Predicting the Next Plant Disease Pandemic

April 5, 2023
9:00AM–6:00PM
Plant Sciences Building,
Centennial Campus

GRIP4PSI

Nusbaum

NC STATE UNIVERSITY
N.C. Plant Sciences Initiative

NC STATE UNIVERSITY
Global One
Health Academy

Emerging Plant Disease and Global Food Security

Agenda
Day 1: Wednesday, April 5
8:15AM—6:00PM

8:15-9:00   Breakfast

9:00-9:20   Opening remarks, *Adrian Percy, Plant Sciences Initiative; Dr. Warwick Arden, Provost NCSU*

9:20-9:40   The Persistent Threat of Emerging Plant Disease to Global Food Security, *Dr. Jean Ristaino, William Neil Reynolds Distinguished Professor of Plant Pathology, Director, Emerging Plant Disease & Global Food Security Cluster, NCSU*

Climate Change and Emerging Diseases
Moderator: Dr. Anna Whitfield, NCSU
9:40-9:55   Climate and Potential Yield Losses to Fungal Plant Pathogens, *Dr. Dan Bebber, Professor, University of Exeter*

9:55-10:15   R2M Rapid Risk Assessment to Support Mitigation of Plant Disease: A Toolbox for National Programs, *Dr. Karen Garrett, Preeminent Professor, University of Florida*

10:15-10:30   Coffee Break

Diagnostics from the Ground Up
Moderator: Dr. Jean Ristaino, NCSU
10:30-10:45   A View from the Ground and Above: A Crops Consultant's Experience with Mapping Farms, Pests, and Pathogens, *Stan Winslow, President, Tidewater Agronomics, Inc.*

10:45-11:00   An Area Agent's Perspective on Pest and Pathogen Emergencies, *Erin Eure, Area Specialized Agent, NC Extension*

11:00-11:15 The Plant Pathogen Confirmatory Diagnostics Laboratory: Safeguarding US Agriculture and Natural Resources, *Dr. John Bienapfl, USDA APHIS*

Diagnostic Networks at the National and International Level
Moderator: Dr. Qingshan Wei, NCSU

11:15-11:30 The National Plant Diagnostic Network, *Dr. Neil McRoberts, Director, National Plant Diagnostic Networks, University of California Davis; Dr. Jim Stack, Director, Great Plains Diagnostic Networks, Kansas State University*

11:30-11:45 The North American and Global Perspective on Understanding and Mitigating the Threats of the Next Plant Health Pandemic, *Dr. Stephanie Bloem, Executive Director, NAPPO*

11:45-12:00 Experiences and Insights for Developing and Delivery Plant Disease Risk Information to Small Stakeholder Farmers in Kenya, *Dr. Bryony Taylor, Digital Development Coordinator, CABI Bioscience, UK*

12:00-12:10 Chancellor remarks, *Dr. Randy Woodson, Chancellor NCSU*

12:10-1:00 Lunch

Modeling, Forecasting, & Decision Support
Moderator: Dr. Ross Meentemeyer, NCSU

1:00-1:15 How Might Spatially Explicit Landscape Scale Models Be Improved?, *Dr. Nik Cunniffe, Head of Theoretical & Computational Epidemiology Group, Cambridge, UK*

1:15-1:30 Slowing the Spread of Sudden Oak Death in Oregon Forests: An Overview of a Landscape Scale Disease Management Program, *Dr. Sarah Navarro, Regional Forest Pathologist, US Forest Service*

1:30-1:45 Effectiveness of management program for Sudden Oak Death in Oregon, *Dr. Chris Jones, Center for Geospatial Analytics, NCSU*

Population Genomics
Moderator: Dr. Iganzio Carbone, NCSU

1:45-2:00 MARPLE Diagnostics: A Pioneering Step in Wheat Rust Management, *Dr. Diane Saunders, John Innes Research Centre, UK*

2:00-2:15 T-BAS: A Tool for Real-time Tracking of Biodiversity Across the Tree of Life, *Dr. Ignazio Carbone, NCSU*

2:15-2:30 RIGEL: A Genomic-Based Biosurveillance Approach, *Dr. Willy A. Valdivia-Granda, Orion Integrated Biosciences Inc.*

Understanding and Mitigating Threats
Moderator: Dr. Peter Ojiambo, NCSU

2:30-2:45 Preventing and Managing Plant Diseases, *Dr. Wendy Jin, USDA, APHIS*

2:45-3:00 Mitigating Biothreat Risk at the Border, *Dr. Romelito Lapitan, Agrobioterrorism Countermeasures, DHS*

3:00-3:15 Assessing the Risk of Cucurbit Downy Mildew Outbreaks in the Eastern United States, *Dr. Peter Ojiambo, NCSU*

3:15-3:30 Coffee Break

3:30-4:00 PlantAid Database Demonstration, *Dr. Chris Jones, Center for Geospatial Analytics, NCSU*

4:00-6:00 Poster Session

5:15-5:45 Plant Sciences Building Tour

Speaker Abstracts

Dr. Jean Ristaino: The Persistent Threat of Emerging Plant Disease to Global Food Security

Plant disease outbreaks are increasing and threaten food security for the vulnerable in many areas of the world. Recently a global human pandemic threatened the health and killed millions of people on our planet. A stable, nutritious food supply will be needed to lift people out of poverty and improve health outcomes. Emerging plant diseases threaten many foods crops including those we eat for breakfast such as coffee, oranges, banana, and potatoes. Plant pathogens cause global losses estimated to be as high as $33 billion per year. Plant diseases, both endemic and recently emerging, are spreading and exacerbated by climate change, transmission with global food trade networks, pathogen spillover, and evolution of new pathogen lineages. The risk of introduction of pathogens into the US with trade requires continued monitoring and improved diagnostic capabilities at our borders. In order to tackle these grand challenges, a new set of tools that include disease surveillance and improved detection technologies including pathogen sensors and predictive modeling and data analytics are needed to prevent future outbreaks. New genetic tools are enabling us to piece together the evolution of emerging plant pathogens and track their spread. Disease surveillance systems have been deployed for *Phytophthora infestans*, the pathogen that caused the Irish famine. The pathogen affects potato production globally and food security. Genomic sequencing tools can be used to track outbreaks and produce maps of disease and pathogen strains. Faster and more reliable methods of detection could greatly reduce time for detection and thus time to action. We have developed field-compatible molecular assays to speed identification of plant pathogens in fields. This will allow growers to respond more rapidly with appropriate fungicide treatments and will allow regulatory agencies to mitigate new outbreaks more effectively. Novel detection technologies combined with disease surveillance, geospatial and bioinformatics tools will help mitigate outbreaks improve deployment of host resistance and inform policy.

Dr. Dan Bebber: Climate and Potential Yield Losses to Fungal Plant Pathogens

Plant diseases are major causes of crop yield losses and exert a financial burden via expenditure on disease control. The magnitude of these burdens varies with biological, environmental and management factors, but this variation is poorly understood. Here we model the effects of weather on potential yield losses due to fungal plant pathogens using experimental trials of fungicide-treated and untreated cereal crops in the UK, and project future potential yield loss under climate change. We find that potential yield loss varies between 10 and 20 % of fungicide-treated yields depending on crop, and increases under warmer winter and wetter spring conditions. Potential yield loss will increase for winter wheat and winter barley under climate change, while declining for spring crops due to drier summers. Mean potential yield loss is comparable to the effects of varietal variation but less than the effect of adverse weather. Analysis of yield differences between fungicide-treated and untreated crops provides a new way to understand climate change responses of plant disease, which complements modelling of infection risk by specific pathogens.

Dr. Karen Garrett: R2M rapid risk assessment to support mitigation of plant disease: A toolbox for national programs

The ability of national agricultural research and extension systems (NARES) and national plant protection organizations (NPPOs) to address emerging pathogen and pest risks is key to national food security. Many countries globally are in the process of improving these systems. R2M is a set of tools for rapid risk assessment and mitigation planning for crop pathogens and pests at the national or regional level. These tools can help countries develop their strategies for effective management of current crop disease problems, as well as new invasive pathogens and pests. R2M tools act as building blocks in the development of a global surveillance and mitigation system for crop disease. The R2M 'meta-tool' for expert knowledge elicitation allows leaders in national programs to create their own tools for evaluating risk and mitigation strategies. R2M also includes geographic risk analysis such as cropland connectivity analysis, and management scenario analysis such as impact network analysis. We provide examples of R2M applications in several countries and introduce the latest R2M options available for new applications.

Stan Winslow: A View from the Ground and Above: A Crops Consultant's Experience with Mapping Farms, Pests, and Pathogens

Tidewater Agronomics is an independent crop consulting and contract research firm located in northeastern NC. Our consulting team provides in-season crop pest management and pre-season soil fertility planning services for nearly 100 different growers in northeastern NC and southeastern VA. Our contract research team, lead by my son Matt, conducts 200 plus trials annually for companies ranging from Bayer, BASF, Syngenta to small start-up companies doing proof of concept testing on new biological products. We are fortunate to be located in an area with a diverse crop mix. This allows us to both consult and conduct research on white potatoes, wheat, corn, soy, peanuts, cotton, sorghum, canola/rapeseed. melons and sweet potato. Our team of 18 full time + 8-12 part time employees move back and forth between the two parts of our business to keep things going during peak work times. Our growers value the help and information we provide and we are blessed to still work for nearly every grower we started with in 1998. Our services are based on providing timely, accurate, un-biased information. This has built trust with the farmers and research study directors which shows itself by the repeat business we receive. We call on Extension Specialists and Agents from both NC and VA for advice quite frequently - again to seek un-biased information. Our business would not be where it is without the support of great Extension Specialists over the years. Please visit www.tidewaterag.com to learn more about us.

Erin Eure: An Area Agent's Perspective on Pest and Pathogen Emergencies

Cooperative Extension Agents are considered boots on the ground for the land grant university system. We serve as an unbiased, research-based source of information for all farmers throughout the state, generally at little to no cost to the farmer. The potential impact of our work hinges largely on the relationships we build with our clientele. Confidentiality, timeliness, and accuracy are key to the success of those relationships. Extension Agents visit with farmers and check fields upon the farmer's request when problems arise, but also check fields at random where strong client-Agent relationships exist, or where on-farm research is hosted. Some pest or disease problems can be identified quickly in the field. Some problems require the use of a microscope or other technology, which may or may not be handled at the local County Extension office. Other problems require a sample be submitted to a diagnostic lab. The County Agent may consult with Area Specialized Agents or Specialists for diagnostic support or up-to-date management recommendations. Agents may need to alert other growers, neighboring County Agents, industry, etc., depending on the potential spread of the pest/pathogen, or where or how the infestation/infection originated. A variety of communication methods are available, but grower confidentiality must often be maintained. The overarching goal of sustaining yields and profits for all farmers requires timely, accurate diagnosis, access to effective management options, and possibly effective communication of potential risk to other stakeholders. Extension Agents are a critical and trusted conduit in this process.

Dr. John Bienapfl: Diagnostics for Regulatory Plant Pathogens

The USDA APHIS PPQ Science and Technology (S&T) Plant Pathogen Confirmatory Diagnostics Laboratory (PPCDL) develops, adapts, validates, and utilizes diagnostic methods for the detection of regulated plant pathogens. The PPCDL is committed to quality in confirmatory molecular diagnostics and is the only Federal Plant Pathology ISO/IEC 17025:2017 accredited laboratory that conducts diagnostics for plant pathogens of regulatory concern. The laboratory uses cutting-edge technologies for accurate and rapid diagnosis of high-consequence plant pathogens, including select agent and exotic pathogens, and conducts molecular confirmation/identification of other plant pathogens of regulatory significance. The PPCDL is instrumental for building and maintaining laboratory testing capacity for screening diagnostic testing, as well as PPQ emergency response and eradication programs through technology transfer of clear-written standard operating procedures and hands-on laboratory training for end users within and outside of PPQ, and through proficiency testing. These activities also support the state of preparedness and rapid response to new incursions. This presentation will describe the PPCDL's functions, activities, and contributions to protect U.S. agriculture and natural ecosystems and its role in supporting national plant biosecurity.

Dr. Neil McRoberts, Dr. Jim Stack: The National Plant Diagnostic Network

The National Plant Diagnostic Network (NPDN) was established under Homeland Security Presidential Directive 9 (HSPD-9) as one of a raft of biosecurity initiatives that were started in the aftermath of the 09/11/2001. The network is funded by discretionary appropriations as part of the Food & Agriculture Defense Initiative, a line item in the budget of USDA-NIFA. HSPD-9 (along with all of the other HSPDs from that era) has now been retired and replaced, as of November 2022, by the National Biosecurity Strategy, which is much broader in perspective, heavily influenced by our recent global experience with COVID-19, and framed by concepts from the domain of One Health. The funding provided by USDA-NIFA allows NPDN to added considerable value to plant diagnostic activities in every US state and several US territories in the Pacific and Caribbean. As an organization, NPDN consists of 5 regional networks of diagnostic labs and the National Data Repository, which is hosted by the Center for Environmental and Regulatory Information Services at Purdue University in Indiana. NPDN works closely with state and federal regulatory agencies to provide US agriculture and other plant-based socio-ecological systems with robust, high quality, diagnostic capability. In the context of the future of the PIPP program, NPDN's 20 year existence may be viewed either as a glittering success story or a dire warning about institutional development and policy implementation in the biosecurity arena. We will discuss why both of these perspectives are true and useful in planning for the future.

Dr. Stephanie Bloem: The North American and Global Perspective on Understanding and Mitigating the Threats of the Next Plant Health Pandemic

Regional and global cooperation and sharing of phytosanitary intelligence to identify and deal with emerging phytosanitary threats are ongoing activities. This presentation will define and highlight the most important initiatives at the North American and global levels.

Dr. Nik Cunniffe: How Might Spatially Explicit Landscape Scale Models be Improved?

Large scale spatially explicit models of plant diseases have now been used for years. This class of model offers policy makers a rational way to understand how best to deploy limited resources for disease detection and control. However, there are various ways in which the underpinning models might be extended to include more realism, or the results of models interrogated more efficiently. Rather than talk about my own work on large scale spread modelling, I will instead reflect on recent work suggesting areas in which landscape scale spread models might perhaps be extended. I will describe recent small-scale models showing how successful disease control can be conditioned on stakeholder behaviour and polygenic differences in pathogen traits. I will also discuss how optimal control theory and techniques from artificial intelligence might be used to understand how, where and when to do disease detection and management most effectively.

Dr. Bryony Taylor: Experiences and Insights for Developing and Delivering Plant Disease Risk Information to Small Stakeholder Farmers in Kenya

In plant pandemics, rapid response is essential. In Sub-Saharan Africa (SSA), 73.8% of farms are < 2ha in size and under certain scenarios there may be a requirement to determine areas of high risk of disease establishment and disseminate rapid response messaging relating to control options. PRISE (Pest Risk Information Service) generates and provides information on the optimum time to intervene against insect pests for smallholders in SSA. The PRISE datacube acquires, stores and handles multiple datasets from reanalysis, meteorological and Earth observation sources, which drive pest models. Outputs are accessed via interfaces (web portals and APIs) and used by third party disseminators in country to deliver "time to act" messages coupled with good agricultural practice information through the most appropriate extension channels. Through PRISE, the feasibility of generating and disseminating plant pathogen risk information was investigated in Kenya. A successful early warning system should ensure that information generated and disseminated is actionable and effective for farmers. In low-income countries, the means to intervene can be resource limited therefore, to investigate how information should be presented to farmers, structured phone surveys were undertaken to investigate whether farmers had encountered key plant pathogens in their growing systems and what means they undertook to prevent or manage them. Here we report initial survey results and barriers to uptake of management practices reported by farmers. Additionally, we present prototype risk maps for *Pseudocercospora griseola*, showing areas at high risk from infection generated using data from the PRISE datacube and disease parameters.

Dr. Sarah Navarro: Death in Oregon Forests: An Overview of a Landscape Scale Disease

Sudden Oak Death (SOD), caused by *Phytophthora ramorum*, is lethal to tanoak (*Notholithocarpus densiflorus*) and threatens this species throughout its range in Oregon. Since the discovery of SOD in coastal southwestern Oregon forests in 2001, an interagency team has attempted to eradicate and slow the spread of disease through a program of a state quarantine, early detection, survey and monitoring, and destruction of infected and nearby host plants. Survey, detection, and monitoring efforts compose of ground, aerial and stream bait surveys. Ground-based detection and delimitation surveys around infested sites are conducted year-round. Aerial surveys, both fixed winged and helicopter, are conducted four times per year; the main surveys occur in July and October when current-year mortality is most visible. Aerial surveys cover a cumulative area of at least 700,000 acres of forest; ground surveys cover 600 acres. Eradication treatments, totaling approximately 8,200 acres, eliminated disease from most infested sites, but the disease continued to spread slowly, mostly in a northward direction. In 2017, a SOD Task Force convened local, state and federal agencies, tribes, industry, and local residents and environmental groups. The mission of the Task Force was to develop a collaborative-based strategic action plan, including securement of additional resources to contain the NA1 strain of *Phytophthora ramorum* and eradicate the EU1 strain of *Phytophthora ramorum* in Curry County, Oregon using the best available science. This presentation will review program developments in treatments, funding, and continued stakeholder involvement in Oregon as well as lessons learned over the last 20 years.

Dr. Chris Jones: Effectiveness of Management Program for Sudden Oak Death in Oregon

We have worked with the Oregon Department of Forestry to analyze how effective previous treatments were at preventing the spread of *Phytophthora ramorum*. We used data from 2015 to 2022 for EU1 and 2002 to 2022 for NA1. We used the PoPS (Pest or Pathogen Spread) modeling framework to simulate both NA1 and EU1 strains of *P. ramorum* in Oregon. The model simulates reproduction, dispersal, and establishment of the disease through space and time based on current infections and environmental data. We calibrated the NA1 model from 2002 to 2015 and validated it from 2016 to 2022. For EU1, we calibrated the model from 2015 to 2020 and validated it with 2021 to 2022 data. We ran the model with two scenarios: 1) using actual treatments that were applied and 2) with no-treatment interventions at all. We compare the total infected area with management to that detected in the field and to the simulation with no treatments in order to quantify the potential prevention in infected area based on the treatments applied by ODF and the Forest Service. We show that the treatment efforts have prevented thousands of acres from being infected far beyond the area that was treated.

Dr. Diane Saunders: MARPLE Diagnostics: A Pioneering Step in Wheat Rust Management

Wheat rusts have been associated with crop failures and famine throughout history. In the last decade, new yellow rust variants have emerged in many locations that are adapted to warmer temperatures, have expanded their ability to infect different wheat varieties and are more aggressive than those previously characterised causing a serious threat to global wheat production. To address this, we set out to improve the speed and resolution of current surveillance and diagnostic systems by developing a new, portable, genomics-based, point-of-care approach for wheat rust diagnostics. This new method termed Mobile And Real-time PLant disEase (MARPLE) diagnostics, utilizes the nanopore sequencer and is specifically tailored for identifying individual strains of the wheat yellow and stem rust pathogens. It enables rapid identification of both newly emergent strains and those with specific properties such as fungicide resistance, generating results within just 48 hours of field sampling. All the components needed to execute the MARPLE diagnostics method are also contained within a single hardcase, providing a truly portable system that can be conducted anywhere irrespective of access to resources. This new strategy has the potential to revolutionise wheat rust diagnostics, changing how emergent threats are identified and tracked into the future.

Dr. Ignazio Carbone: T-BAS: A Tool for Real-Time Tracking of Biodiversity Across the Tree of Life

The Tree-Based Alignment Selector (T-BAS) toolkit is a unique phylogenetic analytic tool that integrates complex microbial biodiversity data and the rich metadata being continuously produced by biologists. This metadata may include metagenomics data on microbial associations with other organisms, phenotypic data, and abiotic or environmental data generated from new sensing technologies. Although tracking the spread of plant pathogens through complex agricultural landscapes remains exceedingly difficult, recent advances in our ability to sequence large numbers of pathogen isolates and analyze population genomic data is providing new insights into pathogen movement. Inspired by the tree of life, the structure of our Plant Aid database will reflect the phylogenetic relationships among sampled taxa, allowing researchers to use the evolutionary insights provided by the tree of life to understand the web of biotic and abiotic interactions and parameters underlying plant performance and resilience.

Dr. Willy A. Valdivia-Granda: RIGEL: A Genomic-Based Biosurveillance Approach

Known and unknown infectious diseases affecting humans, animals, and plants continue to emerge, re-emerge, and persist in different locations worldwide. The risk of these pathogenic agents to global security is exacerbated by the genomic diversity and lethality of manmade hybrid biothreats that represent unknown unknowns, such as threats we are not even aware that we are unaware of. Trade and travel are vulnerable and potential entry pathways to natural, accidental, or intentional introduction of known and unknown biological threats. Here we introduce a data mining and artificial intelligence approach for genomic-based biosurveillance that estimates the risks of specific commodities regarding specific pathogens. RIGEL follows implementation standards for interoperability, integration, and scalability. RIGEL ingest, stores, tracks hourly worldwide information from 102,635 biological facilities working with 9.5 million organisms from a diversity of biological sources, including but not limited to: human, animal, and plant samples; infected or suspect clinical diagnostic material; environmental samples; synthetic constructs, and genetically modified organisms. RIGEL links genomic information from 342 million nucleotide entries, more than 40 million scientific literature articles, and 761,037 patents. This information is aggregated to build worldwide institutional capability annotated in temporal and spatial scales for strategic and tactical analytics. RIGEL captures more than 194,000 officially reported disease outbreaks of agricultural relevance and ingests in near-real-time newsfeeds from 7,000 newspapers from 120 countries. Integration of data streams generated from multiple sources, including genomic and metagenomic sequencing, epidemiological surveys, news, and trade information, can be coupled with artificial intelligence and advanced visualization techniques to generate a more accurate overview of the pandemic potential of pathogens.

Dr. Wendy Jin: Preventing and Managing Plant Diseases

U.S. Department of Agriculture's Animal and Plant Health Inspection Service's (APHIS) Plant Protection and Quarantine (PPQ) safeguards U.S. agriculture and natural resources against the entry, establishment, and spread of economically and environmentally significant pests, and facilitates the safe trade of agricultural products. PPQ uses the latest science and technology to develop methods for detecting, identifying, and keeping harmful plant pests and diseases out of this country. PPQ has established a system of safeguards called the Safeguarding Continuum that begins overseas, continues through U.S. ports of entry, and extends across the nation. PPQ analyzes data from around the world to figure out which pests could harm U.S. agriculture, how these pests might get here, and what we need to do to keep them out of the U.S. PPQ works with State departments of agriculture and others to continuously scan the U.S. landscape and quickly find and respond to new pests and diseases before they can cause large-scale damage to our Nation's farms and forests. When foreign pests become established in the United States, PPQ works closely with Federal, State, Tribal, and industry partners to control and, when possible, eliminate them from our country.

Dr. Romelito Lapitan: Mitigating Biothreat Risk at the Border

The U.S. Customs and Border Protection (CBP) is America's premier law enforcement organization and the guardian of our Nation's borders. CBP's mission is to protect the American people, safeguard our borders, and enhance the nation's economic prosperity. CBP is the frontline of defense against entry of biological threats that may be damaging to American agriculture, natural resources, and public health. On a typical day each year, CBP officers and agriculture specialists inspect thousands of agricultural and biological imports entering through the ports of entry for pests and diseases, and enforce compliance to the regulatory requirements of partner government agencies. While CBP employs a layered screening approach to detection of highly regulated or illicit agricultural commodities, its enforcement capacity is limited by the guidance provided by partner regulatory agencies. The global biological threat landscape is changing at a pace that international sanitary controls and government regulations may not timely adjust; thus, underscores our border's vulnerability to entry of exponential biology. Near-real time surveillance of emerging and immediate biothreats and risk contextualization in trade and travel environments could provide timely decision and operational support to CBP's biothreat exclusion efforts.

Dr. Peter Ojiambo: Mildew Outbreak in the Eastern United States

Outbreaks of cucurbit downy mildew in the eastern US are spatially correlated with time to disease in fields closer together being more similar than in fields farther apart. A Bayesian time-to-event model with spatially correlated random effects following a spatial conditional autoregressive model was fitted to assess the risk of disease outbreak in the eastern United. The model showed clustering of outbreaks at the state level and indicated that states in the mid-Atlantic region have high spatial frailties and a high risk of disease outbreak. Once disease occurs in a field, that field can serve as a source of inoculum for neighboring disease-free fields. Thus, time to disease outbreak and epidemic duration affect each other and understanding this association can aid in managing epidemics. Consequently, we develop a joint Bayesian hierarchical model with spatial correlated random effects. Here, a parametric Weibull distribution to the censored time to disease outbreak data, and a zero-truncated Poisson distribution to disease duration data. In a simulation study, several competing models are considered for the process model. Results show that a generalized multivariate conditionally autoregressive model that includes a correlation and spatial structure is the most preferred model. Using disease records in the 2009, the joint model indicates that states in the mid-Atlantic region tend to have a high risk of disease outbreak. Thus, disease surveillance efforts should concentrate within this region and immediate application of fungicides in the region should substantially reduce the velocity of the epidemic wave front in the eastern US.

Dr. Qingshan Wei: Field Sensors for Mapping Plant Disease and Stress Monitoring

Determination of plant diseases and stresses is currently dependent on time-consuming and complicated measurement technologies that are usually performed in centralized laboratories, which is inadequate for early detection and rapid responses. Recently, we demonstrated a set of miniaturized sensor devices that can perform molecular diagnosis of plant pathogens or monitoring of plant stresses directly in the field. The sensor platforms include a microneedle-smartphone device for performing rapid DNA/RNA extraction and isothermal amplification, and noninvasive volatile organic compound (VOC) sensors based on smartphone or wearable sensor patches. These cost-effective sensors have been thoroughly tested in greenhouse for the detection of a range of tomato pathogens, such as *Phytophthora infestans*, *Alternaria linariae*, and Tomato spotted wilt virus (TSWV) with high detection accuracy. Together, these sensor devices demonstrated the feasibility of in-field detection of plant diseases and stresses of great concern.

Dr. Raju Vatsavai: Near Real-time Decision Making Under Uncertainty for Disease Mapping, Monitoring, and Prediction

Disease mapping, prediction, and management are based on the appropriate data. Farmers are under tremendous pressure to adapt their decision-making to not only changing climate but also due to resource scarcity (e.g., water), reducing arable lands, and crop diseases. Traditional forecasting systems are based on assumptions about pathogens' interactions with the host and the environment. On the other hand, Remote sensing data plays an important role in mapping crop health over time and provides an opportunity to build machine learning-based forecasting systems. By integrating diverse datasets such as weather, local sensor measurements, and on-demand remote sensing data (e.g., UAVs), one could hope for more accurate and timely predictions for farmers with actionable spatial and temporal knowledge (where, when, and by how much) about water, fertilizers, and pesticides. We present ongoing work on incorporating in-situ and remotely sensed measurements into machine learning models, in particular models for making decisions under uncertainty. We will discuss opportunities for integrating this framework with farm equipment (tractors and UAVs) to generate near-real-time actionable knowledge for farmers.

Dr. Laura Tateosian: Case Studies in Mining Text for Plant Pests and Pathogens

Pest observation and distribution data for biosecurity measures and forecasting models commonly come from field observations, official reports, and genetic records consolidated through published literature and databases. While vital, these data can suffer from latency and spatial and temporal sparseness, due to the cost of collecting and collating these data at scale. These limitations have implications for the predictive capabilities of models and the success of control and eradication programs. At the same time, there is a wealth of historical text data as well as growing evidence that Web media could be a valuable source of supplementary data to tap into information for understanding pest encroachments. Gathering data from these sources presents its own challenges. We discuss practical considerations for processing historical text records and collecting online media in order to extract data from text to support pest biosurveillance. We document the presence of mentions of invasive pests and pathogens in these sources through contemporary case studies regarding *Lycorma delicatula*, *Tuta absoluta*, and *Phytophthora infestans* and an exploration of the early history of *P. infestans* through historical documents. Our results using past data demonstrate that these sources provide valuable spatial information describing pest presence and spread.

Posters

1.) Monitoring emerging *Phytophthora ramorum* and *P. kernoviae* in Rhododendron
Amanda Mainello, Amanda Saville, Jyotsna Acharya, Rajesh Paul, Qingshan Wei, Jean Ristaino

2.) An open-access T-BAS phylogeny for emerging *Phytophthora* species
Allison Coomber, Amanda Saville, Ignazio Carbone, and Jean Beagle Ristaino

3.) Distribution and diversity of abaca bunchy top virus and banana bunchy top virus causing bunchy top of abaca in Caraga, Philippines
Mark Paul Selda Rivarez, Jezmeir Porras, Cristal Mae Magadan, Arnaldo Gagula, Rezel Borines, Elizabeth Parac

4.) Economics of Plant Diseases and Disease Management with Application to Field Tomatoes
Daemyung Lee, Kelly Zering

5.) Global surveillance and detection of novel cereal rust virulence
Douglas Luster, Melissa Carter, Pablo Olivera, Yue Jin

6.) Identification of Southern Leaf Blight Infected Corn for Remote-Sensing Field Imagery
Grace Vincent, Cranos Williams, Michael Kudenov, Peter Balint-Kurti

7.) Near Real-time Decision Making Under Uncertainty for Disease Mapping, Monitoring, and Prediction
Raju Vatsavai, Ezio Mei

8.) Development of a LAMP/Cas12a assay to specifically detect the California strain of resistance breaking (RB) - Tomato spotted wilt virus (TSWV) in tomato
Tatsiana Shymanovich, Amanda Saville, Noor Mohammad, Qingshan Wei, Dorith Rotenberg, Anna E. Whitfield, Jean Beagle Ristaino

9.) The Advanced Plant Phenotyping Laboratory: A phenomics platform for dissecting genomics of plant performance and health
Larry M. York, Stan Martin, Mac McLennan, Wellington Muchero, Dave Weston

10.) Automating Severity Assessment of Southern Leaf Blight in Corn Leaves Using Machine Learning.
Chanae Ottley, Cranos Williams

Poster Abstracts

11.) Revolutionizing Plant Pathogen Detection and Monitoring: Portable VOC Fingerprinting and Continuous Monitoring in Agriculture

Oindrila Hossain, Zheng Li, Giwon Lee, Sina Jamalzadegan, Yuxuan Liu, Rajesh Paul, Amanda C. Saville, Tatsiana Shymanovitch, Dorith Rotenberg, Anna E. Whitfield, Jean B. Ristaino, Yong Zhu, Qingshan Wei

12.) Tailoring Named Entity Recognition (NER) to extract pest event data from online news and Tweets

Ariel Saffer, Laura Tateosian, Makiko Shukunobe, Chelsey Walden-Schreiner

13.) Prediction of leaf wetness duration and *Botrytis*, and validation in strawberry fields with multi-sensor arrays

Ashley N. Philbrick, Joshua C. Larsen, Michael W. Kudenov, Tika B. Adhikari, and Roger D. Magarey

14.) Pest or Pathogen Spread Model Case Study with Late Blight

John Polo, Chris Jones, Jean Ristaino, Amanda C. Saville, Inga Meadows, Ella Reeves

1.) Monitoring emerging *Phytophthora ramorum* and *P. kernoviae* in Rhododendron

Amanda Mainello[1] Amanda Saville[1] Jyotsna Acharya[1] Rajesh Paul[2] Qingshan Wei[2] Jean Ristaino[1,3]

[1] Department of Entomology and Plant Pathology, NC State University; [2] Department of Chemical and Biomolecular Engineering, NC State University; [3] Emerging Plant Disease and Global Food Security Cluster, NC State University

Rapid, field-deployable assays such as loop-mediated isothermal amplification (LAMP) are critical for detecting nursery and forest pathogens like *Phytophthora ramorum* and *P.kernoviae* to prevent pathogen spread. We evaluated the specificity and sensitivity of previously published *P. ramorum* and *P. kernoviae* LAMP assays and developed a new LAMP assay for genus-level detection of *Phytophthora spp.* using DNA extracts and infected Rhododendron leaf samples. Sensitivity was measured for each assay by running serial dilutions of target DNA of the pathogen in the thermocycler and real-time LAMP. Products were visualized using colorimetric dyes, gel electrophoresis, on a microfluidic chip on a smartphone device, and as fluorescence curves. All methods can reliably detect 10-1pg/µl of target DNA. Real-time LAMP is being used to measure the target DNA concentration in infected leaf samples over time. The *P. ramorum* LAMP assay accurately detected 14 of 15 inoculated leaves after two days post inoculation. The specificity of the three LAMP reactions is under evaluation using DNA from other *Phytophthora spp.* found on hosts of *P. ramorum* and *P. kernoviae*. Our goal is to run the three LAMP assays together on one microfluidic chip to detect and monitor spread of these important *Phytophthora* species in forest and nursery settings.

2.) An open-access T-BAS phylogeny for emerging *Phytophthora* species

Allison Coomber[1,2] Amanda Saville[1] Ignazio Carbone[1,4] Jean Beagle Ristaino[1,3]

[1.] Department of Entomology and Plant Pathology, NC State University; [2.] Functional Genomics Program, NC State University; [3.] Emerging Plant Disease and Global Food Security Cluster, NC State University; [4.] Center for Integrated Fungal Research, NC State University

Phytophthora species cause severe diseases on food, forest, and ornamental crops. Since the genus was described in 1876, it has expanded to comprise over 190 formally described species. There is a need for an open access phylogenetic tool that centralizes diverse streams of sequence data and metadata to facilitate research and identification of *Phytophthora* species. We used the Tree-Based Alignment Selector Toolkit (T-BAS) to develop a phylogeny of 192 formally described species and 33 informal taxa in the genus *Phytophthora* using sequences of eight nuclear genes. The phylogenetic tree was inferred using the RAxML maximum likelihood program. A search engine was also developed to identify microsatellite genotypes of P. infestans based on genetic distance to known lineages. The T-BAS tool provides a visualization framework allowing users to place unknown isolates on a curated phylogeny of all *Phytophthora* species. Critically, the tree can be updated in real-time as new species are described. The tool contains metadata including clade, host species, substrate, sexual characteristics, distribution, and reference literature, which can be visualized on the tree and downloaded for other uses. This phylogenetic resource will allow data sharing among research groups and the database will enable the global *Phytophthora* community to upload sequences and determine the phylogenetic placement of an isolate within the larger phylogeny and to download sequence data and metadata. The database will be curated by a community of *Phytophthora* researchers and housed on the T-BAS web portal in the Center for Integrated Fungal Research at NC State. The T-BAS web tool can be leveraged to create similar metadata enhanced phylogenies for other Oomycete, bacterial or fungal pathogens.

3.) Distribution and diversity of abaca bunchy top virus and banana bunchy top virus causing bunchy top of abaca in Caraga, Philippines

Mark Paul Selda Rivarez[1,2] Jezmeir Porras[1] Cristal Mae Magadan[1] Arnaldo Gagula[3] Rezel Borines[1] Elizabeth Parac[1]

[1.] Department of Agricultural Sciences, College of Agriculture and Agri-industries, Caraga State University, Ampayon, Butuan City, Agusan del Norte 8600, Philippines. [2.] Department of Entomology and Plant Pathology, College of Agriculture and Life Sciences, North Carolina State University, Raleigh, NC 27607, USA. [3.] Department of Geodetic Engineering, College of Engineering and Geosciences, Caraga State University, Ampayon, Butuan City, Agusan del Norte 8600, Philippines.

The Philippines contributes more than 80% to the world production of abaca (*Musa textilis*) fiber or 'Manila hemp' that is used in various industrial products. However, abaca industry growth is significantly hampered by the bunchy top disease (BTD) caused by abaca bunchy top virus (ABTV) and banana bunchy top virus (BBTV). Herewith, we surveyed major abaca plantations in Caraga region, Philippines using mapping tools complemented with molecular diagnostics, to generate a distribution map for the incidence of abaca BTD. We showed that BTD is present in all Caraga provinces where a total of 395 samples were collected. A subset (n=120) were tested for ABTV/BBTV using duplex PCR tests where 84 samples were positive for BBTV and 66 samples for ABTV. Interestingly, there is a high rate of ABTV/BBTV co-infection, where 49 samples (41%) tested positive for both viruses. Diversity analyses revealed moderate levels of nucleotide diversity for both viruses with evidence of recombination and phylogenetic lineages showed correspondence with the geographic origin of the global isolates. Furthermore, data from PCR tests were used for the MaxEnt analyses that provided predictive insights on the possible spread of the disease in the region. Overall, we contributed novel information on the distribution and diversity of ABTV and BBTV. By using predictive analyses, we advanced the understanding of the epidemiology of abaca bunchy top disease in a major growing region of the Philippines.

4.) Economics of Plant Diseases and Disease Management with Application to Field Tomatoes

Daemyung Lee, Kelly Zering, Department of Agricultural and Resource Economics, NC State University

Linked models are integrated to represent field production, pathogen transmission between fields, effects of disease, and effects of disease management practices. External stochastic factors affect crop production and yield quantity and quality along with revenues, costs, and profit. The models are used to predict probabilistic outcomes for current production practices as well as to predict effects of alternative practices. Predicted value of new technology and practices are derived; at the field level, regionally, nationally, and internationally. Needed adaptations in markets and policy can be identified.

5.) Global surveillance and detection of novel cereal rust virulence

Douglas Luster[1] Melissa Carter[1] Pablo Olivera[2] Yue Jin[3]

[1] USDA-ARS, Foreign Disease-Weed Science Research Unit, Ft. Detrick MD; [2] University of Minnesota, Dept. of Plant Pathology, St. Paul MN; [3] USDA-ARS, Cereal Disease Lab, St. Paul MN

Rust diseases, caused by *Puccinia spp.*, are among the most important causes of yield loss of cereal crops in the US and worldwide. Global surveillance of cereal rusts is an important mitigation strategy to ensure the timely deployment of control measures in vulnerable cereal production areas. The FDWSRU plays a critical role in such efforts, receiving samples of exotic cereal rusts collected by cooperators at institutes in East and North Africa, Europe, and South and Central Asia. Viable rust samples are received, recovered, increased, and archived in the FDWSRU BL-3 facility. A preliminary race analysis is also performed by testing on selected differential lines. Increased rust cultures are shipped to the CDL in St Paul, MN for in-depth phenotypic and genotypic analyses. Analyses derived from these rust cultures have enabled us to monitor the evolution and spread of highly virulent races of the wheat stem rust pathogen, and to identify hot spots around the world where diverse virulence combinations are generated and sustained through sexual cycles of the pathogen. Establishment of sentinel plots will enable us to identify new and highly virulent races promptly as they emerge, providing early warning for potential vulnerability. The new virulent races are being used to identify new sources of resistance for development of durable resistance in cereal crops.

6.) Identification of Southern Leaf Blight Infected Corn for Remote-Sensing Field Imagery

Grace Vincent[1,2*] Cranos Williams[1,2] Michael Kudenov[1,2] Peter Balint- Kurti[3]

[1] NC Plant Sciences Initiative; [2] Department of Electrical and Computer Engineering; [3] Department of Entomology and Plant Pathology; *gmvincen@ncsu.edu

The conventional method of crop disease detection, relying on visible symptoms, is time-consuming and often results in the loss of yield. The ability to detect the effects of these stressors early enables growers to mitigate these losses. This research proposes utilizing machine learning algorithms to develop efficient detection and classification models that recognize patterns in infected and noninfected plants from hyper-spectral bands. This research will use hyper-spectral imagery with corresponding plot-wise disease severity scores assigned by an expert breeder based on visual inspection from a single growing season. For the initial processing, we implement unsupervised clustering to extract pixels and features that correspond to the crops, grass, and background and manually segment plot maps. These components are used to determine the correlation between the visual inspection scores to specific features and plots. Preliminary experiments have shown that the crop-focused segmented data has a strong relationship with the ability to detect the disease. Supplementary statistical tests will be run to provide additional understanding of these relationships. We will then use elastic net regression models to identify specific spectral bands that serve as essential features for distinguishing disease severity. Moreover, we will study the change in intensity of the hyper-spectral wavelengths at different disease severity levels to identify influential frequencies. These results will contribute to the advancement of crop disease management and reducing crop loss. Furthermore, the development of a model that uses hyper-spectral field imagery and machine learning can be applied to other crops and stressors, improving food security and sustainability.

7.) Near Real-time Decision Making Under Uncertainty for Disease Mapping, Monitoring, and Prediction

Raju Vatsavai, Ezio Mei, Department of Computer Sciences, NC State University

Disease mapping, prediction, and management are based on the appropriate data. Farmers are under tremendous pressure to adapt their decision-making to not only changing climate but also due to resource scarcity (e.g., water), reducing arable lands, and crop diseases. Traditional forecasting systems are based on assumptions about pathogens' interactions with the host and the environment. On the other hand, Remote sensing data plays an important role in mapping crop health over time and provides an opportunity to build machine learning-based forecasting systems. By integrating diverse datasets such as weather, local sensor measurements, and on-demand remote sensing data (e.g., UAVs), one could hope for more accurate and timely predictions for farmers with actionable spatial and temporal knowledge (where, when, and by how much) about water, fertilizers, and pesticides. We present ongoing work on incorporating in-situ and remotely sensed measurements into machine learning models, in particular models for making decisions under uncertainty. We will discuss opportunities for integrating this framework with farm equipment (tractors and UAVs) to generate near-real-time actionable knowledge for farmers.

8.) Development of a LAMP/Cas12a assay to specifically detect the California strain of resistance breaking (RB) - Tomato spotted wilt virus (TSWV) in tomato

Tatsiana Shymanovich[1] Amanda Saville[1] Noor Mohammad[2] Qingshan Wei[2] Dorith Rotenberg[1,3] Anna E. Whitfield[1,3] Jean Beagle Ristaino[1,3]

[1.] Department of Entomology and Plant Pathology, NC State University; [2.] Department of Chemical and Biomolecular Engineering, NC State University; [3.] Emerging Plant Disease and Global Food Security Cluster, NC State University

Rapid and accurate detection of strains of plant-pathogenic viruses is critical for disease outbreak surveillance. In California (CA), the widespread use of tomato cultivars with the *Sw-5* tospovirus resistance gene has led to the occurrence and spread of an RB-TSWV strain. The objectives of our study were to 1) compare disease progress and impact on plant growth of the RB to a wild type (non-RB) strain on tomato with (cv. 'Mountain Merit') and without (cv. 'Mountain Fresh Plus') the *Sw-5* gene; 2) determine incidence of detection of RB and non-RB TSWV using microneedle RNA extractions and LAMP; and 3) develop a rapid LAMP/Cas12a assay for detection of the TSWV *NSm* mutation in the RB strain. Susceptible plants showed 15% - 25% stunting when inoculated with either strain compared to non-infected controls. *Sw-5* plants had little disease when inoculated with non-RB but exhibited severe stunting (>50%) when inoculated with RB. The detection of positive LAMP reactions from susceptible tomatoes was higher in non-RB than RB over time. The RB strain remained detectable in susceptible tomato over the 14 days, while non-RB was undetectable by LAMP tests in resistant tomato. We developed a two-step LAMP/Cas12a protocol that differentiates the two strains within one hour that includes colorimetric LAMP followed by Cas12a. Our methods were validated with plants under chamber and field conditions, an indication that this method shows promise for detection of RB-TSWV in the field.

9.) The Advanced Plant Phenotyping Laboratory: A phenomics platform for dissecting genomics of plant performance and health

Larry M. York, Stan Martin, Mac McLennan, Wellington Muchero, and Dave Weston, Oak Ridge National Laboratory, Oak Ridge, TN

The Advanced Plant Phenotyping Laboratory (APPL, pronounced 'apple') houses a conveyor system to automatically move plants through imaging stations for sophisticated measurements of physiological, compositional, and architectural plant properties. The imaging modalities currently include chlorophyll fluorescence, hyperspectral, 3D laser scanning, multispectral, thermal, and RGB color imaging. These modalities allow inference of photosynthetic efficiency, plant leaf area and biomass, and compositional attributes like nitrogen content or specific metabolic profiles. These multimodal data capabilities will allow us to use machine learning approaches and explainable AI to generate unique 'health fingerprints' for every plant. APPL also allows automatic watering and weighing of plants to impose specific water stress regimes. This research highlights recent advancements in the use of this phenomics platform for genome wide association studies (GWAS) in poplar (*Populus trichocarpa*), monitoring of heat-stress tolerance in pennycress (*Thlaspi arvense*), and drought tolerance in switchgrass (*Panicum virgatum*). Central to the success of these projects is the APPL Public Interface (APPL PI, pronounced 'pie') that combines state-of-the-art data management tools and computational infrastructure to facilitate the research. We demonstrate how multiple modalities increase statistical power to uncover gene candidates using GWAS in poplar. Chlorophyll fluorescence uncovers heat tolerance in pennycress. Water use efficiency and leaf temperature from thermal cameras uncover mechanisms of drought tolerance in switchgrass. We will discuss in the context of plant disease epidemics. APPL is a state-of- the-art phenotyping platform allowing researchers to push the boundaries of phenomics and genomics to address challenges of the 21st century.

10.) Automating Severity Assessment of Southern Leaf Blight in Corn Leaves Using Machine Learning.

Chanae Ottley, Cranos Williams, Department of Electrical and Computer Engineering; NC State University

Efficient identification of abiotic and biotic stress experienced in an uncontrolled environment by plants is a prominent issue in agriculture. The use of machine learning approaches with computer vision allows for the estimation of disease progression and the early detection of diseases so that mitigation techniques can be applied before crops become too infected for recovery or before the disease spreads to neighboring plants. This work aims to develop an efficient, objective computational pipeline capable of estimating the disease severity caused by Southern Leaf Blight in images of field-grown maize plants. We collected visible light (RGB) field images of maize leaves from lines susceptible and resistant to southern leaf blight and obtained field severity scores of the maize lines. We have shown a strong correlation, $r(262) = .935$, $p < .0001$, between the field severity scores and the severity score of an image with an individual leaf, indicating that images of a leaf provide consistent grading as would be done in the field for a plot of plants. We propose a multistage approach to quantify infected tissue based on a heatmap produced by a convolutional neural network trained to identify the lesions. This research could provide a road map to early stress detection in the field, which could be used as a decision support tool to identify cultivars that are more resistant to abiotic or biotic stress, monitor epidemics, and understand a plant's stress state such that resources are optimized.

11.) Revolutionizing Plant Pathogen Detection and Monitoring: Portable VOC Fingerprinting and Continuous Monitoring in Agriculture

Oindrila Hossain[1], Zheng Li, Giwon[1] Lee, Sina Jamalzadegan[1], Yuxuan Liu,[1] Rajesh Paul[1], Amanda C. Saville[2], Tatsiana Shymanovitch[2], Dorith Rotenberg[2], Anna E. Whitfield[2,3] Jean B. Ristaino[2,3], Yong Zhu[1], and Qingshan Wei[1,3]

[1.] Department of Chemical and Biomolecular Engineering,[2] Department of Entomology and Plant Pathology, NC State University;   NC State University; [3.] Emerging Plant Disease and Global Food Security Cluster, NC State University

The conventional methods of detecting plant pathogens require complicated molecular assays that are time-consuming and only available in centralized laboratories. To overcome this limitation, a set of cost-effective and miniature volatile organic compound (VOC) sensor platforms were developed for non-invasive diagnosis of plant diseases such as late blight caused by *Phytophthora infestans* in the field. The first platform is based on a smartphone device, which integrates a disposable colorimetric VOC sensor array that can detect key plant volatiles at ppm level within one minute of reaction. The smartphone-based VOC sensor device demonstrated a detection accuracy of ≥95% for both laboratory-inoculated and field-collected tomato leaves, as well as the ability to detect *P. infestans* in symptomless tomato plants in the greenhouse setting. On the other hand, a lower leaf surface-attached multimodal wearable sensor was developed for continuous monitoring of plant physiology. The device integrates multiple sensors for detecting VOC, leaf surface humidity/temperature, and environmental humidity into a single platform. The wearable device can quantitatively detect tomato spotted wilt virus (TSWV) as early as four days after inoculation. The wearable sensor has also been coupled with a machine learning model to integrate multi-channel sensor data and predict the minimally needed sensor number. These in-field sensor technologies have the potential to enhance agricultural productivity by providing real-time information about the plant microenvironment and physiological status.

12.) Tailoring Named Entity Recognition (NER) to extract pest event data from online news and Tweets

Ariel Saffer, Laura Tateosian, Makiko Shukunobe, Chelsey Walden-Schreiner, Center for Geospatial Analytics, NC State University

Plant pest and pathogen (pests, for brevity) observation and distribution data for biosecurity measures and forecasting models commonly come from field observations, official reports, and genetic records consolidated through published literature and databases. While vital, these data can suffer from latency and spatial and temporal sparseness, due to the cost of collecting and collating these data at scale. These limitations have implications for the predictive capabilities of models and the success of control and eradication programs. At the same time, there is growing evidence that Web media, such as online news and Twitter, could be a valuable source of supplementary data to boost coverage and tap into up-to-date information for predicting pest encroachments. We present our results demonstrating the value of data from web media to supplement official records of pest invasions, using Spotted Lanternfly and *Tuta absoluta* as case study species. Our ongoing research explores and evaluates text analysis and Natural Language Processing approaches like Named Entity Recognition (NER) for automating the extraction of structured data from these unstructured sources, with potential for both historical and real-time applications.

13.) Prediction of leaf wetness duration and *Botrytis*, and validation in strawberry fields with multi-sensor arrays

Ashley N. Philbrick[1], Joshua C. Larsen[2], Michael W. Kudenov[2], Tika B. Adhikari[3], Roger D. Magarey[1]

[1.] Center for Integrated Pest Management, North Carolina State University; [2.] Department of Electrical and Computer Engineering, North Carolina State University; [3.] Department of Entomology and Plant Pathology, North Carolina State University

Botrytis cinerea (Botrytis fruit rot) is one of the most destructive pathogens affecting strawberry production in North Carolina. Disease caused by *B. cinerea* is also commonly referred to as gray mold due to the visible colonization of the fungus on plant tissues, most often observed on fruits. *Botrytis cinerea* infection is not limited to the field as symptoms can continue to develop post-harvest affecting strawberry production on the grower, shipper, and consumer level. The ideal environmental conditions for *B. cinerea* infection are cool and wet. Therefore, variables such as temperature, leaf wetness, and relative humidity are important factors to consider when making management decisions. Models like the Bulger infection model, which consider these variables, have proven to be useful tools for predicting the infection risk for *B. cinerea*; however, they are limited by the accuracy of the data gathered from local weather stations, which may differ significantly from the actual conditions observed in the field. Additionally, variables such as leaf wetness can be very difficult to measure, so an alternative is leaf wetness simulation models. An experiment is being conducted to evaluate the leaf wetness and *Botrytis* prediction models using sensors deployed in the field. The field sensors include a Phytos leaf wetness sensor, Temperature, RH, along with custom visual and infrared sensors for detecting leaf wetness. Model predictions made from in-field weather sources will be compared to those made from two local weather stations (ECONet and Wilmington, NC) and a numerical 2.5 km grid weather source NOAA NCEP URMA.

14.) Pest or Pathogen Spread Model Case Study with Late Blight

John Polo[1], Chris Jones[1], Jean Ristaino[2,3], Amanda C. Saville[2], Inga Meadows[2], Ella Reeves[2]

[1.] Center for Geospatial Analytics, NC State University; [2.] Department of Entomology and Plant Pathology, NC State University; [3.] Emerging Plant Disease and Global Food Security Cluster, NC State University

Late blight, a disease caused by the pathogen *Phytophthora infestans*, is a major concern for potato and tomato production around the world. The disease spreads via sporangia that germinate when weather conditions are suitable and can wipe out a field of the host in a matter of days. The Pest or Pathogen Spread model, "PoPS", was developed as a species-agnostic model for forecasting disease or pests in various systems with an explicit spatio-temporal framework. It simulates reproduction, dispersal, and establishment of study organisms based on weather, host, and environmental conditions. It is flexible with scale and resolution in both the spatial and temporal domains. We used Late Blight data from a small field study in Western North Carolina as a case study of the disease with PoPS to calibrate the model and produce a forecast of the spread of the disease, which we validate with data collected during the study.