipetally. Of the 4 leaves tested, average expansion rates were fastest (0.6018 cm/day acropetally and 1.0804 cm/day basipetally) on the eighth true leaf. Incubation period was shortest on the seventh true leaf (7.7831 days). There was no statistical difference between acropetal and basipetal expansion rates. This study, the first to quantify the aggressiveness of *Pantoea stewartii* isolates, serves as a baseline for detecting shifts in pathogen aggressiveness.

P-10 Effect of co-inoculation of *Fusarium virguliforme* and *Phialophora gregata* on soybean. C. MATTUPALLI, P. D. Esker. University of Wisconsin, Madison, WI.

Fusarium virguliforme (*Fv*, causal agent of sudden death syndrome, SDS) and *Phialophora gregata* genotypes A and B (*PgA* and *PgB*, causal agent of brown stem rot, BSR) are two yield-limiting, soil-borne pathogens for Midwest soybean producers. To evaluate the possible interactions between *Fv*, *PgA*, and *PgB* on disease development, a greenhouse study was conducted. Two soybean cultivars, Jack (resistant to *Fv* and *PgA*) and Williams82 (susceptible to *Fv* and *PgA*) were planted in metromix+peat growth medium that was amended with pathogen-infested vermiculite. There were eight inoculum treatments: noninfested controls, *Fv*, *PgA*, *PgB*, *Fv+PgA*, *Fv+PgB*, *PgA+PgB*, and *Fv+PgA+PgB*. Individual pathogens were added in equal parts to yield 10,000 spores cm⁻³ of plant growth medium. Foliar symptoms characteristic of either SDS or BSR were assessed during reproductive stages (R1-R7) as the percentage of plant area infected. Mean area under disease progress curve (AUDPC) ranged from 0%·days for noninfested controls to 518.84%·days for Jack inoculated with *Fv*. Results indicated that there was an effect of variety ($P < 0.0001$), inoculum ($P = 0.0092$) and their interaction ($P = 0.0756$). Multiple comparisons using a Tukey adjustment suggested that Jack inoculated with *Fv+PgA* had greater disease development compared with all Williams82 inoculum treatments. These preliminary results suggest that *Fv* and *PgA* interact with each other and that their effect varies between cultivars.

P-11 Differential regulation of host mRNA translation initiation in the Arabidopsis: TuMV interaction. J. MOELLER. Iowa State University, Ames, IA.

Viruses are known for their ingenuity in reprogramming the host processes of transcription and translation, including use of non-canonical methods of translation initiation. To assess virus-induced changes in host transcription and translational processes, we used the Arabidopsis ATH1 GeneChip oligonucleotide microarray to determine the mRNA species bound to 80S ribosomes versus the mRNA species present in total RNA populations in the Arabidopsis:Turnip mosaic virus (TuMV) interaction. The majority of genes that are either well or poorly loaded onto ribosomes are consistent in their loading behavior between non- and TuMV-infected tissues. However, considerable differential regulation of translation initiation was also found when non- and TuMV-infected tissues were compared. For example, there are numerous genes that are up-regulated upon infection according to their mRNA abundance in total RNA populations but show down-regulation according to the genes' translation initiation status and vice-versa. In support of this finding, 1071 probe sets showed over 4-fold difference when contrasting mRNA from total RNA to mRNA from 80S ribosomes in response to TuMV. This study provides near genome-scale analysis of the regulation of translation initiation in both non- and TuMV-infected states, and it suggests that analyses of mRNA abundance in total RNA may lead to incorrect conclusions about which genes are induced or down-regulated in response to viral infection. Because mRNA associated with 80S ribosomes is expected to be more predictive of the proteome, this approach may provide candidate genes with greater relevance to the Arabidopsis:TuMV interaction.

P-12 Pathotype diversity of *Phytophthora sojae* plant isolates from Iowa. S. M. STEWART, A. E. Robertson. Department of Plant Pathology, Iowa State University, Ames, IA.

Phytophthora root rot (PRR) caused by *Phytophthora sojae* can infect soybeans at all growth stages, causing pre- and post-emergence damping-off and root and stem rot. The most effective way to manage PRR is through the use of *P. sojae*-resistant cultivars however, the pathogen continues to diversify and overcome resistant genes (*Rps*) present in commercial cultivars. This host-pathogen system follows Flor's gene-for-gene hypothesis, and there are 13 known *Rps* genes. Pathotype diversity has been monitored in Iowa since 1966. Prior to 1975, race 1, which is capable of defeating

the resistance gene Rps7, was the only pathotype reported in Iowa however, two decades later 100% of isolates of *P. sojae* recovered from soybean plants were able to infect plants with Rps7. Since only 4.6% of isolates of *P. sojae* in 1976 were able to infect plants with Rps-1k, soybean cultivars with Rps-1k were marketed commercially for PRR management, but by 2004, 73.3% of isolates of *P. sojae* recovered from soybean plants could infect plants with Rps-1k. In 2008, the pathotype diversity of 41 isolates of *P. sojae* recovered from 15 soybean plants sampled from six commercial fields in Iowa was assessed using 14 differentials. The isolates belonged to six unique pathotypes. In four fields, only one unique pathotype was recovered from the plants sampled, while in the other two fields, two unique pathotypes were recovered. In the study, 100% of the isolates were able to infect plants with Rps-7 and 85.4% could infect plants with Rps-1k. As expected, the endemic *P. sojae* population in Iowa continues to diversify and selection pressure posed by commercial *P. sojae*-resistant cultivars results in a greater number of isolates compatible on these cultivars.

P-13 Effectiveness of Brassica short-cycle cover crops in managing *Phytophthora capsici* and *Fusarium* spp. in cucurbit fields. S. THRU PPOYIL, M. Babadoost. University of Illinois, Urbana-Champaign, IL.

A study was conducted in 2008 to determine effectiveness of *Brassica* short-cycle cover crops in managing *Phytophthora capsici* and *Fusarium* spp. in cucurbit fields. Mustard cultivars, Florida Broadleaf (FBL) and Tilney were seeded on 29 April in a field with a history of Phytophthora blight and Fusarium fruit rot of pumpkins and watermelon. The mustard crops were grown for 45 days and then incorporated into top 10-cm layer of the soil after cutting the mustard plants with a disk cultivator. Jack-o-Lantern pumpkin ‘Magic Lantern’, processing pumpkin ‘Dickinson’, and cucumber ‘Eureka’ were grown in the mustard amended area. Incidence and severity of seedling death, leaf spot, vine infection and fruit rot caused by *P. capsici* and *Fusarium* spp. were assessed on a biweekly schedule starting from seedling emergence on 14 July until harvest on 26 September. No seedling infection or leaf spot were observed in the plots. Percentage of vines infected with *P. capsici* in the plots on 19 September were 16.0, 22.5, 23.0, and 27.5% in the plots amended with FBL, Tilney, FBL+Tilney, and control plots, respectively. Similarly, percentage of fruits infected with *P. capsici* on 26 September were 32.2, 33.5, 33.6, and 42.4% in plots amended with FBL, Tilney, FBL+Tilney, and control plots, respectively. No Fusarium infection was detected in the plots.

P-14 Field and greenhouse evaluation of fungicide seed treatment control of sudden death syndrome of soybean. J. D. WEEMS (2), G. Zhang (2), K. A. Ames (2), J. P. Bond (1), C. A. Bradley (2). (1) Southern Illinois University, Carbondale, IL; (2) University of Illinois, Urbana, IL.

Sudden death syndrome (SDS), caused by *Fusarium virguliforme*, is a yield reducing disease common in many soybean producing states. Results of recent research indicated that infection can occur during early radicle emergence, suggesting fungicide seed treatments may provide protection from the pathogen during the early stages of soybean development. In 2008, a field study across two locations and a greenhouse study were conducted to test eleven fungicide seed treatments and an untreated control across four cultivars for effects on *F. virguliforme* infection and development. The southern Illinois location (Valmeyer) was naturally infested with *F. virguliforme*, the central Illinois location (Urbana) was naturally infested with *F. virguliforme* and soil was augmented with sterilized grain sorghum colonized by *F. virguliforme*, and the greenhouse study was artificially infested with *F. virguliforme* inoculum. Roots collected from plots were scanned and analyzed using WinRHIZO. Foliar symptoms of SDS were rated during plant growth and harvest data were collected to monitor disease development. At Valmeyer, SDS was most prevalent and seed treatments had a significant ($P = 0.0002$) effect on early season plant stand, with the untreated control having the lowest stand. Furthermore, roots from untreated plots collected from Valmeyer had significant root tip reductions

($P = 0.0052$) and increased average root diameter ($P = 0.0451$), suggesting lateral root and root hair reduction. Seed treatments had no other significant effect on the pathogen or disease development.

P-15 Bacterial species associated with internally-discolored horseradish roots. J. YU, M. Babadoost. University of Illinois, Urbana-Champaign, IL.

Internal discoloration of horseradish roots is a complex disease, caused by at least three fungal pathogens, *Verticillium dahliae*, *V. longisporum*, and *Fusarium solani*. In addition to the fungal species associated with internally discolored horseradish roots, bacteria have been routinely isolated from the affected roots. This study was conducted to identify bacterial species associated with internally discolored horseradish roots. Horseradish root samples were collected from major horseradish growing areas in North America, including Illinois, Wisconsin, California, and Ontario (Canada), and were assayed for presence of bacteria. The outer layer of the diseased roots were peeled and surface sterilized in a 6% sodium hypochlorite solution for 1 minute, followed by a 95% ethanol concentration for 3 minutes, and then rinsed in sterile-distilled water three times. Five segments from each root were placed onto nutrient agar (NA) plates. The plates were incubated at 22–28°C with 12 h light/12 h darkness. Bacterial growth were observed after 5, 10, 15 days of incubation. Single-cell colonies of each isolated bacterium were grown on NA. Characteristics of each purified colony were recorded. Isolated bacteria were identified using the Biolog program and polymerase chain reaction (PCR)-restriction fragment length polymorphism (RFLP) assay followed by analyzing 16s rDNA sequences. *Pseudomonas fluorescence*, *Bacillus cereus*, and *Erwinia* spp. were the main bacterial species isolated from horseradish root samples.

GENERAL POSTER SESSION

G-1 The effect of foliar fungicide timing on yield and grain fill in high and low aphid pressure environments. N. R. BESTOR (2), D. S. Mueller (2), A. E. Robertson (2), R. Ritson (2), M. O’Neal (1). (1) Department of Entomology, Iowa State University, Ames, IA; (2) Department of Plant Pathology, Iowa State University, Ames, IA.

With the arrival of two invasive pests of soybean, the soybean aphid and soybean rust, there is increasing interest in the use of pesticides for soybean production. Recently, application of foliar fungicides, and to some extent foliar insecticides, to soybean to increase overall “plant health” has been promoted. But the economic benefits of such applications are inconsistent and not well documented. In 2008, the effect of three foliar fungicides (a strobilurin, a triazole and a premix of strobilurin and triazole) applied at growth stages R1 or R3 on seed size and yield was evaluated at two locations in Iowa, one in southeast and one in northwest. Foliar fungicides applied to soybeans in northwest Iowa had a significant positive effect on yield and seed size, while fungicides applied to soybeans in southeast Iowa did not affect yield or seed size. These results were not expected since higher foliar disease levels occurred in southwest Iowa. At both locations, an application of fungicide at R3 resulted in significantly greater yields than an application at R1. In northwest Iowa, no differences in yield were observed between fungicides; however, seed size at this location was significantly greater when a fungicide containing a strobilurin was used. Soybean aphid pressure in northwest Iowa was very high (cumulative aphid days [CAD] = 92,281) while in southeast Iowa, aphid pressure was over 100 fold lower (CAD = 695), which may have been a confounding factor. We plan to investigate the effect of foliar fungicide applications in combination with foliar insecticides under different environmental conditions in subsequent years.

- G-2 Genetic diversity of *Cercospora sojina* revealed by amplified fragment length polymorphism markers.** C. A. BRADLEY (2), A. Wood (3), G. Zhang (2), J. Murray (3), D. Phillips (1), R. Ming (3). (1) University of Georgia, Department of Plant Pathology, Griffin, GA; (2) University of Illinois, Department of Crop Sciences, Urbana, IL; (3) University of Illinois, Department of Plant Biology, Urbana, IL.

Cercospora sojina, a phytopathogenic fungus, causes frogeye leaf spot (FLS) of soybean. Losses caused by this disease in the United States were estimated to range from 6.9 million to 12.7 million bushels annually from 2004 to 2007. The genetic diversity of *C. sojina* isolates collected from three countries was estimated using amplified fragment length polymorphism (AFLP) markers. A total of 64 isolates of *C. sojina* were analyzed by eight AFLP primer combinations, generating 40 markers. The average genetic similarity of the 64 isolates was 0.56 on a scale between 0 and 1, indicating a high degree of genetic diversity within the species. Cluster analysis resulted in two major clusters and seven sub-clusters. Two isolates collected from Georgia were the most closely related, sharing a genetic similarity of 0.97. Two isolates from China were clustered together. Besides these four samples, no clear separation of isolates based on origin was found. This suggests that genetic diversity within a population is as great as between populations based on locations. Our results provide evidence that substantial genetic diversity exists within the species *C. sojina* and that selection for broad spectrum host-resistance should be targeted in soybean breeding programs.

- G-3 Identifying pre-plant risk factors for *Bean pod mottle virus* in Iowa.** E. BYAMUKAMA, A. Robertson, F. Nutter. Iowa State University, Ames, IA.

Integrated disease management requires a thorough understanding of pathogen-plant-environment interactions in order to develop cost-effective management programs. Knowing pre-plant risk factors associated with *Bean pod mottle virus* (BPMV) would enable soybean producers to deploy management practices that delay early season BPMV infection and spread to minimize negative impacts on soybean yield and quality. Potential abiotic and biotic BPMV risk factors identified by correlation analysis were evaluated using regression analysis to quantify the predictive power of single and combined factors at the county scale. We examined thirteen factors: county centroid latitude, longitude, and elevation; soybean planting date, number of soybean farms, and soybean acres; number of alfalfa acres harvested; for the period of October through April, number of days with daily mean temperature $< 0^{\circ}\text{C}$, number of days with snow cover, consecutive days with maximum temperature $< 0^{\circ}\text{C}$, consecutive days with snow cover, and accumulated snow depth; and for March, number of days with mean temperature below 0°C . Variables with highest predictive value for BPMV incidence were days with mean temperatures $< 0^{\circ}\text{C}$ in March and number of soybean farms within Iowa counties, with partial coefficients -4.03 (X_1), and -0.012 (X_2), respectively. The multiple regression model explained 54.5% of the variation in county-scale BPMV incidence; higher BPMV incidence was associated with days in March with mean temperatures $< 0^{\circ}\text{C}$ (X_1) and fewer soybean farms per county (X_2). Thus, we suggest that using the March temperature data and the number of soybean farms/county, potential BPMV incidence can be predicted before planting. Pre-plant predictions can aid soybean growers and seed companies in making management decisions, such as the need for seed and/or foliar insecticide treatments, and selection of planting sites with reduced risk.

- G-4 A survey of *Venturia inaequalis* fungicide resistance in Indiana and Michigan apple orchards.** K. S. CHAPMAN, K. L. Quello, J. L. Beckerman. Purdue University, West Lafayette, IN.

Apple growers rely heavily on fungicides to manage *Venturia inaequalis*, the fungus that causes apple scab. Fungicide resistance has developed as a result. To quantify and assess the levels of fungicide resistance, isolates of *V. inaequalis* were collected from Indiana and Michigan orchards and fungicide resistance was evaluated. Previously published works were used to determine the baseline

concentrations of fungicides and thresholds for growth. Differences were found in the levels of resistance between the two states. In Michigan, 2.0% of the isolates tested were resistant to Sovran (defined as 90% relative growth in the presence of fungicide), but 52.9% were shifted and less sensitive to the fungicide. 63.5% of MI isolates were resistant to Topsin M. With respect to Dodine, 13.5% were resistant (90% relative growth), but 67.3% showed a shift in resistance. 42.3% of isolates tested with Nova were resistant (80% relative growth), and resistance had shifted in 55.8% of isolates. For Indiana, there was no indication of resistance to Sovran. 86.6% of isolates tested had resistance to Topsin M. Dodine testing showed that 7.3% of isolates were resistant and 62.2% had shifted resistance. Of IN isolates tested with Nova, 34.1% were resistant and 57.3% were shifted in their resistance. On a state level this survey will provide the opportunity to educate growers on the degree of fungicide resistance present in local orchards and prevent ineffective fungicide applications.

G-5 Development of a forecasting model to estimate risk of Sclerotinia stem rot development on canola in North Dakota. L. E. DEL RIO. North Dakota State University, Fargo, ND.

Sclerotinia stem rot (SSR) is an important yield reducing disease that is endemic to canola producing areas of North Dakota. SSR, which is caused by *Sclerotinia sclerotiorum* (Lib.) de Bary, is managed mainly through the use of fungicides. Weather conditions play an important role in development of SSR epidemics and thus on the profitability of fungicide applications made to control it. A warning system aimed at estimating the risk of development of SSR epidemics was produced using logistic regression analysis, disease data collected from more than 800 fields through field surveys and weather data collected through a net of 27 weather stations. The selected model had a *c* value of 0.79 and a Somers' D value of 0.58, and identified rain and solar radiation as independent variables of importance. When validated using a data set of similar size that had not been used in model development, the model produced a true positive fraction of 64% and a true negative fraction of 74% and an overall accuracy of 72%. The model was available to canola growers through a website in 2008.

G-6 Low lignin (brown midrib) sorghum genotypes restrict growth of Fusarium spp. as compared with near-isogenic wild-type sorghum. D. L. FUNNELL-HARRIS, J. F. Pedersen, S. E. Sattler. USDA-ARS, Grain, Forage and Bioenergy Research, University of Nebraska, Lincoln, NE.

To increase usability of sorghum for bioenergy and forages, two different brown midrib (*bmr*) genes, *bmr-6* and *bmr-12*, were backcrossed into five elite backgrounds, resulting in reduced lignin near-isogenic genotypes. Field-grown grain from *bmr-6* and *bmr-12* plants had significantly reduced colonization by *Fusarium moniliforme sensu lato* as compared with wild-type grain. *Fusarium* isolates were identified to species using sequence analysis of the translation elongation factor gene. Three of the most commonly identified species, *Fusarium thapsinum*, *Fusarium proliferatum* and *Fusarium verticillioides*, were members of *F. moniliforme* and included sorghum pathogens. Three other commonly isolated species, *Fusarium bullatum*, *Fusarium pallidoroseum* and *Fusarium graminearum*, likely colonize sorghum asymptotically. Chi-square analyses showed that the ratios of *Fusarium* species colonizing *bmr-12* grain were significantly different from those of wild-type, indicating that *bmr-12* affects colonization by *Fusarium* spp. across genetic backgrounds. A thrice-replicated bioassay was conducted in which peduncles of wild-type and near-isogenic *bmr* genotypes in a single background were inoculated with fungi associated with sorghum. *F. thapsinum*, *F. verticillioides*, *Fusarium armeniacum* and *Alternaria alternata* were pathogenic on wild-type plants in most cases. Lesion lengths were significantly reduced on one or both *bmr* genotypes infected by *F. verticillioides*, *F. thapsinum* or *A. alternata* compared to lesions produced on near-isogenic wild-type plants. These data indicate that *bmr-6* and *bmr-12* affect colonization by *Fusarium* spp. and *A. alternata*.

G-7 Improving management of soybean cyst nematode through extension demonstration and outreach. L. J. GIESLER (13), C. Bradley (10), A. Dorrance (8), T. Niblack (9), G. Tylka (1), D. Jardine (2), D. Malvick (11), L. Sweets (12), S. Markell (4), L. Osborne (7), P. Esker (14), G. Bird (3), J. Faghihi (6), A. Tenuta (5). (1) Iowa State University, Ames, IA; (2) Kansas State University, Manhattan, KS; (3) Michigan State University, East Lansing, MI; (4) North Dakota State University, Fargo, ND; (5) Ontario Ministry of Agriculture, Food & Rural Affairs, Ontario, Canada; (6) Purdue University, West Lafayette, IN; (7) South Dakota State University, Brookings, SD; (8) The Ohio State University, Columbus, OH; (9) USDA/ARS/University of Illinois, Urbana, IL; (10) University of Illinois, Urbana-Champaign, IL; (11) University of Minnesota, Minneapolis, MN; (12) University of Missouri, Columbia, MS; (13) University of Nebraska-Lincoln, Lincoln, NE; (14) University of Wisconsin, Madison, WI.

While soybean cyst nematode (SCN) is the most yield limiting pest of soybean in the United States, soybean growers are not always properly managing it. Recent surveys have demonstrated this in Iowa and direct correspondence with growers and commercial agriculture professionals quickly reveals that a major problem exists in that this pest is often ignored. Extension plant pathologists and nematologists from the North Central states are collaborating in this project to deliver a consistent message on management of SCN. As a part of the project, a total of 28 replicated on-farm strip trials were established to evaluate the influence of SCN resistance source on yield and SCN reproduction across the North Central states. Soybean yields were measured, and SCN populations were determined in the spring and fall for all locations. In addition, each location was tested for SCN population HG type, which identifies the ability of the population to reproduce on each of the resistance sources used in the trials. Yield was consistently higher in resistant cultivars compared to susceptible varieties, but response of cultivar varied with location. The yields were highest for varieties utilizing the Peking source of resistance, which had a 5.3 bu/A yield advantage over susceptible varieties averaged over all locations. In fields with high SCN populations ($\geq 3,000$ eggs/100 cc soil), the average yield advantages of varieties utilizing the Peking, PI 88788, and Hartwig sources of resistance were 15.5, 11.8, and 6.3 bu/A better than the susceptible varieties, respectively. In addition to research plots, team members developed extension programs on SCN and delivered SCN information in all states. A total of 30 field days and 33 indoor education programs were delivered to over 5,000 participants in 50 hours of programming.

G-8 Recovery of *Phakopsora pachyrhizi* urediniospores from passive spore trap slides and extraction of their DNA for quantitative PCR. J. S. HAUDENSHIELD (2), P. Chaudhary (2), G. L. Hartman (1). (1) USDA-Agricultural Research Service, Urbana, IL; (2) University of Illinois, Urbana, IL.

Enumeration of rust spores from passive spore traps utilizing white petrolatum-coated slides by traditional microscopic evaluation can represent a serious challenge. Many fungal spores look alike, and clear visualization on the adhesive can be obscured by particulate debris or nonuniformities within the adhesive layer; reports will commonly describe only the number of “rust-like” spores. Molecular methods of *P. pachyrhizi* detection, utilizing both standard PCR and quantitative PCR (qPCR), have been available for several years, but extraction of fungal DNA from petrolatum-embedded spores remained difficult. We now demonstrate the utility of a novel method for recovering the petrolatum layer carrying trapped spores from slides using biodegradable foam strips, with subsequent DNA extraction to yield material suitable for quantification by qPCR. This method permits even single spores of *P. pachyrhizi* to be recovered and detected. False-negative calls were minimized by using a multiplexed exogenous control; no false-positives were observed. This method

was successfully employed to assess spore loads in passive traps located at sentinel plots in the USA during the 2008 soybean growing season.

G-9 Correlation between Fusarium head blight severity and deoxynivalenol in three winter wheat cultivars. J. HERNANDEZ NOPSA, S. Wegulo. University of Nebraska-Lincoln, Lincoln, NE.

Fusarium head blight (FHB), caused by *Fusarium graminearum*, is a damaging disease of wheat. In 2008, a field experiment was conducted to identify relationships between visual assessments of FHB and deoxynivalenol (DON) in three winter wheat cultivars. The cultivars Jagalene, Harry, and 2137 were planted following corn on 27 October 2007. In May 2008, plots were inoculated with 1×10^5 spores/ml of *F. graminearum* at early anthesis and were not irrigated. There also was heavy natural inoculum. Cultivars were arranged in a randomized complete block design with three replications. FHB severity was determined 21 days after inoculation on 20 heads tagged in each of 13 disease severity categories in each plot: 0, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 70, and 90%. There was a significant positive correlation between FHB severity and DON in all three cultivars: Jagalene ($r = 0.92$, $P < .0001$); Harry ($r = 0.64$, $P = 0.0176$); and 2137 ($r = 0.88$, $P < 0.0001$). DON concentration was lower ($P = 0.05$) in 2137 than in Harry or Jagalene; it was highest in Harry (32 $\mu\text{g/g}$) followed by Jagalene (29 $\mu\text{g/g}$) and 2137 (19 $\mu\text{g/g}$). This study demonstrated (i) a positive correlation between FHB severity and DON and (ii) differences among cultivars in the levels of DON they accumulated. Similar results were obtained in 2007.

G-10 Evaluation of winter wheat cultivars for resistance to Fusarium head blight and deoxynivalenol. J. HERNANDEZ NOPSA, S. Wegulo. University of Nebraska-Lincoln, Lincoln, NE.

Fusarium head blight (FHB) of wheat, caused by *Fusarium graminearum*, can cause significant losses. The reaction to FHB and deoxynivalenol (DON) of the winter wheat cultivars Jagalene, Harry, 2137, Hondo, Alliance, Infinity, Goodstreak, Karl 92, Wahoo, Millennium, Wesley, and Overley was evaluated in the field in 2008. In addition to natural inoculum, plots were inoculated with 1×10^5 spores/ml of *F. graminearum* at early anthesis and were not irrigated. FHB index, the percentage of *Fusarium*-damaged kernels (FDK), DON, yield, 1000 kernel weight (1000kwt), and test weight (tw) were measured. Differences among cultivars were significant ($P \leq 0.0068$) for FHB index, FDK, DON, 1000kwt, and yield. Ranges of measured variables were: FHB index: 13% (Harry) to 64% (Overley); FDK: 21% (2137) to 42% (Harry and Wahoo); DON: 3.7 $\mu\text{g/g}$ (Karl 92) to 9.9 $\mu\text{g/g}$ (Harry); yield: 763 kg/ha (Wahoo) to 1,365 kg/ha (Karl 92); 1000 kwt: 24.8 g (Wahoo) to 30.8 g (2137). FDK and DON were positively correlated ($r = 0.59$, $P = 0.0442$). There was a significant ($P \leq 0.05$) negative correlation between FDK and yield ($r = -0.74$), FDK and tw ($r = -0.64$), FDK and 1000 kwt ($r = -0.84$), FHB index and tw ($r = -0.69$), and DON and tw ($r = -0.74$). This study demonstrated differences among winter wheat cultivars in their reaction to FHB and DON. Interestingly, Harry had the lowest FHB index but the highest DON level, implying that cultivars with resistance to FHB may be susceptible to DON accumulation.

G-11 Spatial and temporal analysis to find the epicenters of soybean rust disease foci using remote sensing, GPS and GIS technologies. N. S. HOLAH (1), D. F. Narvaez (2), J. J. Marois (3), D. L. Wright (3), F. W. Nutter (1). (1) Plant Pathology Department, Iowa State University, Ames, IA; (2) Monsanto Co, St. Louis, MO; (3) North Florida Research and Education Center, University of Florida, Quincy, FL.

Exotic plant pathogens have the potential to dramatically impact the U.S. agricultural economy. New plant pathogen threats may be deliberately or accidentally introduced, or may be introduced by a

natural event (e.g., hurricanes). In order to minimize injury to susceptible crops, a precise and accurate early warning system is needed to detect, correctly identify, and quickly respond to new plant pathogen threats. The integration of Global Positioning Systems (GPS), Geographic Information Systems (GIS), and remote sensing technologies offer tremendous opportunities for meeting U.S. agricultural biosecurity needs. The objective of this study was to detect the focal epicenters of Asian soybean rust where this plant pathogen was deliberately introduced to soybean field plots. Pathogen-specific temporal and spatial signatures were extracted from high-resolution satellite images of soybean plots inoculated with Asian soybean rust in Quincy, FL. Disease foci epicenters were determined using high resolution satellite imagery obtained on 27 August, 21 September, and 29 September 2006. Image intensities were extracted from plot images for each date. Contour maps and kriging were used to map and identify the GPS locations of soybean rust disease foci and foci epicenters. The use of integrated GPS, GIS, and remote sensing technologies accurately determined the GPS coordinates where the pathogen was deliberately introduced into plots. The GPS coordinates of the predicted locations of epicenters differed only 1.5 ± 0.92 m from stated inoculation points.

G-12 Aggressiveness of isolates of *Phialophora gregata* genotype B from resistant and susceptible soybean monocultures. T. J. HUGHES, C. R. Grau. Department of Plant Pathology, University of Wisconsin, Madison, WI.

Many soybean accessions described as resistant to brown stem rot (BSR) are preferentially colonized by isolates of *Phialophora gregata* genotype B (*Pg* B). These isolates are generally considered less aggressive than isolates of *Pg* genotype A because they cause mild or no foliar symptoms characteristic of BSR. However, variation in aggressiveness has been observed among isolates of *Pg* B. Monocultures of BSR-resistant or susceptible soybean accessions were planted from 2000 through 2005 to determine if soybean accessions influence the aggressiveness of isolates of *Pg* B. BSR-susceptible Corsoy 79 and BSR-resistant PI 567.157A were inoculated under greenhouse conditions with a total of 39 isolates of *Pg* B obtained from the different monocultures. BSR severity was determined as the percentage of symptomatic foliar and internal stem tissue. Overall, BSR severity was low and did not exceed 20%. Isolates of *Pg* B caused more severe foliar ($P < 0.0001$) and stem ($P = 0.0008$) symptoms on PI 567.157A than Corsoy 79. Analysis of stem symptom severity indicated an interaction ($P = 0.0124$) between soybean accession and the origin of isolates of *Pg*. Isolates of *Pg* B obtained from the monoculture of a BSR-susceptible or resistant accession were more aggressive than isolates from a mixed culture of susceptible and resistant cultivars. The relationship between the origin of isolate of *Pg* B and isolate aggressiveness was more apparent for PI 567.157A than for Corsoy 79.

G-13 Phytophthora root rot-like symptoms on soybeans containing *Rps* 1k in Wisconsin in 2008. T. J. HUGHES (2), P. D. Esker (2), S. P. Conley (1). (1) Department of Agronomy, University of Wisconsin, Madison, WI; (2) Department of Plant Pathology, University of Wisconsin, Madison, WI.

Cool and wet conditions during the early 2008 growing season in Wisconsin were conducive for diseases like Phytophthora root rot (PRR), caused by *Phytophthora sojae* (*Ps*). While conditions had reversed by August and many areas were drought-like, symptoms characteristic of PRR began to appear in several fields. Since many of these fields were planted to cultivars containing *Rps* 1k, serious concern arose over the breakdown of resistance conferred by this gene. To determine if these symptoms were associated with colonization by *Ps*, soybean plants were collected from 22 fields in 7 counties and assayed for the presence of *Ps*. In all plant samples, *Ps* was neither isolated nor observed. Instead, numerous isolates of *Diaporthe phaseolorum* var. *caulivora* (*Dpc*), *D. phaseolorum* var. *sojae* (*Dps*), and *Macrophomina phaseolina* (*Mp*) were obtained. Northern stem canker and pod and stem blight are caused by *Dpc* and *Dps*, respectively, while *Mp* causes charcoal rot. Based on both field observations and plant samples, the PRR-like symptoms observed in

Wisconsin in 2008 were thought to be the result of infection by *Dpc*, *Dps*, or *Mp*. However, greenhouse inoculations with these fungi did not produce symptoms similar to those observed in 2008 on two cultivars containing *Rps* 1k. Whether the PRR-like symptoms were the result of infection by a combination of these fungi or if the plants defense response to *Ps* may have increased susceptibility to *Dpc*, *Dps*, or *Mp*, still remain unknown.

G-14 Using BPMV and SMV vector systems to explore soybean cyst nematode-plant interactions. PARIJAT S. JUVALE (1), Alan Eggenberger (1), Chunquan Zhang (1), John Hill (1), Steve Whitham (1), Melisa Mitchum (2), and Thomas J. Baum (1). (1) Department of Plant Pathology, Iowa State University, Ames, IA, 50010. (2) Division of Plant Sciences and Bond Life Sciences Center, University of Missouri, Columbia, MO, 65211.

Soybean is one of the main sources of oil and an important source of complete protein worldwide. Among the various pathogens that attack soybean, the soybean cyst nematode (SCN) is especially devastating. In spite of sustained research efforts, an elaborate understanding of plant-nematode interaction is still lacking. Since the available methods to generate transgenic soybean plants are time, labor and cost intensive, there is a critical need for adapting innovative approaches for rapid gene expression or gene silencing in soybean roots in a high through-put manner to elucidate nematode-plant interaction. Due to the rapid pace at which virus infection becomes established throughout the plant and the high yield of viral encoded proteins, plant-virus based vectors present promising tools for expressing foreign proteins in soybean. On the other hand, virus-induced gene silencing (VIGS) is an exceptional reverse genetics tool that can be used to generate mutant phenotypes for unknown genes in soybean. We are using a soybean mosaic virus (SMV) vector for expressing previously identified SCN parasitism genes in soybean and a bean pod mottle virus (BPMV) vector for VIGS to elucidate gene functions in nematode resistant soybeans varieties. Since the infection profile of soybean roots by SMV and BPMV is not clearly understood, our primary goal is to study and optimize viral infection of the soybean root system. Currently, we are using reporter genes, GUS and GFP, to study virus movement to the root, optimize conditions to maximize infected root volume and ensure viral particle replication in the nematode feeding site.

G-15 Determining specificity of commercially available ELISAs for *Clavibacter michiganensis* subspecies. K. A. KORUS, A. D. Ziems, A. K. Vidaver, T. A. Jackson. University of Nebraska, Lincoln, NE.

Clavibacter michiganensis (Cm) subsp. *nebraskensis* (Cmn), the bacterium causing Goss's wilt of corn, is currently diagnosed by symptom identification and successful isolation onto CNS selective medium. An ELISA test kit (Agdia®) specific to Cm *michiganensis* (Cmm) reportedly gives a cross-reaction with Cm subspecies. This ELISA would provide a quick and inexpensive method for diagnosis of Cmn. ELISA test kits were provided by Agdia specific to Cmm, Cm *tessellarius* (Cmt), and Cm *sepedonicus* (Cms), respectively. Also, an ELISA test kit (Neogen®) specific to Cmn was included in the study. For each test kit 13 strains of Cmn, 3 Cmm, 5 Cmt, 3 Cms and 1 Cm *insidiosus* (Cmi) were tested for cross-reaction. Cultures were grown on NBY medium for 24 hr, transferred to liquid nutrient broth and agitated for 72 hr, all at 27°C. The CFU/ml was calculated for each isolate and the optimal concentration needed to produce a positive reaction for each strain. Preliminary results conducted at a concentration of 10⁴ CFU/ml from 2 of 4 replications indicate that all 5 subspecies (but not all strains) tested positive on plates coated with antibodies specific to Cmm, Cmn, and Cmt but not on plates coated with antibodies specific to Cms. ELISAs using antibodies specific to Cmm, Cmn and Cmt could be used to give a cross reaction with Cmn. Additional data will be presented on subspecies specificity of Cmm ELISA test strips.

G-16 Optimization of inoculation methods with *Fusarium virguliforme* for virus-induced gene silencing studies on soybean sudden death syndrome. L. LEANDRO, V. Silva.
Department of Plant Pathology, Iowa State University, Ames, IA.

Plant age is important in soybean sudden death syndrome (SDS) since root infection of mature plants may not be conducive to foliar symptoms due to restricted xylem colonization. In order to conduct virus-induced gene silencing (VIGS) studies, a method is needed that allows SDS symptoms to develop in plants inoculated with *Fusarium virguliforme* two weeks after inoculation with the virus. The objective of this study was to develop an inoculation method for VIGS studies on SDS. Roots of 13-day-old soybean plants were wounded by longitudinally splitting the tap root or by cutting the tap and lateral roots 1.25 inches below the soil line, then replanting into soil infested with conidia. To test the effectiveness of the inoculation at different plant ages, roots of 13, 17, 21, 25 day-old plants were wounded with a longitudinal split and replanted into infested soil. Plants were maintained in greenhouse conditions and evaluated for foliar severity over time. In another experiment, 10, 15 and 20 day-old plants with wounded and non-wounded roots were introduced into a *F. virguliforme* cell-free toxin filtrate. Plants were maintained in growth chamber conditions, and foliar severity was evaluated over time. In soil assays, severity of foliar symptoms was similar in split root and cut root methods, and was negatively correlated with plant age. In toxin assays, foliar severity did not differ among wounded and intact roots, but was greater ($P < 0.01$) in the 10-day old plants than in 15 or 20 day-old plants. Toxin assay with intact roots was identified as a simple and effective inoculation method for VIGS studies. We also revealed that soybeans become less susceptible to the *F. virguliforme* toxin as they mature, generating intriguing questions about the role of plant age on SDS.

G-17 Effect of planting density, SCN population, and soil pH on soybean root rot. K. Lim (1), C. GONGORA (1), P. Caragea (2), L. Leandro (1). (1) Department of Plant Pathology, Iowa State University, Ames, IA; (2) Department of Statistics, Iowa State University, Ames, IA.

Root health is essential for crop growth and productivity, but the factors affecting root rot on soybeans are poorly understood. The objective of this study was to investigate the effect of planting density, SCN population, and soil pH on soybean root rot and yield. Field studies were established in 2006 and 2007 following a split-plot design with row spacing (15" and 30") as the main plot and plant population density (100K, 125K, 150K, 175K and 200K seeds/acre) as the split plot. Soil pH and SCN density were assessed in each of the 80 field plots. Roots collected at flowering were assessed for root rot severity, root dry weight and colonization by fungal pathogens. Yield was determined. Regression analysis was conducted accounting for spatial dependence between the variables. A clustered ($P < 0.01$) spatial pattern was found for pH, SCN, root rot and dry weight in 2006 and 2007, and for yield in 2007. Soil pH and SCN showed a similar spatial pattern in the field as root rot severity. Plant population and row spacing did not affect root rot severity. Root dry weight was affected ($P < 0.05$) by row spacing and plant population in 2006, and by plant population in 2007. Soil pH was positively correlated with root rot severity ($r = 0.92$, $P < 0.001$) and ($r = 0.28$, $P = 0.02$), in 2006 and 2007 respectively, and negatively correlated with root dry weight ($r = -0.6$, $P < 0.001$) and yield ($r = -0.3$, $P = 0.07$) in 2007. SCN population was positively correlated with root rot ($r = 0.5$, $P < 0.05$) both years. *Fusarium* was the predominant fungus isolated from roots, and was more frequently isolated from roots with >30% root rot than roots with less severe root rot. This study suggests that soil pH plays an important role in soybean root rot and productivity. The interaction between soil pH and root pathogens warrants further research.

G-18 First report of Fusarium root rot in soybean caused by *Fusarium tricinctum* in Minnesota. P. W. Meyer, M. S. Clancey, I. E. Brose, J. E. KURLE. Dept. of Plant Pathology, University of Minnesota, St. Paul, MN.

Seed, seedling, and root rots of soybean caused by a complex of soilborne fungi are possibly the most important diseases of soybean in Minnesota, causing losses estimated at 380,000 tons in 2005. *F. solani* and *F. oxysporum* are the predominant *Fusarium* species isolated from soybean taproots in Minnesota. For soybeans grown in unamended field soil in a growth chamber at 10 and 16°C, the predominant *Fusarium* species isolated from taproots were *F. solani* and *F. tricinctum*. Three isolates of *F. tricinctum* were obtained from these plants. One of the isolates produced lesions on soybean seedlings after two weeks, using an inoculum layer method in inoculated sterile sand. *F. tricinctum* has been previously reported as pathogenic on soybean in Ontario, Canada. Its preference for lower temperatures might account for the low frequency of isolation from Minnesota grown soybean. Its role in soybean root rot in the field is not known. *F. tricinctum* could contribute to seedling rot early in the season when the soil temperature is below 20°C.

G-19 Engineering payload designs for remote sensing applications for plant pathology using latex weather balloons. MATTHEW E. NELSON (3), J. P. Basart (2), and F. W. Nutter, Jr. (1). (1) Department of Plant Pathology, (2) Electrical and Computer Engineering Department, (3) Space Systems and Controls Lab, Aerospace Engineering Department, Iowa State University, Ames IA.

The High Altitude Balloon Experiments in Technology (HABET) program at the Space Systems and Controls Lab (SSCL) at Iowa State University (ISU) has been flying high altitude balloons in collaboration with the ISU Department of Plant Pathology for over 10 years. Project goals are to obtain real-time imagery of crops under stress from biotic and abiotic agents, as well as to quantify the density of pathogen spore clouds above diseased crops. These flights vary from ground tethered flights to flights reaching altitudes of 30 km or higher. Since 2007, the two teams have been working together to design, build and fly hardware that is capable of acquiring both visible and near-infrared digital images. The engineering design of such hardware presents unique opportunities in building robust, yet accurate and reliable equipment for the detection and accurate identification of various plant diseases. The hardware we are using consists of 2 Digital SLR cameras (Canon 5D cameras with 24-105 mm zoom lenses). However, one of the Canon 5D cameras has been modified for near-infrared operation in the 830 nm near-infrared range. A Single Board Computer is used to remotely control the cameras through a USB connection and allows us to take photographs as well as adjust camera settings while the payload is in the air. The helium balloon platform has also been used to quantify the horizontal and vertical gradients of spore densities being released from disease plant canopies. We have designed and built payloads that are capable of flying 6 Model 20 Rotorod spore collectors which are also remotely controlled from a ground control station. This system allows spore collection at 6 different altitudes to obtain a vertical profile of spore densities. Flights in the near future are being planned for balloons to be released at pre-set altitudes to quantify spore densities horizontally with respect to distance from the source (diseased field).

G-20 Deposition of fungal spores on rotorod collection surfaces is nonrandom. F. W. NUTTER, S. K. Eggenberger, E. Byamukama. Department of Plant Pathology, Iowa State University, Ames, IA.

Numerous types of spore sampling devices have been used by plant pathologists to quantify the diurnal, seasonal, and spatial characteristics of spore densities within and above crop canopies. The collection efficiency of active spore trapping methods is a function of: (i) size and shape of the spore (terminal velocity), (ii) wind speed (which is provided by active spore traps), and (iii) radius of the collection surface of the sampling device (leaf, petiole, monofilament line, glass/plastic slides, tape,

etc.). One assumption commonly made when quantifying spore density is that spore deposition on the collection surface is random. To test this assumption, spores of the wheat leaf rust pathogen, *Puccinia recondita* f. sp. *tritici*, were collected using rotorod spore samplers in a settling tower in the greenhouse and below a helium weather balloon positioned above a wheat field. In both environments, wheat leaf rust spores were deposited in higher numbers toward the center of a collection rod, with significantly fewer toward the outer edge of the rod; in these instances, spore deposition on rotorods was non-random. This information should be considered when making decisions regarding sampling pattern and number of microscope fields to count. Our results indicate that to minimize sampling error, a systematic sampling design should be employed to quantify spore densities.

G-21 Aggressiveness of different *Fusarium graminearum* chemotypes on wheat cultivars with different level of resistance to Fusarium head blight. K. D. PURI, S. Zhong. North Dakota State University, Fargo, ND.

Fusarium head blight (FHB), caused by *F. graminearum* Schw., is a destructive disease of wheat and barley throughout the world. The disease is responsible for both direct yield reduction and mycotoxin contamination of grains. The major mycotoxins produced by the pathogen include deoxynivalenol (DON) and its derivatives [3-acetyl deoxynivalenol (3-ADON) and 15-acetyl deoxynivalenol (15-ADON)] as well as nivalenol (NIV), which pose health hazards to human and animals. The relative aggressiveness of 132 isolates collected during 1980 to 2000 in North Dakota, 43 isolates collected in 2008 from different counties of North Dakota and 59 isolates from China were evaluated after their chemotype. PCR assay indicated that 124 (93.9%) isolates from the old collection (1980 to 2000) and 24 (55%) from the new collection (2008) were of 15-ADON chemotype, and 46 (77.9%) from China were of NIV chemotype. Fourteen isolates from each of 15-ADON and 3-ADON chemotypes, and two from the NIV chemotype were tested for aggressiveness on three wheat cultivars/line (Grandin, Steele-ND and ND 2710), which are susceptible, moderately susceptible and moderately resistant to FHB, respectively. Mean disease severity induced by the isolates varied from 13.5 to 55.6% and difference in aggressiveness among isolates were highly significant ($P = 0.0001$). Majority of 3-ADON producing isolates had higher disease severity compared to 15-ADON or NIV isolates, but no isolate/variety interaction was detected. The results indicate that the 3-ADON chemotype isolates of *F. graminearum* have increased in the population of North Dakota and in general were more aggressive than 15-ADON and NIV isolates.

G-22 Extended-duration row covers to suppress bacterial wilt on muskmelon: Optimizing a new management strategy. E. SAALAU ROJAS, M. L. Gleason, J. C. Batzer. Iowa State University, Ames, IA.

Bacterial wilt (pathogen: *Erwinia tracheiphila*) causes major losses on muskmelon in the Midwest U.S. Extending the period during which plants are covered by spunbond row covers may shield crops from cucumber beetles, which vector the pathogen. Experiments at two Iowa State University research farms (Muscatine and Gilbert, IA) in 2008 validated the ability of extended-duration row covers to suppress incidence of bacterial wilt on muskmelon. Treatments in a latin square design were: 1) no row cover; 2) row cover removed at the beginning of anthesis (start of bloom); 3) row covers removed 10 days after anthesis, with row cover ends opened at anthesis to allow pollination; and 4) row covers removed 10 days after anthesis, with bumble bee boxes inserted under row covers at anthesis to provide pollination. In both trials, wilt incidence in the non-covered control was much higher than in the row-covered treatments. Yield in the extended-duration row cover treatments was similar when row ends were opened or when a bumble bee box was inserted under the cover. At Muscatine, the extended-duration row covers significantly reduced incidence of bacterial wilt at harvest compared to row cover removal at anthesis. At Gilbert, where melons were transplanted 3 weeks later than at Muscatine, all row cover treatments resulted in similar levels of wilt suppression.

The results suggest that row covers can effectively suppress cucurbit bacterial wilt, and that timing of transplanting may determine whether extending the row-covered period provides an additional margin of wilt protection.

G-23 Virulence and genetic diversity of *Phakopsora pachyrhizi* in Nigeria. M.

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Soybean rust, caused by *Phakopsora pachyrhizi*, is a major disease in many soybean-producing areas in Nigeria. To determine the virulence and the genetic structure of Nigerian field populations of the soybean rust pathogen, a total of 116 purified isolates established from infected leaves randomly collected from soybean fields in four agroecological zones in 2005 was used. The virulence variability of the isolates was determined using a set of four soybean accessions with Rpp1, Rpp2, Rpp3, and Rpp4 resistance genes, two highly resistant and two highly susceptible genotypes. Principal component and cluster analyses on the number of uredinia per cm² of leaf tissue separated the rust isolates into seven pathotype clusters. Isolates in cluster III were the most virulent, while those in cluster IV were the least virulent. In a follow-up study, 18 simple sequence repeat markers were used to study the genetic diversity using the same 116 isolates and an additional 146 isolates collected from infected plants in two fields (73 isolates in each field) located 292 km apart. There was a high genetic variation in Nigerian *P. pachyrhizi* populations. Eighty-four distinct genotypes were identified among isolates from the three agroecological zones, while 48 distinct genotypes were identified from 146 isolates analyzed from both fields. Nei's average genetic diversity across geographical regions was 0.22 while for both fields was 0.09. Hierarchical analysis of molecular variance revealed significant ($P < 0.05$) and low genetic differentiation among all populations of *P. pachyrhizi*. However, the majority (> 90%) of the genetic diversity was distributed within a soybean field, while almost 6% was distributed among fields within geographic regions. The phylogenetic analysis showed three groups in Nigerian rust populations with one major group comprising more than 90% of the isolates. However there was a poor correlation between virulence and genetic variation. This work will be useful in breeding and management of soybean rust by facilitating the deployment of rust-resistant cultivars.

G-24 Performance of SCN-resistant soybean varieties in fields infested with different soybean cyst nematode HG types. G. L. TYLKA, G. D. Gebhart, C. C. Marett. Department of Plant Pathology, Iowa State University, Ames, IA.

There are hundreds of soybean varieties resistant to the soybean cyst nematode (SCN). These varieties vary in yield and the ability to control SCN populations. The HG type test is a greenhouse test that assesses SCN reproduction on the different sources of resistance used in breeding SCN-resistant soybean varieties. Each year, we evaluate the agronomic performance and SCN control of SCN-resistant soybean varieties in field experiments, and results reveal how the HG type of an SCN population relates to performance of SCN-resistant soybean varieties in the field. There are nine experimental locations statewide annually, three each in northern, central, and southern Iowa. Plots are four rows wide, spaced 76 cm (30 inches) apart and 5.2 meters (17 feet) long. Each variety is replicated four times per location. Soil samples are collected from each plot at planting to verify the presence of SCN and to determine the initial SCN population density. Also, an HG type test is

conducted on the SCN population obtained from the spring soil samples at each location. At harvest, another soil sample is collected from each plot to determine SCN population densities. The center two rows of each plot are harvested, and yield and SCN population densities are averaged for each variety at each location. The highest-yielding SCN-resistant varieties often are those with a source of resistance on which there was low (<5 percent) SCN reproduction in the HG type test. But in some experiments, the highest yielding SCN-resistant soybean varieties are those with a source of resistance on which there was relatively high (>20 percent) SCN reproduction in the HG type test. Also, in some experiments, SCN population densities declined or did not increase during the growing season on varieties with sources of SCN resistance on which there was >20% reproduction in the HG type test.

- G-25 Discovery of genes underlying soybean QTLs conferring partial resistance to *Phytophthora sojae*.** H. WANG (4), L. Waller (5), S. Tripathy (5), S. K. St. Martin (3), L. Zhou (5), K. Krampis (5), D. M. Tucker (1), I. Hoeschele (2), S. Maroof (1), B. Tyler (5), A. E. Dorrance (4). (1) Department of Crop and Soil Environmental Sciences, Virginia Polytechnic Institute and State University, Blacksburg, VA; (2) Department of Statistics, Virginia Polytechnic Institute and State University, Blacksburg, VA; (3) The Department of Horticulture and Crop Science, The Ohio State University, Columbus, OH; (4) The Department of Plant Pathology, The Ohio State University, Wooster, OH; (5) Virginia Bioinformatics Institute, Virginia Polytechnic Institute and State University, Blacksburg, VA.

Phytophthora sojae causes soybean root and stem rot, resulting in an annual loss of 1–2 billion dollars in soybean production worldwide. Partial resistance confers a broad-spectrum durable resistance to *P. sojae* and is currently thought to be a more stable alternative than single gene mediated resistance. Few QTLs have been mapped for soybean partial resistance to *P. sojae* and little is known about the molecular mechanisms behind it. In this study, five potential QTLs on Chromosomes 12, 13, 14, 17 and 19, each explaining 4–7% of phenotypic variation, were identified from 186 RIL of a F_{4:7} population from a cross of the partially resistant cultivar ‘Conrad’ and the susceptible cultivar ‘Sloan’ by composite interval mapping. Global expression profiling identified a large number of genes showing expression contrast between ‘Conrad’ and ‘Sloan’ either after inoculation or constitutively. Of these, 55 genes map to the QTL regions and include defense-related proteins such as auxin response factors, heat shock proteins, transcription factors, membrane transporters, NBS-LRR proteins, pyruvate decarboxylase, cytochrome P450, cysteine protease and H(+)/calcium ATPase. Eighteen of the 55 (32.7%) proteins are either unknown or have uncharacterized functions. Fifteen genes under QTLs were selected and their expression was confirmed by qRT-PCR. The results indicate the possibility of a complex QTL-mediated resistance network and provide the clues for further functional studies of soybean partial resistance to *P. sojae*. These genes could also be used as markers for breeding and thus improving soybean production.

- G-26 The 2007 and 2008 Fusarium head blight epidemics in Nebraska.** S. WEGULO, P. Baenziger, L. Nelson, J. Hernandez Nopsa, J. Millhouse, N. Mengistu, J. Breathnach. University of Nebraska-Lincoln, Lincoln, NE.

Because of a variable climate, including drought during some years, Fusarium head blight (FHB) occurs sporadically in Nebraska. In 2007 and 2008, FHB epidemics occurred in the state for the first time in more than a decade. Infection of wheat heads by *Fusarium graminearum* was favored by excessive rainfall before and during flowering. The most affected areas were the south central and eastern parts of the state. However, in 2008, FHB was observed as far west as Imperial in the southwestern part of the state where irrigated fields were more severely affected. Northwest, the Nebraska Panhandle was spared in both years due to dry conditions. A shift towards reduced tillage or no-till to conserve water and soil and inclusion of corn and wheat in crop rotation schemes has led to buildup of FHB inoculum in Nebraska. Yields were reduced not only by FHB but by other foliar

diseases favored by wet weather. The major foliar diseases were *Septoria tritici* blotch, powdery mildew, and tan spot. In addition to reducing yield and grain quality, FHB caused accumulation of the mycotoxin deoxynivalenol (DON) in grain. Yield losses of up to 20% were estimated in the most severely affected areas in the south central and eastern parts of the state. In 2007, the overall loss statewide in grain yield was estimated at 2.0% or 1.68 million bushels valued at \$9.4 million based on a June 11, 2007 wheat price of \$5.57/bushel. In 2008, the overall loss statewide was estimated at 2.3% or 1.64 million bushels valued at \$13.3 million based on an August 28, 2008 wheat price of \$8.11/bushel. Additional losses were incurred in reduced prices for the infected grain with high levels of DON. In the most severely affected areas in both years, DON concentrations of more than 18 ppm were recorded in the most susceptible cultivars.

G-27 Detection of *Melon necrotic spot virus* in *Oplidium* sp. infested cucumbers. C. D. WOLTJEN, D. J. Lewandowski. The Ohio State University, Columbus, OH.

Melon necrotic spot virus (MNSV) is an important pathogen of cucumbers and melons that can lead to a reduction in fruit quality and economic losses. MNSV is vectored by zoospores of *Oplidium* sp. and can also be mechanically transmitted. In 2008, we received a call from a greenhouse cucumber grower in Ohio with a high percentage of symptomatic cucumber (*Cucumis sativus*) plants exhibiting large necrotic foliar lesions. Leaf samples from symptomatic cucumbers tested positive for MNSV by DAS-ELISA. Roots of symptomatic plants were found to be infested with *Oplidium* sp. The objectives of our research were to compare the sequence of this Ohio MNSV isolate to other known MNSV isolates and to determine the susceptibility of several cucurbit species. Sap from MNSV-infected cucumber leaves was rub-inoculated onto the cotyledons of three *C. melo* and seven *C. sativus* cultivars. Necrotic local lesions on cotyledons of all ten cultivars were confirmed to be MNSV-positive by DAS-ELISA. MNSV was also transmitted from the original *Oplidium* sp. infested substrate to one *C. sativus* variety. cDNA was synthesized from total RNA extracted from MNSV-infected leaves using an MNSV primer complementary to the 3'-UTR. The coat protein (CP) ORF was amplified with PCR using the same 3' primer and a primer located upstream of the CP ORF. The gel-purified PCR product was sequenced and compared to other known isolates of MNSV. The CP of the Ohio MNSV isolate is 84–94% and 74–97% identical to the other isolates of MNSV at the nucleotide and amino acid levels, respectively.

G-28 Genetic variation of *Phytophthora sojae* populations from Ohio and South Dakota. L. X. ZELAYA-MOLINA (1), M. A. Draper (2), A. E. Dorrance (1). (1) Dept. of Plant Pathology, OARDC, Wooster, OH; (2) formerly Plant Science Department, South Dakota State University, Brookings, SD.

Phytophthora sojae is an important plant pathogen of soybean and negatively impacts yield each year in the north central region. Understanding how the pathogen population is evolving will assist in developing effective management strategies. Our objective was to assess the population variation of *P. sojae* isolates collected from 2 states, OH and SD and 2 intensively sampled fields within OH, Sandusky and Wood, with 21 polymorphic SSR markers. The average number of alleles was 3.6 per loci for the OH population, and 2 of the 32 isolates were putative heterozygotes for 2 SSRs. Seventeen alleles were exclusive to the OH population. SD population had fewer alleles, 2.9; while one isolate was heterozygous for one SSR, and 4 alleles were exclusive. The Sandusky and Wood populations had an average of 3.1 and 3.3 alleles, respectively; Wood population had two heterozygous isolates. Nei's genetic distance and Fst analysis indicates a moderate genetic differentiation between the populations. The results agree with previous reports of low level of outcrossing in these populations that could account for the generation of different pathotypes in the field.