This article was listed in Forest Nursery Notes, Summer 2007

88. Excised shoots of top-pruned red pine (*Pinus resinosa*), a source of inoculum of the shoot blight pathogen *Diplodia pinea*. Munck, I. A. Phytopathology 97(7)Suppl:S81. 2007.

based management of dry land agriculture. As such, development of elite cultivars necessitates synchronous identification of genetic factors conferring tolerance and resistance to drought and *M. phaseolina*. Fifty seven F_8 cowpea recombinant inbred lines derived from a cross between two parents contrasting for drought tolerance and ashy stem blight resistance were screened in greenhouse and field experiments. Recovery dry weights and mortality counts were used as phenotypic indices in drought and ashy stem blight experiments respectively. A cowpea linkage map was constructed with 359 amplified fragment length polymorphisms and 12 restriction fragment length polymorphisms derived from the population. QTL analysis was carried out using the Kruskall-Wallis and MQM packages of MapQTL 4.0 software. Four QTL accounting for 14.4, 15.4, 23.3, and 27.6% of the phenotypic variance to ashy stem blight were identified. Ten QTL accounting for between 6 and 28% of the phenotypic variance were mapped for drought tolerance. QTL for both phenotypes showed no apparent association. These results provide a foundation for further isolation of genes and molecular markers for genetic based management of drought and ashy stem blight in cowpea.

The effects of temperature on urediniospore production in *Phakopsora pachyrhizi* and development of national risk maps

E. MUMMA (1), R. W. Schneider (1), C. L. Robertson (1), C. G. Giles (1)
(1) Dept. Plant Pathology, Louisiana State University Agricultural Center, Baton Rouge, LA, USA
Phytopathology 97:S81

The primary objective of this research was to determine the temperature range that is most conducive to the production and release of urediniospores of *Phakopsora pachyrhizi*, causal agent of Asian soybean rust. Quantitative spore trapping data from diseased fields in Quincy, FL were collected for two years, and the results were related to different diurnal temperature parameters. In addition, isothermal growth chamber studies were conducted with field-collected leaves to determine the optimal temperature for urediniospore production and to assess the sensitivity of this process to less than optimal temperatures, including exposure to temperatures above 32°C. Results from these studies and archived daily temperatures for each county in the U.S. were used to construct color-coded maps that show areas of high and low risk for infection and spread of the disease for each month of the season.

Excised shoots of top-pruned red pine (*Pinus resinosa*), a source of inoculum of the shoot blight pathogen *Diplodia pinea*

I. A. MUNCK (1), G. R. Stanosz (1)
(1) Department of Plant Pathology, UW-Madison, WI, USA
Phytopathology 97:S81

Diplodia pinea causes shoot blight and collar rot diseases that kill or otherwise render nursery pine seedlings unmarketable. *D. pinea* sporulates abundantly on needles and stems it has colonized and killed. Nursery managers sometimes top prune pine seedlings to reduce their height. In late summer 2005, *D. pinea* pycnidia were observed on excised shoots present in red pine seedling beds that had been top pruned earlier during that third season of growth. This prompted a survey of top-pruned beds at two nurseries to determine incidence and abundance of *D. pinea* conidia from excised shoots. At each nursery, excised shoots were collected from the seedling canopy in two subplots and adjacent alleyway ground surface in each of five beds (plots). A washing and filtration technique was used to quantify conidia extracted from colonized shoots. Excised shoots from both nurseries abundantly bore *D. pinea* pycnidia and conidia. Excised shoots collected from the seedling canopy yielded more conidia than shoots collected from the ground. Most conidia from shoots in the canopy and from the ground germinated on water agar. Species-specific PCR primers were used to confirm the identity of the pathogen. Removal of excised shoots from top-pruned pine nursery seedlings should be considered as a means to reduce inoculum in nurseries where *D. pinea* is present.

Landscape scale variation in *Diplodia* spp. conidia from cones and asymptomatic persistence of Diplodia shoot blight fungi on red pine

I. MUNCK (2), T. Sickley (1), D. Smith (2), G. R. Stanosz (2)
(1) Department of Forest Ecology and Management, UW-Madison, WI, USA; (2) Department of Plant Pathology, UW-Madison, WI, USA
Phytopathology 97:S81

Diplodia pinea and *D. scrobiculata* sporulate abundantly on cones of many pine hosts. Variation in incidence and abundance of potential inoculum from cones and frequency of asymptomatic persistence on or in shoots was examined for sites differing in dominant presettlement vegetation in Bayfield and Douglas counties in northern Wisconsin. Collections were made in each county from six mature red pine (*Pinus resinosa*) plantations, three each in areas dominated in presettlement times by jack (*P. banksiana*) and red pine. At each site, five cones were collected from each of five red pines and 10 shoots were collected from up to five red pines. Conidia from cones were quantified with a water wash and filtration technique. *Diplodia* spp. were cultured from surface-disinfested asymptomatic shoots. *Diplodia* specific PCR was used to identify *Diplodia* spp. Cones and asymptomatic shoots from each county yielded *D. pinea* and *D. scrobiculata*. More conidia were obtained from cones from Douglas Co., where there is a history of severe shoot blight damage, than from Bayfield Co. In Douglas Co., more conidia were obtained from plantations in areas of presettlement jack pine dominance than those in areas of presettlement red pine dominance. The numbers of conidia and frequencies of cultural detection of *Diplodia* spp. from asymptomatic shoots at a site were positively correlated.

Inter-row cover crops to reduce aphid-borne plant virus disease in pumpkin

J. F. MURPHY (1), J. Mosjidis (1), M. D. Eubanks (1), G. J. Buda (2), J. Masiri (1)
(1) Auburn University, AL, USA; (2) Clarkson University, NY, USA
Phytopathology 97:S81

Inter-row cover crops (*Sericia lespedeza* and Sunn Hemp) were evaluated comparatively with a conventional, bare soil treatment for their ability to reduce the aphid-borne virus, *Watermelon mosaic virus* (WMV), incidence and associated yield losses in pumpkin. It was hypothesized that inter-row cover crops would provide consistency in color or reflectance observed by incoming aphids thereby being less attractive than the high contrast between pumpkin plants and soil. In addition, upon landing on the cover crop, the viruliferous aphids would lose virus during test probes of leaves to determine suitability as a food source. These aphids would then be virus-free upon moving to pumpkin. WMV incidence in pumpkin plants did not differ among treatments, although fewer plants were infected in Sericia treatments (69, 25 and 49% for conventional, Sericia and Sunn Hemp treatments, respectively). WMV titer in pumpkin leaf samples, however, was significantly less in the Serecia cover crop. Interestingly, significantly more aphids occurred on pumpkin plants in the Sericia treatment than on pumpkin plants in the other treatments. No differences in pumpkin yield were observed among treatments.

Baseline levels of aflatoxin contamination of peanuts from western Kenya

C. K. Mutegi (1), H. K. NGUGI (2)
(1) Kenya Agricultural Research Institute, P. O. Box 57811, Nairobi, Kenya; (2) Penn State University, Fruit Research & Extension Center, Biglerville, PA, USA
Phytopathology 97:S81

Aflatoxin contamination of peanuts poses a risk to human health and has been identified as a major constraint to trade in peanuts in eastern Africa. As part of a project to control aflatoxins, a survey was carried out to obtain baseline data on levels of aflatoxin in peanuts from major production regions of western Kenya. A total of 389 and 375 samples from Busia and Homa Bay districts, respectively, were obtained and analyzed for aflatoxin content with a direct competitive ELISA protocol. Levels of aflatoxin ranged from 0 to 2688 and 7525 ppb in samples from Busia and Homa Bay, respectively. Of the total 764 samples, 87.8% contained < 4 ppb of aflatoxin, 5.1% had between 4 and 20 ppb, while 7.1% exceeded the Kenya's regulatory limit of 20 ppb. There was a highly significant ($\chi^2 = 16.03$; $P < 0.0001$) association between district of origin and sample aflatoxin levels whereby, 10.3% of the samples from Busia exceeded 20ppb compared with 3.7% of the samples from Homa Bay. This observation is supported by a significant ($\chi^2 = 10.13$; $P = 0.0015$) association between levels of aflatoxin and agroecological zones; only 3.2% of the samples from the dryer LM3 zone had >20 ppb compared with 9.4% of the samples from the wetter LM1 zone. This high variability in levels of aflatoxin between samples and regions underscores the need for proper sampling procedures for regulatory purposes.

Metagenomics for identification of novel plant viruses

V. MUTHUKUMAR (1), G. B. Wiley (2), M. L. Pierce (1), B. A. Roe (2), U. Melcher (1)
(1) Oklahoma State University, Stillwater OK, USA; (2) University of Oklahoma, Norman OK, USA
Phytopathology 97:S81

The number of virus species identified by the ICTV is likely to be far less than the actual number of viruses present. A metagenomic approach is being taken to discover novel viruses from plants. Aliquots of plant material were subjected to homogenization and differential centrifugation to isolate virus-like particles. The pellet obtained was treated successively with DNase-I to remove contaminating plant DNA and proteinase-K, sodium dodecyl sulfate to digest the DNase-I and capsid proteins. The VNA was amplified by reverse transcription and PCR using degenerate primers. The sequences obtained from cloned PCR products were assembled and characterized by comparison with known viral sequences. To date, 100 plants were analyzed; of these 41 were PCR positive. Of the 20 sequence sets available to date, 40% suggested the presence of 5 viruses, all previously uncharacterized by sequence analysis. Two double infections were found. Polymorphisms in the sequence of a