NC STATE UNIVERSITY

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Ph.D. Symposium, NCSU Department of Plant Pathology

Friday 22 April 2016, Talley Governance Chamber, Room 4140

8:00 - 8:30	**Refreshments**
8:30 - 8:45	**Welcome** Drs. Eric Davis and Marc Cubeta
8:45 - 9:15	**Luis O. Lopez-Zuniga,** Peter J. Balint-Kurti, Randall J. Wisser, and Petra Wolters. Production of chromosome segment substitution lines for the identification of multiple disease resistance loci in maize.
9:15 - 9:45	**Katie N. Neufeld,** Frank Louws, Barbara Shew, Todd Wehner, and Peter Ojiambo. Predicting within-season infection risk of cucurbits by *Pseudoperonospora cubensis* and validation of the CDM ipmPIPE forecasting system.
9:45 - 10:15	**BREAK**
10:15 - 10:45	**Sean Bloszies**, Chris Reberg-Horton and Shuijin Hu. Alternatives to tillage and synthetic fertilizers: effects of alternative farming systems on soil organic matter pools and nitrous oxide emissions.
10:45 - 11:15	**Alsayed Mashaheet,** David Marshall, Kent Burkey, Shuijin Hu, and David Livingston. The effects of O_3 and CO_2 on wheat interactions with leaf and stem rust pathogens.
11:15 - 12:15	**Deborah R. Fravel,** Alumnus Enrichment Speaker, USDA-ARS National Program Leader for Plant Health, emeritus. Discovering your path at the USDA-ARS.

Abstracts

Production of chromosome segment substitution lines for the identification of multiple disease resistance loci in maize

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Southern leaf blight (SLB), northern leaf blight (NLB), and gray leaf spot (GLS) caused by *Cochliobolus heterostrophus, Exserohilum turcicum*, and *Cercospora zeae-maydis* respectively, are among the most important corn diseases worldwide. Previously, strong genetic correlations between resistance levels to each of these diseases in a population of 282 diverse maize inbred lines were demonstrated. The goal of this study is to identify loci underlying elite levels of resistance observed in four of the multiply disease resistant (MDR) lines identified previously. These lines were identified by the creation of chromosome segment substitution line (CSSL) populations in which a whole genome tiling path of introgressions from MDR lines was captured in multiple disease susceptible (MDS) genomic backgrounds. Four MDR lines (NC304, NC344, Ki3 and NC262) were used as donor parents and two MDS lines (Oh7B, H100) as recurrent parents, to produce eight $BC_3F_{4:5}$ CSSL populations comprising 1,750 inbred lines in total. Each population was assessed for SLB, NLB and GLS in replicated trials in two environments. Moderate to high levels of heritability (0.32 to 0.83) were observed. Several lines in each population were significantly more resistant than the susceptible parental lines for each disease. For most populations and most disease combinations, significant correlations were observed between disease scores and marker effects and the number of lines that were resistant to more than one disease was significantly higher than would be expected by chance. QTLs for disease resistance were detected; 36 for SLB, 16 for NLB, and 20 for GLS. Among these, 30 QTLs were associated with variation in resistance to a single disease, 18 to two disease (SLB/NLB: 6, SLB/GLS: 7, NLB/GLS: 5), and 4 QTLs were associated with resistance to all three diseases.

Predicting within-season infection risk of cucurbits by *Pseudoperonospora cubensis* and validation of the CDM ipmPIPE forecasting system

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Pseudoperonospora cubensis which causes cucurbit downy mildew is considered the most damaging pathogen of cucurbits worldwide. The pathogen propagates via sporangia that are aerially dispersed and can cause infection depending on prevailing weather. The CDM ipmPIPE forecasting system integrates data on disease outbreaks and trajectories of sporangia transport to predict the risk of disease outbreaks in the United States but the forecasting system has yet to be validated. Validation was conducted by relating predicted risks to the presence of sporangia and disease onset. Rainwater samples from eight states were collected from planting to first disease report in experimental fields from 2013 to 2015 and presence of sporangia verified using PCR. The forecasting system correctly classified disease onset in 60 to 85% of the cases, while forecasts correctly classified presence of sporangia in 43 to 87% of the cases. To develop a model to predict within-season infection risk of cucurbits, cucumber plants were exposed to field conditions and naturally occurring inoculum over a 24- and 48-h period in Clayton, NC and Charleston, SC, in multiple experiments from 2012 to 2015. Disease severity was assessed 7 days after exposure, and weather variables during exposure were recorded. Using data collected in NC, 67 and 128 defined weather variables for the 24- and 48-h period, respectively, were examined to identify variables favorable for disease development. Binary logistic regression models with hours of relative humidity >80% and average daily temperature over the 24- and 48-h period had superior predictive ability with correct classification rates >80%, while sensitivity rates were >88%. Independent validation of the 48-h model using data collected in SC showed very good model performance with a true skill statistic of 0.84.

Alternatives to tillage and synthetic fertilizers: effects of alternative farming systems on soil organic matter pools and nitrous oxide emissions

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A majority of the anthropogenic nitrous oxide (N_2O) emissions in world come from agricultural soils. Since emissions levels depend on a combination of factors including soil organic matter (SOM) levels and mineral N availability, it is not clear how farm management strategies may affect net production of this potent greenhouse gas. Furthermore, it is vital to understand which of the several diverse SOM pools is driving N_2O emissions. The objectives of this study were to examine different rotations for their impact on soil N_2O emissions, and to elucidate the soil C and N dynamics driving these differences. Both organic and conventional annual cropping systems have been managed since 1999 in the Coastal Plain of North Carolina using reduced-till (RT), clean till (CT), or a 3 year rotation with pasture (LR). Data collected from field soil (0-15cm) included microbial biomass carbon and nitrogen (MBC/MBN), and dissolved organic carbon (DOC). Laboratory incubations were also conducted to quantify N_2O emissions, soil respiration, and N mineralization from the same samples. Preliminary results indicate that the farming systems differ in the size of the flush of N_2O that occurs following rewetting soils (70% WFPS) collected in early spring and at soybean harvest, but not during the growing season. Conventional CT soil N_2O emissions exceeded organic LR and CT at both time points. MBN of organic LR also exceeded that of conventional CT in early spring, while in organic RT, MBN was higher than that of conventional NT at harvest. No differences in MBN or DOC were observed among rotations in the study.

The effects of O_3 and CO_2 on wheat interactions with leaf and stem rust pathogens

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Elevated O_3 and CO_2 associated with climate change, affect wheat and interactions between wheat and leaf and stem rust pathogens. Understanding these effects is thus, important for maintaining or increasing global yields of wheat. However, there is very limited information on the effects of these gases, in relation to the treatment dose and timing, the host's growth-stage, and rust-resistance. We screened a wide range of winter- and spring-wheat germplasm for O_3 responses to identify suitable host varieties for wheat/gas/rust studies. Using four selected winter wheat cultivars (Coker 9553, NC Neuse, Jamestown and NuEast), near-ambient O_3 concentration of 50 ppb was found to increase disease severity and pustule size, and to hasten sporulation of leaf rust on O_3-sensitive Coker 9553. Severity of stem rust on Coker 9553 also increased at near-ambient O_3 concentration but not at higher concentrations (70 or 90 ppb). Increase in disease severity was also dependent upon pre-exposure of plants to the gas treatment prior to inoculation, indicating a complex plant-ozone-disease interaction. We confirmed the differential O_3 responses of Coker 9553 and O_3-tolerant MD01W28-8-11 using seedlings and adult plants, and screened the doubled haploid population of the cross between these two for rust resistance. These results could facilitate selection of high yielding, rust-resistant, O_3-tolerant varieties. O_3-screening studies also were conducted to narrow down the genetic control of observed O_3 tolerance in the cultivar Chinese Spring at the chromosomal level, and to identify the effects of 43 leaf rust resistance genes in near isogenic lines developed from the O_3-sensitive cultivar Thatcher.